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FUNDAMENTAL VA AMALIY MIKROBIOLOGIYANING BUGUNGI HOLATI VA RIVOJLANISH ISTIQBOLLARI: YOSH OLIMLAR NIGOHI

RESPUBLIKA ILMIY-AMALIY ANJUMAN

STATUS AND DEVELOPMENT PROSPECTS OF FUNDAMENTAL AND APPLIED MICROBIOLOGY: THE VIEWPOINT OF YOUNG SCIENTISTS

REPUBLICAN SCIENTIFIC AND PRACTICAL CONFERENCE

СОСТОЯНИЕ И ПЕРСПЕКТИВЫ РАЗВИТИЯ ФУНДАМЕНТАЛЬНОЙ И ПРИКЛАДНОЙ МИКРОБИОЛОГИИ: ТОЧКА ЗРЕНИЯ МОЛОДЫХ УЧЕНЫХ

РЕСПУБЛИКАНСКАЯ НАУЧНО-ПРАКТИЧЕСКАЯ КОНФЕРЕНЦИЯ

MATERIALLAR TO‘PLAMI



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MIKROBIOLOGIYA INSTITUTI

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СОСТОЯНИЕ И ПЕРСПЕКТИВЫ РАЗВИТИЯ ФУНДАМЕНТАЛЬНОЙ И ПРИКЛАДНОЙ МИКРОБИОЛОГИИ: ТОЧКА ЗРЕНИЯ МОЛОДЫХ УЧЁНЫХ

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ANNOTATSIYA · АННОТАЦИЯ · ABSTRACT

To‘plamda O‘zbekiston Respublikasi Fanlar akademiyasi Mikrobiologiya instituti tomonidan Research Focus xalqaro ilmiy jurnali hamkorligida o‘tkazilgan «Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi» mavzusidagi Respublika ilmiy-amaliy anjumani materiallari — 138 ta ilmiy maqola va tezis jamlangan. Materiallar oltita yo‘nalish bo‘yicha guruhlangan: fundamental va amaliy mikrobiologiya; biotexnologiya, molekulyar biologiya va bioinformatika; probiotiklar, oziq-ovqat va farmatsevtik mikrobiologiya; tuproq, suv, ekologiya va sanitariya mikrobiologiyasi; infeksion kasalliklar, immunologiya va laborator diagnostika; yosh olimlar tadqiqotlari va innovatsion ishlanmalar. To‘plam mikrobiologiya, biotexnologiya va turdosh sohalarda faoliyat yuritayotgan olimlar, doktorantlar, magistrantlar va talabalar uchun mo‘ljallangan.

Сборник включает 138 научных статей и тезисов Республиканской научно-практической конференции «Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных», проведённой Институтом микробиологии Академии наук Республики Узбекистан совместно с международным научным журналом Research Focus. Материалы сгруппированы по шести направлениям и предназначены для учёных, докторантов, магистрантов и студентов в области микробиологии, биотехнологии и смежных наук.

The volume contains 138 research papers and abstracts presented at the Republican Scientific and Practical Conference “Status and Development Prospects of Fundamental and Applied Microbiology: The Viewpoint of Young Scientists”, held by the Institute of Microbiology of the Academy of Sciences of the Republic of Uzbekistan in partnership with Research Focus International Scientific Journal. The materials are grouped into six thematic sections and are intended for researchers, doctoral and master’s students and undergraduates in microbiology, biotechnology and related fields.

ANJUMAN TASHKILIY QO‘MITASI RAISI

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To‘plamga kiritilgan maqola va tezislarning mazmuni, keltirilgan ma’lumot va natijalarning to‘g‘riligi hamda aniqligi uchun mualliflar javobgar. Materiallar imlo va bezak jihatidan yagona talablar asosida tahrir qilindi.

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SO‘ZBOSHI

Jahon miqyosida kechayotgan ijtimoiy-iqtisodiy va ekologik o‘zgarishlar, aholi sonining ortishi, iqlim o‘zgarishi, oziq-ovqat xavfsizligi va biologik resurslardan oqilona foydalanish masalalari zamonaviy ilm-fan oldiga yangi vazifalarni qo‘ymoqda. Ushbu muammolarga ilmiy asoslangan yechimlar ishlab chiqishda mikrobiologiya, virusologiya va biotexnologiya fanlari alohida o‘rin egallaydi. Mikroorganizmlarning ulkan genetik va metabolik imkoniyatlarini o‘rganish fundamental biologik qonuniyatlarni anglash bilan bir qatorda, qishloq xo‘jaligi, tibbiyot, farmatsevtika, sanoat va atrof-muhit muhofazasi uchun samarali texnologiyalar yaratish imkonini bermoqda.

So‘nggi yillarda molekulyar biologiya, genomika, metagenomika, proteomika, metabolomika va bioinformatika sohalarida erishilgan yutuqlar mikrobiologik tadqiqotlarni sifat jihatidan yangi bosqichga olib chiqdi. Mikroorganizmlarning genetik xilma-xilligini aniqlash, mikrob jamoalarining funksional imkoniyatlarini baholash, biologik faol metabolitlarni tadqiq qilish, patogenlarning molekulyar diagnostikasini takomillashtirish hamda istiqbolli shtammlar asosida biotexnologik mahsulotlar yaratish sohaning ustuvor yo‘nalishlariga aylanmoqda.

Mamlakatimizda ham ilm-fanning iqtisodiyot va jamiyat taraqqiyotidagi o‘rnini kuchaytirish, fundamental tadqiqotlar natijadorligini oshirish, ilmiy infratuzilmani modernizatsiya qilish va yuqori malakali ilmiy kadrlar tayyorlashga qaratilgan huquqiy hamda institutsional islohotlar amalga oshirilmoqda.

Jumladan, O‘zbekiston Respublikasi Prezidentining 2020-yil 29-oktabrdagi PF-6097-sonli «Ilm-fanni 2030-yilgacha rivojlantirish konsepsiyasini tasdiqlash to‘g‘risida»gi Farmoni bilan ilm-fanni rivojlantirishning uzoq muddatli strategik yo‘nalishlari va maqsadli ko‘rsatkichlari belgilandi. Konsepsiyada 2030-yilga qadar ilm-fanga yo‘naltiriladigan mablag‘larning yalpi ichki mahsulotga nisbatan ulushini boshlang‘ich darajaga nisbatan 10 baravarga oshirish, ilmiy-tadqiqot va tajriba-konstruktorlik ishlarini moliyalashtirishda xususiy sektor ulushini 30 foizga yetkazish vazifalari nazarda tutilgan.

Mazkur vazifalar ilmiy tadqiqotlarni moliyalashtirish manbalarini diversifikatsiyalash, fan va ishlab chiqarish o‘rtasidagi hamkorlikni mustahkamlash, ilmiy ishlanmalarni tijoratlashtirish hamda tadqiqot natijalarining amaliy samaradorligini oshirish zaruratini ko‘rsatadi.

O‘zbekiston Respublikasi Prezidentining 2023-yil 11-sentabrdagi PF-158-sonli Farmoni bilan tasdiqlangan «O‘zbekiston-2030» strategiyasida ham inson kapitalini rivojlantirish, yoshlarning intellektual salohiyatini ro‘yobga chiqarish, sifatli ta’lim va innovatsion faoliyat uchun imkoniyatlarni kengaytirish ustuvor vazifalar sifatida belgilangan.

Mamlakatimiz ilm-fani taraqqiyotida muhim ahamiyatga ega bo‘lgan navbatdagi huquqiy hujjat – O‘zbekiston Respublikasi Prezidentining 2025-yil 27-dekabrdagi PQ-390-sonli «O‘zbekiston Respublikasi Fanlar akademiyasi faoliyatini takomillashtirish chora-tadbirlari to‘g‘risida»gi qaroridir. Mazkur qaror Fanlar akademiyasi tizimida fundamental va amaliy tadqiqotlar sifatini oshirish, ilmiy muassasalarning xalqaro raqobatbardoshligini ta’minlash,

ilm-fan va ishlab chiqarish integratsiyasini mustahkamlash hamda yoshlarni akademik ilm-fanga keng jalb etishning aniq mexanizmlarini belgilab berdi.

Qarorda 2030-yilga qadar Fanlar akademiyasi ilmiy xodimlari tarkibida yoshlar ulushini 60 foizgacha oshirish, nufuzli xalqaro ilmiy nashrlarda chop etiladigan maqolalar sonini 4 baravarga, xalqaro hamkorlikda amalga oshiriladigan ilmiy tadqiqotlar sonini 3 baravarga, yangi ilmiy ishlanmalar va ularni tijoratlashtirishdan olinadigan mablag‘lar hajmini 3 baravarga oshirish maqsad qilib qo‘yilgan.

Shuningdek, Fanlar akademiyasi ilmiy muassasalarida ilmiy xodimlar shtat birliklari sonini 2025-yildagi 1 408 tadan 2030-yilda 2 138 taga yetkazish rejalashtirilgan. Ushbu ko‘rsatkichlar ilmiy salohiyatni mustahkamlash, yangi tadqiqot yo‘nalishlarini rivojlantirish va yosh kadrlarni akademik ilm-fanga jalb etish uchun muhim tashkiliy asos yaratadi.

Ayniqsa, mazkur qarorda yosh olimlarni qo‘llab-quvvatlashga qaratilgan amaliy mexanizmlarning belgilanganligi e’tiborga molik. Jumladan, davlat granti loyihalari shtat jadvalida yosh olimlar ulushini kamida 30 foizga yetkazish, ular uchun akademik va amaliy treninglar, ilmiy seminarlar, tanlovlar, ko‘rgazmalar, konferensiyalar hamda forumlar tashkil etish, ilmiy tadqiqotlarda yuqori natijalarga erishgan yoshlarni rag‘batlantirish nazarda tutilgan.

Mazkur qaror asosida ilmiy tadqiqotlarni qo‘llab-quvvatlash, yosh olimlarni jalb qilish va strategik ahamiyatga ega ilmiy yo‘nalishlarni barqaror moliyalashtirish maqsadida Fanlar akademiyasi jamg‘armasini tashkil etish belgilangan. Jamg‘arma uchun Davlat byudjetidan har yili 80 milliard so‘m mablag‘ ajratilishi nazarda tutilganligi ilmiy faoliyatni moliyaviy qo‘llab-quvvatlashning aniq mexanizmlaridan biridir.

Bunday chora-tadbirlar yosh tadqiqotchilar uchun yangi imkoniyatlar yaratish bilan birga, ularning ilmiy faoliyatiga nisbatan mas’uliyatni ham oshiradi. Zamonaviy yosh olim faqat ilmiy ma’lumotlarni o‘zlashtiruvchi mutaxassis emas, balki mustaqil ilmiy g‘oyalarni shakllantiruvchi, zamonaviy tadqiqot metodologiyasini qo‘llay oladigan, natijalarni xalqaro ilmiy mezonlar asosida tahlil qiladigan va o‘z ishlanmalarini amaliyotga yo‘naltira oladigan tadqiqotchi bo‘lishi zarur.

Mikrobiologiya va biotexnologiya sohalarining rivojlanishi ham mamlakatimizda qabul qilingan strategik hujjatlar bilan bevosita bog‘liqdir. Xususan, O‘zbekiston Respublikasi Prezidentining 2020-yil 25-noyabrdagi PQ-4899-sonli «Biotexnologiyalarni rivojlantirish va mamlakatning biologik xavfsizligini ta’minlash tizimini takomillashtirish bo‘yicha kompleks chora-tadbirlar to‘g‘risida»gi qarorida biotexnologik tadqiqotlarni kengaytirish, mahalliy ilmiy ishlanmalarni qo‘llab-quvvatlash, biologik xavfsizlikni ta’minlash va biotexnologik mahsulotlarni ishlab chiqarishga joriy etish vazifalari belgilangan.

Ushbu vazifalarning amaliy ahamiyati, ayniqsa, qishloq xo‘jaligida yaqqol namoyon bo‘ladi. Tuproqlarning sho‘rlanishi, suv tanqisligi, qurg‘oqchilik, mineral o‘g‘itlar va pestitsidlardan intensiv foydalanish oqibatida yuzaga kelayotgan ekologik muammolar resurs tejamkor, ekologik xavfsiz va ilmiy asoslangan agrotexnologiyalarni ishlab chiqishni talab etmoqda.

Azot fiksatsiyalovchi, fosfatlarni mobilizatsiyalovchi, o‘simliklarning o‘sishi va rivojlanishini rag‘batlantiruvchi, fitopatogenlarga nisbatan antagonistik faollikka ega mikroorganizmlar asosida biopreparatlar yaratish mazkur muammolarga istiqbolli biotexnologik yechimlardan biri hisoblanadi. Shu bilan birga, pestitsidlar va boshqa ksenobiotik birikmalar

bilan ifloslangan muhitlarni biologik usullarda tiklash, mikroorganizmlarning biodegradatsiya salohiyatini oʻrganish va bioremediatsiya texnologiyalarini takomillashtirish ekologik mikrobiologiyaning dolzarb vazifalaridandir.

Oʻsimliklarning virusli kasalliklarini erta aniqlash, fitopatogenlarning molekulyar-genetik xususiyatlarini oʻrganish, infeksion jarayonlarning rivojlanish mexanizmlarini tadqiq qilish va kasalliklarning oldini olishga qaratilgan samarali chora-tadbirlarni ishlab chiqish ham qishloq xoʻjaligi xavfsizligini ta’minlashda muhim ilmiy ahamiyatga ega.

Oʻzbekiston Respublikasi Fanlar akademiyasi Mikrobiologiya institutida olib borilayotgan fundamental va amaliy tadqiqotlar mazkur ustuvor yoʻnalishlar bilan uzviy bogʻliqdir. Institutda mikroorganizmlarning fiziologik-biokimyoviy, genetik va biotexnologik xususiyatlarini oʻrganish, istiqbolli mahalliy shtammlarni ajratib olish, mikrobiologik preparatlar yaratish, ekologik muammolarning biologik yechimlarini izlash, sanoat uchun ahamiyatli mikroorganizmlar va ularning metabolitlarini tadqiq qilish, shuningdek, fitovirusologiya sohasida ilmiy izlanishlar olib borilmoqda.

Institutning ilmiy salohiyatini yanada rivojlantirishda tajribali olimlar tomonidan shakllantirilgan ilmiy maktablar an’analarini saqlash, ularning davomiyligini ta’minlash va yosh tadqiqotchilarni zamonaviy ilmiy yoʻnalishlarga jalb etish muhim ahamiyat kasb etadi. Bunda ustoz-shogird an’analarini mustahkamlash, ilmiy natijalarning ishonchliligi va takrorlanuvchanligini ta’minlash, akademik halollik tamoyillariga rioya qilish, fanlararo hamkorlikni kengaytirish hamda tadqiqot natijalarini xalqaro ilmiy hamjamiyatga taqdim etish ustuvor vazifalardan hisoblanadi.

Shu nuqtai nazardan, Oʻzbekiston Respublikasi Fanlar akademiyasi Mikrobiologiya instituti tomonidan 2026-yil 30-oktabr kuni «Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi» mavzusida tashkil etilayotgan Respublika ilmiy-amaliy anjumani alohida ahamiyat kasb etadi.

Mazkur anjuman yosh olimlarning ilmiy izlanishlarini qoʻllab-quvvatlash, ularning tadqiqot natijalarini ilmiy jamoatchilik muhokamasiga taqdim etish, ilmiy maktablar oʻrtasida tajriba almashish hamda fundamental va amaliy mikrobiologiyaning istiqbolli yoʻnalishlarini belgilash maqsadida tashkil etilmoqda.

Anjumanga jami 138 ta ilmiy maqola va tezis qabul qilinganligi uning ilmiy qamrovini tavsiflovchi muhim koʻrsatkichdir. Mazkur materiallarda mikrobiologiya, virusologiya, biotexnologiya va ular bilan bogʻliq fanlararo yoʻnalishlarda olib borilayotgan tadqiqotlar natijalari oʻz aksini topgan.

Toʻplamda jamlangan ilmiy ishlar mikroorganizmlarning biologik xususiyatlarini tadqiq qilish, molekulyar-genetik usullarni qoʻllash, qishloq xoʻjaligi va ekologik mikrobiologiya, sanoat biotexnologiyasi, biologik faol moddalar hamda biotexnologik mahsulotlar yaratish bilan bogʻliq masalalar yuzasidan ilmiy fikr almashish imkonini beradi.

Anjumanning muhim jihatlaridan biri – yosh tadqiqotchilarning ilmiy natijalarini tajribali olimlar ishtirokida muhokama qilish, tadqiqot metodologiyasini takomillashtirish, yangi ilmiy gʻoyalarni shakllantirish va kelgusidagi hamkorlik yoʻnalishlarini belgilash imkoniyatidir. Bu esa Fanlar akademiyasi faoliyatini takomillashtirishga qaratilgan PQ-390-sonli qarorda belgilangan yoshlarni akademik ilm-fanga keng jalb etish, ularning ilmiy tashabbuslarini qoʻllab-quvvatlash

va ilmiy salohiyatini rivojlantirish vazifalari bilan bevosita uyg‘unlashadi.

Shuni alohida ta’kidlash lozimki, ilmiy anjumanlarning ahamiyati faqat taqdim etilgan maqolalar soni bilan emas, balki ularda ilgari surilgan g‘oyalarning ilmiy yangiligi, metodologik asoslanganligi, amaliy ahamiyati va keyingi tadqiqotlar uchun yaratadigan imkoniyatlari bilan belgilanadi. Shu bois mazkur anjuman materiallari kelgusidagi ilmiy izlanishlar, fanlararo hamkorlik va innovatsion ishlanmalar uchun muhim ilmiy-axborot manbai bo‘lib xizmat qilishiga ishonamiz.

Bugungi kunda yosh olimlar oldida turgan asosiy vazifa – mavjud ilmiy bilimlarni o‘zlashtirish bilan cheklanib qolmasdan, yangi ilmiy natijalarga erishish, zamonaviy eksperimental va tahliliy usullardan samarali foydalanish, xalqaro ilmiy hamkorlikni rivojlantirish hamda tadqiqot natijalarini mamlakatimiz taraqqiyotiga xizmat qiluvchi amaliy ishlanmalarga aylantirishdan iboratdir.

Ishonchimiz komilki, ushbu Respublika ilmiy-amaliy anjumani yosh tadqiqotchilarning ilmiy faolligini oshirish, ustoz va shogirdlar o‘rtasidagi ilmiy muloqotni mustahkamlash, fundamental va amaliy mikrobiologiya sohasidagi dolzarb muammolarga yangi yondashuvlarni shakllantirish hamda ilmiy hamkorlik aloqalarini yanada kengaytirishga xizmat qiladi.

Fursatdan foydalanib, anjumanni tashkil etishda ishtirok etgan barcha hamkor tashkilotlarga, tashkiliy qo‘mita a’zolariga, o‘z ilmiy ishlari bilan anjuman mazmunini boyitgan olimlar, yosh tadqiqotchilar, doktorantlar, mustaqil izlanuvchilar, magistrantlar va talabalarga samimiy minnatdorchilik bildiraman.

«Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi» mavzusidagi Respublika ilmiy-amaliy anjumani ishtirokchilariga samarali ilmiy muloqot, yangi g‘oyalar, muvaffaqiyatli tadqiqotlar va kelgusidagi ilmiy faoliyatlarida ulkan yutuqlar tilayman.

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MUNDARIJA

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BO‘LIM · SECTION · СЕКЦИЯ

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32
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SOYA O‘SIMLIGINING TUGANAK BAKTERIYALARINING XILMA-XILLIGI, SIMBIOTIK XUSUSIYATLARI VA ISTIQBOLLI SHTAMMLARINI TANLASH: ZAMONAVIY TADQIQOTLAR SHARHI

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Annotatsiya: Ushbu maqolada oxirgi yillarda e’lon qilingan ilmiy tadqiqotlar asosida soya tuganak bakteriyalarining biologik xususiyatlari, taksonomik xilma-xilligi, ajratib olish va identifikatsiya qilish usullari, *16S rRNA*, *nodC* va *nifH* genlaridan foydalanish, simbiotik samaradorlikni baholash, mahalliy shtammlarning abiotik stresslarga chidamliligi hamda biologik o‘g‘itlar ishlab chiqishdagi istiqbollari tahlil qilingan. Zamonaviy tadqiqotlarda soya o‘simligi uchun asosiy simbiotik mikroorganizmlar sifatida *Bradyrhizobium* avlodi qayd etilgan, ammo ayrim hududlarda *Rhizobium*, *Ensifer* va boshqa rizobiyalar ham soyada tuganaklarini hosil qilishi mumkinligi ko‘rsatilgan.

Kalit so‘zlar: soya (Glycine max), tuganak bakteriyalari, Bradyrhizobium, simbioz, biologik azot fiksatsiyasi, 16S rRNA, nodC, nifH, simbiotik samaradorlik.

Аннотация: В статье на основе научных исследований, опубликованных в последние годы, проанализированы биологические свойства клубеньковых бактерий сои, их таксономическое разнообразие, методы выделения и идентификации, использование генов *16S rRNA*, *nodC* и *nifH*, оценка симбиотической эффективности, устойчивость местных штаммов к абиотическим стрессовым факторам, а также перспективы их применения при разработке биологических удобрений. Современные исследования показывают, что основными симбиотическими микроорганизмами сои являются представители рода *Bradyrhizobium*. Вместе с тем установлено, что в отдельных регионах клубеньки на корнях сои могут также формировать представители родов *Rhizobium*, *Ensifer* и других групп ризобий.

Ключевые слова: соя (Glycine max), клубеньковые бактерии, Bradyrhizobium, симбиоз, биологическая фиксация азота, 16S rRNA, nodC, nifH, симбиотическая эффективность.

Abstract: This article reviews recent scientific studies on the biological characteristics of soybean-nodulating bacteria, their taxonomic diversity, methods of isolation and identification, the use of *16S rRNA*, *nodC*, and *nifH* genes, assessment of symbiotic effectiveness, tolerance of indigenous strains to abiotic stresses, and their prospects for application in the development of biofertilizers. Recent studies indicate that members of the genus *Bradyrhizobium* are the major symbiotic microorganisms associated with soybean. However, studies from different regions have also shown that representatives of the genera *Rhizobium*, *Ensifer*, and other rhizobial groups can form nodules on soybean roots.

Keywords: soybean (Glycine max), nodule bacteria, Bradyrhizobium, symbiosis, biological nitrogen fixation, 16S rRNA, nodC, nifH, symbiotic efficiency.

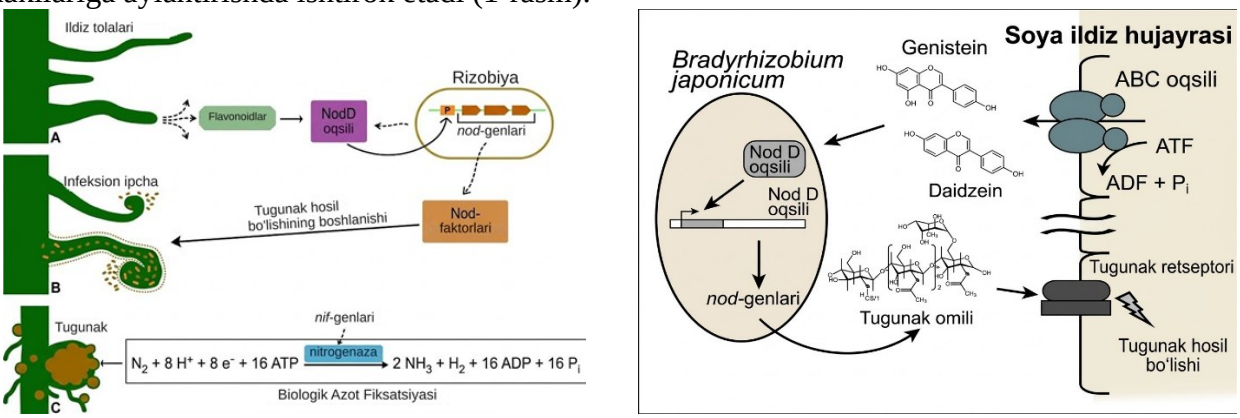
Ma’lumki, soya (*Glycine max* L.) o‘simligi qishloq xo‘jaligida muhim dukkakli ekinlardan biri bo‘lib, yuqori oqsil va moy miqdori bilan oziq-ovqat, yem-xashak va sanoat uchun qimmatli xomashyo hisoblanadi. Soyaning yuqori mahsuldorligini ta’minlashda azot bilan ta’minlanish muhim omillardan biridir. Azotning muhim qismi o‘simlik va rizobiyalar o‘rtasidagi simbiotik munosabat

IQTIBOS UCHUN
Juraeva R.N., Islomova M.N. Soya o‘simligining tuganak bakteriyalarining xilma-xilligi, simbiotik xususiyatlari va istiqbolli shtammlarini tanlash: zamonaviy tadqiqotlar sharhi // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 19–22.
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natijasida biologik azot fiksatsiyasi orqali ta’minlanishi mumkin. Soyaning o‘sishi va hosildorligida biologik azot fiksatsiyasi bilan bir qatorda fosfor bilan ta’minlanish ham muhim ahamiyatga ega bo‘lib, *Bradyrhizobium* bilan inokulyatsiya qilish va fosfor qo‘llash nodulyatsiya, azot o‘zlashtirilishi va hosildorlikni yaxshilashi mumkin [1].

Soya ildiz tizimi bilan simbioz holda tuganak bakteriyalar atmosferadan azotni o‘zlashtirib, ildiz tuganaklarining shakllanishini ta’minlaydi. Bunday mikroorganizmlarning samaradorligi bakteriya turi va shtammiga, soya genotipiga, tuproq xususiyatlariga, harorat, namlik, sho‘rlanish va boshqa ekologik omillarga bog‘liq. Zamonaviy tadqiqotlar soya rizobiyalarining xilma-xilligi avval qabul qilinganidan ancha murakkab ekanligini ko‘rsatmoqda. Oldin soya bilan simbiozning asosiy vakili sifatida *Bradyrhizobium japonicum* qaralgan bo‘lsa, molekulyar-genetik tadqiqotlar *B. diazoefficiens*, *B. elkanii*, *B. ottawaense* va boshqa taksonomik guruhlarning ham soya bilan samarali simbioz hosil qilishi mumkinligini ko‘rsatdi [2,3].

Soya va tuganak bakteriyalarining simbiotik munosabati. Soya–rizobiya simbiozi o‘simlik ildizidan ajraladigan kimyoviy birikmalar va bakteriyalarning maxsus signal molekulalari o‘rtasidagi o‘zaro ta’sirdan boshlanadi. Rizobiyalar ildiz sohasiga jalb qilinadi, ildiz tukchalari bilan o‘zaro ta’sirga kirishadi va natijada bakteriyalarning o‘simlik to‘qimalariga kirishi uchun infeksiya jarayoni boshlanadi [2,3]. Keyinchalik ildiz tuganagi shakllanadi va bakteriyalar tuganak hujayralarida maxsus simbiotik muhitda faoliyat ko‘rsatadi [2,4]. Azot fiksatsiyasi jarayonida bakteriyalarning nitrogenaza ferment tizimi atmosferadagi N_2 ni o‘simlik o‘zlashtira oladigan azot shakllariga aylantirishda ishtirok etadi (1-rasm).



1-rasm. *Bradyrhizobium japonicum* tuganak bakteriyasining nodulyatsiya jarayonining boshlanish mexanizmining sxematik tasviri

O‘simlik esa bakteriyalarni uglerod manbalari va energiya bilan ta’minlaydi. Simbiozning samaradorligi har bir bakteriya shtammida bir xil emas. Shuning uchun faqat tuganak hosil qilish qobiliyati emas, balki o‘simlik biomassasi, tuganaklar soni va massasi, azot to‘planishi hamda nazorat variantiga nisbatan o‘sish ko‘rsatkichlari ham baholanishi kerak [2,5].

Soya tuganak bakteriyalarining taksonomik va genetik xilma-xilligi. Soya bilan simbiotik munosabat hosil qiluvchi rizobiyalar orasida *Bradyrhizobium* turkumi alohida ahamiyatga ega. Ammo, 2022-yilda e’lon qilingan keng qamrovli adabiyotlar sharhida soya bilan simbioz hosil qiluvchi rizobiyalarning ekologiyasi, genetik xilma-xilligi, identifikatsiya usullari va simbiotik xususiyatlari tahlil qilingan. Mualliflar *Bradyrhizobium* bilan bir qatorda *Rhizobium*, *Ensifer* va *Mesorhizobium* kabi avlodlarning ayrim vakillari ham soyani nodulyatsiya qilishi mumkinligini qayd etgan [2]. Xitoy Xalq Respublikasining Xeylunszyan provinsiyasida o‘tkazilgan tadqiqotlarda soya bilan bog‘liq 74 ta rizobiya izolyati ajratib olingan. PCR-RFLP tahlili ularni 9 ta genotipga ajratgan, 16S rRNA, *recA*, *atpD* va *gyrB* genlari asosida o‘tkazilgan ko‘p lokusli filogenetik tahlil natijasida *Bradyrhizobium japonicum*, *B. diazoefficiens* va *B. ottawaense* turlari hamda alohida *Bradyrhizobium* guruhi aniqlangan [3]. Ayniqsa, ushbu tadqiqotda aniqlangan izolyatlarning 64%i hali to‘liq tavsiflanmagan *Bradyrhizobium* guruhiga kirishi mahalliy rizobiyalar genetik zahirasi juda keng bo‘lishi mumkinligini ko‘rsatadi. Shuningdek, *nodC* va *nifH* genlari bo‘yicha filogenetik tahlillar esa

izolyatlarning *symbiovar glycinearum* bilan bog‘liqligini ko‘rsatgan [3]. Mahalliy tuganak bakteriyalarini o‘rganishning birinchi bosqichi soya ildizlaridan yaxshi rivojlangan va tashqi ko‘rinishi sog‘lom bo‘lgan tuganaklarni tanlashdan iborat.

Molekulyar identifikatsiya: 16S rRNA, nodC va nifH genlari. Soya rizobiyalarini zamonaviy identifikatsiya qilishda 16S rRNA geni muhim markerlardan biri hisoblanadi. Bunda bakteriyalarning filogenetik o‘rnini dastlabki aniqlash imkonini beradi. Biroq 16S rRNA geni yaqin qarindosh *Bradyrhizobium* turlarini bir-biridan aniq ajratish uchun har doim ham yetarli emas. Shu sababli, zamonaviy tadqiqotlarda *recA*, *atpD* va *gyrB* kabi qo‘shimcha genlardan ham foydalanilmoqda [2,3]. Shuningdek, 2026-yilda nashr etilgan maqolalarda tadqiqotning aynan shu ko‘p lokusli yondashuv *Bradyrhizobium* izolyatlarini yanada aniqroq tavsiflash uchun qo‘llanilgan [3]. Simbiotik xususiyatni baholashda esa *nodC* va *nifH* genlari alohida ahamiyatga ega, *nodC* geni tuganak hosil bo‘lish jarayoni bilan bog‘liq bo‘lsa, *nifH* azot fiksatsiyasida ishtirok etuvchi nitrogenaza kompleksi bilan bog‘liq genlardan hisoblanadi [2,3].

Mahalliy va tijorat shtammlarini taqqoslash. Tijoratda tuganak bakteriyalar asosida biopreparatlar ma’lum sharoitlarda yuqori samara berishi mumkin. Biroq tashqi muhitga kiritilgan shtammlarning samaradorligi tuproqning fizik-kimyoviy xususiyatlari, harorat, namlik, mahalliy mikrobiota va tabiiy rizobiyalar bilan raqobatiga bog‘liq [5,7]. Shu sababli, mahalliy sharoitdan ajratilgan rizobiyalarni o‘rganish va ularning simbiotik hamda adaptiv xususiyatlarini baholash muhim ahamiyatga ega [3,6]. 2026-yilda o‘tkazilgan tadqiqotda mahalliy *Bradyrhizobium* izolyatlarining simbiotik samaradorligi va abiotik stresslarga chidamliligi o‘rganilgan. Tadqiqot natijalaridan mahalliy shtammlarning ishqoriy muhit, yuqori harorat va PEG yordamida modellashtirilgan qurg‘oqchilik sharoitlariga chidamliligi turlicha ekanligi aniqlangan. Ayrim shtammlarda yuqori simbiotik samaradorlik va stressga chidamlilik bir vaqtda kuzatilgan. Xususan, SH16 shtammi yuqori simbiotik samaradorlikni stresslarga chidamlilik bilan birlashtirgan. Bu natijalar mahalliy rizobiyalarni muayyan hudud sharoitiga mos biologik inokulyantlar yaratish uchun tanlash istiqbolli ekanligini ko‘rsatadi [3].

Qurg‘oqchilik, sho‘rlanish va boshqa stresslarga chidamlilik. Global iqlim o‘zgarishi sharoitida yuqori harorat, qurg‘oqchilik va tuproq sho‘rlanishi soya–rizobiya simbiozi samaradorligiga salbiy ta’sir ko‘rsatishi mumkin. Rizobiya shtammini tanlashda faqat laboratoriyadagi o‘sish qobiliyatini emas, balki uning stress sharoitida yashovchanligi va soya bilan simbiozni saqlab qolish qobiliyatini ham baholash muhim. Shu nuqtai nazardan, 2026-yilgi tadqiqotda *Bradyrhizobium* izolyatlarining ishqoriylik, yuqori harorat va PEG-induksiyalangan qurg‘oqchilikka chidamliligi o‘rganilgan. Ayrim shtammlarda yuqori simbiotik samaradorlik bilan birga stressga chidamlilik xususiyati ham qayd etilgan [3].

Rizosfera mikroorganizmlari va soya mahsuldorligi. So‘nggi yillarda soya mahsuldorligini shakllantirishda rizosfera mikroorganizmlarining roliga ham katta e’tibor qaratilmoqda. Rizosferadagi mikroorganizmlar o‘simlikning oziqlanishi, o‘sishi va stresslarga moslashuviga ta’sir ko‘rsatishi mumkin. Turli tuproq sharoitlarida tuganak bakteriya bilan inokulyatsiya qilish soya ildiz tuganaklarining shakllanishi va rizosferadagi bakteriyalar jamoasi tarkibiga ta’sir qilishi mumkin [5]. Shuningdek, rizosferaga xos mikrobiom va o‘simlik–mikroorganizm o‘zaro ta’sirlari soya mahsuldorligini oshirishda muhim omillardan biri sifatida qaralmoqda [6]. Mikroorganizmlardan foydalanish, jumladan, tuganak bakteriyalar va boshqa foydali mikroorganizmlarni qo‘llash, barqaror qishloq xo‘jaligi tizimlarida kimyoviy resurslarga bo‘lgan ehtiyojni kamaytirish va o‘simliklarning oziqlanishini yaxshilash imkonini beradi [6].

Xulosa

Soya tuganak bakteriyalarini o‘rganishda fenotipik tavsiflashdan molekulyar va ko‘p lokusli filogenetik tahlillarga o‘tish kuzatilmoqda. Zamonaviy ma’lumotlar soya rizobiyalarining genetik xilma-xilligi keng ekanligini va *Bradyrhizobium* turkumi bilan bir qatorda boshqa rizobiya guruhlarining ham ayrim hududlarda soya bilan simbioz hosil qilishi mumkinligini ko‘rsatmoqda. Mahalliy tuproq sharoitidan ajratilgan shtammlar orasida yuqori simbiotik samaradorlikka va abiotik

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stresslarga chidamli bo‘lgan bakteriyalarni aniqlash soya yetishtirishda biologik inokulyantlardan foydalanish uchun muhim ilmiy asos bo‘lib xizmat qiladi [3,5]. Ayniqsa, 16S rRNA, recA, atpD, gyrB, nodC va nifH kabi molekulyar markerlarni birgalikda qo‘llash istiqbolli shtammlarni yanada ishonchli tanlash imkonini beradi [2,3].

Kelgusida O‘zbekistonning turli tuproq-iqlim zonalaridan soya tuganaklarini yig‘ish, mahalliy tuganak bakteriyalarini ajratish, ularning taksonomik va simbiotik xususiyatlarini o‘rganish hamda yuqori samarador shtammlar asosida biologik inokulyantlar yaratish muhim amaliy ahamiyat kasb etadi. Bunday yondashuv mahalliy sharoitga mos, samarali va barqaror mikrobiologik preparatlarni ishlab chiqish uchun ilmiy asos bo‘lishi mumkin.

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CAROXYLON DENDROIDES O‘SIMLIGI GALOTOLERANT BAKTERIYALARINING FUSARIUM TURKUMI VAKILLARIGA QARSHI ANTAGONISTIK FAOLLIGI

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Annotatsiya: Fitopatogen zamburug‘lar qishloq xo‘jaligi barqarorligiga jiddiy tahdid soladi, bu katta iqtisodiy yo‘qotishlarga va oziq-ovqat sifatining pasayishiga olib keladi. Natijada, kasalliklarni boshqarish strategiyalarini muqobil o‘rganish, ayniqsa antagonistik potensialga ega tabiiy mikroorganizmlardan foydalanish juda muhimdir.

Tadqiqotimizda Sirdaryo viloyati Sayxunobod tumani sho‘rlangan tuproqlarida uchrovchi Sho‘rbuta (*Caroxylon dendroides (Pall.) Tzvelev)* o‘simligidan ajratib olingan galotolerant bakteriya shtammlarining o‘simliklarning o‘sishini rag‘batlantiruvchi xususiyatlari baholandi. Eng kuchli faollik bergan izolyatlar MALDI-TOF tahliliga ko‘ra**,** *Bacillus atrophaeus* 20, *Bacillus rugosus* 29 ekanligi aniqlandi. Ushbu tanlab olingan izolyatlarning *Fusarium oxysporum, F. gossypinum, F. graminearum, F. brachygibbosum* zamburug‘lariga qarshi antagonistik faolligi baholandi.

Kalit so‘zlar: *Caroxylon dendroides*, zamburug‘, *Fusarium*, galotolerant bakteriya, antagonizm.

Аннотация: Фитопатогенные грибы представляют серьёзную угрозу для устойчивого развития сельского хозяйства, приводя к значительным экономическим потерям и снижению качества сельскохозяйственной продукции. В связи с этим особую актуальность приобретает поиск альтернативных стратегий борьбы с фитопатогенами, в частности, с использованием природных микроорганизмов, обладающих антагонистическим потенциалом.

В данном исследовании оценивали ростстимулирующие свойства галотолерантных бактериальных штаммов, выделенных из галофитного растения *Caroxylon dendroides* (Pall.) Tzvelev (шўрбута), произрастающего на засолённых почвах Сайхунабадского района Сырдарьинской области Республики Узбекистан. По результатам MALDI-TOF-анализа наиболее перспективные изоляты были идентифицированы как Bacillus atrophaeus штамм 20 и Bacillus rugosus штамм 29. В дальнейшем была оценена антагонистическая активность отобранных изолятов в отношении фитопатогенных грибов *Fusarium oxysporum, F. gossypinum, F. graminearum u F. brachygibbosum.*

Ключевые слова: *Caroxylon dendroides*, грибы, *Fusarium*, галотолерантные бактерии, антагонизм.

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Abstract: Phytopathogenic fungi pose a serious threat to agricultural sustainability, causing substantial economic losses and reducing food quality. Therefore, exploring alternative disease management strategies, particularly those involving naturally occurring microorganisms with antagonistic potential, is of considerable importance.

In this study, the plant growth-promoting properties of halotolerant bacterial strains isolated from the halophyte *Caroxylon dendroides* (Pall.) Tzvelev, commonly known as Sho‘rbuta, growing in saline soils of Saykhunabad District, Syrdarya Region, Uzbekistan, were evaluated. Based on MALDI-TOF analysis, the most promising isolates were identified as Bacillus atrophaeus strain 20 and Bacillus rugosus strain 29. The antagonistic activity of these selected isolates against the phytopathogenic fungi *Fusarium oxysporum, F. gossypinum, F. graminearum, and F. brachygibbosum* was subsequently assessed.

Keywords: *Caroxylon dendroides*, fungi, *Fusarium*, halotolerant bacteria, antagonism.

Kirish

Global iqlim o‘zgarishi va ekin maydonlarining degradatsiyasi kabi ikki tomonlama bosim ostida qishloq xo‘jaligining barqaror rivojlanishi jiddiy qiyinchiliklarga duch kelmoqda. Xususan, patogen mikroorganizmlar keltirib chiqaradigan zarar va sho‘r-ishqoriy stress tufayli yuzaga keladigan cheklovlar don ekinlarining xavfsiz yetishtirilishini cheklovchi ikki muhim omil sifatida paydo bo‘ldi [1].

Fitopatogen o‘simlik zamburug‘lari o‘simlik kasalliklarining 70% dan 80% gacha bo‘lgan qismini keltirib chiqaradi, bu esa global qishloq xo‘jaligi mahsuldorligiga doimiy tahdid soladi, natijada hosildorlikning keskin pasayishi va asosiy ekin sifatining yomonlashishiga olib keladi [2;3;4].

Fusarium turkumidagi zamburug‘lar don ekinlarining asosiy patogenlari bo‘lib, don hosildorligi va sifatini pasaytiradigan fito- va mikotoksinlarni ishlab chiqaradi. Shuning uchun o‘simlik bilan bog‘liq bakteriyalar orasida samarali biologik nazorat vositalarini izlash dolzarb soha hisoblanadi [5].

Antagonistik bakteriyalar zararli fitopatogenlarning o‘sishini tabiiy ravishda cheklash orqali o‘simliklar salomatligi va ekologik muvozanatni saqlashda muhim o‘rin tutadi [6]. Bakteriyalar o‘simlik ildizi atrofi va ichki to‘qimalarida yashab, ozuqa moddalari va joy uchun raqobat, antibiotiklar, lipopeptidlar (masalan, surfaktin, iturin va fengitsin) va poliketidlarni o‘z ichiga olgan antimikrob birikmalar ishlab chiqarish va patogen hujayra devorlarini parchalaydigan gidrolitik fermentlarning sekretsiyasi kabi turli mexanizmlar orqali himoya ta’sirini ko‘rsatadi [7;8]. Bu bioaktiv birikmalar zamburug‘ hujayra membranalarini buzish, asosiy metabolik jarayonlarga xalaqit berish yoki sporalarning rivojlanishini blokirovka qilish orqali zamburug‘larning o‘sishini ingibitsiya qilishi mumkin [9;10].

Materiallar va usullar

Sirdaryo viloyati Sayxunobod tumani sho‘rlangan tuproqlarida uchraydigan dominant galofit *Sho‘rbuta* (*Caroxylon dendroides (Pall.) Tzvelev*) o‘simligi tadqiqot obyekti sifatida tanlab olindi. O‘simlik turli qismlaridan ajratib olingan bakteriya izolyatlarining galotolerantlik hamda o‘simliklarning o‘sishini rag‘batlantirish xususiyati baholandi [11]. Eng kuchli faollik namoyon qilgan bakteriya izolyatlari MALDI-TOF usuli bilan identifikatsiya qilindi. Ushbu izolyatlar *B. atrophaeus* 20, *B. rugosus* 29 ekanligi aniqlandi.

Ushbu shtammlarning fitopatogen zamburug‘lar *F. oxysporum, F. gossypinum, F. graminearum, F. brachygibbosum* turkumi vakillariga nisbatan antagonistik faolligini baholash uchun tarkibi 50 % ozuqa agar va 50 % kartoshka saxarozali agar tutgan ozuqa muhiti tayyorlandi. Shtammlar tomonidan zamburug‘ mitseliysi o‘sishini ingibitsiya qilishini aniqlash uchun bakteriya o‘sish chegarasi va zamburug‘lar o‘sishi chegarasi orasidagi masofa hisoblandi [12]. Zamburug‘ mitseliysining o‘sishini ingibitsiya qilishi quyidagi tenglama yordamida baholandi: I(%) = (1 − a/b)

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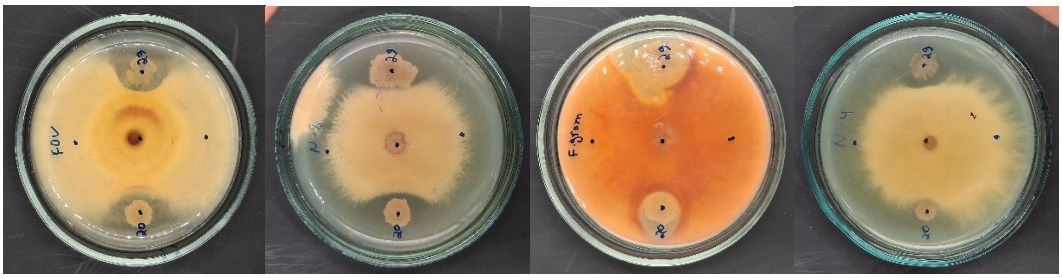
× 100. Bunda: a — zamburug‘lar koloniyasi markazidan bakterial tomondan zamburug‘larning o‘sish chekkasigacha bo‘lgan masofa; b — zamburug‘ koloniyasini ingibirlash radiusi.

Olingan natijalar

Tadqiqot davomida *B. atrophaeus* 20 va *B. rugosus* 29 bakteriya shtammlarining *Fusarium* turkumiga mansub fitopatogen zamburug‘larga nisbatan antagonistik faolligi baholandi. Olingan natijalarga ko‘ra, har ikkala bakteriya shtammi ham sinovdan o‘tkazilgan to‘rtta fitopatogen zamburug‘ning o‘sishini sezilarli darajada ingibirlashi qayd etildi. Biroq ularning antagonistik faolligi fitopatogen zamburug‘ turiga qarab farq qilishi kuzatildi.

Yuqoridagi keltirilgan formula bo‘yicha hisoblash olib borilganda, *B. atrophaeus* 20 shtammi *F. oxysporum* o‘sishini 65,25 %, *F. gossypinumni* 55,25 %, *F. graminearumni* 58,75 %, F. *brachygibbosumni* esa juda kuchsiz ingibitsiya qilganligi aniqlandi.

B. rugosus 29 shtammi *F. oxysporum* o‘sishini 52,5 %, *F. gossypinumni* 66,25 %, *F. graminearumni* 40,75 %, F. *brachygibbosumni* esa 62 % ingibirlashi aniqlandi (1-rasm).



1-rasm. *B. atrophaeus* 20 va *B. rugosus* 29 shtammlarining antagonistik xususiyatini baholash

Ushbu natijalar *B. atrophaeus* 20 va *B. rugosus* 29 shtammlarining fitopatogen zamburug‘larga nisbatan antagonistik faolligi turlicha ekanligini ko‘rsatadi. *B. atrophaeus* 20 shtammi *F. oxysporum* o‘sishini 65,25 % ga ingibitsiya qilib, eng yuqori antagonistik faollikni namoyon etdi. Shuningdek, ushbu shtamm *F. graminearum* va *F. gossypinum* o‘sishini 58,75 % va 55,25 % ga kamaytirdi. Biroq, *F. brachygibbosum*ga nisbatan antifungalligi nisbatan past ekanligi aniqlandi.

B. rugosus 29 shtammi esa *F. gossypinum* o‘sishini 66,25 % ga ingibirlab, mazkur zamburug‘ga qarshi eng yuqori faollikni ko‘rsatdi. Bundan tashqari, ushbu shtamm *F. brachygibbosum, F. oxysporum va F. graminearum* turlariga nisbatan 62 %, 52,5 % va 40,75 % gacha antagonistlik hosil qildi. *B. rugosus* 29 shtammining antagonistik faolligi zamburug‘ turiga bog‘liq bo‘lib, u *F. gossypinum* va *F. brachygibbosum*ga nisbatan yuqoriroq ingibitorlik ta’sirini namoyon etdi.

Xulosa

Olib borilgan tadqiqotlar natijasida sho‘rlangan tuproqlarda tabiiy holda o‘suvchi Sho‘rbuta *(Caroxylon dendroides (Pall.) Tzvelev)* o‘simligi mikroflorasida sho‘rlanishga chidamli va biologik faol bakteriya izolyatlaridan eng kuchli faollik namoyon qilgan izolyatlar fitopatogen *Fusarium* turkumi vakillariga nisbatan antagonistik xususiyatlari baholandi va turlicha antagonistik faollikni namoyon etdi.

Olingan natijalar kelgusida tanlab olingan izolyatlarning antagonistik xususiyatlarini chuqurroq o‘rganish, ularni turli fitopatogen zamburug‘larga nisbatan kompleks biopreparatlar tarkibiga kiritish hamda dala sharoitidagi samaradorligini baholash uchun ilmiy asos bo‘lib xizmat qiladi.

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WICKERHAMOMYCES ANOMALUS 95 SHTAMMINING FITOPATOGEN ZAMBURUG‘LARGA QARSHI ANTAGONIST POTENSIALI VA UCHUVCHAN METABOLITLAR PROFILI

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Annotatsiya: Mazkur tadqiqotda mahalliy *Wickerhamomyces anomalus* achitqi shtammlarining fitopatogen zamburug‘larga (*Penicillium expansum*, *Aspergillus flavus*, *Fusarium oxysporum*) qarshi antagonistik faolligi o‘rganildi. Skrining natijalariga ko‘ra, *W. anomalus* 120 va 95 shtammlari eng yuqori antagonistik samaradorlikni (87,2–88,3%) ko‘rsatdi. Gaz xromatografiyasi–mass-spektrometriyasi (GC-MS) tahlili yuqori antagonist *W. anomalus* 95 shtammi ekstraktida 38 ta metabolitni, jumladan, kuchli antifungal xususiyatga ega 2-feniletanol va fenolik birikmalarni aniqladi. Olingan natijalar ushbu shtammlar asosida qishloq xo‘jaligi mahsulotlarini saqlashda qo‘llaniladigan samarali biofungitsidlar yaratish istiqbolli ekanligini tasdiqlaydi.
Kalit so‘zlar: *Wickerhamomyces anomalus*, biokontrol, antagonistik faollik, GC-MS, 2-feniletanol.

Аннотация: В данном исследовании изучена антагонистическая активность местных штаммов дрожжей *Wickerhamomyces anomalus* против фитопатогенных грибов (*Penicillium expansum*, *Aspergillus flavus*, *Fusarium oxysporum*). По результатам скрининга штаммы *W. anomalus* 120 и 95 показали наибольшую эффективность подавления (87,2–88,3%). Газохроматографический масс-спектрометрический (GC-MS) анализ экстракта штамма *W. anomalus* 95 выявил 38 метаболитов, включая 2-фенилэтанол и фенольные соединения с выраженными противогрибковыми свойствами. Полученные результаты подтверждают перспективность создания эффективных биофунгицидов на основе данных штаммов для защиты сельскохозяйственной продукции при хранении.
Ключевые слова: *Wickerhamomyces anomalus*, биоконтроль, антагонистическая активность, GC-MS, 2-фенилэтанол.

Abstract: This study evaluated the antagonistic activity of native *Wickerhamomyces anomalus* yeast strains against phytopathogenic fungi (*Penicillium expansum*, *Aspergillus flavus*, *Fusarium oxysporum*). Screening results showed that *W. anomalus* strains 120 and 95 exhibited the highest antagonistic efficacy (87,2–88,3%). Gas chromatography–mass spectrometry (GC-MS) analysis of the *W. anomalus* 95 extract revealed 38 metabolites, including 2-phenylethanol and phenolic compounds with pronounced antifungal properties. These findings confirm the potential of developing effective biofungicides based on these strains for postharvest protection of agricultural products.
Keywords: *Wickerhamomyces anomalus*, biocontrol, antagonistic activity, GC-MS, 2-phenylethanol.

Hosildan keyingi davrda uchraydigan zamburug‘li kasalliklar qishloq xo‘jaligi mahsulotlarining sezilarli darajada yo‘qotilishiga, ularning tovar ko‘rinishi va sifati pasayishiga olib keluvchi asosiy sabablardan biri hisoblanadi. Dunyoda ko‘plab yig‘ib olingan hosilning salmoqli qismi aynan saqlash va tashish jarayonida fitopatogenlar ta’sirida yaroqsiz holga kelishi kuzatiladi

IQTIBOS UCHUN
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[1]. O‘simliklarni himoya qilishda an’anaviy tarzda kimyoviy fungitsidlar keng qo‘llanib kelinayotgan bo‘lsa-da, ularning muntazam ishlatilishi patogen mikroorganizmlarda chidamlilikning shakllanishiga hamda bir qator jiddiy ekologik va toksikologik muammolarni keltirib chiqarishga sabab bo‘lmoqda [2]. Bundan tashqari, qishloq xo‘jaligi mahsulotlari tarkibida kimyoviy pestitsidlar qoldiqlarining to‘planishi iste’molchilar salomatligi uchun jiddiy xavf tug‘diradi [3]. Shu munosabat bilan fitopatogen zamburug‘larga qarshi kurashishda samarali, xavfsiz va ekologik toza biologik vositalardan foydalanish zamonaviy biotexnologiya va o‘simliklarni himoya qilish tizimining muhim va dolzarb yo‘nalishlaridan biri hisoblanadi [4].

Antagonistik achitqilar tez o‘sish, ekologik bo‘shliqlarni muvaffaqiyatli egallash va turli mexanizmlar yordamida patogenlarning rivojlanishini to‘xtatish qobiliyati tufayli biologik nazoratning istiqbolli vositalari sifatida qaraladi [5]. Ularning bakteriyalarga nisbatan afzalligi shundaki, achitqilar inson va atrof-muhit uchun xavfsiz bo‘lib, zaharli toksinlar sintez qilmaydi [6]. Eng istiqbolli shtammlar qatoriga *Wickerhamomyces anomalus* (sinonimi: *Pichia anomala, Hansenula anomala, Candida pelliculosa*) turi kuchli antimikrob faolligi va yuqori ekologik moslashuvchanligi bilan ajralib turadi [7]. Ushbu tur keng diapazonli harorat, pH va osmotik bosim sharoitlarida ham o‘z hayotchanligini va antagonistik xususiyatlarini saqlab qolish qobiliyatiga ega [8]. Mazkur tur oziq-ovqat, qishloq xo‘jaligi va biotexnologiya sohalarida bionazorat potensiali yuqori bo‘lgan biologik agent hisoblanadi [9]. Turli tadqiqotlarda *W. anomalus* shtammlarining *Botrytis cinerea, Penicillium expansum, P. digitatum, P. italicum, Alternaria alternata, Aspergillus flavus*, *Monilinia* spp. hamda *Colletotrichum* spp. kabi iqtisodiy jihatdan muhim fitopatogen zamburug‘larga qarshi yuqori antagonistik faollik ko‘rsatishi aniqlangan [10–12].

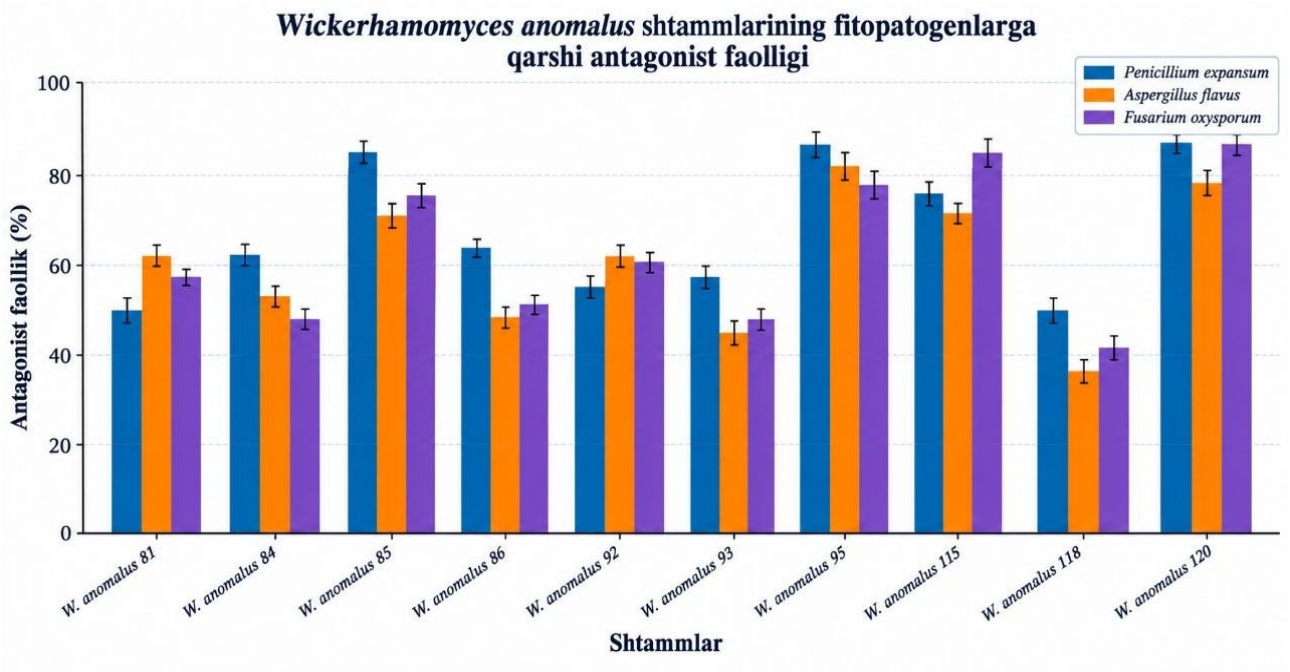
Ushbu achitqining antagonistik ta’siri ozuqa moddalari va makon uchun raqobat qilish, bioplyonka hosil qilish, killer-toksinlar, hujayradan tashqari gidrolitik fermentlar (xususan, ko‘plab fitopatogen zamburug‘larning hujayra devoridagi β-glyukanlar va xitinni parchalay oladigan β-1,3-glyukanazalar va xitinazalar) hamda uchuvchan organik birikmalar sintez qilish kabi bir nechta mexanizmlarning birgalikdagi ta’siri bilan izohlanadi [11,13,14]. Bunday ko‘p qirrali (polifunksional) ta’sir mexanizmi patogenlarda biologik agentga nisbatan rezistentlik (chidamlilik) rivojlanishining oldini oladi [15].

Shu sababli, O‘zR FA Mikrobiologiya instituti “Mikroorganizmlar to‘plami”da saqlanayotgan mahalliy *Wickerhamomyces anomalus* shtammlarining fitopatogen zamburug‘larga qarshi antagonistik xususiyatlarini o‘rganish hamda ular tomonidan sintez qilinadigan uchuvchan metabolitlarning kimyoviy tarkibini aniqlash ushbu shtammning metabolik imkoniyatlarini har tomonlama tavsiflash va uning biokontrol xususiyatlarini amaliyotga tatbiq etish muhim ilmiy-amaliy ahamiyat kasb etadi.

Tadqiqot natijalari

O‘tkazilgan skrining natijasida tadqiq qilingan 10 ta *Wickerhamomyces anomalus* shtammining barchasi *Penicillium expansum*, *Aspergillus flavus* va *Fusarium oxysporum* fitopatogen zamburug‘lariga nisbatan antagonistik faollik namoyon qildi (1-rasm).

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1-rasm. *Wickerhamomyces anomalus* shtammlarining fitopatogen zamburug‘lar o‘sishiga ingibirlovchi ta’siri (%)

Taqdim etilgan diagrammada mahalliy ekotizimlardan ajratib olingan *Wickerhamomyces anomalus* achitqi shtammlarining asosiy fitopatogen zamburug‘lar — *Penicillium expansum*, *Aspergillus flavus* va *Fusarium oxysporum* mitseliysining o‘sishiga qarshi antagonistik faollik darajasi (%) keltirilgan. Olingan natijalarning tahliliga ko‘ra, tadqiq etilgan shtammlar orasida *W. anomalus* 120 va *W. anomalus* 95 shtammlari barcha sinovdan o‘tkazilgan fitopatogenlarga nisbatan eng yuqori (87,2-88,3%) antagonistik faollikni namoyon etdi. Shuningdek, *W. anomalus* 85 shtammi ham barcha patogenlarga nisbatan 72–85% oralig‘idagi yuqori ko‘rsatkichlarda aniqlandi. Boshqa shtammlar (*W. anomalus 81, 84, 86, 92, 93, 115* va *118*) ham muayyan darajada antagonistik faollikka ega bo‘lib, ularning ko‘rsatkichlari o‘rtacha 37,0% dan 86,0% gacha o‘zgarib turdi. Umuman olganda, olingan eksperimental natijalar mahalliy shtammlar orasida yuqori bionazorat salohiyatiga ega bo‘lgan shtammlar mavjudligini tasdiqlaydi. Jumladan, *W. anomalus* 120 va *W. anomalus* 95 shtammlarining keng spektrli fitopatogenlarga qarshi yuqori faollik ko‘rsatishi ularni qishloq xo‘jaligi mahsulotlarini saqlashda biofungitsid sifatida amaliyotga joriy etish istiqbolli ekanligidan dalolat beradi.

Keyingi tajribalarimizda faol yuqori antagonist *W. anomalus* 95 shtammi ikkilamchi metabolitlari tarkibidagi uchuvchan birikmalar GC-MS usulida tahlil qilinganda, 30 daqiqa davomida 38 ta xromatografik pik aniqlandi (retensiya vaqti: 2,118–26,828 min). Mass-spektral kutubxona yordamida asosiy uchuvchan va yarim uchuvchan metabolitlar identifikatsiya qilindi. Gaz xromatografiyasi–mass-spektrometriyasi (GC-MS) natijalariga ko‘ra, *Wickerhamomyces anomalus* 95 shtammi ekstraktida yuqori mass-spektral moslikka (85–98%) ega bo‘lgan asosiy uchuvchan va yarim uchuvchan metabolitlar aniqlandi. Aniqlangan birikmalar qatoriga aromatik spirtlar (masalan, 2-feniletanol), fenol birikmalari (tirozol va uning atsetat hosilalari), organik va aminokislota hosilalari, shuningdek, yuqori biologik faollikka ega bo‘lgan diketopiperazinlar hamda to‘yinmagan yog‘ kislotalari kiradi (1-jadval). Bu metabolitlarning mavjudligi shtammning keng spektrli fitopatogen zamburug‘larga qarshi yuqori antagonistik va fungitsid xususiyatlarini belgilovchi asosiy kimyoviy omillardan biri hisoblanadi.

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1-jadval. *Wickerhamomyces anomalus 95* shtammi ekstraktida yuqori darajadagi mass-spektral moslik bilan aniqlangan metabolitlar

№	Birikma	Kimyoviy formulasi	Retension vaqti, min	MS mosligi, %	Metabolit guruhi
1	D-Piroglutamin kislotasi	$C_5H_7NO_3$	3.816	98	Aminokislota hosilasi
2	2-Feniletanol	$C_8H_{10}O$	5.311	98	Aromatik spirt
3	Fenilsirka kislotasi	$C_8H_8O_2$	8.027	97	Aromatik organik kislota
4	Tirozol (4-gidroksifeniletanol)	$C_8H_{10}O_2$	10.797	98	Fenolik birikma
5	Tirozol atsetati	$C_{10}H_{12}O_3$	12.821	98	Fenolik ester
6	4-Gidroksifenilsirka kislotasi	$C_8H_8O_3$	13.631	97	Fenolik kislota
7	3-(2-Metilpropil)pirolo[1,2-a]pirazin-1,4-dion	$C_{11}H_{18}N_2O_2$	18.146	85	Diketopiperazin hosilasi
8	Linol kislotasi	$C_{18}H_{32}O_2$	20.235	92	To‘yinmagan yog‘ kislotasi
9	3-Benzil-2,5-piperazindion	$C_{11}H_{12}N_2O_2$	21.256	98	Diketopiperazin
10	3-Benzil-6-izopropil-2,5-piperazindion	$C_{14}H_{18}N_2O_2$	21.962	90	Diketopiperazin

Ekstraktning uchuvchan organik birikmalar profili asosan aromatik spirt va esterlarning mavjudligi bilan tavsiflanadi. Jumladan, 2-feniletanol 5.311 minutlik retension vaqtida 98% mass-spektral moslik bilan aniqlanib, uchuvchan organik birikmalar guruhidagi eng ishonchli komponentlardan biri bo‘ldi. 2-Feniletanol atirgul hidiga ega bo‘lgan aromatik spirt bo‘lib, ko‘plab mikroorganizmlar tomonidan ishlab chiqariladi va bir qator patogen mikroorganizmlarga qarshi antifungal faollik ko‘rsatgan. U fitopatogen zamburug‘lar mitseliy tuzilishini buzishi, oksidlovchi stressni yuzaga keltirishi, hujayra membranalarining yaxlitligini izdan chiqarishi va hosildan keyingi mevalarning sifatini saqlab qolishga yordam berishi aniqlangan. Tadqiqotlarda *Botrytis cinerea* patogeni mitseliylarining o‘sishini bostirish bo‘yicha eng kuchli birikmalardan biri sifatida qulupnay va pomidordagi kulrang chirishga qarshi samarali ta’sir ko‘rsatgan [16].

Shuningdek, fenilsirka kislotasining etil efiri 7.421 minutda 85% va 2-feniletil atsetat 7.658 minutda 91% moslik bilan aniqlandi. 3-Metilbutan kislotasi (izovalerian kislotasi) esa 2.118 minutda 93% moslik bilan qayd etilib, ekstraktning uchuvchan organik kislotalar komponenti sifatida baholandi.

O‘tkazilgan tahlillar *Wickerhamomyces anomalus* shtammlari sintez qiladigan uchuvchan organik birikmalar (UOB) postharvest kasalliklarga qarshi kurashda muhim ahamiyatga ega ekanligini ko‘rsatdi. Xususan, aniqlangan asosiy komponentlardan biri — 2-feniletanol (5.311 min, 98% moslik) atirgul hidiga ega aromatik spirt bo‘lib, ko‘plab mikroorganizmlar tomonidan ishlab chiqariladi va kuchli antifungal faollik namoyon etadi. U fitopatogen zamburug‘lar mitseliysining tuzilishini buzib, oksidlanish stressini keltirib chiqaradi va hujayra membranalarini izdan chiqaradi [16].

Adabiyot ma’lumotlari ham *W. anomalus* shtammlarining UOB profili asosan spirtlar va esterlardan (jl. *2-feniletanol, etil atsetat, izoamil atsetat, feniletil atsetat*) iborat ekanligini tasdiqlaydi [17]. Masalan, *B. cinerea* va *P. expansum*ga qarshi kurashda bu birikmalar spora unishi hamda

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mitseliy o‘sishini samarali bostirishi ko‘rsatilgan [18]. Ushbu metabolitlarning miqdori va tarkibi shtammning biologik xususiyatlari hamda o‘stirish sharoitiga bog‘liq bo‘lib, mahalliy shtammlarning metabolik profili ularning yuqori biokontrol salohiyatini ilmiy jihatdan asoslaydi.

Xulosa

Gaz xromatografiyasi–mass-spektrometriyasi (GC-MS) natijalari *Wickerhamomyces anomalus* 95 shtammi ekstraktida aromatik spirtlar, fenolik birikmalar, organik hamda yog‘ kislotalari va siklik dipeptidlar mavjudligini ko‘rsatdi. Ayniqsa, 2-feniletanol va tirozol hosilalari kabi yuqori mass-spektral moslikka ega birikmalar shtammning fitopatogenlarga qarshi yuqori antagonistik va fungitsid ta’sirini belgilovchi asosiy metabolitlar sifatida baholanadi. Olingan natijalar mahalliy shtammlar asosida hosildan keyingi kasalliklarga qarshi biofungitsidlarni yaratishda istiqbolli ekanligini tasdiqlaydi.

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СРАВНЕНИЕ МЕТОДОВ ВЫЯВЛЕНИЯ ЭКЗОПОЛИСАХАРИД-ПРОДУЦИРУЮЩИХ БАКТЕРИЙ И ОБОСНОВАНИЕ ВЫБОРА МЕТОДА СКРИНИНГА ДЛЯ ПОЧВЕННЫХ ИЗОЛЯТОВ

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Аннотация: Для первичного отбора экзополисахарид-продуцирующих (ЭПС) бактерий из почвенных образцов сравнены методы: визуальная оценка мукоидных колоний, скрининг на среде с конго красным, сканирующая электронная микроскопия, а также выделение ЭПС осаждением этанолом с количественным определением. Для первичного скрининга выбран метод конго красного агара в варианте, описанном корейской группой *Shaffique* и соавт. (2023): среда LB с 5% сахарозы и 0,8 г/л конго красного, инкубация 5 суток при 30-35 °C. Метод прост, подходит для массового просмотра колоний и совпадает по условиям с нашей схемой выделения. Его главное ограничение — качественный характер результата, поэтому отобранные изоляты нужно проверять выделением и количественным определением ЭПС.

Ключевые слова: экзополисахариды, конго красный агар, скрининг, почвенные бактерии, сравнение методов.

Ekzopolisaxarid ishlab chiqaruvchi bakteriyalarni aniqlash usullarini taqqoslash va tuproq izolatlari uchun skrining usulini tanlash asoslari

Annotatsiya: Tuproq namunalaridan ekzopolisaxarid ishlab chiqaruvchi (EPS) bakteriyalarni birlamchi tanlash uchun quyidagi usullar taqqoslandi: mukoid koloniyalarni vizual baholash, Kongo qizilini o‘z ichiga olgan muhitda skrining qilish, skanerlovchi elektron mikroskopiya va miqdoriy aniqlash bilan etanol cho‘ktirish orqali EPSni ajratish. Birlamchi skrining uchun Koreya guruhi *Shaffique* va boshqalar (2023) tomonidan tasvirlangan Kongo qizil agar usuli tanlandi: 5% saxaroza va 0,8 g/L Kongo qizili bo‘lgan LB muhit, 30-35 °C da 5 kun davomida inkubatsiya qilingan. Bu usul oddiy, koloniyalarni keng ko‘lamli skrining qilish uchun mos keladi va bizning izolyatsiya sxemamiz shartlariga mos keladi. Uning asosiy cheklovi natijaning sifat jihatidan xarakteri; shuning uchun tanlangan izolatlar EPSni ajratish va miqdoriy aniqlash orqali tekshirilishi kerak.

Kalit so‘zlar: ekzopolisaxaridlar, Kongo qizil agari, skrining, tuproq bakteriyalari, usullarni taqqoslash.

Comparison of methods for detecting exopolysaccharide-producing bacteria and justification for the choice of a screening method for soil isolates

Abstract: To select exopolysaccharide (EPS)-producing bacteria from soil samples, several methods were compared: visual assessment of mucoid colonies, screening on Congo red medium, scanning electron microscopy, and EPS isolation via ethanol precipitation followed by quantification. The Congo red agar method — specifically the variant described by the Korean research group *Shaffique* et al. (2023) — was selected for primary screening; this involves using LB medium supplemented with 5% sucrose and 0.8 g/L Congo red, with incubation for 5 days at 30-35°C. This method is simple, suitable for high-throughput colony screening, and compatible with the conditions

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Кудратуллаева Д.О., Тоштемирова М.Ж. Сравнение методов выявления экзополисахарид-продуцирующих бактерий и обоснование выбора метода скрининга для почвенных изолятов // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 33–36.
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of our isolation protocol. Its main limitation is that it yields qualitative results; therefore, selected isolates require further verification through EPS isolation and quantification.

Keywords: exopolysaccharides, Congo red agar, screening, soil bacteria, method comparison.

Введение

От выбора метода первичного скрининга зависит, какие изоляты попадут в дальнейшую работу, поэтому метод нужно обосновывать, а не брать по привычке. Бактерии, способные расти при низкой водной активности, используют синтез ЭПС как главную защиту от высыхания и засоления, а ЭПС-продуценты аридных регионов считаются перспективными для агротехнологий [1]. Для почв Узбекистана такой поиск только начинается, и первым шагом остаётся быстрый и недорогой скрининг колоний. Общие сведения о свойствах и методах получения бактериальных ЭПС изложены в нашем обзоре [2].

Цель статьи — сравнить методы, которыми выявляют ЭПС-продуцирующие бактерии, и обосновать выбор метода для скрининга почвенных изолятов.

Сравниваемые методы

Методы различаются тем, что именно они показывают: наличие ЭПС, их количество или структуру. Первые два дают быстрый отбор колоний, остальные подтверждают и измеряют результат.

Таблица 1. Сравнение методов выявления ЭПС-продуцирующих бактерий

Метод	Что показывает	Преимущества	Ограничения
Мукоидные колонии на среде с сахарозой	Слизистость колоний	Дёшево, не нужно оборудование	Не все продуценты мукоидны, оценка субъективна
Конго красный агар	Тёмные или чёрные колонии на красном фоне при продукции ЭПС	Быстро, много колоний на одной чашке, колонии остаются живыми	Качественный подтверждающий тест; создан для стафилококков
Сканирующая электронная микроскопия	ЭПС-матрица вокруг клеток	Прямое подтверждение	Сложная подготовка образцов, нужен микроскоп
Осаждение этанолом, диализ, сухая масса	Выход ЭПС	Просто, подходит для больших объёмов	Соосаждение белков и нуклеиновых кислот, сухая масса включает примеси
Фенол-серный метод	Общее содержание углеводов (490 нм, стандарт глюкоза)	Точный, простой, чувствительный	Неспецифичен, учитывает и сахара среды
HPLC, FTIR, NMR	Моносахаридный состав и структура	Детальная характеристика полимера	Сложность и стоимость

Корейский метод: протокол Shaffique и соавторов

Метод конго красного агара предложен для выявления слизеобразования у стафилококков: среда содержала 37 г/л бульона BHI, 50 г/л сахарозы, 10 г/л агара и 0,8 г/л конго красного, чашки инкубировали 24 ч при 37 °C, а чёрные колонии с сухой кристаллической консистенцией считали положительными [6]. Группа из Национального университета Кёнпук (Тэгу, Южная Корея) адаптировала его для почвенных бактерий в работе по биопраймингу пшеницы при засухе [7].

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Протокол.

1. Среда: LB-бульон 25 г/л, агар 2%, сахароза 5%, конго красный 0,8 г/л; все компоненты смешивают и автоклавируют.
2. Посев и инкубация: 5 суток при 30-35 °C.
3. Учёт: чёрные колонии на красном фоне подтверждают наличие полисахаридов.
4. Подтверждение: сканирующая электронная микроскопия показала бактерии, погружённые в ЭПС-матрицу, а в среде определяли сахарозу методом HPLC.

Из ризосферной почвы вокруг *Artemisia vulgaris* (пляж Похан, около Тэгу) выделено 73 изолята; для штамма SH-8 установлена принадлежность к *Klebsiella aerogenes* (сходство 99,93% по 16S рРНК, номер GenBank OM535901). Штамм образовывал ЭПС, который в таблице обозначен как «+++», то есть без числовых значений [7].

Обоснование выбора метода

Для первичного скрининга почвенных изолятов выбран конго красный агар по протоколу [7] по следующим причинам.

1. Масштаб. На одной чашке оценивают много колоний без экстракции и центрифугирования, что важно для десятков почвенных образцов.
2. Совместимость с нашей схемой. Среда на основе LB с 5% сахарозы и инкубация 5 суток при 30-35 °C соответствуют условиям, которые мы использовали при выделении бактерий из почвы.
3. Адаптация к почвенным бактериям. В отличие от первоначальной версии для клинических штаммов (24 ч при 37 °C) [6], протокол [7] рассчитан на почвенную микробиоту.
4. Полная схема работы. В [7] скрининг сочетали с идентификацией по 16S рРНК и электронной микроскопией, и такую последовательность можно повторить.

Метод качественный: в [7] ЭПС оценён как «+++» без количественных данных, а конго красный агар в целом считают подтверждающим, но не количественным тестом [8]. Поэтому после скрининга нужно выделить ЭПС осаждением этанолом с диализом и определить выход, например фенол-серным методом, помня, что он учитывает все углеводы [4,8]. Схема такого выделения (удаление белков трихлоруксусной кислотой, осаждение холодным этанолом, диализ, лиофилизация, FTIR и UHPLC) описана корейской группой в [9]. Кроме того, результаты на среде LB нужно проверять на разных образцах, так как данные [8] получены для молочнокислых бактерий, а [6] — для стафилококков.

Применение метода к почвам Учкудукского района

Отобрано 14 образцов почвы в окрестностях Кулкудука и Зафарабада (Навоийская область) в мае 2025 г. (13 мая - 5 образцов, 14 мая - 5, 18 мая - 4) вдоль маршрута от окрестностей Кулкудука (точка 1) через центральную часть маршрута (точка 2) к окрестностям Зафарабада (точка 3). После посева на среду с конго красным доля $ЭПС^+$ колоний составила 20-30% в одной группе образцов и 10-15% в другой; всего учтено 9 колоний, из них $ЭПС^+$ 5. Выявлены тёмно-синие, малиновые и чёрные колонии, по совокупности признаков (окраска, слизистая консистенция, растекающийся край, крупный размер) отобрано 5 перспективных изолятов [10]. Это предварительные данные: цвет колоний не позволяет определить тип полисахарида, поэтому изоляты нужно довести до чистых культур и проверить выделением ЭПС.

Выводы

Методы выявления ЭПС делятся на быстрые качественные (мукоидные колонии, конго красный агар) и подтверждающие (микроскопия, выделение ЭПС, фенол-серный метод, HPLC, FTIR, NMR). Для первичного скрининга почвенных изолятов выбран конго красный агар по протоколу Shaffique и соавт. (2023) как простой, массовый и совместимый с нашей схемой выделения.

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Метод даёт только качественную оценку, поэтому отобранные изоляты необходимо проверить выделением ЭПС и количественным определением.

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BUG‘DOY O‘SIMLIGIDAN AJRATIB OLINGAN *FUSARIUM GRAMINEARUM* FITOPATOGEN ZAMBURUG‘INING MORFO-BIOLOGIK XUSUSIYATLARI VA UNI ANIQLASH

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Annotatsiya: Mazkur maqolada qishloq xo‘jaligi ekinlari namunalaridan ajratib olingan fitopatogen zamburug‘ — *Fusarium graminearum* shtammining morfologik va biologik xususiyatlari, ozuqa muhitlaridagi o‘sish darajasi va mikroskopik tahlil natijalari yoritilgan. Tadqiqot jarayonida zamonaviy mikologik aniqlagichlar yordamida izolyatning *Fusarium graminearum* turiga mansubligi aniqlandi. Shuningdek, olingan shtammni laboratoriya sharoitida saqlash, uning patogenlik xususiyatlarini o‘rganish hamda "Fitopatogen va boshqa mikroorganizmlar kolleksiyasi" noyob obyekti genofondini mahalliy izolyatlar bilan boyitishning ilmiy-amaliy ahamiyati asoslab berildi.

Kalit so‘zlar: *Fusarium graminearum*, fitopatogen zamburug‘, kolleksiya, morfo-biologik xususiyatlar, KDA ozuqa muhiti, taksonomiya.

Аннотация: В данной статье освещены морфологические и биологические особенности, скорость роста на питательных средах и результаты микроскопического анализа штамма фитопатогенного гриба *Fusarium graminearum*, выделенного из образцов сельскохозяйственных культур. В ходе исследования с помощью современных микологических определителей была подтверждена принадлежность изолята к виду *Fusarium graminearum*. Также были обоснованы научно-практическое значение хранения полученного штамма в лабораторных условиях, изучения его патогенных свойств, а также пополнения генофонда уникального объекта «Коллекция фитопатогенных и других микроорганизмов» местными изолятами.

Ключевые слова: *Fusarium graminearum*, фитопатогенный гриб, коллекция, морфо-биологические особенности, питательная среда КДА (картофельно-декстрозный агар), таксономия.

Abstract: This article highlights the morphological and biological characteristics, growth rates on nutrient media, and microscopic analysis results of the phytopathogenic fungus *Fusarium graminearum* strain isolated from agricultural crop samples. During the research, using modern mycological identifiers, the isolate was identified as belonging to the species *Fusarium graminearum*. Furthermore, the scientific and practical significance of preserving the obtained strain in laboratory conditions, studying its pathogenic properties, and enriching the gene pool of the unique object "Collection of Phytopathogenic and Other Microorganisms" with local isolates was substantiated.

Keywords: *Fusarium graminearum*, phytopathogenic fungus, collection, morpho-biological characteristics, PDA (Potato Dextrose Agar) nutrient medium, taxonomy.

Kirish

Hozirgi kunda global miqyosda qishloq xo‘jaligi ekinlari yetishtirishda eng jiddiy muammolardan biri o‘simlik kasalliklari, xususan, zamburug‘lar keltirib chiqaradigan kasalliklar hisoblanadi. G‘allachilik maydonlarida keng tarqalgan va qishloq xo‘jaligi o‘simliklariga jiddiy

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iqtisodiy zarar keltiruvchi xavfli kasalliklardan biri bu boshoq qorayishi yoki qizil boshoq hisoblanadi. Mazkur kasallikning asosiy qo‘zg‘atuvchisi *Fusarium graminearum* fitopatogen zamburug‘i bo‘lib, u nafaqat don hosildorligini 30-50% gacha kamaytiradi, balki don tarkibida xavfli mikotoksinlar (deoksinivalenol, zearalenon) to‘planishiga olib keladi. Bu esa o‘z navbatida oziq-ovqat xavfsizligiga jiddiy xavf tug‘diradi.

Ilmiy-tadqiqot institutlarida, xususan, Genetika va o‘simliklar eksperimental biologiyasi institutining "Fitopatogen va boshqa mikroorganizmlar kolleksiyasi" noyob obyektida bunday patogen mikroorganizmlarning genofondini yig‘ish, saqlash, pasportlashtirish va ularning biologik xususiyatlarini chuqur o‘rganish ustuvor vazifalardan hisoblanadi. Shu bois, qishloq xo‘jaligi o‘simliklaridan yangi fitopatogen izolyatlarni ajratib olish va ularni aniqlash dolzarb ahamiyat kasb etadi.

Adabiyotlar tahlili

Ilmiy adabiyotlarga ko‘ra, *Fusarium* turkumiga mansub zamburug‘lar tuproqda va o‘simlik qoldiqlarida saprotrof yoki parazit sifatida keng tarqalgan. Leslie va Summerell hamda Domsch va boshqalar tomonidan olib borilgan tadqiqotlarda *Fusarium graminearum* turlarining morfologik tuzilishi, xususan, ularning makrokonidiyalari va sporalarining tuzilishiga qarab aniqlanishi batafsil bayon etilgan [1,2].

Mahalliy olimlarning tadqiqotlari shuni ko‘rsatadiki, O‘zbekistonning tuproq-iqlim sharoitida g‘alla ekinlarining zararlanishi har yili ob-havo sharoitiga qarab o‘zgarib turadi. Shu sababli, har bir mintaqaga xos bo‘lgan fitopatogen shtammlarni aniqlash, ularning irsiy va fenotipik xususiyatlarini o‘rganish dolzarb ilmiy muammo bo‘lib qolmoqda [3].

Tadqiqot materiali va usullari

Tadqiqotlar O‘zbekiston Respublikasi FA Genetika va o‘simliklar eksperimental biologiyasi institutida laboratoriya sharoitida olib borildi. Namunalarni yig‘ish jarayonida kasallik alomatlari yaqqol ko‘ringan bug‘doy boshoqlari va poyalari respublikaning turli hududlaridan yig‘ib olindi va laboratoriyaga keltirildi.

Kasallangan bug‘doy to‘qimalari dastlab oqadigan suvda tuproq qoldiqlaridan tozalandi va 0.5 sm hajmdagi kichik bo‘laklarga bo‘lindi. To‘qimalar sirtidagi suvsizlanishning oldini olish hamda dezinfeksiyalovchi eritmaning bir tekis ta’sir qilishini ta’minlash uchun dastlab Tvin-80 (Tween-80) eritmasida ishlov berildi. Shundan so‘ng namunalar ketma-ket ravishda 0.1% li natriy gipoxlorit (NaClO) eritmasida va 50% li etil spirtida yuza qismi sterillandi. Oxirida to‘qima parchalari qoldiq kimyoviy moddalardan tozalash maqsadida uch marta sterillangan distillangan suvda yaxshilab yuvildi [4].

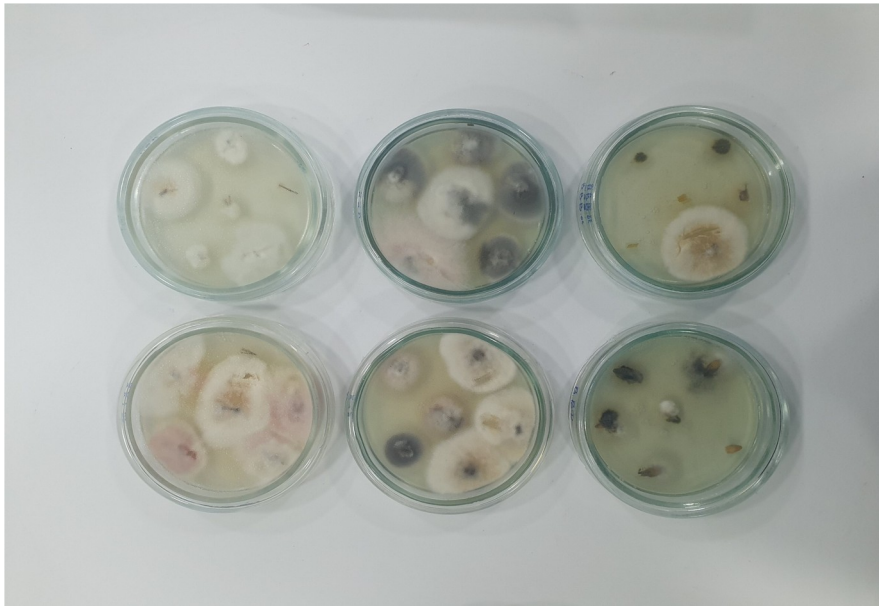
Ozuqa muhitiga ekish va sof kulturalarni ajratish. Sterillangan to‘qima bo‘laklari patogenlarni o‘stirish uchun universal hisoblangan kartoshka-dekstroza agar (PDA - Potato Dextrose Agar) ozuqa muhitiga steril sharoitda petri idishlarga ko‘chirib ekiladi. O‘simlikning zararlangan qismidan ajratib olib ekilgan fragmentlar inkubatorga joylashtirilib, 26 °C da optimal haroratda saqlanadi.

Morfologik va mikroskopik tahlil. O‘sgan koloniyalarning tashqi ko‘rinishi (rangi, tuzilishi, o‘sish tezligi) qayd etildi (1-rasm). Mikroskopik tadqiqotlar yorug‘lik mikroskopi yordamida amalga oshirildi. Mikroskopik morfologik belgilar John F. Leslie va Brett A. Summerell tomonidan tayyorlangan *The Fusarium Laboratory Manual* qo‘llanmasida keltirilgan *Fusarium* vakillarining diagnostik belgilariga muvofiq tahlil qilindi. Mazkur qo‘llanmada *Fusarium* turlarini aniqlashda makrokonidiyalarning shakli, septalanishi, mikrokonidiyalarning morfologiyasi hamda boshqa ikkilamchi belgilar muhim diagnostik mezonlar sifatida ko‘rsatilgan.

Tadqiqot natijalari va ularning muhokamasi

Tadqiqot davomida o‘simlik namunalaridan jami bir nechta zamburug‘ izolyatlari ajratib olindi va ulardan birining *Fusarium graminearum* turiga mansubligi to‘liq tasdiqlandi.

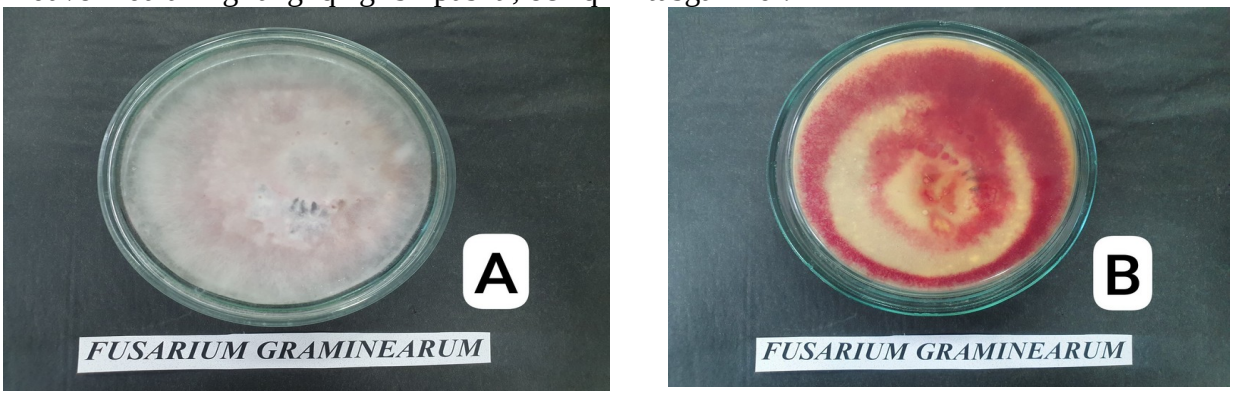
DOI: 10.66073/ReFocus-Conf/3010005



1-rasm. Bug‘doy o‘simligidan ajratib olingan zamburug‘ koloniyalari

Kultural xususiyatlari.

KDA ozuqa muhitida o‘stirilgan zamburug‘ koloniyasi tez o‘sishi bilan ajralib turdi. Dastlabki kunlarda mitseliy oqish, och pushti rangli tuzilishda rivojlandi. Koloniya rivojlanishi davomida 7-10 kun davomida uning rangi qizg‘ish-pushti, och qizil tusga kirdi.

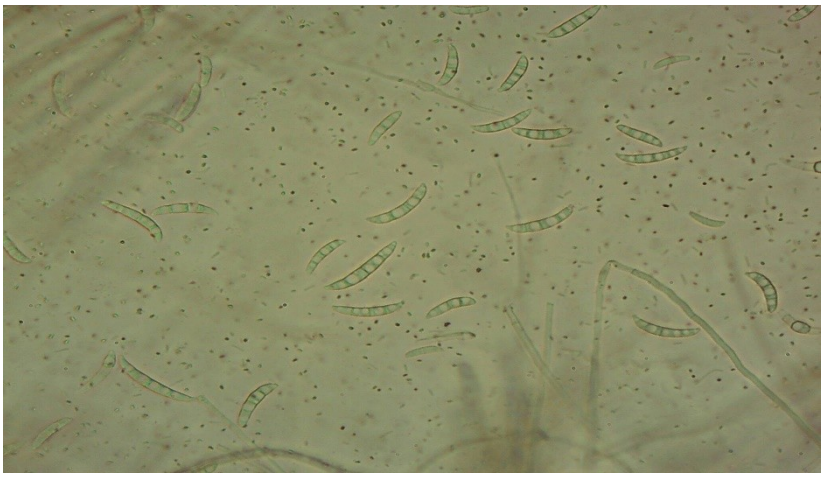


2-rasm. KDA ozuqa muhitida o‘sayotgan *Fusarium graminearum* sof kulturasining umumiy ko‘rinishi: a) ustki qismi, b) orqa tomoni

Ozuqa muhitining orqa tomoni ham qizg‘ish-jigarrang tusda bo‘lishi kuzatildi, bu ushbu turning muhim diagnostik belgilaridan biridir (2-rasm).

Mikroskopik xususiyatlari. *Fusarium* turkumiga mansub izolyatlarning mikroskopik tekshiruvi NLCD-307B optik mikroskopi yordamida $10^{\times}100$ kattalashtirishda amalga oshirildi. Mikroskopik tahlillar shuni ko‘rsatdiki, ajratib olingan shtamm o‘roqsimon egilgan makrokonidiyalar bilan ajralib turadi. Makrokonidiyalar o‘rtacha 3-5 ta ko‘ndalang to‘siqli (hujayrali) bo‘lib, ularning uchlari biroz ingichkalashgan shakli ko‘rildi (3-rasm). Mikrokonidiyalar bu tur uchun deyarli kuzatilmasligi aniqlandi. Olingan morfologik ko‘rsatkichlar xalqaro aniqlagichlardagi ta’riflarga 98-100% mos keldi.

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3-rasm. *Fusarium graminearum* zamburug‘ining mikroskopik tuzilishi: o‘roqsimon makrokonidiyalar 10x100 kattalashtirilgan ko‘rinishi

Muhokama. Olingan natijalar shuni ko‘rsatadiki, qishloq xo‘jaligi o‘simliklari namunalaridan ajratib olingan *Fusarium graminearum* izolyatlari klassik morfologik belgilariga ko‘ra standart shtammlar bilan to‘liq mos keladi. Bu esa ushbu patogenni laboratoriya sharoitida muvaffaqiyatli saqlash va kelgusida qishloq xo‘jaligi kasalliklariga qarshi kurashish chora-tadbirlarini ishlab chiqishda foydalanish imkonini beradi.

Xulosa

O‘simlik namunalaridan sof kultura holatiga ajratib olingan fitopatogen zamburug‘ zamonaviy mikologik aniqlagichlar yordamida tahlil qilinib, uning *Fusarium graminearum* turiga mansubligi isbotlandi.

PDA ozuqa muhitidagi kultural va mikroskopik xususiyatlari (o‘roqsimon makrokonidiyalar va pushti qizg‘ish koloniya rangi) ushbu turning klassik ta’riflariga mos kelishi aniqlandi.

Aniqlangan va o‘rganilgan ushbu shtamm Genetika va o‘simliklar eksperimental biologiyasi institutining "Fitopatogen va boshqa mikroorganizmlar kolleksiyasi" noyob obyekti genofondini boyitish hamda kelgusidagi fitopatologik tadqiqotlar uchun ishonchli manba bo‘lib xizmat qiladi.

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KASALLANGAN OLMA NAMUNALARIDAN *COLLETOTRICHUM* TURKUMI ZAMBURUG‘LARINI AJRATISH VA IDENTIFIKATSIYA QILISH

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Annotatsiya: Ushbu maqolada kasallangan olma (*Malus domestica*) namunalaridan *Colletotrichum* turkumiga mansub fitopatogen zamburug‘larni ajratib olish va identifikatsiya qilishning asosiy usullari yoritilgan. Shuningdek, kasallik belgilari kuzatilgan olma namunalaridan fitopatogen zamburug‘larni ajratish, sof kulturaga olish va keyingi *Colletotrichum* izolyatlarini morfologik hamda molekulyar jihatdan aniqlashga qaratilgan tadqiqotning dastlabki metodik bosqichlari yoritiladi. Tadqiqot davomida kasallik belgilari kuzatilgan olma mevalaridan namunalar olinib, laboratoriya sharoitida zamburug‘larning sof kulturalari ajratib olinadi. Ajratilgan izolyatlarning o‘sish xususiyatlari, koloniya rangi, mitseliy tuzilishi, sporalari, konidiyalar va appressoriyalarning morfologik belgilari mikroskopik usulda o‘rganiladi. Shuningdek, *Colletotrichum* turkumi zamburug‘lari o‘simliklarda antraknoz kasalliklarini keltirib chiqaruvchi eng xavfli fitopatogenlardan biri hisoblanadi. Mazkur tadqiqot natijalari olma kasalliklarini keltirib chiqaruvchi *Colletotrichum* turkumi vakillarini aniqlash, ularning biologik xususiyatlarini o‘rganish hamda kasalliklarga qarshi samarali kurash choralarini ishlab chiqish uchun ilmiy asos bo‘lib xizmat qilishi mumkin.

Kalit so‘zlar: *Colletotrichum*, olmaning achchiq chirishi, appressoriy, fitopatogen, antraknoz, sof kultura, ITS, morfologik identifikatsiya, molekulyar identifikatsiya.

Аннотация: В данной статье рассмотрены основные методы выделения и идентификации фитопатогенных грибов рода *Colletotrichum* из образцов поражённых яблок (*Malus domestica*). Кроме того, освещены первоначальные методические этапы исследования, направленного на выделение фитопатогенных грибов из образцов яблок с признаками заболевания, получение чистых культур и последующую морфологическую и молекулярную идентификацию изолятов *Colletotrichum*. В ходе исследования образцы отбираются из плодов яблони с выраженными признаками заболевания, после чего в лабораторных условиях проводится выделение чистых культур грибов. Изучаются особенности роста выделенных изолятов, окраска и структура колоний, строение мицелия, спор, конидий и аппрессориев с использованием микроскопических методов. Кроме того, представители рода *Colletotrichum* относятся к числу наиболее опасных фитопатогенных грибов, вызывающих заболевания антракнозного типа у растений. Результаты данного исследования могут послужить научной основой для выявления представителей рода *Colletotrichum*, вызывающих заболевания яблони, изучения их биологических особенностей, а также разработки эффективных мер борьбы с данными заболеваниями.

Ключевые слова: *Colletotrichum*, горькая гниль яблок, аппрессории, фитопатоген, антракноз, чистая культура, ITS, морфологическая идентификация, молекулярная идентификация.

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Abstract: This article reviews the main methods for the isolation and identification of phytopathogenic fungi belonging to the genus *Colletotrichum* from diseased apple (*Malus domestica*) samples. It also describes the initial methodological stages of the study aimed at isolating phytopathogenic fungi from apple samples showing disease symptoms, obtaining pure cultures, and subsequently identifying *Colletotrichum* isolates using morphological and molecular approaches. During the study, samples are collected from apple fruits exhibiting visible disease symptoms, followed by the isolation of pure fungal cultures under laboratory conditions. The growth characteristics of the isolated strains, colony colour and structure, mycelial characteristics, spores, conidia, and appressoria are examined using microscopic methods. In addition, fungi of the genus *Colletotrichum* are considered among the important and potentially destructive phytopathogens responsible for anthracnose diseases in plants. The results of this study may provide a scientific basis for identifying representatives of the genus *Colletotrichum* that cause apple diseases, studying their biological characteristics, and developing effective measures for disease control.

Keywords: *Colletotrichum*, apple bitter rot, appressoria, phytopathogen, anthracnose, pure culture, ITS, morphological identification, molecular identification.

Kirish

Bugungi kunda insoniyatning ozuqa manbai hisoblangan o‘simliklarga zarar keltiradigan fitopatogenlar bilan kurashish, ayniqsa, hozirgi davrda dolzarb muammolardan biri bo‘lib qolmoqda. Olma (*Malus domestica*) dunyoda keng yetishtiriladigan va iqtisodiy jihatdan muhim mevali ekinlardan biri hisoblanadi. Olma hosildorligi va meva sifatiga turli bakterial, virusli va zamburug‘li kasalliklar salbiy ta’sir ko‘rsatadi. Shunday kasalliklardan biri *Colletotrichum* turkumiga mansub zamburug‘lar bilan bog‘liq antraknoz va achchiq chirish kasalliklaridir. Ushbu turkum vakillari ko‘plab ekinlarda antraknoz, meva chirishi, barg va poya zararlanishlarini yuzaga keltiradi.

Colletotrichum turkumi turlarining patogenlik darajasi va ekologik moslashuvi bir xil emasligi sababli kasallik qo‘zg‘atuvchisini tezda aniqlash kasallik epidemiologiyasi va nazorat strategiyasini ishlab chiqishda muhim hisoblanadi. Shuningdek, olma yetishtirishda *Colletotrichum* bilan bog‘liq *bitter rot* — achchiq chirish kasalligi muhim muammolardan biridir. Zamonaviy tadqiqotlarda olma mevalaridan ajratilgan *Colletotrichum* izolyatlari orasida *C. fioriniae*, *C. chrysophilum*, *C. fructicola* va boshqa turlar aniqlangan; ayrim tadqiqotlarda yangi turlar ham tavsiflangan [1].

Colletotrichum turkumi vakillari ko‘plab qishloq xo‘jaligi ekinlarida kasallik keltirib chiqaruvchi muhim fitopatogen zamburug‘lar guruhiga kiradi. Ushbu turkumning taksonomiyasi murakkab bo‘lib, morfologik jihatdan bir-biriga o‘xshash turlar mavjudligi sababli ularni faqat tashqi belgilar asosida aniq ajratish har doim ham mumkin emas. Zamonaviy tadqiqotlarda morfologik belgilar bilan bir qatorda molekulyar-filogenetik usullarni qo‘llash *Colletotrichum* turlarini aniqlashning muhim qismi hisoblanadi [2].

Olmada *Colletotrichum* bilan bog‘liq kasalliklar ko‘pincha mevalarda yumaloq yoki biroz cho‘zinchoq, botiq, jigarrangdan to‘q ranggacha bo‘lgan chirish dog‘larining hosil bo‘lishi bilan namoyon bo‘ladi. Kasallik rivojlangan sari zararlangan joylar kengayib, mevaning ichki to‘qimalariga ham tarqalishi mumkin. Nam sharoitda zararlangan to‘qimalarda zamburug‘ning sporalarini hosil qiluvchi tuzilmalari rivojlanishi kuzatiladi [3].

Kasallik rivojlanganda zararlangan joylarda zamburug‘ning sporulyatsiya tuzilmalari paydo bo‘ladi. Ayrim *Colletotrichum* turlari olma barglarida ham dog‘lanish kasalliklari bilan bog‘liq. AQShning Nyu-York hududida olib borilgan katta hajmdagi tadqiqotlarni kuzatadigan bo‘lsak, bunda olma mevalaridan yuzlab izolyatlar yig‘ilib, ularning bir qismi morfologik guruhlarga ajratilgan va keyinchalik ko‘p-lokusli filogenetik tahlil yordamida tur darajasida identifikatsiya qilingan. Olma mevalaridan *Colletotrichum* izolyatlarini ajratish bo‘yicha adabiyotlarda turli geografik hududlarda turli *Colletotrichum* turlari aniqlangani qayd etilgan. Shu jumladan, Janubiy

Koreyada o‘tkazilgan tadqiqotda kasallangan olma mevalaridan izolyatsiya qilingan shtammlar morfologik belgilar, o‘sish xususiyatlari va ko‘p-lokusli ketma-ketlik ma’lumotlari asosida aniqlangan [4].

Materiallar va usullar

Tadqiqot materiali va namuna yig‘ish

Tadqiqot materiali sifatida kasallik belgilari kuzatilgan olma mevalari hamda barglari olindi. Namuna yig‘ish jarayonida chirigan yoki nekrotik belgilari mavjud mevalar hamda barglar tanlanib, laboratoriyaga alohida maxsus idishlarda olib kelindi. Har bir namuna uchun kelib chiqish hududi, yig‘ilgan sana, xo‘jayin o‘simlik va kuzatilgan kasallik belgilari qayd etildi.

Zamburug‘larni ajratish

Kasallangan olma barglari va mevalaridan zamburug‘larni ajratish uchun namunalar 2 soat oqar suvda yuvildi va keyinchalik distillangan suv bilan yana qayta yuvildi. Tayyorlangan namunalar filtr qog‘ozi joylashtirilgan Petri idishlariga qo‘yilib, 28 °C haroratda 72 soat davomida inkubatorda inkubatsiya qilindi. Inkubatsiya jarayonida namunalar yuzasida hosil bo‘lgan zamburug‘ mitseliylari va sporulyatsiya belgilari kuzatildi. Rivojlangan zamburug‘ koloniyalari keyingi bosqichda sof kulturani ajratish hamda morfologik va molekulyar-genetik identifikatsiya qilish uchun foydalaniladi.

Ekish va kultivatsiya qilish

Sterillangan to‘qima bo‘laklari filtr qog‘ozida quritilib, tarkibida bakteriyalarga qarshi streptomitsin (50 mg/L) saqlovchi Kartoshka-Dekstroza Agar (KDA) muhitiga o‘tkaziladi. Petri idishlari inkubatorda 25-28 °C haroratda 4-7 kun davomida saqlanadi.

Sof kulturalarni olish

O‘simlik barglarida o‘sib chiqqan zamburug‘ gifalari steril igna yordamida yangi KDA idishlariga ko‘chiriladi. O‘sib chiqqan zamburug‘ koloniyalari muntazam kuzatib borildi. Birlamchi koloniyalar orasidan morfologik jihatdan *Colletotrichum*ga o‘xshash koloniyalardan kichik mitseliy bo‘lagi olinib, yangi KDA ozuqa muhitiga qayta ekildi. Bu jarayon bir xil morfologik xususiyatga ega sof kultura hosil bo‘lguncha davom ettiriladi, ya’ni, bir xil va monospora izolyat holiga kelguncha bu jarayon takrorlanadi.

Tadqiqot natijasi va muhokama

Ilmiy izlanish davomida *Colletotrichum* turkumi zamburug‘larini kasallangan olma daraxtlarining to‘qimalaridan ajratish va monokonidial izolyatlari olinadi, ajratib olingan izolyatlar mikroskopik va molekulyar-genetik identifikatsiya qilinadi. *Colletotrichum* izolyatlarining koloniyalari turga va izolyatga qarab oq, kulrang, och kulrang, zaytunsimon yoki to‘q kulrang ranglarda bo‘lishi mumkin. Ayrim izolyatlarda nazar tashlaydigan bo‘lsak, koloniya markazida to‘q pigmentatsiya va konsentrik zonalar kuzatiladi. Kasallangan olma mevasida *Colletotrichum* infeksiyasi ko‘pincha yumaloq yoki biroz cho‘zinchoq, botiq, jigarrangdan to‘q ranggacha bo‘lgan nekrotik dog‘lar bilan namoyon bo‘ladi. Nam sharoitda sporalarining strukturalari hosil bo‘lib, konidial massa ko‘rinishi kuzatiladi. Biroq, bunday belgilarni faqat ko‘z bilan baholash tur darajasida ishonchli identifikatsiya uchun yetarli emas. Bu belgilar zamburug‘li kasallik jarayoni bilan mos kelishi mumkin, biroq faqat tashqi simptomlarga asoslanib *Colletotrichum* turkumini tasdiqlash mumkin emas. Oxirgi aniq xulosa sof kultura va keyingi morfologik hamda molekulyar identifikatsiya natijalari asosida chiqariladi. Mikroskopik tekshirishda preparatlar tayyorlanadi va mitseliy, konidiofor, konidiya va appressoriylarning mavjudligi hamda shakli kuzatiladi. *Colletotrichum* vakillarida konidiyalar odatda rangsiz, bir hujayrali, silliq devorli bo‘lib, ko‘pincha silindrsimon, tuxumsimon yoki biroz duksimon shaklga ega bo‘ladi. Sof kultura olingach, koloniya diametri, ranglanishi, pigment hosil qilishi, spora hosil qilishi, konidiya shakli va o‘lchami kabi belgilar qayd etiladi. Ushbu ma’lumotlar keyinchalik molekulyar natijalar bilan birlashtirilib, izolyatning kompleks identifikatsiyasi amalga oshirilishida muhim ahamiyat kasb etadi. Chunki, bir namuna tarkibida bir nechta zamburug‘ yoki boshqa mikroorganizmlar mavjud bo‘lishi mumkin.

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Xulosa

Olib borilgan tadqiqotlar va ilmiy adabiyotlar tahlili asosida kasallangan olma namunalaridan *Colletotrichum* turkumiga mansub zamburug‘larni ajratib olishda kasallangan to‘qimalardan sof kultura olish va KDA oziqa muhitidan foydalanish samarali yondashuvlardan biri ekanligi aniqlandi. Ajratilgan kulturalarni morfologik jihatdan baholashda koloniya rangi, mitseliy zichligi, o‘sish xarakteri, konidiyalarning shakli va o‘lchami hamda appressoriylarning morfologik xususiyatlari muhim diagnostik belgilar hisoblanadi. *Colletotrichum* turkumining ayrim vakillari morfologik jihatdan bir-biriga juda yaqin bo‘lganligi sababli, morfologik identifikatsiya natijalarini molekulyar ma’lumotlar bilan tasdiqlash maqsadga muvofiqdir. Umuman olganda, kasallangan olma namunalaridan *Colletotrichum* izolyatlarini ajratish va identifikatsiya qilish mahalliy fitopatogen zamburug‘lar xilma-xilligini o‘rganish, kasallik qo‘zg‘atuvchilarini aniqlash hamda olma yetishtirishda biologik va agrotexnik himoya choralarini takomillashtirish uchun muhim ilmiy-amaliy ahamiyatga ega.

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CUCUMIS SATIVUS L. O‘SIMLIGINI KASALLANTIRUVCHI ASOSIY VIRUSLARNING BIOLOGIK XUSUSIYATLARI

БИОЛОГИЧЕСКИЕ ОСОБЕННОСТИ ОСНОВНЫХ ВИРУСОВ, ПОРАЖАЮЩИХ CUCUMIS SATIVUS L.

BIOLOGICAL CHARACTERISTICS OF THE MAJOR VIRUSES INFECTING CUCUMIS SATIVUS L.

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Annotatsiya: Ushbu ishda bodringni zararlovchi CMV, ZYMV va CGMMVning biologik xususiyatlari haqida ma’lumotlar keltirilgan. Ularning tasnifi, xo‘jayinlar doirasi, kasallik alomatlari va yuqish yo‘llari ko‘rib chiqilgan. Viruslarni farqlashda tashqi alomatlar bilan birga biologik xususiyatlarni hisobga olish infeksiya manbalarini aniqlash va tarqalishni cheklash uchun muhimdir.
Kalit so‘zlar: *Cucumis sativus* L., CMV, ZYMV, CGMMV, virus genomi, mozaika, shira orqali yuqish, urug‘ orqali yuqish, fitosanitariya.

Аннотация: В данном обзоре литературы обобщены биологические особенности CMV, ZYMV и CGMMV, поражающих огурец. Рассмотрены их классификация, круг растений-хозяев, симптомы заболеваний и пути передачи. Учёт биологических особенностей наряду с внешними симптомами при дифференциации вирусов важен для выявления источников инфекции и ограничения её распространения.
Ключевые слова: *Cucumis sativus* L., CMV, ZYMV, CGMMV, вирусный геном, мозаика, передача тлями, передача семенами, фитосанитария.

Abstract: This literature review summarizes the biological characteristics of CMV, ZYMV, and CGMMV infecting cucumber. Their classification, host range, disease symptoms, and transmission routes are examined. Considering biological characteristics alongside visible symptoms when differentiating these viruses is important for identifying infection sources and limiting their spread.
Keywords: *Cucumis sativus* L., CMV, ZYMV, CGMMV, viral genome, mosaic, aphid transmission, seed transmission, phytosanitation.

Kirish

Bodring o‘simligini dunyo bo‘yicha 20 dan ortiq fitopatogen viruslar kasallantirib katta iqtisodiy zarar keltiradi. Ularning orasidan bodring mozaikasi, qovoqchaning sariq mozaikasi va bodringning yashil dog‘li mozaika viruslari keng tarqalgan viruslar qatoriga kiradi. Shuning uchun ushbu ishda ushbu viruslar haqida kengroq ma’lumotlar keltirishni asosiy maqsad qilib olindi. Bodring mozaikasi virusi *Bromoviridae* oilasining *Cucumovirus* turkumiga mansub, diametri taxminan 28–30 nm bo‘lgan ikosaedrik o‘simlik virusidir. Mochizuki va Ohki (2012) sharhida qayd etilishicha, 1916-yilda Doolittle va Jagger bodring hamda boshqa qovoqdosh o‘simliklarda bodring

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mozaikasi kasalligining dastlabki holatlarini qayd etgan [1]. Ushbu adabiyotlar sharhining maqsadi bodringni kasallantiruvchi CMV, ZYMV va CGMMVning biologik xususiyatlarini ilmiy manbalar asosida taqqoslash hamda ularning xo‘jayin o‘simliklar doirasi, kasallik alomatlari va yuqish yo‘llaridagi farqlarni umumlashtirishdan iborat.

Bodring mozaikasi virusi (CMV). CMV butun dunyoda, asosan, mo‘tadil iqlimdan tropik iqlimgacha bo‘lgan hududlarda tarqalgan. U 100 ta o‘simlik oilasiga mansub 1200 dan ortiq turni, jumladan, bir urug‘pallali va ikki urug‘pallali o‘simliklarni zararlaydi. CMV infeksiyasi keltirib chiqaradigan alomatlar xo‘jayin o‘simlik turi yoki virus shtammiga qarab farqlanadi. Ular mozaika, xloroz, pakanalik, barglarning noto‘g‘ri shakllanishi va tizimli nekrozni o‘z ichiga oladi. CMV kasalligi, asosan, shiralar orqali nopersistent usulda tarqaladi. CMV, asosan, qovoqdoshlar (*Cucurbitaceae*), ituzumdoshlar (*Solanaceae*), dukkakdoshlar (*Leguminosae*), karamdoshlar (*Brassicaceae*) va boshoqdoshlar (*Gramineae*) oilalarida, shuningdek, boshqa ko‘plab o‘simlik turlarida mozaika va o‘sishdan qolish kasalliklarini keltirib chiqaradi. Uning genomi uchta musbat qutbli bir zanjirli RNK segmentidan tashkil topgan [1]. Bodring mozaikasi virusi (CMV) ekologiyasi muhim qishloq xo‘jaligi ekinining barqarorligiga virus qanday ta’sir ko‘rsatishi mumkinligini ko‘rsatuvchi dolzarb misol sifatida keltiriladi. Hozirgi vaqtda shunday qarash keng tarqalganki, zamonaviy qishloq xo‘jaligida qo‘llaniladigan texnologiyalar ishlab chiqarish tizimlarini shunday tashkil etishni ta’minlashi kerakki, bunda atrof-muhitga zarar yetkazilmagan holda mahsulot sifati yillar davomida saqlanib qolsin. Gallitelli (2000) ma’lumotiga ko‘ra, o‘simliklarning yangi va yuqori hosildor navlarini joriy etishdan kutilgan foyda mahalliy virus populyatsiyasi tarkibini keskin o‘zgartira oladigan yangi virus shtammlarining hamrohlikda kirib kelishi tufayli tezda yo‘qqa chiqishi mumkin. Barqarorlikka erishishda o‘simlik ko‘paytirish materiallarini karantin nazoratidan o‘tkazish va gen muhandisligi samarali vositalar sifatida taklif etiladi [4].

Qovoqchaning sariq mozaikasi virusi (ZYMV). Qovoqchaning sariq mozaikasi virusi (ZYMV) *Potyviridae* oilasining *Potyvirus* turkumiga mansub. ZYMV musbat, bir zanjirli RNK tutuvchi virusidir. Kasallik alomatlari: tabiiy va tajriba sharoitidagi zararlanish asosan *Cucurbitaceae* — qovoqdoshlar oilasi vakillarida qayd etilgan. Tajriba sharoitida mahalliy zararlanish o‘choqlari hosil bo‘ladigan xo‘jayin o‘simliklarga *Chenopodium amaranticolor*, *C. quinoa* va *Gomphrena globosa* kiradi. ZYMVning ayrim shtammlari *Ranunculus sardous*, *Nicotiana benthamiana* va *Sesamum indicum* kabi o‘simliklarda alomatsiz infeksiyani yuzaga keltiradi. ZYMV qovoqdosh o‘simliklarning o‘sishdan qolishiga, barglarining kuchli deformatsiyalanishiga, ularda to‘q yashil pufaksimon bo‘rtmalar va mozaika belgilarining paydo bo‘lishiga sabab bo‘ladi. Keyinchalik barglar ipsimon shaklga kiradi. Umuman olganda, qovoqdosh o‘simliklarda kasallik alomatlari kuchli namoyon bo‘ladi va mevalarning jiddiy deformatsiyasi tufayli hosildorlik keskin kamayadi. Virionlari uzunligi 680–730 nm, diametri 11–13 nm bo‘lgan egiluvchan ipsimon zarrachalardir. Ular hisoblangan molekulyar massasi 31 kDa bo‘lgan yagona turdagi oqsilning taxminan 2000 ta subbirligidan tashkil topgan. Genom RNKsining uzunligi 9,6 kb bo‘lib, uning 5′ uchiga virus tomonidan kodlanadigan oqsil — VPg kovalent bog‘langan, 3′ uchida esa poli(A) dumi mavjud. Nukleotidlar ketma-ketligining 5′ uchi adenin va uratsilga boy bo‘lib, ularning ulushi 69% ni tashkil etadi. U shiralar orqali nopersistent usulda va mexanik yo‘l bilan yuqadi [2].

Bodringning yashil dog‘li mozaika virusi (CGMMV). Bodringning yashil dog‘li mozaika virusi (CGMMV) *Virgaviridae* oilasining *Tobamovirus* turkumiga mansub. Virus ilk bor 1935-yilda bodringda aniqlangan va o‘rganilgan dastlabki o‘simlik viruslaridan biridir. U dastlab Angliyadan boshqa mamlakatlarga tarqalgan, so‘ngra Angliya va ushbu mamlakatlardan boshqa davlatlarga ham yoyilgan. Ushbu tarqalish jarayoni 1935–1985-yillar oralig‘ida sekin, 1986–2006-yillarda tezroq, 2007–2016-yillarda esa juda tez sur’atlarda kechgan. Virusning qovoqdoshlar (shu jumladan, tarvuz) hosildorligi va meva sifatini pasaytirishi aniqlangach, kasallik eng ko‘p zarar yetkazgan mamlakatlarda keng ko‘lamli tadqiqotlar olib borila boshlandi. Bu sa’y-harakatlar virus zarrachasi va genom xususiyatlari, uning evolyutsiyasi hamda epidemiologiyasini o‘rganishni o‘z ichiga oldi. Tobamoviruslarga xos bo‘lgan zarracha barqarorligi, kontakt orqali oson yuqish va urug‘ orqali tarqalish xususiyatlari virusning murakkab kasallik siklini hamda hech qanday tashuvchisiz

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(vektorsiz) ham mahalliy yoki uzoq masofalarga tarqalish qobiliyatini izohlab berdi. Kasallik etiologiyasi va epidemiologiyasi bo‘yicha olingan bilimlar turli fitosanitariya choralariga asoslangan kasalliklarga qarshi kurashning kompleks usullarini ishlab chiqishga imkon yaratdi. Dombrovsky va hammualliflar (2017) ta’kidlashicha, tropik yoki subtropik mamlakatlarda yetishtirilgan qovoqdoshlar urug‘lari bilan bog‘liq infeksiyaning xalqaro urug‘ savdosi orqali tarqalishi CGMMV ning dunyo bo‘ylab tez yoyilishida muhim rol o‘ynagan [3].

Xulosa qilib aytganda, bodring o‘simligini zararlovchi CMV, ZYMV va CGMMVni farqlashda kasallik alomatlari bilan birga ularning biologik xususiyatlari va yuqish yo‘llarini ham hisobga olish zarurligini ko‘rsatadi. CMV va ZYMV asosan shiralar orqali nopersistent usulda tarqaladi, CGMMVning tarqalishida esa mexanik kontakt va zararlangan urug‘lar muhim o‘rin tutadi. Ushbu farqlar infeksiya manbalarini aniqlash va tarqalishni cheklash choralarini tanlashga asos bo‘ladi. Ko‘rib chiqilgan xalqaro manbalar asosida bu viruslarning O‘zbekistondagi tarqalish darajasini belgilab bo‘lmaydi, buning uchun mahalliy tadqiqotlar zarur ekanligi ma’lum bo‘ladi.

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THE ROLE OF BACTERIAL EXOPOLYSACCHARIDES IN MICROBIOLOGICAL CALCIFICATION

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Abstract: Microbiological calcification is a biologically mediated process in which microorganisms promote the precipitation of calcium carbonate ($CaCO_3$) through their metabolic activities and interactions with their surrounding environment. Among the microbial factors involved, bacterial exopolysaccharides (EPS) play an important role in regulating mineral nucleation, crystal growth, and calcium carbonate deposition. These extracellular polymers contain functional groups capable of binding calcium ions, providing nucleation sites, and creating localized microenvironments favorable for biomineralization. Furthermore, EPS contribute to bacterial adhesion, biofilm formation, and the stabilization of mineral structures. Understanding the relationship between EPS production and microbiological calcification is essential for developing sustainable biotechnological applications, including self-healing concrete, soil stabilization, and the remediation of porous materials. This review summarizes the principal mechanisms through which bacterial EPS influence calcium carbonate precipitation and discusses their potential applications and current research challenges.

Keywords: bacterial exopolysaccharides, microbiological calcification, calcium carbonate, biomineralization, microbial-induced calcium carbonate precipitation, extracellular polymeric substances.

1. Introduction

Microbiological calcification is an important form of biologically mediated mineral formation in which microorganisms facilitate the precipitation of calcium carbonate under suitable environmental conditions. This process occurs in natural ecosystems, including soils, sediments, saline environments, and aquatic habitats, and contributes to carbonate cycling, sediment lithification, and the formation of mineral structures. Microbial-induced calcium carbonate precipitation (MICP) has attracted considerable scientific interest because of its potential applications in environmental biotechnology, geotechnical engineering, and sustainable construction materials [1].

The formation of calcium carbonate is influenced by several interconnected factors, including microbial metabolism, calcium ion availability, pH, dissolved inorganic carbon, and the physicochemical characteristics of microbial cell surfaces. In addition to these factors, bacterial extracellular polymeric substances, particularly exopolysaccharides (EPS), can substantially influence the initiation and development of mineral precipitation. EPS are high-molecular-weight

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polymers secreted by microorganisms and commonly consist of polysaccharides, proteins, extracellular DNA, and other organic compounds. Their chemical composition and structural properties determine their interactions with mineral ions and growing crystals [2].

Although bacterial metabolic activity is a major driver of MICP, EPS provide an additional mechanism through which microorganisms regulate mineral nucleation, crystal morphology, and the spatial distribution of calcium carbonate. Consequently, understanding EPS-mediated biomineralization is important for optimizing microbial calcification processes and developing efficient biological mineralization technologies [3].

2. Mechanisms of EPS-Mediated Microbiological Calcification

2.1. Calcium binding and mineral nucleation

One of the principal functions of bacterial EPS in microbiological calcification is their ability to bind calcium ions (Ca^{2+}). Many extracellular polysaccharides contain negatively charged functional groups, including carboxyl, hydroxyl, and, in some cases, sulfate and phosphate groups (fig. 1). These functional groups can interact with calcium ions through electrostatic interactions and coordination processes, resulting in localized calcium accumulation within the extracellular matrix [4].

The accumulation of calcium ions creates favorable conditions for the initial stages of mineral nucleation when sufficient carbonate ions are available. As the local solution becomes supersaturated with respect to calcium carbonate, nucleation and subsequent crystal growth may occur on EPS-associated sites. The extracellular matrix therefore acts as a potential template for mineral deposition, facilitating the formation of mineral structures in close association with bacterial cells and biofilms [5].

However, EPS do not invariably promote precipitation. Depending on their concentration, molecular structure, and degree of ionization, they may also bind calcium strongly enough to inhibit crystal nucleation or delay crystal growth (fig. 2).

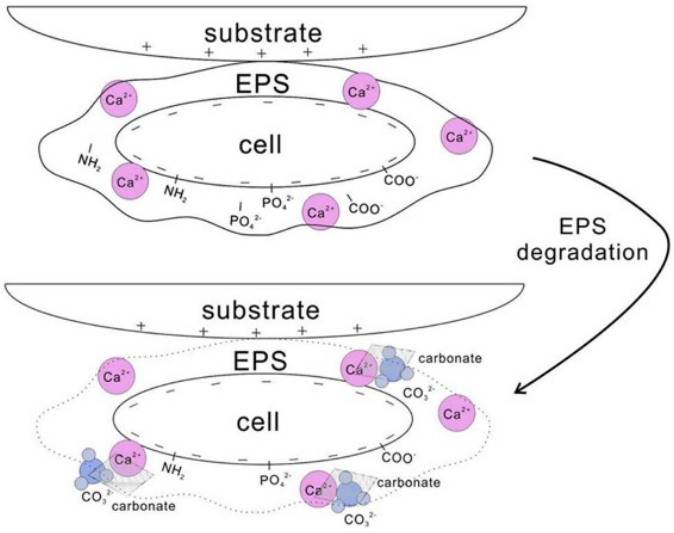


Figure 1. Schematic representation of calcium binding by bacterial extracellular polymeric substances (EPS) and subsequent calcium carbonate precipitation associated with EPS degradation

Thus, the effect of EPS on calcification depends on the balance between calcium sequestration, nucleation-site availability, and solution supersaturation [6].

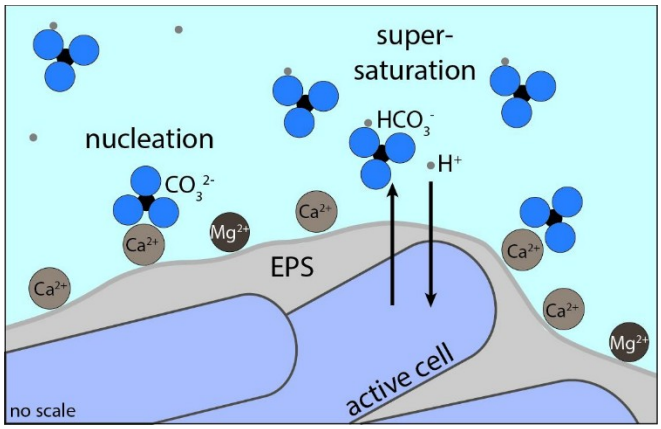


Figure 2. Schematic representation of EPS-associated calcium carbonate nucleation under supersaturated conditions, illustrating the interactions of calcium and carbonate species with the bacterial extracellular matrix

2.2. Regulation of crystal growth and morphology

In addition to facilitating nucleation, EPS influence the growth and morphology of calcium carbonate crystals. Their polymeric structure provides a three-dimensional matrix in which mineral particles can accumulate and interact. EPS may adsorb onto specific crystal surfaces, modifying crystal growth rates, particle aggregation, and the development of different calcium carbonate morphologies [6, 7].

Calcium carbonate can occur in several mineral forms, including calcite, aragonite, and vaterite. The resulting polymorph depends on multiple factors, including temperature, pH, calcium and carbonate concentrations, and the composition of the surrounding organic matrix. EPS may influence these processes through selective ion binding, surface adsorption, and spatial confinement of mineral growth [2, 6, 8].

The extracellular matrix can also contribute to the formation of composite structures consisting of organic polymers and inorganic minerals. Such structures may exhibit improved cohesion and stability compared with mineral particles formed in the absence of an organic matrix. Nevertheless, the precise effects of individual EPS components on calcium carbonate polymorphism remain dependent on the microorganism and the experimental conditions [6, 9].

2.3. Interaction between EPS production and bacterial metabolism

EPS-mediated calcification is closely connected with bacterial physiological activity. In ureolytic bacteria, the hydrolysis of urea generates ammonia and dissolved inorganic carbon, generally increasing the pH and favoring carbonate availability. In the presence of sufficient calcium ions, these changes can promote calcium carbonate precipitation [10, 11].

EPS complement this metabolic process by providing calcium-binding sites and a matrix for mineral nucleation. They may also facilitate bacterial attachment to surfaces and biofilm development, creating localized microenvironments in which mineral precipitation occurs. However, the contribution of EPS must be distinguished from the effects of urease activity, pH changes, and carbonate generation because these factors can independently influence the quantity and characteristics of the resulting mineral [10, 12].

The relationship between EPS production and calcium carbonate precipitation is therefore not necessarily linear (fig. 3).

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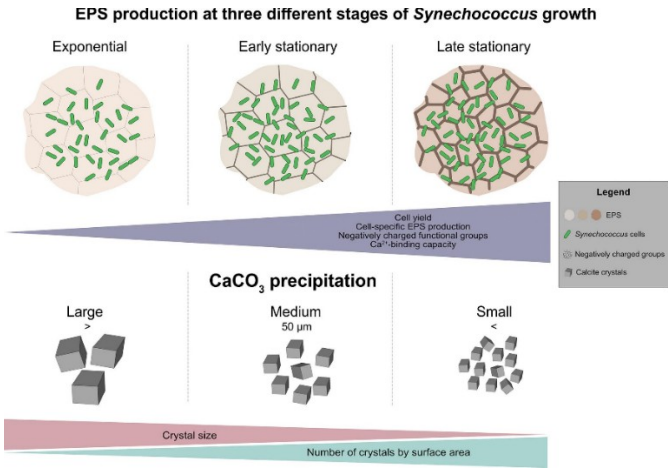


Figure 3. Schematic representation of growth-phase-dependent EPS production and its potential influence on calcium carbonate precipitation and crystal size

Moderate EPS production may enhance nucleation and mineral retention, whereas excessive polymer accumulation may restrict ion diffusion or alter calcium availability. Determining the optimal balance between bacterial metabolism and EPS synthesis is consequently an important consideration in the development of efficient biomineralization systems [2, 13].

3. Biotechnological Applications of EPS-Mediated Calcification

The ability of bacterial EPS to facilitate mineral formation has important implications for several biotechnological applications. In construction engineering, MICP is being investigated as a means of producing bio-based materials, sealing cracks, and reducing the permeability of porous structures (fig. 4). The diagram illustrates the effects of nutrient availability and seawater Mg^{2+}/Ca^{2+} ratios on mineral precipitation and polymorph formation. Bacterial urease activity promotes urea hydrolysis, generating carbonate species that react with calcium ions to form calcium carbonate minerals. Extracellular polymeric substances (EPS) may contribute to bacterial attachment, ion retention, and mineral nucleation, supporting the deposition of minerals within concrete cracks. EPS can support bacterial attachment, retain mineral particles, and contribute to the cohesion of calcium carbonate deposits. When combined with appropriate bacterial strains and mineralization conditions, these properties may improve the effectiveness of biological crack repair and soil consolidation [14, 15].

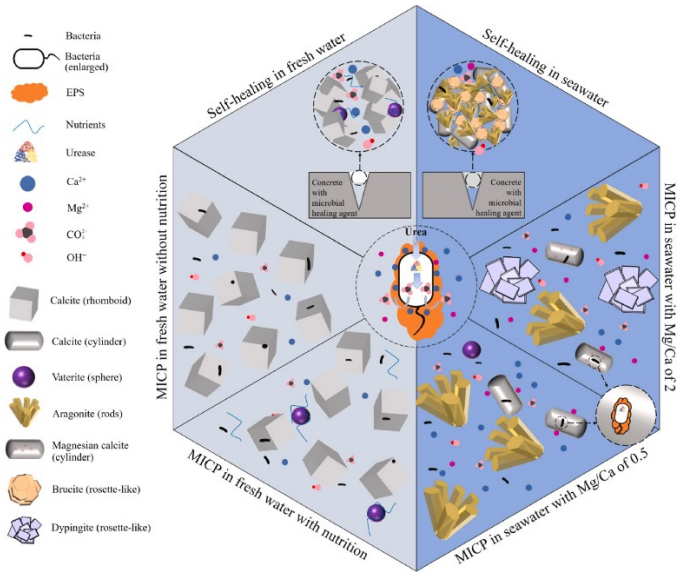


Figure 4. Schematic representation of microbially induced calcium carbonate precipitation (MICP) and its applications in concrete self-healing under different environmental conditions

In environmental applications, EPS-mediated calcification may contribute to the stabilization of soil particles, the reduction of pore connectivity, and the immobilization of selected contaminants through mineral precipitation or adsorption. The potential for these processes to improve soil structure is particularly relevant in environments affected by erosion, salinity, or degradation. However, their effectiveness depends on soil chemistry, microbial survival, mineralization rates, and the long-term stability of the precipitated minerals [16-19].

EPS-producing bacteria also represent promising candidates for developing sustainable biomineralization technologies. For example, strains of *Bacillus* and other mineral-forming bacteria may combine urease activity with extracellular matrix production, supporting calcium carbonate deposition under controlled conditions. Nevertheless, the suitability of individual strains must be established experimentally by evaluating EPS composition, urease activity, calcium carbonate yield, crystal morphology, and the mechanical properties of the resulting materials [15, 17, 18, 20].

4. Conclusions and Future Perspectives

Bacterial exopolysaccharides are important structural and biochemical components of microbiologically induced calcium carbonate precipitation. Their principal contributions include calcium ion binding, provision of potential nucleation sites, regulation of crystal growth, and stabilization of mineral deposits within microbial extracellular matrices. Through interactions with bacterial metabolism and environmental conditions, EPS can influence both the efficiency and the characteristics of biological calcification.

Despite substantial progress in understanding microbial biomineralization, further research is required to clarify the relationships between EPS composition, polymer concentration, urease activity, and calcium carbonate production. Integrated investigations combining quantitative EPS analysis, mineralogical characterization using X-ray diffraction (XRD), morphological examination using scanning electron microscopy (SEM), and elemental analysis using energy-dispersive X-ray spectroscopy (EDS) would provide a more comprehensive understanding of these interactions.

Overall, elucidating the mechanisms of EPS-mediated calcification may facilitate the development of environmentally sustainable technologies for construction, soil stabilization, and environmental remediation. In particular, investigating bacterial strains isolated from extreme ecosystems may reveal novel combinations of mineralization activity and extracellular polymer production that are valuable for applications under challenging environmental conditions.

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О ВОЗМОЖНОСТИ РЕГУЛЯЦИИ СТРУКТУРЫ G-КВАДРУПЛЕКСОВ МЕТОДАМИ РАДИАЦИОННОЙ ТЕХНОЛОГИИ

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Аннотация: рассмотрены молекулярные структуры и электронное строение G-квадруплексов в ДНК и РНК, очерчена область их функционального действия, а также некоторые области в биологии и медицине. Описаны радиационно-технологические Оже-процессы в таких структурах, способные влиять на электрон-атомное строение G-квадруплексов и регулировать их функции в нужном направлении.

Ключевые слова: G-квадруплексы, структура, электронное строение, радиационная технология, Оже-процессы.

Введение

Объемная структура вторичной укладки РНК или ДНК, образующейся в местах, богатых гуанином, в виде плоских G-квартетов, называется G-квадруплексом (G4). Такие квадратные образования, состоящие из 4 молекул гуанина, связываются друг с другом по кругу с помощью хугстиновских водородных связей, формируя прочный пространственный «столбик», внутри которого образуется центральный канал, где находятся моновалентные металлические катионы [1]. Последние, в различной степени ($K^+ > Na^+ > Li^+$) нейтрализуя электростатическое отталкивание четырех атомов карбонильного кислорода (O6), образующих отрицательно заряженное ядро в центре G-квартета, могут прочно сшивать структуру G4. Причем стабильность структуры G4 оказалась настолько высокой, что даже температура его плавления in vitro превышает физиологический диапазон [2].

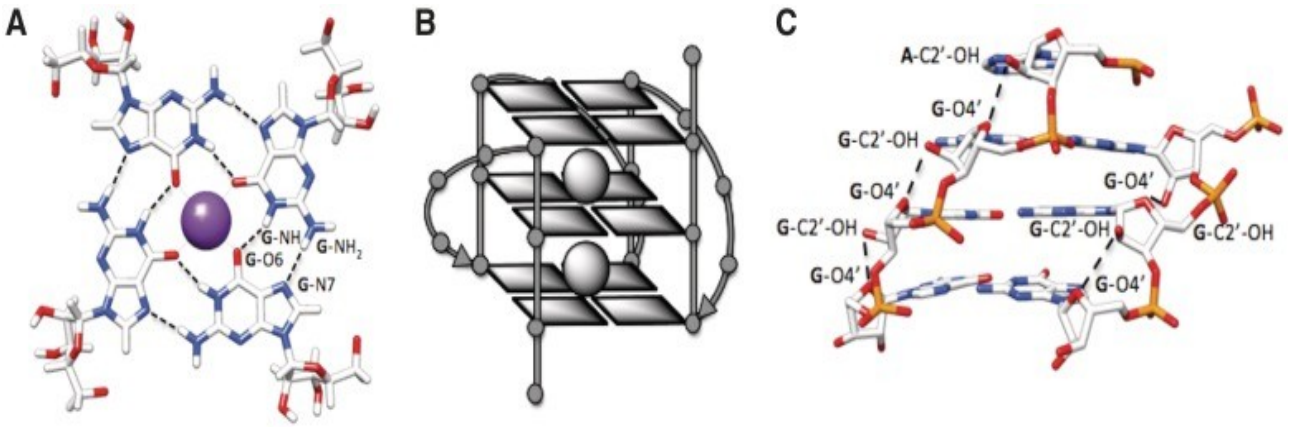


Рисунок 1. (A) Схема структуры G-квартета и (B) структуры G-квадруплекса нуклеиновых кислот, (C) расположение межмолекулярной водородной связи (обозначено пунктиром) между ОН группами рибозы C2′ и кислородом O4′ в G-квартете РНК

ДЛЯ ЦИТИРОВАНИЯ

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Именно в этой области и было выявлено существование зоны высокой возможности регуляции структуры G-квадруплексов, раскрытие процесса которого, в силу ряда обстоятельств, приобретает в настоящее время большую актуальность.

Впервые молекулярная структура G-квартета была выявлена Gellert и коллегами с помощью рентгеновской дифракции в 1962 г. [2]. Позже (в 1988 году) была открыта биологическая значимость структуры ДНК G-квадруплекса в области теломер и иммуноглобулинов. В течение последующих двух десятилетий работами многих авторов были установлены пути регуляции структуры G4 в виде их сворачивания или раскрывания с помощью нескольких белков, способных связываться с G4 [1].

В 2007 году выявлено формирование РНК G-квадруплекса у бактерий, однако их количество оказалось чрезвычайно малым у бактерий, в отличие от клеток млекопитающих [2]. Поскольку искусственное вставление rG4 в систему гена репортеров бактерий приводит к снижению роста бактерий, ряд авторов предположили [3], что в ходе эволюции G4 у них элиминируются. Из-за низкой выявляемости естественных rG4 у бактерий исследования в этой области в настоящее время очень ограничены.

С другой стороны, в последние годы, особенно в период коронавирусной пандемии, было проведено всестороннее предсказание G4 в геноме всех известных ДНК- и РНК-вирусов, способных заражать человека, и показано их характерное наличие и расположение для каждой семьи и вида вирусов [4].

В 2016 году было проведено первое общетранскриптомное картирование G4 в человеческом геноме и к настоящему времени обнаружено более 700 000 ДНК G4 в >97% генов. А в целом было выявлено более 3 миллионов G4, которые соответствуют примерно 30 000 генам млекопитающих [1].

Выявлено, что G4 участвуют в самых различных биологических процессах в вирусной системе, а именно: в прямой и обратной транскрипции, репликации и трансляции. И это показывает, что они являются перспективными мишенями для разработки противовирусных препаратов. Относительно бактериальных rG4, исследования выявили как положительную, так и отрицательную регуляторную роль в трансляции, которая зависит от стабильности и положения rG4, а также от контекста фланкирующей последовательности соответствующего транскрипта [1].

В клетках млекопитающих РНК G4 могут появляться и существовать как в ядре, так и в цитоплазме, только при определённых условиях, например, на определённых стадиях клеточного цикла, при специфических стрессовых стимулах (повреждение ДНК), заболеваниях или в клеточно-специфическом виде в нейронах, оказывая широкий спектр влияния на метаболизм РНК. Особенно важной оказалась связь G4 с ключевыми биологическими процессами в онкологии — от транскрипции и трансляции онкогенов и супрессоров опухолей до поддержания теломер и нестабильности генома.

Исследования показали, что РНК G4 в нормальных условиях *in vivo*, в основном, разворачиваются. Однако какова бы ни была роль G4, оба процесса: и сворачивание, и разворачивание, происходят с помощью белков, которые при мутации ДНК/РНК не могут выполнять свои нормальные функции [2].

Поэтому в плане регуляции структурного состояния G4 основные работы проводятся в плане выявления любых биомолекул или новых белков, связывающих G4, а также транскриптомного картирования РНК G4 при различных условиях функционирования клеток. В настоящее время таким образом проводится поиск новых методов лечения многих заболеваний, особенно таких грозных, как злокачественные опухоли, нейродегенеративные заболевания, паразитарные и вирусные инфекции [1,2].

Также в этом отношении разрабатываются специфические инструменты селективного нацеливания функционально важных rG4 для различных применений. Так, на основе конформационных изменений G4 была установлена возможность их использования в качестве аптамерных зондов для обнаружения молекул белка или нуклеиновых кислот, а также ионов

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металлов, pH, молекулярной скученности и т.д. в клетках млекопитающих, вирусах и бактериях. Например, для обнаружения *Staphylococcus aureus* применялся G4-аптамер, нацеленный на белок A поверхности клетки [5].

В целом, однако, нужно заметить, что для проведения всех этих исследований было бы желательно разработать новые инструменты воздействия на структуру G4 физического плана. Одним из таких, возможно, наиболее сильных методов является радиационная технология, уже сыгравшая и играющая огромную роль в молекулярной биологии и медицине.

Методы исследования и результаты

Современные методы радиационной технологии чрезвычайно многообразны, но с большой степенью общности можно выделить как особые возможности варьировать энергии, интенсивность, хиральность, комбинированность, дозы воздействия облучающих частиц, включая фотоны и различные типы корпускулярного излучения: электроны, ионы, нейтроны, мюоны. Для биомедицинских целей особенно важное значение представляет возможность моделирования облучаемого объекта с помощью так называемых иерархических структур (напр., связанные электроны, валентные электроны, молекулы, структуры из них, органы и более крупные объекты различной размерности и размера). Чрезвычайно существенно, что можно использовать как одиночные излучения, так и комбинированные, что позволяет либо постепенно, в первом случае, либо одновременно воздействовать на различные платформы иерархических структур. Очень существенно следующее обстоятельство: радиация может действовать чрезвычайно локально, передавая очень большую энергию в первичном повреждении, так что перемещение возбуждения к меньшим энергиям («снизу-вверх») уменьшает степень локальности, но увеличивает количество вторичных дефектов. И так – до прохождения всей иерархической структуры, которая и демонстрирует ожидаемый макроэффект, не углубляясь в детали радиационной физики и химии (в частности, биополимеров) – а эти наука и практика развиты чрезвычайно детально и широко (начиная с 1852г!). Остановимся на самом важном – применительно к G-квадруплексам. Варьируя выше отмеченным параметром радиации (например, рентгеновское излучение), можно использовать так называемый Оже-эффект, открытый в 1926 году (Пьером Оже) и ныне внедренный широчайшим образом в радиационную онкологию [6]. В нашем случае его возможности также многогранны. Так, если перед нами стоит задача уничтожить квадруплекс, то следует ионизовать самую глубокую (K-) оболочку ионов, , то это приводит к Оже-каскаду, завершающемуся ионизацией целой группы ионов вокруг и кулоновскому взрыву, т.е. уничтожению целого кусочка структуры РНК или ДНК. Именно таким способом было найдено решение дезактивировать РНК вируса SARS-2V и радиационным путем подавлять Covid-19 [7]. Именно этот механизм Оже-деструкции лежит в основе рентгеновской онкологии ряда опухолей. Если первичная ионизация происходит в более высокой L оболочке (а этого можно добиться, уменьшая энергию фотона X-лучей), то разрушение квадруплекса будет неполным. Если же начать облучение с M оболочки, то эффект дезорганизации структуры будет меньшим. На сегодняшний день эта мощная рентгеновская терапия осуществляется с помощью так называемого синхротрона и широко используется, например, на Западе. Для учета хиральности структуры облучаемого биообъекта, синхротроном подобрать требуемую хиральность. Менее «грандиозные разрушения» G-квадруплекса, причем направленные на определенные химические связи, можно осуществить различной лазерной радиацией. Важно отметить, поскольку лазерный свет поглощается вблизи поверхности объекта, то используется красивый «трюк»: объект насыщается особыми примесями, осаждающимися вблизи квадруплекса, которые возбуждаются рентгеновским лучом, то есть проходящим глубоко, а его флуоресценция (частичное выбрасывание фотона) приводит уже к тому, что именно этот фотон (уже на глубине!) уничтожает нужные валентные связи и глобально не нарушается структура G-квадруплекса. Особенно привлекательной представляется возможность уничтожения

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квадруплекса, переносящего части РНК опухолей, ликвидируя процессы метастазирования. Подобным образом, используя различные манипуляции, можно, по существу, управлять, в частности регулировать, процессы, в которых участие G-квадруплексов, как оказывается, абсолютно необходимо и перспективно.

Заключение

Что касается теоретических исследований в проблемах G-квадруплексов, то они проходят в последние годы на уровне квантово-химического моделирования, хотя первые исследования в области петлеобразования столь необходимого для G-квадруплексов по теории были произведены около 25 лет тому назад, причем именно в глубоко теоретическом плане [8]. Проделанные нами расчёты согласуются с работой [8] и указанными исследованиями по квантовой химии, т.е. они являются мостиком двух подходов.

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ISOLATION AND PHYSIOLOGICAL CHARACTERIZATION OF AN L-METHIONINE-OVERPRODUCING BACTERIAL STRAIN FROM INDUSTRIAL WASTEWATER

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1. Introduction

L-methionine is a high-value, sulfur-containing essential amino acid widely used as a feed additive in livestock production and as a key ingredient in pharmaceutical and cosmetic formulations. While chemical synthesis yields a racemic DL-mixture, fermentation-based production offers a cleaner, more sustainable alternative — one that selectively delivers only the biologically active L-enantiomer. Industrial environments — particularly the soils surrounding manufacturing facilities and their associated wastewater systems — represent some of the harshest ecological niches found in nature. Persistent chemical pollution, heavy organic loading, and fluctuating sulfur gradients create intense selective pressure on resident microbial communities. The bacteria that manage to thrive under these conditions often develop remarkable metabolic adaptations, including an enhanced capacity to overproduce amino acids. With this in mind, the present study undertakes a systematic effort to isolate, molecularly identify, and physiologically characterize wild-type bacterial strains recovered from industrial soils and manufacturing plant effluents — with the ultimate goal of establishing a scalable bioprocess for extracellular L-methionine production.

2. Materials and Methods

Bacterial isolates were selectively recovered from industrial soil core samples and liquid effluent collected at active drainage points of manufacturing facilities. To assess their technological and physiological potential, a purpose-built minimal cultivation medium — designated Medium No. 2 — was formulated. The medium was specifically designed to amplify sulfur metabolic flux, incorporating ammonium sulfate ($(NH_4)_2SO_4$, 5.0 g/L) as a combined nitrogen and sulfur source, alongside D-glucose (20.0 g/L) as the primary carbon and energy substrate. Fermentation was carried out over a 96-hour window at 30°C on an orbital shaker running at 180 RPM. Growth kinetics were tracked continuously via optical density measurements at 600 nm (OD_{600}) using a UV-Vis spectrophotometer, while glucose consumption and culture pH were monitored dynamically throughout. Extracellular amino acid accumulation was quantified by High-Performance Liquid Chromatography (HPLC) following removal of bacterial biomass through high-speed refrigerated centrifugation.

3. Results and Discussion

Screening of eight bacterial isolates from industrial soils and wastewater canals revealed considerably different growth and amino acid secretion of the isolates in ammonium sulfate-amended medium. Such a physiological turning point approximately occurs during the late exponential and

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stationary phases at 48-72 hours of cultivation. In this context, Isolate-1, the most promising overproducer of all the isolated strains, was isolated from an industrial wastewater discharge point. Showing a high biomass productivity and a strong secretion rate of amino acids, quantitative HPLC measurements indicated that a total of 0.783 mg/g pure L-methionine was secreted into the culture supernatant of Isolate-1, indicating active methionine secretion in this strain. The custom designed Medium No. 2 helped the predominant isolates to eliminate their lag phase, and promoting good viability for long times of culture, even in the face of the progressive sulfate accumulation in the culture medium that markedly decreases the viability of old cultures. The presence of stabilizing agents $CaCl_2$ (0.01 g/L) and $MgSO_4$ (0.5 g/L) protects the membrane from rupture during osmotic pressure. The presence of methionine in the supernatant and its absence in the cells indicates that Isolate-1 has an active membrane efflux mechanism, which could be useful for further research. These specialized amino acid exporter pumps seem to constantly excrete the newly synthesized methionine out of the cytoplasm and prevent the formation of an intracellular methionine pool that would enable feedback inhibition. This allows for unimpeded methionine overproduction because the transporting machines to extend the metabolic pathway are always being pushed.

4. Conclusion

This study successfully established a practical workflow for isolating and evaluating wild-type bacterial strains with high L-methionine production. The custom culture device used in this workflow is low-cost. The Isolate-1 strain, which was screened from an industrial waste habitat, can secrete 0.783 mg/g of L-methionine into the culture supernatant. This secretory production model eliminates the costly and labor-intensive cell lysis step, greatly simplifies downstream processing, and provides a solid, industrially feasible foundation for subsequent bioprocess development. Looking ahead, future work will focus on the molecular identification of Isolate-1 via 16S rRNA gene sequencing, followed by a stepwise scale-up in laboratory bioreactors to assess its performance under pilot-scale conditions.

Keywords: L-methionine, Industrial soils, Manufacturing wastewater, Ammonium sulfate minimal medium, Extracellular secretion, HPLC validation.

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PAENIBACILLUS SP. BAKTERIYASIDA EKZOPOLISAXARID HOSIL BO‘LISHI VA ANTIFUNGAL FAOLLIKNING EPS AJRATILGANDAN KEYINGI FRAKSIYADA ANIQLANISHI

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Annotatsiya: Ushbu tadqiqotda *Paenibacillus sp.* bakteriyasining turli suyuq ozuqa muhitlarida o‘sishi va *Fusarium oxysporum f. sp. vasinfectum* ga qarshi antifungal faollik namoyon qiluvchi fraksiyalarni dastlabki aniqlash masalasi o‘rganildi. Bakteriya Nutrient Broth (NB), Luria–Bertani (LB), Potato Dextrose (PD), Tryptone Soy Broth (TSB), ISP2 va Corn Steep Liquor (CSL) muhitlarida 28 °C haroratda, 150 ayl/min tezlikda 5 kun davomida kultivatsiya qilindi. Olingan ekstraktlarning dastlabki tekshiruvlarida sezilarli antifungal ta’sir aniqlanmadi. ISP2 muhitida ekzopolisaxarid (EPS) hosil bo‘lishi kuzatildi va u etanol yordamida ajratildi. Alohida tekshirilganda, EPS fraksiyasi *F. oxysporum f. sp. vasinfectum* o‘sishini ingibitsiya qilmadi, EPS ajratilgandan keyin qolgan fraksiya esa zamburug‘ mitseliysi o‘sishini susaytirdi. Natijalar faollikni namoyon qiluvchi birikmalarni keyingi bosqichlarda xromatografik usullar bilan ajratish va kimyoviy tabiatini aniqlash zarurligini ko‘rsatadi.

Kalit so‘zlar: *Paenibacillus sp.*, *Fusarium oxysporum f. sp. vasinfectum*, antifungal faollik, ekzopolisaxarid, EPS dan keyingi fraksiya, biologik nazorat.

Kirish

Fitopatogen zamburug‘lar qishloq xo‘jaligi ekinlarida kasalliklar keltirib chiqarib, hosildorlik va mahsulot sifatiga salbiy ta’sir ko‘rsatadi. *Fusarium* turkumiga mansub zamburug‘lar o‘simliklarda so‘lish va ildiz kasalliklari bilan bog‘liq muhim fitopatogenlar qatoriga kiradi [1, 2]. Kimyoviy fungitsidlardan uzoq muddat foydalanish agroekotizimlarga salbiy ta’sir ko‘rsatishi mumkinligi sababli, mikroorganizmlar asosidagi biologik nazorat usullarini o‘rganish dolzarbdir [3]. *Paenibacillus* turkumiga mansub bakteriyalar biologik faol birikmalar ishlab chiqarish qobiliyati tufayli bunday tadqiqotlar uchun istiqbolli obyekt hisoblanadi. Ishning maqsadi *Paenibacillus sp*. bakteriyasidan olingan ekstraktlarning *F. oxysporum f. sp. vasinfectum* ga qarshi faolligini dastlabki baholash va faollik aniqlangan fraksiyani keyingi tadqiqotlar uchun belgilashdan iborat.

Materiallar va metodlar

Tadqiqot obyekti sifatida *Paenibacillus sp*. bakteriya izolyati, test-organizm sifatida esa *Fusarium oxysporum f. sp. vasinfectum* zamburug‘i ishlatildi. Bakteriya NB, LB, PD, TSB, ISP2 va CSL suyuq ozuqa muhitlarida 28 °C haroratda, 150 ayl/min tezlikda 5 kun davomida o‘stirildi.

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Kultivatsiyadan so‘ng biomassa va kultural suyuqlik ajratilib, ekstraktlar tayyorlandi. Ekstraktlarning antifungal faolligi agar-diffuziya usuli yordamida baholandi. ISP2 muhitida hosil bo‘lgan EPS etanol yordamida cho‘ktirilib, EPS fraksiyasi va cho‘ktirishdan keyin qolgan fraksiya alohida tekshirildi.

Natijalar va muhokama

Dastlabki tajribalarda turli ozuqa muhitlaridan tayyorlangan ekstraktlar hamda turli erituvchilarda olingan namunalarda *F. oxysporum f. sp. vasinfectum* ga qarshi sezilarli ingibitsiya kuzatilmadi. Keyingi tajribalarda ISP2 muhitida *Paenibacillus sp*. tomonidan EPS hosil bo‘lishi qayd etildi. EPS ajratib olingach, uning o‘zi zamburug‘ o‘sishini susaytirmadi, biroq EPS ajratilgandan keyin qolgan fraksiyada antifungal ta’sir kuzatildi. Bu kuzatuv faol komponent(lar) EPS fraksiyasida to‘planmagan, balki etanol bilan cho‘kmagan qolgan fraksiyada bo‘lishi mumkinligini ko‘rsatadi. Biroq mavjud natijalar faol moddaning kimyoviy tuzilishi yoki aniq sinfini belgilash uchun yetarli emas. Shuning uchun ushbu fraksiyani xromatografik ajratish, fraksiyalar faolligini qayta tekshirish va keyinchalik instrumental tahlil yordamida tavsiflash zarur.

Xulosa

O‘rganilgan sharoitlarda ISP2 muhitida hosil bo‘lgan EPS fraksiyasi antifungal faollik ko‘rsatmadi, EPS ajratilgandan keyingi fraksiyada *esa F. oxysporum f. sp. vasinfectum* o‘sishining susayishi kuzatildi. Ushbu dastlabki natija *Paenibacillus sp*. bakteriyasining antifungal ta’sirini yuzaga keltiruvchi birikmalarni EPS dan keyingi fraksiyadan izlash va ularni keyingi xromatografik hamda kimyoviy tahlillar orqali aniqlash uchun asos bo‘lib xizmat qiladi.

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INVESTIGATION OF THE ANTIMICROBIAL PROPERTIES OF N,N-BIS(BENZYLIDENE)-o-PHENYLENEDIAMINE ZINC ACETATE COMPLEX

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Abstract: Schiff bases and their transition metal complexes represent a class of compounds of significant biological and industrial importance. The primary objective of this study is to investigate the antimicrobial, anticorrosion, and anti-wear properties of the N,N-Bis(benzylidene)-o-phenylenediamine ligand—synthesized from benzaldehyde and o-phenylenediamine—along with its zinc-acetate complex in cutting fluids, fuels, and lubricating oils. The structure of the synthesized compounds was confirmed by IR spectroscopy, revealing characteristic absorption bands for the azomethine C=N group at 1620 cm^{-1} for the ligand and 1663 cm^{-1} for the zinc-acetate complex. The antimicrobial and fungicidal activities of the compounds were evaluated using the well-diffusion method in accordance with GOST 9.052-88 and GOST 9.023-74 standards against Mycobacterium phlei, Pseudomonas aeruginosa bacteria, and Aspergillus niger, Cladosporium resinae fungi. The results demonstrated that the zinc-acetate complex at a concentration of 0.5% exhibits high fungicidal activity against Cladosporium resinae in cutting fluids and gasoline, with inhibition zones of 2.2–2.2 cm and 3.8–3.9 cm.

Keywords: Schiff bases, zinc complex, antimicrobial biocide, cutting fluids.

Annotatsiya: Shiff asoslari va ularning o‘tish metalli komplekslari yuqori biologik va sanoat ahamiyatiga ega bo‘lgan birikmalar sinfidir. Ushbu tadqiqotning asosiy maqsadi benzaldegid va o-fenilendiamin asosida sintez qilingan N,N'-Bis(benziliden)-o-fenilendiamin ligandi hamda uning rux-atsetat kompleksining sovutuvchi-kesuvchi suyuqliklarda (SKS), yoqilg‘i va moylash materiallarida mikroblarga qarshi, korroziyaga qarshi va yeyilishga qarshi xossalarini o‘rganishdan iborat. Sintez qilingan birikmalarning tuzilishi IQ spektroskopiyasi yordamida tasdiqlangan bo‘lib, azometin C=N guruhining yutilish chiziqlari ligandi uchun 1620 sm^{-1} da, rux-atsetat kompleksi uchun esa 1663 sm^{-1} chastotada kuzatilgan. Birikmalarning mikroblarga qarshi va fungitsid faolligi GOST 9.052-88 va GOST 9.023-74 standartlariga muvofiq diffuziya zonasi usuli yordamida *Mycobacterium phlei*, *Pseudomonas aeruginosa* bakteriyalari hamda *Aspergillus niger*, *Cladosporium resinae* zamburug‘lariga qarshi aniqlangan. Tadqiqotlar shuni ko‘rsatdiki, rux-atsetat kompleksi 0.5% konsentratsiyada sovutuvchi-kesuvchi suyuqliklar va benzin yoqilg‘isida Cladosporium resinae zamburug‘iga qarshi yuqori fungitsid faollik ko‘rsatadi (infeksiyani bostirish zonalari mos ravishda 2.2-2.2 sm va 3.8-3.9 sm).

Аннотация: Основания Шиффа и их переходные металлокомплексы представляют собой класс соединений, имеющих высокую биологическую и промышленную значимость. Основной целью исследования является изучение антимикробных, антикоррозионных и противоизносных свойств лиганда N,N-Бис(бензилиден)-о-фенилендиамина, синтезированного на основе бензальдегида и о-фенилендиамина, а также его цинк-ацетатного комплекса в смазочно-охлаждающих жидкостях (СОЖ), топливах и смазочных маслах.

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Gasimli G.R., Babayev E.R., Eyvazova I.M., İbrahimova T.M. et al. Investigation of the antimicrobial properties of N,N-bis(benzylidene)-o-phenylenediamine zinc acetate complex // Proceedings of the Republican Scientific and Practical Conference “Status and Development Prospects of Fundamental and Applied Microbiology: The Viewpoint of Young Scientists”. – Tashkent, 2026. – P. 62–65.
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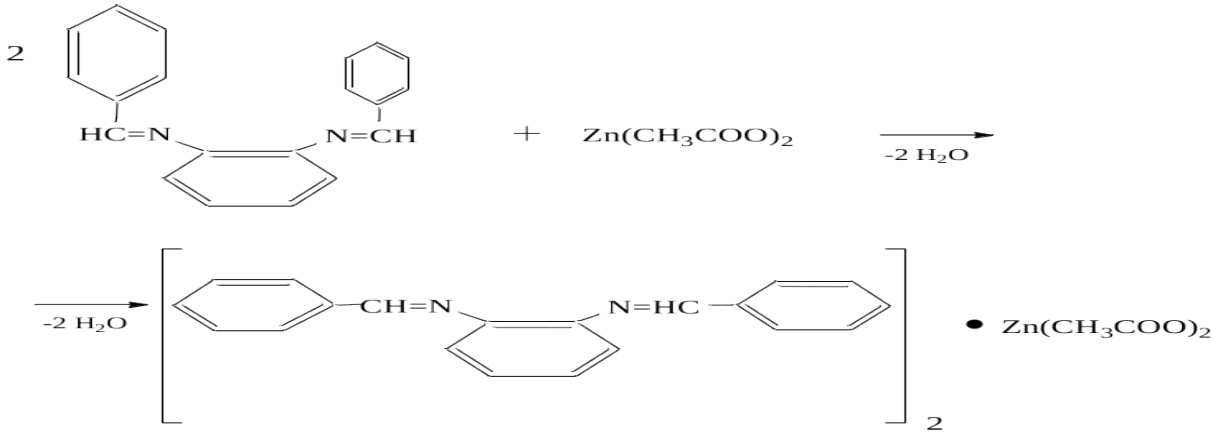
Структура синтезированных соединений подтверждена методом ИК-спектроскопии: полосы поглощения азометиновой группы (C=N) наблюдаются при частоте 1620 $см^{-1}$ для лиганда и 1663 $см^{-1}$ для цинк-ацетатного комплекса. Антимикробная и фунгицидная активность соединений определялась методом диффузии в лунки в соответствии со стандартами ГОСТ 9.052-88 и ГОСТ 9.023-74 в отношении бактерий Mycobacterium phlei, Pseudomonas aeruginosa и грибов Aspergillus niger, Cladosporium resinae. Исследования показали, что цинк-ацетатный комплекс при концентрации 0.5% проявляет высокую фунгицидную активность против гриба *Cladosporium resinae* в СОЖ и бензине (зоны угнетения составляют соответственно 2.2–2.2 см и 3.8–3.9 см).

Introduction

Recent studies indicate that transition metal complexes incorporating Schiff bases possess unique physicochemical properties with significant potential in pharmaceutical, biological, and industrial fields. Due to the presence of the azomethine group (–C=N–) alongside active heteroatoms (nitrogen, oxygen, sulfur), these compounds readily adsorb onto metal surfaces, forming protective films that provide high efficacy in protecting carbon steel from corrosion in aggressive environments. Furthermore, owing to the synergistic effect between metal ions (such as zinc) and organic ligands, these complexes display enhanced antimicrobial and fungicidal activities, making them effective biocide additives for industrial fluids and fuels.

Methods

The ligand N,N-Bis(benzylidene)-o-phenylenediamine was synthesized via the condensation of benzaldehyde and o-phenylenediamine in a 2:1 molar ratio. It represents a dark brown crystalline compound with a melting point of $T_{mp} = 90^0C$. The subsequent interaction of this Schiff base with zinc acetate salt yielded the corresponding zinc-acetate complex.



The antimicrobial and fungicidal performances were evaluated via the well-diffusion method in accordance with GOST 9.052-88 and GOST 9.023-74 standards.

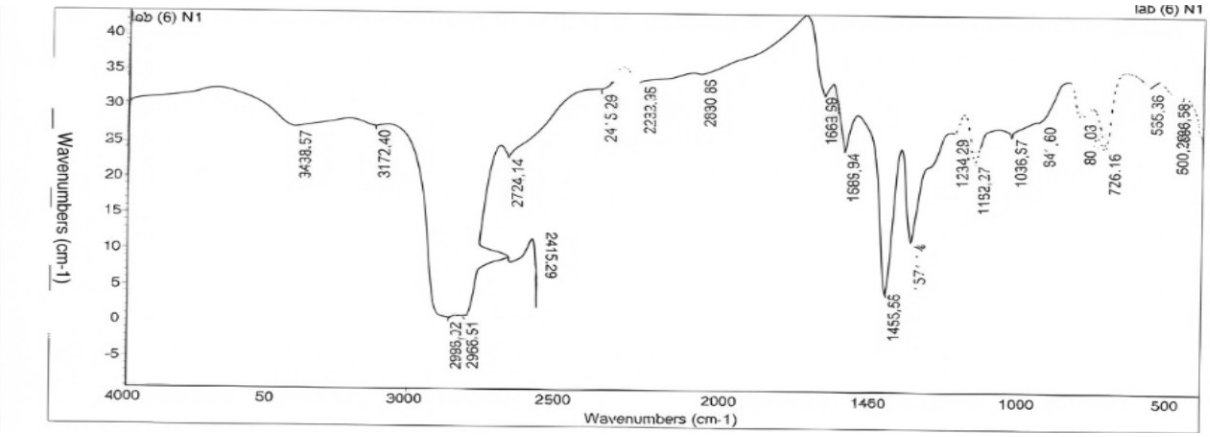


Figure 1. IR spectrum of the N,N-bis(benzylidene)-o-phenylenediamine zinc acetate complex

The intense absorption band observed at 1663.99cm $^{-1}$ corresponds to the stretching vibrations of the azomethine group C=N characteristic of the Schiff base. The shift in the frequency of this band compared to the initial ligand is one of the key indicators proving that the nitrogen atom is coordinated with the metal ion.

The antimicrobial properties of the synthesized compounds were evaluated using the well-diffusion method in accordance with GOST 9.052-88 and GOST 9.023-74 standards. The Schiff base derived from benzaldehyde and o-phenylenediamine yielded favorable results in lubricating-cooling fluids (LCFs**)** and fuel systems, specifically targeting *Cladosporium resinae*. Testing was conducted at a concentration of 0.5% in both media. The resulting derivative (at a 2:2 ratio) exhibited prominent fungicidal properties, displaying inhibition zones of 2.8–2.8 cm in lubricating-cooling fluids and 3.5–3.8 cm in fuel.

The antimicrobial performance of the evaluated organic compounds in fuel and lubricating-cooling fluids (LCFs) is summarized in Table 1:

Table 1. Antimicrobial activity of the studied compounds in lubricating-cooling fluids (LCFs) and fuel

№	compound	Diameter of the micro-organism destruction zone, cm					
		LCF			Fuel		
		Concentration%	Bacteria (*Mycobacterium phlei*, *Pseudomonas aeruginosa*)	Fungus (*Aspergillus niger*)	Concentration%	Bacteria (*Pseudomonas aeruginosa*)	Fungus (*Cladosporium resinae)*
1	Benzylidene-o-phenylenediamine zinc acetate complex salt	1,0	+++	2,2-2,2	0,5	2,3-2,4	3,8-3,9
2	Benzylidene-o-phenylenediamine	1,0	+++	2,0-2,0	0,5	2,3-2,4	2,4-2,4

The shift of the C=N absorption band in the IR spectra from 1620cm^{-1} (in the free ligand) to 1663 cm^{-1} (in the complex) explicitly confirms successful coordination between the nitrogen atom and the zinc center. Biological evaluations demonstrate that the 0.5% zinc-acetate complex exhibits remarkable fungicidal properties against *Cladosporium resinae*, particularly in fuel systems (showing

an inhibition zone of 3.8–3.9 cm). This enhanced efficacy stems from the synergistic interplay between the metal ion and the organic ligand. Additionally, the presence of active heteroatoms facilitates the formation of a protective adsorption layer on metal interfaces, efficiently lowering corrosion rates and sediment accumulation in MC-20 lubricating oil.

The N,N-Bis(benzylidene)-o-phenylenediamine ligand and its zinc-acetate complex were successfully synthesized and structurally validated via IR spectroscopy through characteristic azomethine C=N band shifts. Biological assays confirmed that the zinc-acetate complex serves as an exceptional antimicrobial and fungicidal biocide, showing high potency against *Cladosporium resinae*. The synthesized derivatives demonstrate strong anticorrosion and antioxidant performance in MC-20 lubricating oil by significantly mitigating metal corrosion and sediment creation.

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PIGMENT HOSIL QILUVCHI AKTINOMITSET SHTAMMLARINI TURLI USULLARDA SAQLASHDA HAYOTCHANLIK VA PIGMENT SINTEZLASH XUSUSIYATINING BARQARORLIGI

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Annotatsiya: Sanoat uchun muhim mikroorganizmlar kulturalari to‘plamida saqlanayotgan pigment hosil qiluvchi *Streptomyces iakyrus* ACT-P-20 va *Amycolatopsis lurida*-51 shtammlarining turli usullar (davriy qayta ekish, distillangan suv, vazelin moyi qatlami ostida, steril qum, steril tuproq, glitserin) da 1 yil davomida saqlangandagi hayotchanligi, pigment hosil qilish xususiyati o‘rganilgan.
Kalit so‘zlar: aktinomitsetlar, pigmentlar, *Streptomyces*, *Amycolatopsis*, saqlash usullari, hayotchanlik, liofilizatsiya.

Abstract: The viability, pigment-forming ability, and antagonistic activity of the pigment-producing actinomycetes *Streptomyces iakyrus* ACT-P-20 and *Amycolatopsis lurida*-51, held in the Collection of Industrially Important Microorganisms, were studied after 1 year of storage by different methods (distilled water, mineral oil overlay, sterile sand, sterile soil, glycerol).
Keywords: actinomycetes, pigments, *Streptomyces*, *Amycolatopsis*, preservation methods, viability.

Kirish

Sintetik bo‘yoqlarning inson salomatligi va atrof-muhitga salbiy ta’siri haqidagi ma’lumotlar ko‘payib borayotgani sababli oziq-ovqat, farmatsevtika, to‘qimachilik va kosmetika sohalarida tabiiy pigmentlarga bo‘lgan ehtiyoj ortib bormoqda [1]. Mikroorganizmlar, jumladan aktinomitsetlar bunday pigmentlarning istiqbolli manbai hisoblanadi: ular ikkilamchi metabolitlar, xususan, eruvchan va melanoid pigmentlar hamda antibiotik moddalar sintez qiladi [2,3,4,5].

Pigment hosil qiluvchi shtammlarning biotexnologik qiymati ularning pigment sintezlash xususiyati saqlanib qolishiga bog‘liq. Davriy qayta ekish usulida shtammning tez-tez bo‘linishi natijasida genetik o‘zgaruvchanlik, pigment hosil qilish xususiyatining pasayishi va ozuqa muhitining qurib qolishi mumkin, shu sababli kolleksiyalarda saqlashning muqobil usullarini qo‘llash va ularning samaradorligini taqqoslash muhim ahamiyatga ega [6,7,8].

Tadqiqot maqsadi – O‘zbekiston Respublikasi Fanlar akademiyasi Mikrobiologiya instituti kolleksiyasida saqlanayotgan pigment hosil qiluvchi *Streptomyces iakyrus* ACT-P-20 va *Amycolatopsis lurida*-51 shtammlarining morfologik-kultural xususiyatlarini, turli usullarda saqlashdagi hayotchanligi va pigment hosil qilish barqarorligini qiyosiy baholash.

Obyekt va usullar

Tadqiqot obyekti sifatida O‘zbekiston Respublikasi Fanlar akademiyasi Mikrobiologiya instituti sanoat uchun muhim mikroorganizmlar kulturalari kolleksiyasida 1 yil davomida turli usullarda saqlanayotgan *Streptomyces iakyrus* ACT-P-20 va *Amycolatopsis lurida*-51 shtammlari tanlandi.

IQTIBOS UCHUN
Bekmuxamedova N.K., Husanova S.M. Pigment hosil qiluvchi aktinomitset shtammlarini turli usullarda saqlashda hayotchanlik va pigment sintezlash xususiyatining barqarorligi // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 66–69.
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Aktinomitsetlarning kultural belgilari (havo va substrat mitseliysining rangi, eruvchan va melanoid pigmentlarning mavjudligi) Gauze usuli bo‘yicha Gauze, Chapek, glitserin-nitratli va saxaroza-nitratli agar, suli agari (OA), pepton-achitqili agar hamda sof agar muhitlarida 28°C da 7–14 kun davomida yorug‘likda Bondarsev ranglar shkalasi yordamida 7, 14 va 21-kunlarda baholandi [9,10]. Hujayralar morfologiyasi yorug‘lik mikroskopi ostida o‘rganildi.

Shtammlar davriy qayta ekish bilan birga vazelin moyi qatlami ostida, distillangan suvda, steril qumda, steril tuproqda, glitserinda (−20°C) saqlashga qo‘yilgan. Hayotchanlik ketma-ket suyultirish usuli bilan (10^1–10^4) har bir suyultirishdan 0,1 ml ozuqa muhiti yuzasiga ekib, 28°C da 7–14 kun inkubatsiya qilingandan so‘ng o‘sib chiqqan koloniyalarni sanash orqali aniqlandi va KHB/ml hisobida ifodalandi ($N = C \times 10^n/V$, bunda C — koloniyalarning o‘rtacha soni, 10^n — suyultirish darajasi, V — ekilgan hajm, ml). Hayotchanlik darajasi 2026-yil fevral oyida (2 yildan so‘ng) nazoratga nisbatan foizlarda baholandi.

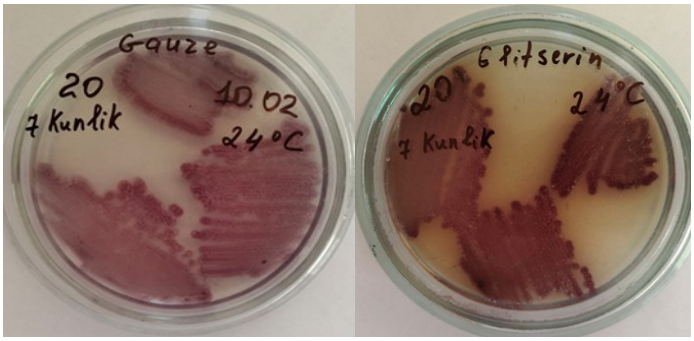
Natijalar va muhokama

Saqlashdan 1 yil o‘tgach shtammlar ozuqa muhitlariga ekilganda hayotchanligini va pigment hosil qilish xususiyatini saqlab qolganligi aniqlandi. *Streptomyces iakyrus* ACT-P-20 shtammi turli ozuqa muhitlarida qizildan to‘q qizilgacha bo‘lgan eruvchan pigmentlar hosil qildi (1-jadval).

1-jadval. *Streptomyces iakyrus* ACT-P-20 shtammining turli ozuqa muhitlarida pigment hosil qilishi

№	Ozuqa muhiti	Havo mitseliysi (HM)	Substrat mitseliysi (SM)
1	Gauze	qizil	to‘q qizg‘ish
2	Glitserin-nitratli agar	qizil	to‘q qizg‘ish
3	Chapek	to‘q pushti	och sariq
4	OA (suli agar)	to‘q pushti	to‘q qizg‘ish
5	Organik agar	to‘q kulrang	to‘q jigarrang

Shtammda spiral shakldagi spora tashuvchilar kuzatildi. Gauze va glitserin-nitratli agarda 20°C da to‘q qizil, 24°C da qizil yoki och pushti pigment hosil bo‘ldi.



1-rasm. Streptomyces iakyrus ACT-P-20 shtammining pigment hosil qilishi (20^0C va 24^0C)

Streptomyces iakyrus ACT-P-20 shtammining rivojlanishida ozuqa muhiti bilan birga harorat va yorug‘lik muhim ekanligi kuzatildi. Unga ko‘ra 20^0C haroratda, tashqi muhitda shtammning o‘sishi va pigment ajratishi kuzatildi. Shtammning jadal o‘sishi va o‘ziga xos ochdan to‘q qizg‘ishgacha pigment hosil qilishi kuzatildi (1-rasm). Nafaqat tashqi muhit sharoitida, balki termostatda 24^0C haroratda 7 kun davomida kuzatilganda ham o‘ziga xos och pushti pigment hosil qilganligini ko‘rish mumkin.

Amycolatopsis lurida-51 shtammi barcha o‘rganilgan ozuqa muhitlarida eruvchan pigmentlar hosil qildi (2-jadval). Saxaroza-nitratli suyuq muhitda tebranish rejimida (180 ayl/min) o‘stirilganda muhit to‘q binafsha (indigo) rangga bo‘yaldi. Temir sitrat saqlagan pepton-achitqili agarda 14 kunda qora melanoid pigment hosil bo‘lishi shtammning tirozinaza faolligidan dalolat

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beradi. Saxaroza-nitratli agarda 28°C da shtamm o‘sdi, ammo pigment hosil qilmadi, +4°C da saqlanganda esa pigment sekin-asta sintezlandi, bu pigment hosil qilishning haroratga bog‘liqligini ko‘rsatadi.

2-jadval. *Amycolatopsis lurida*-51 shtammining turli ozuqa muhitlarida pigment hosil qilishi

№	Ozuqa muhiti	Havo mitseliysi (HM)	Substrat mitseliysi (SM)
1	Saxaroza-nitratli agar	havorang	to‘q ko‘k
2	Saxaroza-nitratli suyuq muhit	to‘q binafsha	to‘q binafsha
3	Pepton-achitqili agar	to‘q jigarrang	Qora
4	OA (suli agar)	havorang	to‘q ko‘k
5	Gauze	havorang	ko‘k
6	Glitserin-nitratli agar	to‘q ko‘k	to‘q ko‘k

Saqlash usullarining samaradorligi 1 yildan so‘ng KHB/ml bo‘yicha baholandi. *S. iakyrus* ACT-P-20 va *A. lurida*-51 shtammlari uchun eng yuqori hayotchanlik distillangan suvda ($3{,}0\times10^5$: $3{,}0\times10^6$ KHB/ml) qayd etildi. Vazelin moyi qatlami ostida saqlashda shtammlar hayotchanlik ko‘rsatkichi faol namoyon bo‘lgan bo‘lsa-da, pigment hosil qilish xususiyati nisbatan past bo‘ldi ($3{,}0\times10^2$ va $5{,}0\times10^3$ KHB/ml). Steril tuproqda saqlash ikkala shtamm uchun eng past natijani berdi (10^2), pigmentatsiya esa saqlanib qoldi. Glitserinda (−20°C) saqlash ushbu shtammlar uchun kutilgan natijani bermadi.

Xulosa

Pigment hosil qiluvchi *Streptomyces iakyrus* ACT-P-20 va *Amycolatopsis lurida*-51 shtammlari 1 yil davomida turli usullarda saqlanganda asosiy morfofiziologik ko‘rsatkichlari va pigment hosil qilish xususiyatini saqlab qoldi. Hayotchanlik bo‘yicha distillangan suvda, steril qumda va vazelin moyi qatlami ostida saqlash, steril tuproqda saqlashga nisbatan samaraliroq bo‘ldi. Glitserin (−20°C) da saqlash aynan ushbu shtammlar uchun natija bermadi. Olingan shtammlar uzoq muddatli saqlash usullarini takomillashtirish va ular asosida biopreparatlar yaratish imkoniyatlarini baholash uchun qiziqish uyg‘otadi.

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TUZLI STRESS SHAROITIDA *STREPTOMYCES ROCHEI* N4 SHTAMMINING EKZOPOLISAXARID SINTEZI

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Annotatsiya: Antropogen ifloslanish va ikkilamchi sho‘rlanishga uchragan tuproqdan ajratilgan *Streptomyces rochei* N4 shtammining tuzli stress sharoitida ekzopolisaxaridlar (EPS) sintezi baholandi va natijalar xalqaro ilmiy adabiyotlar bilan solishtirildi. 300 mM NaCl saqlagan muhitda EPS miqdori nazoratga nisbatan 47% ga oshib, 21,6 ± 1,2 mg/ml ni tashkil etdi. Natijalar shtammdan sho‘rlangan tuproqlarda o‘simliklar chidamliligini qo‘llab-quvvatlovchi mikrobli inokulyantlar yaratishda foydalanish istiqbollarini o‘rganish uchun asos bo‘lib xizmat qiladi.

Kalit so‘zlar: *Streptomyces rochei*, ekzopolisaxarid, tuzli stress, NaCl, sho‘rlangan tuproq.

Tuproq sho‘rlanishi ekinlar o‘sishini cheklovchi muhim abiotik omil bo‘lib, yer degradatsiyasi va cho‘llanishni kuchaytiradi (Tarolli va boshqalar, 2024). Shu bois, sho‘rlanishga chidamli, o‘simlik o‘sishini rag‘batlantiruvchi mikroorganizmlar va ularning ekzopolisaxaridlar (EPS) sintez qilish mexanizmlarini o‘rganish ekologik biotexnologiyada muhim ahamiyatga ega.

Ekzopolisaxaridlar (EPS) mikroorganizmlar sintezlaydigan polimerlar bo‘lib, mikrob hujayralari va ularning atrof-muhit bilan o‘zaro ta’sirida muhim rol o‘ynaydi. Ular mikroorganizmlar hamda xo‘jayin o‘simliklarni qurg‘oqchilik, sho‘rlanish va og‘ir metallar ta’siri kabi abiotik stress omillaridan himoya qilishga yordam beradi (Joe va boshqalar, 2026). Tajriba ma’lumotlari ham shuni tasdiqlaydi: tuzga chidamli Halomonas variabilis va Planococcus rifietoensis shtammlarida sho‘rlanish oshgan sari biofilm hosil bo‘lishi va EPS to‘planishi kuchaygan, shtammlar bilan inokulyatsiya esa no‘xat o‘sishini yaxshilab, ildiz atrofida tuproq agregatlari hosil bo‘lishini rag‘batlantirgan (Qurashi & Sabri, 2012).

Aktinomitsetlar, jumladan, *Streptomyces* izolyatlarining sho‘rlanishga chidamliligi va o‘simlik o‘sishini rag‘batlantirish xususiyati aniqlangan. 300 mM NaCl sharoitida bir izolyatda IAA ishlab chiqarilishi 2,4 dan 4,7 µg/ml gacha oshgan va u bilan ishlov berish bug‘doy o‘sishini yaxshilagan (Sadeghi va boshqalar, 2011). Dengiz cho‘kindilaridan ajratilgan Streptomyces maritimus SST3 shtammi 800 mM NaCl sharoitida 5,73 mg/ml EPS sintez qilgan va pomidor o‘simligining sho‘rlanish stressiga chidamliligini oshirishga yordam bergan (Silambarasan va boshqalar, 2024). Shu bilan birga, sho‘rlangan tuproqlardan ajratilgan mikroorganizmlarda EPS sintezining nazorat va tuzli stress sharoitlarida o‘zgarishini shtamm darajasida miqdoriy baholashga oid ma’lumotlarni yanada kengaytirish zarurati mavjud.

Streptomyces shtammi glyukoza-achitqi ekstraktli agarda 28 °C da 5–7 kun o‘stirildi. EPS sintezi glyukoza (30 g/l), achitqi ekstrakti (5 g/l), $NaNO_3$ (3 g/l), $MgSO_4 \cdot 7H_2O$ (0,5 g/l), K_2HPO_4 (1 g/l) va $CaCO_3$ (1 g/l) saqlagan, pH 7,0 ga keltirilgan suyuq muhitda o‘rganildi. Nazorat va tajriba variantlariga mos ravishda NaCl qo‘shilmadi yoki 300 mM NaCl kiritildi. Kulturalar 28 °C da, 150 ayl/min tezlikda 4 kun inkubatsiya qilindi. Kultura suyuqligi sentrifugalangach, supernatantga uch hajm sovuq absolyut etanol qo‘shildi va 4 °C da bir sutka saqlandi. Hosil bo‘lgan EPS cho‘kmasi ajratilib, quritildi va uning miqdori quruq massa asosida aniqlandi. Natijalar nazorat varianti bilan taqqoslandi (Sardari va boshqalar, 2016).

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300 mM NaCl sharoitida S. rochei N4 shtammining EPS sintezi nazoratga nisbatan 46,9% ga oshib, 21,6 ± 1,2 mg/ml ni tashkil etdi (nazoratda 14,7 ± 1,0 mg/ml). Ushbu natija shtammning tuzli stress sharoitida EPS ishlab chiqarish salohiyati ortishini ko‘rsatadi. Mazkur o‘zgarish osmotik stressga moslashuv bilan bog‘liq bo‘lishi mumkin, biroq bu taxminni tasdiqlash uchun qo‘shimcha tadqiqotlar zarur.

Olingan natijalar *S. rochei* N4 shtammining tuzli stress sharoitida EPS sintez qilish salohiyatini ko‘rsatib, sho‘rlanishga chidamli mikroorganizmlar bo‘yicha adabiyotlarda keltirilgan ma’lumotlarga mos keladi. Ushbu shtammni sho‘rlangan tuproqlarda mikrobli inokulyant sifatida qo‘llash istiqbollarini baholash uchun uning o‘simlik o‘sishi va sho‘rlanishga chidamliligiga ta’sirini laboratoriya hamda vegetatsion tajribalarda tekshirish zarur.

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LONG-TERM PRESERVATION AND BIOLOGICAL PROPERTIES OF *BACILLUS THURINGIENSIS* STRAINS MAINTAINED IN A MICROORGANISM CULTURE COLLECTION

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Introduction

Spore-forming bacteria belonging to the genus *Bacillus* have been widely studied because of their physiological diversity, environmental adaptability, and broad biotechnological applications. Among them, *Bacillus thuringiensis* (Bt) is particularly important in sustainable agriculture as a biological control agent against insect pests and is also known for its antifungal and plant growth-promoting activities. During sporulation, Bt produces parasporal crystal proteins (Cry and Cyt toxins) that exhibit specific toxicity against target insect groups.

The long-term preservation of industrially and scientifically valuable bacterial strains while maintaining their phenotypic stability is a fundamental task of microbial culture collections. An effective preservation method should ensure high cell viability while retaining essential physiological and biological characteristics for future research and practical applications. However, prolonged storage may lead to physiological changes or reduced metabolic activity, depending on the preservation conditions and strain-specific characteristics. Therefore, evaluating the functional stability of long-term preserved strains is essential for selecting appropriate preservation methods. This study aimed to evaluate the viability, morphological stability, halotolerance, and antagonistic activity of *B. thuringiensis* strains maintained in a microbial culture collection for 15 years using different preservation methods.

Materials and Methods

Five *Bacillus thuringiensis* strains (Bt 62-5, Bt 70-5, Bt LM 18, Bt LM 24, and Bt LM 3) maintained in the Microorganism Culture Collection were examined after 15 years of storage using three preservation methods: lyophilization, mineral oil overlay, and storage in the dry spore state under ambient conditions. Strain viability (CFU/mL), cultural and morphological characteristics, halotolerance at NaCl concentrations ranging from 0 to 15%, and antagonistic activity against three phytopathogenic fungi (*Verticillium dahliae*, *Fusarium oxysporum*, and *Fusarium solani*) were evaluated.

Results and Discussion

The results demonstrated that the preservation method substantially influenced the viability of *B. thuringiensis* strains after 15 years of storage. Among the methods evaluated, lyophilization was the most effective in maintaining viability. Strain Bt 62-5 exhibited 98.0% viability, with a reported viable cell titre of 56×10^8, whereas strain Bt 70-5 retained 95.0% viability, with a viable cell titre of 49×10^8. These findings indicate that lyophilization effectively maintained the viability of the investigated strains over the extended storage period.

The strains preserved under mineral oil exhibited lower viability, at 88.0% and 72.6%, respectively. Their viable cell titres also decreased by approximately one to two orders of magnitude

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compared with the initial level of 10^9. The lowest viable counts were observed in strains stored as dry spores under ambient conditions, ranging from 22 to 75 × 10^5 CFU after 15 years. These differences highlight the importance of preservation conditions in maintaining the viability of spore-forming bacteria.

The cultural and morphological characteristics of the strains were generally retained during long-term storage. On meat-peptone agar, the investigated strains formed round, grey or white colonies with slightly wrinkled surfaces, approximately 2–3 mm in diameter. The cells were Gram-positive, while growth in liquid medium was characterized by sediment formation and the development of a surface pellicle. Sporulation and parasporal crystal formation on solid medium were observed within 3–5 days. However, strains preserved under mineral oil required two to three successive subcultures to restore their typical cellular morphology. This finding suggests that the recovery period following preservation may depend on the storage method.

Halotolerance varied among the investigated strains. At 10% NaCl, the highest optical density (OD) values were recorded for Bt 62-5 (0.98 ± 0.03) and Bt 70-5 (0.95 ± 0.07). At 15% NaCl, Bt 70-5 exhibited the highest OD (0.83 ± 0.05), whereas Bt LM 3 showed no detectable growth. The growth of Bt LM 18 and Bt LM 24 also decreased as salinity increased. These results indicate that Bt 70-5 exhibited the highest salt tolerance among the tested strains under the conditions examined.

After 15 years of storage, Bt 70-5 demonstrated the highest antagonistic activity against the tested phytopathogenic fungi, with inhibition zones ranging from 32 ± 0.4 to 35 ± 2.7 mm. For Bt 62-5, the inhibition zones ranged from 20 ± 1.2 to 30 ± 1.5 mm. Bt 70-5 inhibited the growth of *V. dahliae*, *F. oxysporum*, and *F. solani*, indicating that its antagonistic activity was retained after long-term preservation.

Conclusion

Lyophilization was the most effective method for maintaining the long-term viability and phenotypic stability of *B. thuringiensis* strains over a 15-year storage period. The retention of high halotolerance and antagonistic activity against phytopathogenic fungi highlights the biotechnological potential of strains Bt 70-5 and Bt 62-5 for agricultural biological control applications.

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ANTIMICROBIAL SCREENING AND MOLECULAR IDENTIFICATION OF ACTIVE ENDOPHYTIC BACTERIAL ISOLATES FROM *FERULA VARIA*

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Abstract: Endophytic bacteria from medicinal plants are a promising source of antimicrobial metabolites, and this study evaluated the endophytic isolates of Ferula varia (more than 40 isolates from roots, stems, leaves, and flowers) against Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa, Bacillus subtilis, and Candida albicans. Six isolates showed antimicrobial activity and were identified by 16S rRNA gene sequencing as Bacillus pumilus, B. atrophaeus, B. rugosus, and Serratia odorifera, with the sequences deposited in NCBI GenBank. Four of these isolates (FV1i, FV3i, FVP1.1, and FVB1) were active against all five test organisms, making them promising candidates for further study of their bioactive metabolites.

Keywords: *Ferula varia*, endophytic bacteria, antimicrobial activity, inhibition zone, 16S rRNA gene sequencing, molecular identification, antimicrobial metabolites.

Introduction

Endophytic bacteria are microorganisms that live within the internal tissues of plants, usually without causing disease symptoms in the host plant, and are regarded as a promising source of biologically active metabolites. Medicinal plants play an important role in studying the diversity of endophytic microorganisms and in the search for new antimicrobial agents. Studying the antimicrobial properties of endophytic bacteria associated with *Ferula varia* makes it possible to identify biotechnologically significant microorganisms. The aim of this study was to evaluate the antimicrobial activity of endophytic bacteria isolated from *F. varia* against selected bacterial and fungal test organisms and to identify the active isolates at the molecular level using 16S rRNA gene sequencing.

Materials and Methods

In the primary screening, more than 40 endophytic bacterial isolates obtained from the roots, stems, leaves, and flowers of *F. varia* were tested for antimicrobial activity against *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Bacillus subtilis*, and *Candida albicans*. Antimicrobial activity was determined by measuring the diameters of the growth inhibition zones of the test organisms. The active isolates were identified at the molecular level by 16S rRNA gene sequencing, and the resulting nucleotide sequences were analyzed to determine the taxonomic affiliation of the isolates.

Results and Discussion

Among the endophytic bacteria isolated from *F. varia*, isolates FV1i, FV3i, FV8i, FVP2, FVP1.1, and FVB1 exhibited antimicrobial activity against the test organisms (Table 1) and were selected for further studies.

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Table 1. Antimicrobial activity of the isolates (diameter of the growth inhibition zone)

Isolates	S. aureus (mm)	Ps. aeruginosa (mm)	B. subtilis (mm)	E. coli (mm)	C. albicans (mm)
FV1i	20	28	20	29	16
FV3i	21	29	26	33	16
FV8i	–	–	–	12	–
FVP2	–	–	12	18	–
FVP1.1	33	12	14	12	12
FVB1	27	14	18	28	14

The selected isolates were identified at the molecular level using the 16S rRNA gene marker. According to the identification results, five of the six selected isolates belonged to the genus *Bacillus* and one to the genus *Serratia*. The resulting nucleotide sequences were deposited in the NCBI GenBank database under the accession numbers listed in Table 2.

Table 2. Results of the molecular identification of the isolates based on the 16S rRNA gene

Isolated Strains Sequences Deposited in GenBank		Closest Match among Bacteria (16S rRNA Genes) (GenBank)		
Strains	**Accession Number**	**Species**	**Source**	**ID%**
FV1i	PZ582851	*Bacillus pumilus*	*F. varia*	100%
FV3i	PZ583085	*Bacillus atrophaeus*	*F. varia*	100%
FV8i	PZ583143	*Bacillus atrophaeus*	*F. varia*	99,86%
FVP2	PZ583123	*Bacillus rugosus*	*F. varia*	99,38%
FVP1.1	PZ054243	*Bacillus rugosus*	*F. varia*	99,86%
FVB1	PZ331847	*Serratia odorifera*	*F. varia*	99,93%

Conclusion

In this study, six active isolates of endophytic bacteria associated with *F. varia* were investigated with respect to their antimicrobial activity and molecular identification. The activity of the isolates against the test organisms *E. coli*, *S. aureus*, *P. aeruginosa*, *B. subtilis*, and *C. albicans* was evaluated, and 16S rRNA gene sequencing showed that five of them belonged to the genus Bacillus and one to the genus *Serratia*. These data provide a basis for the further characterization of these isolates, a more detailed investigation of their antimicrobial potential, and the identification of their biologically active metabolites.

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OLMA (MALUS DOMESTICA) FITOPATOGEN ZAMBURUG‘LARI VA ULARGA QARSHI ANTAGONIST MIKROORGANIZMLARNI TANLASH

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Annotatsiya: Ushbu tezisda olma (Malus domestica) o‘simligida uchraydigan asosiy fitopatogen zamburug‘lar va ularning tarqalish xususiyatlari yoritilgan. Shuningdek, ularga qarshi antagonist mikroorganizmlarni tanlash va biologik kurash usullarining istiqbollari ko‘rib chiqilgan. Tadqiqot natijalari fitopatogenlar zararlanish darajasi va biologik nazoratning samaradorligini ko‘rsatadi. Ekologik xavfsiz himoya usullarini joriy etishning ahamiyati asoslab berilgan.

Kalit so‘zlar: Malus domestica, fitopatogen zamburug‘lar, Venturia inaequalis, Penicillium expansum, Alternaria alternata, Monilinia spp., biologik nazorat, antagonist mikroorganizmlar, Trichoderma, Bacillus.

Kirish

Olma daraxti (Malus domestica) dunyo qishloq xo‘jaligida muhim meva ekinlaridan biri bo‘lib, oziq-ovqat xavfsizligi va eksport salohiyatini oshirishda katta ahamiyatga ega. Biroq, olma bog‘larida turli fitopatogen zamburug‘lar tomonidan chaqiriladigan kasalliklar hosildorlikning keskin pasayishiga olib keladi. Venturia inaequalis, Podosphaera leucotricha va Penicillium expansum kabi patogenlar barg, meva va saqlash davridagi to‘qimalarni zararlab, katta iqtisodiy yo‘qotishlarga sabab bo‘ladi.

Kimyoviy fungitsidlarning keng qo‘llanilishi ekologik muammolarni keltirib chiqarmoqda. Shu sababli biologik kurash usullarini ishlab chiqish, ayniqsa antagonist mikroorganizmlardan foydalanish dolzarb yo‘nalish hisoblanadi.

Shu nuqtai nazardan, fitopatogen zamburug‘larga qarshi biologik kurash vositalarini izlash va ularning samaradorligini baholash zamonaviy fitopatologiyaning ustuvor yo‘nalishlaridan biri hisoblanadi. Antagonist mikroorganizmlar fitopatogenlarning o‘sishi va rivojlanishini tabiiy yo‘l bilan cheklab, o‘simliklarning kasalliklarga chidamliligini oshiradi. Ayniqsa, Trichoderma, Bacillus va Pseudomonas turkumlariga mansub mikroorganizmlar o‘zining yuqori antagonistik faolligi bilan ajralib turadi. Ular fitopatogenlarga qarshi antibiotik moddalar ishlab chiqarishi, oziqa muhiti uchun raqobatlashishi hamda parazitizm xususiyatlarini namoyon qilishi bilan muhim ahamiyatga ega. Bugungi kunda ekologik toza mahsulot yetishtirish va kimyoviy preparatlardan foydalanishni kamaytirish qishloq xo‘jaligining asosiy vazifalaridan biri hisoblanadi. Shu sababli olma daraxtlarida uchraydigan fitopatogenlarni aniqlash va ularga qarshi samarali antagonist mikroorganizmlarni tanlash ilmiy hamda amaliy jihatdan katta ahamiyat kasb etadi. Olingan natijalar kelgusida mahalliy sharoitga mos biologik preparatlar yaratish uchun ilmiy asos bo‘lib xizmat qiladi.

Tadqiqot metodlari

Fitopatogen zamburug‘larni ajratib olish va identifikatsiya qilishda klassik mikologik usullardan foydalanildi. Zamburug‘larning morfologik va kultural xususiyatlari bo‘yicha aniqlash ishlari Barnett H.L. va Hunter B.B. tomonidan tavsiya etilgan mikologik aniqlagichlar asosida amalga

IQTIBOS UCHUN
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oshirildi. Mikroskopik belgilari va koloniya xususiyatlarini baholashda Watanabe T. metodikasidan foydalanildi. Fitopatogenlarning patogenligini aniqlashda Robert Koch tomonidan ishlab chiqilgan Kox postulatlari asosida infeksiyalash tajribalari o‘tkazildi. Antagonist mikroorganizmlarning fitopatogenlarga qarshi faolligini baholashda ikkilamchi ekish (dual culture) usuli qo‘llanildi. Ushbu usul Dennis C. va Webster J. tomonidan tavsiya etilgan metodika asosida amalga oshirildi.

Tajriba natijalarini statistik qayta ishlashda R.A. Fisher tomonidan ishlab chiqilgan dispersion tahlil (ANOVA) usullaridan foydalanildi.

Tadqiqot davomida kasallangan olma daraxtlaridan fitopatogen zamburug‘lar ajratib olindi. Ularning morfologik va kultural xususiyatlari mikroskopik tahlil orqali o‘rganildi. Fitopatogenlarning patogenlik darajasi laboratoriya sharoitida aniqlandi.

Antagonist mikroorganizmlar sifatida Trichoderma spp., Bacillus spp. va boshqa foydali bakteriyalar ajratib olinib, dual culture metodi orqali ularning fitopatogenlarga qarshi antagonistik faolligi baholandi. Statistik tahlil asosida zararlanish va inhibisiya darajalari hisoblandi.

Olingan natijalar va ularning tahlili

Tadqiqot natijalariga ko‘ra, olma bog‘larida eng keng tarqalgan fitopatogenlar Venturia inaequalis (60–85%), Penicillium expansum (40–70%), Alternaria alternata (35–65%), Botrytis cinerea (30–60%) va Monilinia spp. (25–50%) ekanligi aniqlandi.

Zararlanish darajasi bo‘yicha eng yuqori ko‘rsatkich Penicillium expansumga tegishli bo‘lib (50–80%), u saqlash davrida mevalarning to‘liq chirishiga sabab bo‘ladi. Venturia inaequalis esa barg va mevalarda qora qo‘tir kasalligini keltirib chiqarib, hosildorlikka sezilarli zarar yetkazadi.

Antagonist mikroorganizmlar orasida Trichoderma spp. va Bacillus spp. yuqori inhibisiya faolligini ko‘rsatib, fitopatogenlarning o‘sishini 60–85% gacha kamaytirishi aniqlandi. Bu ularning biologik nazorat vositasi sifatida yuqori istiqbolga ega ekanligini ko‘rsatadi.

Tadqiqotlar davomida ajratib olingan fitopatogen zamburug‘larning morfologik va kultural xususiyatlari ham o‘rganildi. Venturia inaequalis koloniyalari zaytun-yashil rangda bo‘lib, sekin o‘sishi bilan ajralib turdi. Alternaria alternata esa to‘q rangli mitseliy hosil qilib, tez o‘sish xususiyatini namoyon etdi. Laboratoriya sharoitida o‘tkazilgan ikkilamchi kultura (dual culture) tajribalarida Trichoderma spp. fitopatogen koloniyalarining o‘sishini faol ravishda cheklashi kuzatildi. Bacillus spp. shtammlari esa antibiotiksimon moddalar ishlab chiqarishi hisobiga patogenlarning rivojlanishini susaytirdi. Antagonist mikroorganizmlar ta’sirida patogenlarning mitseliy o‘sishi va spora hosil qilish qobiliyati sezilarli darajada kamaydi. Olingan natijalar biologik agentlarning nafaqat fitopatogenlarni bostirishda, balki o‘simliklarning tabiiy himoya mexanizmlarini faollashtirishda ham muhim ahamiyatga ega ekanligini ko‘rsatdi. Bu esa kelgusida mahalliy shtammlar asosida ekologik xavfsiz biopreparatlar yaratish va ularni olma bog‘larida amaliyotga joriy etish imkoniyatini kengaytiradi. Biologik kurash usullarini qo‘llash kimyoviy fungitsidlarga bo‘lgan ehtiyojni kamaytirishga hamda atrof-muhit barqarorligini saqlashga xizmat qiladi.

Xulosa

Olma o‘simligida uchraydigan fitopatogen zamburug‘lar hosildorlik va meva sifatiga jiddiy zarar yetkazadi. Kimyoviy usullar ekologik muammolarni keltirib chiqarganligi sababli biologik kurash usullariga ehtiyoj ortib bormoqda. Tadqiqot natijalari antagonist mikroorganizmlar, xususan Trichoderma va Bacillus turlari fitopatogen zamburug‘larni samarali bostirishini ko‘rsatdi. Bu esa ekologik xavfsiz, barqaror va samarali himoya tizimini yaratishda muhim ilmiy asos bo‘lib xizmat qiladi.

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ANTIFUNGAL ACTIVITY OF VOLATILE ORGANIC COMPOUNDS FROM SOIL-DERIVED ACTINOMYCETE ISOLATES AGAINST *FUSARIUM OXYSPORUM* AND *RHIZOCTONIA SOLANI*

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Introduction

Phytopathogenic fungi, in particular the wilt and root rot diseases caused by representatives of the genera *Fusarium* and *Rhizoctonia*, are inflicting substantial economic damage on agricultural crops worldwide. Since the use of chemical fungicides against these pathogens gives rise to environmental problems and leads to the development of resistance in the pathogens, interest in developing biological control agents based on soil microorganisms, and in particular on actinomycetes (especially members of the genus *Streptomyces*), has been growing in recent years.

Actinomycetes are known as a rich source of secondary metabolites, among which volatile organic compounds (VOCs) are of particular importance. Certain VOCs produced by actinomycetes possess the ability to inhibit the mycelial growth and development of phytopathogenic fungi.

The aim of the study was to evaluate the antifungal activity of volatile organic compounds produced by soil-derived actinomycete isolates against *Fusarium oxysporum* and *Rhizoctonia solani*.

Materials and methods

For this study, four isolates that had exhibited the highest activity — *Streptomyces* sp. 2/1, *Streptomyces* sp. 3, *Streptomyces* sp. 7 and *Streptomyces* sp. S4 — were selected from among soil actinomycetes whose antagonistic properties towards phytopathogenic fungi had been assessed in earlier experiments. In the experiments carried out for this selection, the actinomycete isolates were streaked onto the nutrient medium and agar–mycelium blocks of the phytopathogenic fungi were placed opposite them, and antagonistic activity was assessed on the basis of the degree of inhibition of the pathogens' mycelial growth. The strains *Fusarium oxysporum* 21 and *Rhizoctonia solani* 38, isolated in our previous study from diseased potato tubers during the storage period, were used as test pathogens.

The antifungal activity of the volatile organic compounds (VOCs) of the actinomycete isolates was evaluated by the double dish (sealed plate) method. Potato dextrose agar (PDA) medium was poured into both Petri dishes. An agar–mycelium disc 5 mm in diameter, taken from an actively growing culture of the pathogen, was placed in the centre of one dish, while the actinomycete isolate was streaked onto the second dish. The lids were then removed and the bases of the dishes were placed face to face and sealed tightly with parafilm, yet without coming into direct contact with each other. The paired dishes were incubated at 25 °C for 7 days. In the control variant, the dish inoculated with the pathogen was paired with a dish containing only sterile PDA medium, without any actinomycete.

Inoculation of the actinomycete was performed according to two schemes: (1) simultaneous inoculation — the actinomycete and the pathogen were inoculated at the same time and the dishes

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were paired immediately (isolate *Streptomyces* sp. 3 was tested under this scheme); (2) pre-incubation — the actinomycete was first grown separately for 2 days and then paired with a freshly inoculated pathogen dish (isolates *Streptomyces* sp. 2/1, S4 and 7 were tested under this scheme). Isolate *Streptomyces* sp. 2/1 was additionally tested under the simultaneous inoculation scheme as well; in this case the growth of strain *R. solani* 38 was measured on day 3 (when the control had reached 35 mm).

After 7 days of incubation (on day 3 for the simultaneous variant of *Streptomyces* sp. 2/1), the diameter of the pathogen colony was measured and compared with that of the control variant. The degree of inhibition of mycelial growth was calculated using the following formula:

$$Inhibition\ (\%) = [(Dc - Dt) / Dc] \times 100$$

where: Dc — diameter of the pathogen in the control dish (mm); Dt — diameter of the pathogen in the experimental dish (mm).

Results

After seven days of incubation, the colony diameter of strain *F. oxysporum* 21 in the control variant was 35 mm. Under the influence of isolate *Streptomyces* sp. 7, the pathogen colony diameter decreased to 20 mm, and 42.86% inhibition was recorded. Under the influence of isolates *Streptomyces* sp. 3 and 2/1, the colony diameter was 25 mm, and 28.57% antifungal activity was observed for both isolates. Under the influence of isolate *Streptomyces* sp. S4, however, no inhibition of the growth of strain *F. oxysporum* 21 was observed.

In the experiment conducted with strain *R. solani* 38, the diameter of the control colony was 45 mm. Under the influence of *Streptomyces* sp. 3, the colony diameter decreased to 35 mm and 22.22% inhibition was determined. Under the influence of isolates *Streptomyces* sp. 2/1 and *Streptomyces* sp. 7, which had been pre-grown for two days, the colony diameter of strain *R. solani* 38 was 40 mm, and 11.11% inhibition was recorded. In the case of isolate *Streptomyces* sp. S4, the growth of the pathogen colony did not differ from the control and no antifungal activity was observed.

The activity of isolate *Streptomyces* sp. 2/1 against *R. solani* 38 was also evaluated under conditions of simultaneous inoculation. While on day 3 of the experiment the pathogen colony diameter in the control variant had reached 35 mm, under the influence of the VOCs of isolate *Streptomyces* sp. 2/1 its diameter was 15 mm, and 57.14% inhibition was recorded.

Conclusion

The results obtained showed that the volatile organic compounds produced by soil-derived actinomycete isolates possess the ability to inhibit the mycelial growth of strains *F. oxysporum* 21 and *R. solani* 38 under non-contact conditions. The highest activity against *F. oxysporum* 21 was exhibited by isolate *Streptomyces* sp. 7 (42.86%), and against *R. solani* 38 by isolate *Streptomyces* sp. 2/1 under simultaneous inoculation (57.14%). The results demonstrate that the VOC-mediated antifungal effect differs depending on the actinomycete isolate, the phytopathogen species and the inoculation conditions.

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ФИТОХИМИЧЕСКИЙ АНАЛИЗ БИОЛОГИЧЕСКИ АКТИВНЫХ СОЕДИНЕНИЙ ЭНДОФИТНЫХ ГРИБОВ

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Аннотация: Эндофитные грибы являются перспективным источником биологически активных вторичных метаболитов, обладающих различными фармакологическими свойствами. Особый интерес представляют соединения, способные ингибировать панкреатическую липазу — ключевой фермент пищеварения, участвующий в расщеплении жиров. Целью исследования является изучение качественных характеристик эндофитных грибов, выделенных из лекарственных растений, и оценка их метаболического потенциала для выявления перспективных продуцентов ингибиторов панкреатической липазы. Полученные результаты могут послужить основой для дальнейшего поиска биологически активных соединений с потенциальным гиполипидемическим действием.

Ключевые слова: эндофитные грибы, лекарственные растения, вторичные метаболиты, панкреатическая липаза, ингибиторы ферментов, гиполипидемическая активность.

Annotatsiya: Endofit zamburug‘lar turli farmakologik xususiyatlarga ega bo‘lgan biologik faol ikkilamchi metabolitlarning istiqbolli manbai hisoblanadi. Ayniqsa, yog‘larning parchalanishida ishtirok etuvchi muhim hazm fermenti — pankreatik lipazani ingibirlash xususiyatiga ega birikmalar alohida ilmiy qiziqish uyg‘otadi. Tadqiqotning maqsadi dorivor o‘simliklardan ajratib olingan endofit zamburug‘larning sifat ko‘rsatkichlarini o‘rganish hamda pankreatik lipaza ingibitorlarini ishlab chiqaruvchi istiqbolli shtammlarni aniqlash uchun ularning metabolik salohiyatini baholashdan iborat. Olingan natijalar kelgusida potensial gipolipidemik faollikka ega biologik faol birikmalarni izlab topish uchun asos bo‘lib xizmat qilishi mumkin.

Kalit so‘zlar: endofit zamburug‘lar, dorivor o‘simliklar, ikkilamchi metabolitlar, pankreatik lipaza, ferment ingibitorlari, gipolipidemik faollik.

Abstract: Endophytic fungi are a promising source of biologically active secondary metabolites with diverse pharmacological properties. Compounds capable of inhibiting pancreatic lipase, a key digestive enzyme involved in fat hydrolysis, are of particular scientific interest. This study aims to investigate the qualitative characteristics of endophytic fungi isolated from medicinal plants and to assess their metabolic potential for identifying promising producers of pancreatic lipase inhibitors. The findings may provide a basis for further screening of biologically active compounds with potential hypolipidemic activity.

Keywords: endophytic fungi, medicinal plants, secondary metabolites, pancreatic lipase, enzyme inhibitors, hypolipidemic activity.

Введение

Ожирение и связанные с ним метаболические нарушения, включая сахарный диабет 2-го типа и сердечно-сосудистые заболевания, являются актуальной проблемой современного здравоохранения. Одним из подходов к их коррекции является ингибирование панкреатической липазы — фермента, участвующего в гидролизе пищевых жиров. Однако

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побочные эффекты существующих ингибиторов обусловливают необходимость поиска альтернативных природных соединений [1, 2].

Перспективным источником таких соединений являются эндофитные грибы, обитающие во внутренних тканях растений и продуцирующие разнообразные вторичные метаболиты, включая алкалоиды, флавоноиды, терпеноиды и фенольные соединения. Некоторые из этих метаболитов обладают биологической активностью, в том числе способностью ингибировать панкреатическую липазу [3, 4].

Качественный анализ эндофитных грибов позволяет оценить их метаболический потенциал и отобрать перспективные штаммы для дальнейших биохимических и фармакологических исследований. В связи с этим изучение липазоингибирующей активности вторичных метаболитов эндофитных грибов, выделенных из лекарственных растений, представляет интерес для поиска новых природных соединений с потенциальной гиполипидемической активностью.

Материалы и методы

Определение качественного состава экстрактов вторичных метаболитов эндофитных грибов. Фитохимический состав экстрактов определяли по методике Prabhavathi R.M. и соавт. [5]. Таннины и фенольные соединения выявляли с помощью 10% $FeCl_3$ по изменению окраски. Терпеноиды определяли реакцией экстракта с хлороформом и концентрированной H_2SO_4. Гликозиды выявляли с использованием ледяной уксусной кислоты, $FeCl_3$ и концентрированной H_2SO_4. Алкалоиды определяли реактивом Вагнера по образованию бурого осадка. Наличие флавоноидов устанавливали по появлению интенсивно-жёлтой окраски после добавления 20% NaOH и её исчезновению после подкисления 70% HCl. Белки и пептидные соединения выявляли биуретовой реакцией с 40% NaOH и 1% $CuSO_4$ по появлению фиолетовой окраски.

Результаты и их обсуждение

В ходе проведённого исследования была оценена ингибиторная активность изолятов эндофитных грибов в отношении панкреатической липазы, а также выполнен качественный анализ их вторичных метаболитов. По результатам скрининга были отобраны пять штаммов Тысячелистник желтый (Achillea tomentosa) AT8S, Алоэ (*Aloe vera)* AV7R, Одуванчик *(Taraxacum officinale)* TO12L, *Allium longicuspis* AL135L и Гинкго билоба (Ginkgo *biloba)* GB7S, продемонстрировавшие выраженную липазоингибирующую активность.

С целью установления возможной взаимосвязи между выявленной биологической активностью и химическим составом продуцируемых соединений проведён качественный фитохимический анализ исследуемых изолятов.

Анализ результатов качественного фитохимического исследования показал, что все изученные изоляты эндофитных грибов характеризуются наличием терпеноидов, фенольных соединений (включая танины), а также сердечных гликозидов. Данные группы метаболитов потенциально могут быть связаны с выявленной липазоингибирующей активностью исследуемых штаммов.

Пептидные соединения были обнаружены только у штаммов AV7R и AL135L, что указывает на определённые различия в их метаболическом профиле. В то же время сапонины, алкалоиды, флавоноиды и антрахиноны в исследованных образцах выявлены не были.

Следует отметить, что в рамках данного исследования был проведён именно качественный анализ, позволяющий установить факт наличия или отсутствия определённых классов соединений, без оценки их количественного содержания. Тем не менее, полученные данные свидетельствуют о сходстве метаболического профиля исследуемых штаммов и подтверждают их потенциал как источников биологически активных вторичных метаболитов.

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Таким образом, выявленные особенности химического состава создают основу для дальнейших исследований, направленных на выделение, идентификацию и количественную оценку отдельных соединений, а также изучение механизмов их биологического действия.

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MIKROBIOLOGIYA FANINING SHAKLLANISHI, UNING AMALIY AHAMIYATI VA TARIXIY RIVOJLANISH BOSQICHLARI

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Annotatsiya: Ushbu tezisda mikrobiologiya fanining shakllanishi, tarixiy rivojlanish bosqichlari va amaliy ahamiyati adabiyotlar tahlili asosida yoritilgan. Mikroorganizmlarning biologik xilma-xilligi, tabiatdagi moddalar aylanishidagi ishtiroki hamda tibbiyot, qishloq xo‘jaligi va sanoatdagi ahamiyati umumlashtirilgan. Antoni van Levenguk, Lui Paster va Robert Koxning ilmiy ishlari mikrobiologiyaning kuzatuvga asoslangan bilimlardan eksperimental fan darajasiga ko‘tarilishidagi muhim omillar sifatida tavsiflangan. Fan taraqqiyoti empirik, mikroskopik, eksperimental hamda molekulyar-biotexnologik bosqichlar orqali tizimlashtirilgan. Mikrobiologiyaning rivojlanishi tadqiqot usullarining takomillashuvi va amaliy ehtiyojlar bilan uzviy bog‘liqligi asoslangan.

Kalit so‘zlar: mikrobiologiya, mikroorganizmlar, mikroskopiya, sof kultura, bijg‘ish, pasterizatsiya, mineralizatsiya, biotexnologiya.

Аннотация: В данной тезисной работе на основе анализа литературы освещены формирование, исторические этапы развития и практическое значение микробиологии. Обобщены биологическое разнообразие микроорганизмов, их участие в круговороте веществ в природе, а также их значение в медицине, сельском хозяйстве и промышленности. Научные труды Антони ван Левенгука, Луи Пастера и Роберта Коха охарактеризованы как ключевые факторы трансформации микробиологии из науки, основанной на наблюдениях, в экспериментальную дисциплину. Прогресс науки систематизирован по эмпирическому, микроскопическому, экспериментальному и молекулярно-биотехнологическому этапам. Обоснована неразрывная связь развития микробиологии с совершенствованием методов исследований и практическими потребностями.

Ключевые слова: микробиология, микроорганизмы, микроскопия, чистая культура, брожение, пастеризация, минерализация, биотехнология.

Abstract: Based on a literature review, this paper highlights the establishment, historical stages of development, and practical significance of microbiology. The biological diversity of microorganisms, their participation in global nutrient cycles, and their importance in medicine, agriculture, and industry are summarized. The scientific works of Antonie van Leeuwenhoek, Louis Pasteur, and Robert Koch are characterized as crucial factors in elevating microbiology from an observational discipline into an experimental science. The development of the discipline is systematized into empirical, microscopic, experimental, and molecular-biotechnology stages. It is demonstrated that the advancement of microbiology is intrinsically linked to the refinement of research methods and practical demands.

Keywords: microbiology, microorganisms, microscopy, pure culture, fermentation, pasteurization, mineralization, biotechnology.

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Kirish

Mikrobiologiya mikroorganizmlarning morfologik, fiziologik, genetik va metabolik xususiyatlarini, ularning tarqalishi hamda boshqa organizmlar bilan o‘zaro munosabatlarini o‘rganuvchi fundamental va amaliy fan hisoblanadi. Uning tadqiqot obyektlariga bakteriyalar, arxeyalar, zamburug‘lar va bir hujayrali eukariotlar kiradi. Hujayrasiz tuzilishga ega bo‘lgan viruslar ham mikrobiologiya doirasida o‘rganiladi [1].

Mikrobiologik bilimlarning shakllanishi insoniyatning oziq-ovqat tayyorlash, mahsulotlarni saqlash va kasalliklarning oldini olishga bo‘lgan ehtiyojlari bilan bog‘liq. Dastlab tajribaga asoslangan usullarning biologik mohiyati noma’lum bo‘lgan. Mikroskopik kuzatishlar va nazoratli tajribalar rivojlanishi natijasida mikroorganizmlarning mavjudligi, ularning bijg‘ish, parchalanish va ayrim kasalliklardagi roli ilmiy asosda tushuntirildi [1, 2].

Mavzuning dolzarbligi mikrobiologiyaning tarixiy yutuqlari zamonaviy biologiya, ishlab chiqarish va ekologik tadqiqotlarning metodologik asoslarini tashkil etishi bilan belgilanadi. Mikroorganizmlarning xususiyatlarini tushunish ularning foydali imkoniyatlaridan foydalanish va zararli ta’sirlarini cheklash uchun zarur.

Ishning maqsadi mikrobiologiya fanining shakllanishini tarixiy ketma-ketlikda tahlil qilish, rivojlanish bosqichlarini tizimlashtirish va amaliy ahamiyatini umumlashtirishdan iborat.

Metodlar

Ushbu maqola adabiyotlar sharhi shaklida tayyorlandi. Tahlilda 2000-yildan keyin nashr etilgan mikrobiologiya va oziq-ovqat texnologiyasiga oid manbalar, mikroorganizmlarning ekologik ahamiyatini yorituvchi ilmiy maqola hamda Institut Pasteurning tarixiy materiallaridan foydalanildi.

Manbalar mavzuga aloqadorligi, bibliografik ma’lumotlarining tekshirilishi va mikrobiologiya taraqqiyotini tushuntirishdagi ahamiyatiga ko‘ra tanlandi. Tarixiy-xronologik usul orqali asosiy kashfiyotlarning ketma-ketligi ko‘rib chiqildi. Qiyosiy tahlil yordamida turli davrlardagi tadqiqot yondashuvlari solishtirildi, umumlashtirish orqali fanning amaliy yo‘nalishlari ajratildi.

Davrlashtirish mezonlari sifatida ustuvor tadqiqot usullari, ilmiy tushunchalarning rivojlanishi va amaliy qo‘llanish imkoniyatlarining kengayishi olindi.

Natijalar

Tahlil mikrobiologiya fanining rivojlanishini o‘zaro bog‘liq to‘rtta bosqich orqali yoritish imkonini berdi. Ushbu davrlashtirish mazkur sharhning tahliliy tuzilmasi bo‘lib, bosqichlar chegarasi shartli hisoblanadi.

Empirik bosqich. Mikroorganizmlar kashf etilishidan avval insonlar non tayyorlash, mahsulotlarni bijg‘itish va saqlash amaliyotlaridan foydalangan. Bu jarayonlarning sababini tushuntiruvchi ilmiy bilimlar mavjud bo‘lmasa-da, to‘plangan tajriba keyingi mikrobiologik tadqiqotlar uchun zamin yaratgan. Mazkur bosqichda jarayonlarning natijalari kuzatilgan, biroq ularni yuzaga keltiruvchi biologik sabablar aniqlanmagan [1].

Mikroskopik bosqich. XVII asrda optik asboblarning takomillashuvi mikroskopik organizmlarni bevosita kuzatish imkonini yaratdi. Antoni van Levengukning kuzatishlari mikroorganizmlar mavjudligini ko‘rsatishda muhim ahamiyat kasb etdi. Ushbu davrda tadqiqotlar asosan mikroblarning shakli, harakati va tashqi belgilarini tavsiflashga yo‘naltirilgan edi [1].

Eksperimental bosqich. XIX asrning ikkinchi yarmida mikroorganizmlarning faoliyatini nazoratli tajribalar orqali o‘rganish kuchaydi. Lui Paster bijg‘ish jarayonlarining mikroorganizmlar faoliyatiga bog‘liqligini ko‘rsatdi. Uning oziqli muhitlar bilan o‘tkazgan tajribalari odatiy sharoitda mikroorganizmlar jonsiz muhitdan o‘z-o‘zidan paydo bo‘ladi degan qarashni rad etdi [2]. Ushbu xulosani Yerda hayotning dastlabki kelib chiqishi haqidagi barcha gipotezalarning inkori sifatida talqin qilish mumkin emas.

Paster tadqiqotlari oziq-ovqat mahsulotlariga issiqlik bilan ishlov berishni ilmiy asoslashga xizmat qildi. Pasterizatsiya mahsulot turiga mos harorat va vaqt rejimi orqali patogen hamda mahsulotni buzuvchi mikroorganizmlar miqdorini kamaytiradi. U to‘liq sterilizatsiyadan farq qiladi.

Shuningdek, ayrim mahsulotlar ishlovdan keyin ham tegishli saqlash sharoitini talab etadi [2, 3]. Paster va hamkorlarining quturishga qarshi emlash ishlari immunoprofilaktikaning rivojlanishiga ham muhim hissa qo‘shdi [2].

Robert Kox va uning ilmiy maktabi mikroorganizmlarni o‘stirish, sof kulturani ajratish va muayyan qo‘zg‘atuvchi bilan kasallik o‘rtasidagi sababiy bog‘liqlikni tekshirish yondashuvlarini rivojlantirdi. Natijada mikroblarni tavsiflash bilan birga ularning biologik rolini tajribada asoslash imkoniyati kengaydi [1].

Molekulyar va biotexnologik bosqich. XX asrda mikroorganizmlarning genetik va biokimyoviy xususiyatlarini o‘rganish fan taraqqiyotining muhim yo‘nalishiga aylandi. Keyinchalik molekulyar usullar mikroorganizmlarni aniqlash, ularning irsiy farqlarini baholash va metabolik jarayonlarini tushuntirish imkoniyatlarini kengaytirdi. Zamonaviy mikrobiologiyada mikrobiomni o‘rganish organizm va uning mikrob hamjamiyati o‘rtasidagi munosabatlarga e’tiborni kuchaytirdi [1, 4].

Tahlilda mikrobiologik obyektlarning tuzilishi va funksiyalarini farqlash zarurligi ham aniqlandi. Bakteriyalar va arxeyalar prokariot organizmlar hisoblanadi. Ko‘pchilik bakteriyalarning hujayra devorida peptidoglikan mavjud, ammo hujayra devorisiz bakteriyalar ham uchraydi. Mikroskopik zamburug‘lar, mikroalgalar va bir hujayrali protistlar eukariot tuzilishga ega. Viruslar esa prokariotlarga kirmaydi. Ular genomi kapsid bilan himoyalangan hujayrasiz tuzilmalar bo‘lib, ko‘payishi xo‘jayin hujayrasiga bog‘liq [1].

Mikrobiologiyaning amaliy ahamiyati ishlab chiqarish va ekologik jarayonlarda namoyon bo‘ladi. Mikroorganizmlar oziq-ovqat ishlab chiqarishining biologik asoslarini tashkil etadi. Mikrobiologik nazorat esa mahsulotlarning xavfsizligi va saqlanishini ta’minlashga xizmat qiladi [3]. Tabiiy muhitda mikroorganizmlar organik moddalarni parchalash, oziq elementlarini qayta aylantirish va ekotizimlar faoliyatini ta’minlashda muhim o‘rin tutadi [5].

O‘zbekistonda mikrobiologiya rivojlanishida mahalliy ilmiy maktablarning shakllanishi muhim o‘rin tutadi. Xususan, S. A. Asqarova mikrobiologik tadqiqotlarni tashkil etishga, A. M. Muzaffarov eksperimental algologiya va mikrosuvo‘tlardan amaliy foydalanish yo‘nalishiga, M. I. Mavloniy xamirturushlar sistematikasiga, A. G. Xolmurodov esa mikroorganizmlarda fiziologik faol birikmalar biosintezini o‘rganishga hissa qo‘shgan. Ularning ishlari respublikada fundamental mikrobiologiya va amaliy biotexnologiya rivojlanishiga xizmat qilgan [6].

Muhokama

Mikrobiologiyaning shakllanishi kuzatish, tajriba va amaliy ehtiyojlarning o‘zaro ta’siri orqali kechgan. Mikroskopiya mikroorganizmlarni tadqiqot obyektiga aylantirgan bo‘lsa, eksperimental usullar ularning muayyan jarayonlardagi rolini aniqlashga xizmat qildi. Molekulyar yondashuvlar esa ushbu jarayonlarning irsiy mexanizmlarini o‘rganishga imkon berdi.

Pasterning ishlari fundamental tadqiqotning amaliy muammolar bilan bog‘liqligini ko‘rsatadi. Bijg‘ishning biologik tabiatini tushuntirish oziq-ovqat ishlab chiqarishni boshqarishga, mikroorganizmlarning tarqalishini o‘rganish esa gigiyena va aseptik yondashuvlarning rivojlanishiga yordam berdi [2].

Mikroorganizmlarni foydali va zararli guruhlarga ajratishda ularning turi, shtammi, xo‘jayin organizm va muhit sharoitlari hisobga olinishi lozim. Ayrim turlar mahsulotni buzishi yoki toksin hosil qilishi mumkin, boshqalari esa foydali biologik xususiyatlarga ega [1].

Ekologik nuqtayi nazardan mikroorganizmlarning faoliyati faqat organik qoldiqlarni parchalash bilan cheklanmaydi. Ular uglerod va azot aylanishi, o‘simliklar bilan o‘zaro munosabatlar hamda issiqxona gazlarining hosil bo‘lishi va sarflanishida ishtirok etadi [5].

Xulosa

Mikrobiologiya empirik tajribalardan mikroskopik kuzatishlarga, eksperimental tadqiqotlarga va molekulyar tahlilga o‘tish jarayonida shakllangan. Levenguk, Paster va Koxning ilmiy ishlari

mikroorganizmlarning mavjudligi, faoliyati va kasalliklar bilan bog‘liqligini tushuntirishda muhim asos yaratgan.

Mikrobiologiya fanining amaliy ahamiyati mikroorganizmlarning hayot faoliyatini o‘rganish va ularning foydali xususiyatlaridan foydalanishda namoyon bo‘ladi. Bu bilimlar oziq-ovqat mahsulotlarining xavfsizligini ta’minlash, yuqumli kasalliklarning oldini olish, biologik mahsulotlar ishlab chiqarish va tabiatdagi moddalar aylanishini tushunish uchun zarur. Fan tarixini o‘rganish esa mikroorganizmlar haqidagi kashfiyotlar qanday tadqiqotlar orqali amalga oshirilgani va ularning natijalari amaliyotda qanday qo‘llanilganini tushunishga yordam beradi.

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EVALUATION OF PROTEASE AND LIPASE ACTIVITIES OF INDIGENOUS ENTOMOPATHOGENIC FUNGAL ISOLATES

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Introduction

The whitefly, *Bemisia tabaci* (Gennadius), is one of the most economically important insect pests affecting tomato, cotton, and numerous other agricultural crops. The repeated use of chemical insecticides against this pest may promote the development of insecticide resistance and cause a range of environmental problems. Therefore, the use of entomopathogenic fungi as biological control agents represents a promising alternative approach.

Entomopathogenic fungi constitute an important group of microorganisms with considerable potential for the biological control of insect pest populations. Fungal infection involves a sequence of processes, including adhesion of conidia to the insect cuticle, conidial germination, formation of penetration structures, and enzymatic degradation of the cuticular barrier. Since the insect cuticle is composed of complex structural components, including proteins, lipids, and chitin, extracellular hydrolytic enzymes produced by entomopathogenic fungi are considered important factors involved in the infection process.

Purpose

The aim of this study was to qualitatively evaluate the proteolytic and lipolytic activities of indigenous *Beauveria* and *Metarhizium* isolates, compare their enzymatic indices, and screen isolates with promising enzymatic potential for further investigation.

Materials and Methods

Entomopathogenic fungi were isolated from soil samples collected from a cotton agroecosystem in the Syrdarya region and from insect sources. Larvae of *Galleria mellonella* L. and *Leptinotarsa decemlineata* Say were used as insect sources. After removal of the surface soil layer, samples were collected from a depth of approximately 5 cm and stored at 4 °C until laboratory examination.

Preliminary identification of the fungal isolates was based on their macro- and micromorphological characteristics. Colony growth characteristics and morphology, as well as microscopic structures, were examined. Based on preliminary screening of their morphological and cultural characteristics, four *Beauveria* sp. isolates and one *Metarhizium* sp. isolate were selected for the assessment of enzymatic activity.

Proteolytic activity of the isolates was qualitatively assessed on casein-containing agar medium. The hydrolysis zone formed around the fungal colony as a result of substrate degradation was used as an indicator of protease activity. Lipolytic activity was evaluated on Tween 80-containing

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medium. Following incubation, the diameters of the fungal colonies and the surrounding reaction zones were measured and recorded.

To compare the enzymatic characteristics of the isolates, the enzymatic index (EI) was calculated based on the diameters of the fungal colony and the surrounding hydrolysis zone as follows:

The enzymatic index (EI) was calculated as the ratio of the total diameter of the fungal colony and the surrounding hydrolysis zone to the diameter of the fungal colony.

The resulting EI values were used for the preliminary qualitative or semi-quantitative comparison of the proteolytic and lipolytic potential of the fungal isolates.

Results and Discussion

Enzymatic screening demonstrated variation among the indigenous entomopathogenic fungal isolates in their ability to produce proteases and lipases. Positive proteolytic and lipolytic activities were detected in 80% of the five isolates **examined**, indicating that most of the isolates possessed the potential to hydrolyze protein- and lipid-based substrates.

The enzymatic index for lipolytic activity ranged from 1.07 to 2.81, demonstrating a relatively broad variation in lipolytic activity among the isolates.

For proteolytic activity, EI values ranged from 1.03 to 1.30. Compared with lipolytic activity, the protease EI values varied within a narrower range. Nevertheless, the combined assessment of proteolytic and lipolytic activities allowed differentiation among the isolates according to their overall enzymatic potential.

Based on the combined evaluation of protease and lipase activities, *Beauveria* sp. 2 was identified as one of the promising isolates because of its overall enzymatic profile. Although *Beauveria* sp. 1 exhibited high lipolytic activity, no detectable proteolytic activity was observed. In contrast, *Beauveria* sp. 3, *Beauveria* sp. 4, and the *Metarhizium* sp. isolate showed comparatively lower proteolytic and lipolytic activities. These findings support the selection of *Beauveria* sp. 2 for further quantitative evaluation of enzyme production and more detailed investigation of its biological characteristics.

The enzymatic index is primarily a screening parameter; therefore, the results obtained should be interpreted as indicators of the qualitative or semi-quantitative enzymatic potential of the isolates rather than as direct measurements of enzyme concentration or catalytic activity.

Because several hydrolytic enzymes contribute to the penetration of entomopathogenic fungi through the insect cuticle, protease and lipase activities alone are insufficient to draw definitive conclusions regarding isolate virulence. Nevertheless, these enzymes may serve as useful physiological indicators for the preliminary screening of promising isolates. Further assessment of chitinase activity would provide a more comprehensive characterization of the cuticle-degrading enzymatic potential of the selected isolates.

Conclusion

The present study demonstrated variability in proteolytic and lipolytic characteristics among indigenous *Beauveria* and *Metarhizium* isolates. Positive protease and lipase activities were detected in 80% of the isolates examined. The enzymatic index ranged from 1.07 to 2.81 for lipase and from 1.03 to 1.30 for protease, indicating greater variability in lipolytic activity than in proteolytic activity among the isolates.

Based on the combined evaluation of protease and lipase activities, *Beauveria* sp. 2 was identified as an isolate with promising enzymatic characteristics. These findings can be used for the preliminary characterization of the enzymatic potential of indigenous entomopathogenic fungi and for the selection of promising isolates for subsequent biological studies.

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KASALLANGAN KARTOSHKA TUGANAGIDAN AJRATILGAN FITOPATOGEN *FUSARIUM SAMBUCINUM* UZ-PH 34 SHTAMMINING KIMYOVIY PREPARATLARGA *IN VITRO* SHAROITIDA SEZGIRLIGINI BAHOLASH

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Annotatsiya: Saqlash davrida kasallangan kartoshka tuganaklaridan ajratib olingan *Fusarium sambucinum* Uz-Ph34 shtammining to‘rtta tijorat kimyoviy preparatiga sezgirligi *in vitro* sharoitida baholandi. Preparatlar 0,1; 1; 10 va 100 mg/l konsentratsiyalarda kartoshka-dekstrozali agar muhitida sinovdan o‘tkazildi. Имикар, КС barcha konsentratsiyalarda mitselial o‘sishni 100% ingibitsiya qildi, boshqa preparatlarning ta’siri esa konsentratsiyaga qarab farqlandi.

Kalit so‘zlar: kartoshka, *Fusarium sambucinum*, quruq chirish, kimyoviy preparatlar, *in vitro*, tuganak, konsentratsiya.

Аннотация: В условиях in vitro была оценена чувствительность штамма *Fusarium sambucinum* Uz-Ph34, выделенного из пораженных клубней картофеля во время хранения, к четырем коммерческим химическим препаратам. Препараты тестировали на картофельно-декстрозном агаре в концентрациях 0,1; 1; 10 и 100 мг/л. Имикар (КС) ингибировал рост мицелия на 100% при всех концентрациях, в то время как эффект других препаратов различался в зависимости от концентрации.

Ключевые слова: картофель, *Fusarium sambucinum*, сухая гниль, химические препараты, in vitro, клубень, концентрация.

Abstract: The sensitivity of a *Fusarium sambucinum* strain (Uz-Ph34), isolated from infected potato tubers during storage, to four commercial chemical agents was evaluated in vitro. The agents were tested on potato dextrose agar at concentrations of 0.1, 1, 10, and 100 mg/L. Imikar (KS) inhibited mycelial growth by 100% at all tested concentrations, whereas the effects of the other agents varied depending on their concentration.

Keywords: potato, *Fusarium sambucinum*, dry rot, chemical preparation, in vitro, tuber, concentration.

Kirish

Kartoshka (*Solanum tuberosum* L.) asosiy oziq-ovqat ekinlaridan biri bo‘lib, yetishtirilgan hosilning iste’molbopligi va urug‘lik sifatini saqlab qolish muhim ahamiyatga ega. Tuganaklar hosil yig‘ib olingandan keyin ham turli etiologiyali kasalliklar ta’sirida zararlanishi mumkin. Ayniqsa, saqlash davrida namoyon bo‘ladigan zamburug‘li kasalliklar mahsulotning tovarlik qiymati va urug‘lik sifatining pasayishiga olib keladi [1].

Bunday kasalliklar orasida *Fusarium* turkumi vakillari qo‘zg‘atadigan fuzarioz quruq chirish alohida o‘rin tutadi. Kasallikning rivojlanishi va keltirib chiqaradigan yo‘qotishlari saqlash sharoitlari, tuganaklarning shikastlanish darajasi va qo‘zg‘atuvchilar tarkibiga qarab farqlanadi [1]. Kartoshkani himoyalashda kimyoviy preparatlardan foydalaniladi, biroq ularning fitopatogenlarga ta’siri hamisha bir xil bo‘lmaydi. Xususan, *Fusarium* izolyatlarining fungitsidlarga sezgirligi tur va shtamm darajasida sezilarli farq qilishi mumkin [2, 4]. Shu bois mahalliy fitopatogen shtammga bir

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necha preparatning turli konsentratsiyalardagi ta’sirini *in vitro* sharoitida solishtirish keyingi amaliy sinovlar uchun istiqbolli variantlarni tanlashda muhimdir.

Tadqiqotning maqsadi. Kasallangan kartoshka tuganaklaridan ajratib olingan *F. sambucinum* Uz-Ph34 shtammining Имикар, КС, Селест Топ, КС, Maksim va Maksim XL preparatlariga *in vitro* sharoitida sezgirligini aniqlash.

Tadqiqot materiallari va metodlari

Tadqiqot obyekti sifatida saqlash davrida kasallangan kartoshka tuganaklaridan ajratib olingan va tuganaklarda o‘tkazilgan dastlabki patogenlik tajribalarida yuqori agressivligi bilan ajralib turgan *F. sambucinum* Uz-Ph34 shtammi olindi. Mitselial o‘sishning kimyoviy preparatlar ta’sirida susayishi kartoshka-dekstrozali agar (KDA) muhitida, nazoratga nisbatan koloniya diametrini taqqoslash usulida baholandi [3].

Sinovlarda Имикар, КС (imidakloprid 280 g/l + tiabendazol 80 g/l), Селест Топ, КС (tiametoksam 262,5 g/l + difenokonazol 25 g/l + fludioksonil 25 g/l), Maksim (fludioksonil asosidagi) va Maksim XL (fludioksonil + metalaksil-M asosidagi) preparatlaridan foydalanildi. Preparatlar KDA muhitiga tijorat preparatining umumiy miqdori bo‘yicha 0,1; 1; 10 va 100 mg/l konsentratsiyalarda kiritildi. Nazorat sifatida preparat qo‘shilmagan KDA ozuqa muhitidan foydalanildi.

Petri idishlari markaziga faol o‘sayotgan zamburug‘ kulturasining mitseliyli agar bo‘lagi ko‘chirilib, 25 °C haroratda 7 sutka inkubatsiya qilindi. Har bir variant bitta tajriba seriyasida uchta parallel Petri idishida bajarildi. Koloniyalar diametri, mitselial o‘sish ingibitsiyasi quyidagi formula asosida hisoblandi.

$$I = [(Dk - Do) / Dk] \times 100$$

bunda Dk – nazoratdagi, Do – preparatli variantdagi koloniya diametri (mm).

Natijalar

Yetti sutkalik inkubatsiyadan so‘ng nazorat variantida *F. sambucinum* Uz-Ph34 koloniyasining diametri 75 mm ni tashkil etdi. Kimyoviy preparatlar qo‘llangan variantlarda o‘sishning ingibitsiya darajasi preparat va konsentratsiyaga qarab turlicha bo‘ldi (1-jadval).

1-jadval. *F. sambucinum* UzPh 34 shtammi mitselial o‘sishining ingibitsiyasi, %

Preparat	0,1 mg/l	1 mg/l	10 mg/l	100 mg/l
Имикар, КС	100	100	100	100
Селест Топ, КС	37,79	34,23	34,23	16,45
Maksim	73,33	23,56	82,23	16,45
Maksim XL	2,23	6,67	10,21	15,55

Имикар, КС preparati ta’sirida 0,1-100 mg/l konsentratsiyalarning barchasida koloniya o‘sishi kuzatilmadi (0 mm), ya’ni ingibitsiya 100% bo‘ldi. Селест Топ, КС preparatida ingibitsiya 16,45-37,79% oralig‘ida bo‘lib, barcha variantlarda mitselial o‘sish saqlanib qoldi. Maksim preparatida eng yuqori ingibitsiya 10 mg/l konsentratsiyada (82,23%; koloniya diametri 13,33 mm), eng past qiymat esa 100 mg/l da (16,45%) qayd etildi. Maksim XL da 0,1 mg/l da ingibitsiya 2,23% bo‘ldi, 1-100 mg/l da koloniya diametri nazoratdagidan ortdi.

Muhokama

Natijalar *F. sambucinum* Uz-Ph34 shtammining o‘rganilgan preparatlarga javobi bir xil emasligini ko‘rsatdi. Имикар, КС sinovdagi barcha konsentratsiyalarda barqaror to‘liq ingibitsiyani ta’minladi, qolgan preparatlarda esa konsentratsiya ortishi bilan ta’sir kuchayishining izchil qonuniyati kuzatilmadi. Adabiyotlarda ham *Fusarium* izolyatlarining fungitsidlarga sezgirligi bir-biridan farqlanishi ko‘rsatilgan [2, 4]. Ushbu natijalar tijorat preparatlari uchun olingan bo‘lib, ular tarkibidagi alohida faol moddalarning ta’sirini mustaqil ravishda ifodalamaydi. Tajriba bitta mustaqil seriya doirasida o‘tkazilgani sababli natijalar laboratoriya skriningi sifatida baholanadi.

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Xulosa

Tadqiqot natijalariga ko‘ra, *F. sambucinum* Uz-Ph34 shtammining kimyoviy preparatlarga sezgirligi bir xil emasligi aniqlandi. Имикар, КС 0,1; 1; 10 va 100 mg/l konsentratsiyalarning barchasida mitselial o‘sishni 100% ingibitsiya qilib, sinovdan o‘tgan preparatlar orasida eng barqaror ta’sirni namoyon etdi. Селест Топ, КС da ingibitsiya 16,45-37,79% ni tashkil etgan bo‘lsa, Maksimning eng yuqori ta’siri 10 mg/l da (82,23%) qayd etildi. Maksim XL ning 1-100 mg/l konsentratsiyalarida esa koloniyalar nazoratdagidan kattaroq bo‘ldi.

Natijalar preparatlarni tanlashda aynan shtammning sezgirligini va konsentratsiya ta’sir munosabatining o‘zgaruvchanligini hisobga olish zarurligini ko‘rsatadi.

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TUPROQ BAKTERIYALARINING ANTIMIKROB FAOLLIGINI BAHOLASH

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Annotatsiya: Ushbu tadqiqotning maqsadi tuproqdan ajratib olingan bakteriya shtammlarining antimikrob faolligini o‘rganishdan iborat. Tuproqdan 20 dan ortiq bakteriya shtammlari ajratib olindi. Ularning antimikrob faolligi quyidagi mikroorganizmlar *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans* va *Bacillus subtilis* ga nisbatan agarli blok usuli orqali baholandi. Natijada 11 ta izolyat *S. aureus* ga qarshi faollik ko‘rsatdi; o‘sishni ingibitsiya qilish zonasi 15-30 mm ni tashkil etdi. Qolgan izolyatlarda test-mikroorganizmlarga qarshi faollik kuzatilmadi.

Kalit so‘zlar: tuproq bakteriyalari, antimikrob faollik, bakterial izolyatlar, patogen mikroorganizmlar, biologik nazorat.

Kirish

Tuproq turli xildagi mikroorganizmlar yashaydigan tabiiy muhit bo‘lib, unda bakteriyalar orasida boshqa bir mikroorganizmlarning o‘sishiga ta‘sir ko‘rsatuvchi xususiyatlarga ega vakillar ham uchraydi. Bunday bakteriyalarni aniqlash hamda ularning biologik faolligini o‘rganish mikroorganizmlarning biotexnologik imkoniyatlarini baholashda muhim ahamiyatga ega. Ayniqsa, bakteriya izolyatlarining patogen mikroorganizmlarga qarshi antagonistik faolligini aniqlash ularning keyingi tadqiqotlar uchun istiqbolliligini baholashga imkon beradi.

Material va metodlar

Bakteriya shtammlarining antimikrob faolligi ikki qavatli agar usuli yordamida baholandi. Dastlab, tuproqdan ajratilgan bakteriya shtammlari Nutrient Agar (NA) muhitida 28 °C haroratda 24 soat davomida o‘stirildi. Test-patogen mikroorganizmlar esa 37 °C haroratda 24 soat davomida o‘stirildi. Ular quyidagilar: *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans* va *Bacillus subtilis.* Shundan so‘ng, izolyatlar o‘stirilgan Petri kosachalaridan maxsus o‘yiqchalar tayyorlanib, oldindan o‘stirilgan patogen test mikroorganizmlar o‘stirilgan chashkalarga joylashtirildi. Inkubatsiyadan so‘ng patogenlarning o‘sishi to‘xtagan zonalar diametri millimetrda o‘lchanib, shtammlarning antagonistik faolligi baholandi.

Natija va muhokama

Tadqiqot natijalariga ko‘ra, tekshirilayotgan 20 ta bakteriya izolyatining 11 tasi (105,108,110,115,117,118,120,122,123,124,126) *S. aureus* ga qarshi antagonistik faollik namoyon etdi. Faol izolyatlarda o‘sishni to‘xtatish zonasi 15-30 mm oralig‘idagi o‘lchamlarga ega bo‘ldi. Eng yuqori o‘lchamdagi ko‘rsatkich 110-sonli izolyatda 30 mm ni, eng past ko‘rsatkich esa 120-sonli izolyatda 15 mm ni namoyon etdi. Alohida izolyatlar bo‘yicha *S. aureus* ga qarshi o‘sishni ingibitsiya qilish zonalari quyidagicha bo‘ldi: 105-sonli izolyatda 17 mm, 108-da 24 mm, 110-da 30 mm, 115-da

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26 mm, 117-da 24 mm, 118-da 24 mm, 120-da 15 mm, 122-da 17 mm, 123-da 24 mm, 124-da 20 mm hamda 126-da 16 mm. 104, 106, 109, 111, 112, 113, 114, 116 va 119-sonli izolyatlarda antagonistik faollik aniqlanmadi. Shuningdek, *C. albicans*, *P. aeruginosa*, *E. coli* va *B. subtilis* ga qarshi faollik kuzatilmadi. Olingan natijalar tuproqdan ajratib olingan bakteriya shtammlarining ayrimlari *S. aureus* ning o‘sishini cheklash xususiyatiga ega ekanligini ko‘rsatdi.

Xulosa

Tekshirilgan izolyatlarning antagonistik faolligi o‘rganilganligi ushbu bakteriyalarni keyingi tadqiqotlar uchun tanlab olish mumkinligini ko‘rsatadi. Ammo mazkur natijalar bakteriyalarning turini, faol moddaning tabiatini aniqlamaydi. Shuning uchun istiqbolli izolyatlarni taksonomik identifikatsiya qilish shu bilan birgalikda ularning biologik xususiyatlarini batafsil o‘rganish zarurligini anglatadi.

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ISSIQXONADA YETISHTIRILGAN KASALLANGAN POMIDOR KO‘CHATLARIDAN AJRATILGAN BAKTERIYALARNING TAKSONOMIK XILMA-XILLIGI

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Annotatsiya: Xorazm viloyatidagi issiqxonada yetishtirilgan kasallangan pomidor ko‘chatlaridan bakterial izolyatlar ajratildi. Ular morfo-kultural va mikroskopik belgilar bo‘yicha tavsiflanib, MALDI-TOF MS usulida identifikatsiya qilindi. Izolyatlar *Micrococcus*, *Lysinibacillus*, *Ralstonia*, *Serratia*, *Pseudomonas* va *Rothia* avlodlariga mansub ekanligi aniqlandi.

Kalit so‘zlar: pomidor, issiqxona, bakterial izolyatlar, MALDI-TOF MS, mikroflora.

Аннотация: Из поражённых сеянцев томата, выращенных в теплице Хорезмской области, выделены бактериальные изоляты. Их охарактеризовали по морфолого-культуральным и микроскопическим признакам и идентифицировали методом MALDI-TOF MS. Обнаружены представители родов *Micrococcus*, *Lysinibacillus*, *Ralstonia*, *Serratia*, *Pseudomonas* и *Rothia*.

Ключевые слова: томат, теплица, бактериальные изоляты, MALDI-TOF MS, микрофлора.

Abstract: Bacterial isolates were recovered from diseased tomato seedlings grown in a greenhouse in Khorezm Region, Uzbekistan. The isolates were characterized morphologically and microscopically and identified using MALDI-TOF MS. They were assigned to the genera *Micrococcus, Lysinibacillus, Ralstonia, Serratia, Pseudomonas,* and *Rothia*.

Keywords: tomato, greenhouse, bacterial isolates, MALDI-TOF MS, microflora.

Kirish

Pomidor (Solanum lycopersicum) muhim sabzavot ekini bo‘lib, issiqxona sharoitida o‘simliklar bilan assotsiatsiyalangan bakteriyalarni o‘rganish fitosanitar monitoring uchun ahamiyatlidir[1]. Kasallangan to‘qimalarda patogenlar bilan birga boshqa ekologik guruhlarga mansub bakteriyalar ham uchrashi mumkin[2]. Tadqiqotning maqsadi kasallangan pomidor ko‘chatlaridan bakteriyalarni ajratish va ularning taksonomik mansubligini aniqlashdan iborat.

Materiallar va metodlar

Tadqiqotlar 2024-yilda Xorazm viloyati Tuproqqal’a tumanidagi “Greenhouse Company” MChJ issiqxonasida yetishtirilgan “De Ruiter” navli pomidor ko‘chatlarida olib borildi. Kasallik belgilari kuzatilgan o‘simlik qismlari yuvilib, etil spirti va steril suvning 3:1, 1:1 va 1:3 nisbatdagi aralashmalarida bir minutdan ishlov berildi. So‘ng steril suvda yuvilgan to‘qimalardan 1,5–2 sm bo‘laklar kesilib, go‘sht-peptonli agar muhitiga ekildi va 28–29 °C da inkubatsiya qilindi. Morfologik farqlanuvchi koloniyalar qayta ekish orqali sof kulturaga ajratildi. Mikroskopik preparatlar Gram usulida bo‘yalib, N-300M mikroskopida 100× immersion obyektiv yordamida ko‘rildi. Taksonomik identifikatsiya MALDI-TOF MS spektrlarini referens ma’lumotlar bazasi bilan taqqoslash asosida bajarildi.

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Natijalar

Kasallangan pomidor ko‘chatlaridan morfo-kultural belgilari bilan farqlanuvchi bakterial izolyatlar ajratildi. Koloniyalar oq, qaymoqrang va sarg‘ish tuslarda bo‘lib, yuzasi hamda chetlarining tuzilishi jihatidan farqlandi. MALDI-TOF MS tahlili izolyatlarning *Micrococcus, Lysinibacillus, Ralstonia, Serratia, Pseudomonas* va *Rothia* avlodlariga mansubligini ko‘rsatdi.

Muhokama

Mazkur avlodlar turli ekologik va funksional xususiyatlarga ega bakteriyalarni birlashtiradi. Biroq MALDI-TOF MS asosidagi taksonomik mansublikning o‘zi ajratilgan izolyatlarning kasallik qo‘zg‘atuvchisi yoki biologik himoya agenti ekanligini isbotlamaydi. Kasallangan o‘simlik to‘qimalarida uchragan bakteriyalarning haqiqiy rolini aniqlash uchun patogenlik, antagonistik faollik va molekulyar identifikatsiyaga oid qo‘shimcha sinovlar zarur. Identifikatsiya aniqligi referens spektrlar bazasining qamroviga ham bog‘liq [1, 2].

Xulosa

Kasallangan pomidor ko‘chatlaridan ajratilgan bakteriyalar oltita avlodga mansub ekani ko‘rsatildi. Olingan natijalar issiqxona pomidor ko‘chatlari bilan assotsiatsiyalangan kultivatsiyalanuvchi bakteriyalarning taksonomik xilma-xilligini tavsiflaydi va ularning fitopatologik ahamiyatini keyingi tadqiqotlarda baholash uchun asos yaratadi.

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ISOLATION, METAGENOMIC PROFILING, AND BIOTECHNOLOGICAL POTENTIAL OF INDIGENOUS METHANOTROPHIC BACTERIA IN UZBEKISTAN

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Methanotrophs are a unique group of bacteria possessing the remarkable ability to utilize methane as their sole source of carbon and energy. They are widely distributed in nature and have been isolated from a variety of environments, including soils, sediments, freshwater, marine sediments, seawater, acidic peat bogs, hot springs, and cold environments such as Antarctica. Methane represents a promising next-generation carbon feedstock for industrial biotechnology, as it is abundant and cost-effective. The biological conversion of methane into high-value products offers a potential solution to mitigate greenhouse gas (GHG) emissions associated with methane releases. Single-cell proteins (SCP) produced from these microorganisms contain 30–80% protein, as well as essential amino acids, vitamins, and minerals, making them highly effective feed additives in livestock and poultry diets. Soil and substrate samples were collected from diverse ecological regions of Sirdaryo, Qashqadaryo, and Surxondaryo regions to isolate and cultivate resilient methanotrophic bacterial strains of biotechnological importance. After 10–15 days of incubation in serum bottles and desiccators inoculated into NMS (Nitrate Mineral Salts) liquid medium under a CH_4: air (1:1 and 1:4) gas-phase mixture, signs of microbial growth, including turbidity of the culture medium and an increase in sample biomass, were observed. Application of a high-temperature regime (45 °C) inhibited the growth of mesophilic companion microbiota and enriched the population of target thermotolerant methanotrophic bacteria. Total metagenomic DNA was extracted from cumulative and enriched liquid cultures using a commercial kit (DNeasy PowerSoil Pro Kit, Qiagen, Germany) in accordance with the manufacturer's instructions. The concentration and purity of the extracted DNA were evaluated using a Qubit 4.0 Fluorometer and a NanoDrop spectrophotometer. A metagenomic library was prepared, and high-throughput shotgun sequencing was performed on the Illumina platform. The obtained raw reads underwent quality control and were filtered using bioinformatic software tools (FastQC, Trimmomatic). For taxonomic classification and determination of relative abundance, sequences were aligned against the NCBI and GTDB (Genome Taxonomy Database) databases. According to the analysis results, members of the class Gammaproteobacteria (phylum Proteobacteria) exhibited absolute dominance in both samples, accounting for 74.04% in the sample collected from the gas mines of the Qashqadaryo region (H1) and 75.37% in the sample from the Sirdaryo region (H2). The second most abundant class was Betaproteobacteria (15.99%) in sample H1 and Alphaproteobacteria (16.15%) in sample H2. The obtained results confirm that the cultivation conditions successfully enriched the population of methanotrophic bacteria belonging to the class Gammaproteobacteria.

Analysis of the 16S rRNA gene of methanotrophic bacteria isolated from samples collected in the Surxondaryo region (oil wells of the Boysun district) revealed a 99.4% sequence identity with *Methylocaldum gracile*.

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Based on the obtained results, scientific research is consistently ongoing. At the present stage, applied research is being conducted to evaluate the biocatalytic and biotechnological potential of the isolated thermotolerant methanotrophic bacterial strains, specifically focusing on the efficiency of methane biotransformation and microbial biomass (protein) biosynthesis.

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RHIZOSPHERE SOIL SAMPLING FOR THE ISOLATION OF MICROMYCETES WITH ANTIBACTERIAL AND ANTIFUNGAL ACTIVITY

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Abstract: This paper describes the appropriate procedures for rhizosphere soil sampling, emphasizing the importance of proper sample collection, handling, and transportation for the isolation of micromycetes with antibacterial and antifungal activity.
Keywords: *Alhagi maurorum, Karelinia caspia, Tamarix spp., Halostachys caspica*, micromycetes, rhizosphere, sterility, transportation.

Annotatsiya: Ushbu tezisda antibakterial va antifungal faollikka ega mikromitsetlarni ajratib olish uchun rizosfera tuprog‘idan namuna olishning tegishli usullari bayon etilgan. Bunda namunalarni to‘g‘ri yig‘ish, saqlash va tashishning ahamiyatiga alohida e’tibor qaratilgan.
Kalit so‘zlar: *Alhagi maurorum, Karelinia caspia, Tamarix spp., Halostachys caspica*, mikromitsetlar, rizosfera, sterillik, tashish.

Аннотация: В статье описываются соответствующие методы отбора проб ризосферной почвы для выделения микромицетов, обладающих антибактериальной и антифунгальной активностью. Особое внимание уделяется важности правильного сбора, хранения и транспортировки образцов.
Ключевые слова: *Alhagi maurorum, Karelinia caspia, Tamarix spp., Halostachys caspica*, микромицеты, ризосфера, стерильность, транспортировка.

Introduction

Micromycetes, or microscopic fungi, represent a diverse group of organisms that inhabit a wide range of environments, including soil and plant-associated habitats. They play important ecological roles in organic matter decomposition, nutrient cycling, and interactions with plants and other microorganisms [2,7]. In addition to their ecological significance, certain micromycetes produce secondary metabolites with antibacterial and antifungal properties, making them promising candidates for biotechnological applications [10].

The rhizosphere is a particularly interesting environment for studying microscopic fungi because plant roots influence the composition and activity of associated microbial communities. Studies have demonstrated that filamentous fungi isolated from plant rhizosphere soil may exhibit antibacterial activity against selected bacterial pathogens [1]. Furthermore, research on

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micromycetes has shown that antimicrobial activity can vary among fungal isolates, highlighting the importance of systematic isolation and screening procedures [10].

Therefore, appropriate rhizosphere soil sampling is an essential initial step in the search for micromycetes with antibacterial and antifungal potential. Careful sample collection, handling, transportation, and subsequent fungal isolation can support the recovery of viable fungal cultures for further antimicrobial screening.

Materials and methods

Sampling site selection is an important step in soil microbiological research because soil characteristics, vegetation, environmental conditions, and human activities may influence the composition of microbial communities [3,9]. Sciurba et al. [12] emphasized the importance of clearly documenting sampling locations, sampling procedures, and sample-handling conditions to improve the reliability and reproducibility of microbiological studies. For investigations of rhizosphere microorganisms, researchers select suitable plants and collect their roots together with the soil adhering to them, as the rhizosphere is a biologically active zone in which plant roots interact with diverse microorganisms [4,13].

During sample collection, researchers use clean sampling tools and separate containers for individual samples to minimize cross-contamination. Information such as the sampling location, collection date, and plant species is recorded to ensure sample traceability [12]. The collected roots and their associated rhizosphere soil are then transported to the laboratory for further processing and microbial isolation.

Prompt transportation and appropriate storage conditions are important because temperature and storage duration can affect soil microbial community composition and metabolic activity. Dickie et al. [6] described cooling and suitable storage conditions as important considerations for maintaining sample integrity. In a study by Cui et al. [5], different soil-storage methods were found to influence microbial community structure and metabolic activity, while fresh soil was considered preferable for investigations involving microbial metabolic activity. Therefore, researchers are encouraged to minimize the interval between sample collection and laboratory processing. Following arrival at the laboratory, rhizosphere soil can be prepared for the isolation of micromycetes and subsequent screening for antibacterial and antifungal activity.

Results

Plant samples were collected from a field site in Amudarya District, Republic of Karakalpakstan, Uzbekistan. A total of four plant species were sampled, including their roots and associated rhizosphere soil: *Alhagi maurorum, Karelinia caspia, Tamarix* spp., and *Halostachys caspica*.

The plants were carefully excavated together with their root systems and associated soil using sterilized tools [8]. Each plant sample was placed in a separate sterile bag to prevent cross-contamination. The bags were securely sealed and labelled to identify the samples and their collection locations.

During transportation to the laboratory, precautions were taken to protect the samples from direct sunlight, excessive heat, and freezing. These measures were intended to minimize environmental influences that could affect the viability and composition of the microorganisms associated with the plant roots [14].

Upon arrival at the laboratory, loosely attached soil was gently removed from the roots by shaking. Soil adhering closely to the root surfaces, representing the rhizosphere soil fraction, was then carefully collected using sterile techniques and transferred into separate sterile containers [11]. The collected rhizosphere soil samples were prepared for subsequent laboratory procedures aimed at isolating micromycetes and screening the obtained fungal isolates for antibacterial and antifungal activity.

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Discussion

The collected plant–rhizosphere soil samples provide a basis for investigating rhizosphere-associated micromycetes. Previous research has described methods for studying microbial communities in soil, rhizosphere, and root samples [11]. Fungi are also recognized as potential sources of antibacterial and antifungal substances [2]. Therefore, further laboratory isolation and screening are necessary to determine whether the collected samples contain micromycetes with these biological activities.

Conclusion

Proper selection and collection of plant roots and rhizosphere soil samples are essential initial steps in research aimed at isolating micromycetes with antibacterial and antifungal activity. Appropriate sampling, handling, storage, and transportation help preserve sample quality and support reliable results during subsequent laboratory isolation and screening procedures.

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PHENOTYPIC DIVERSITY OF THE MICROBIOTA OF THE MEDICINAL KHOJAIPOK MINERAL LAKE

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Abstract: In this article, based on the physicochemical parameters of the highly mineralized and sulfur-rich Khojaipok lake located in the Kashkadarya region, pure cultures of microorganisms were isolated, and their phenotypic characteristics were analyzed.

Keywords: extremophilic microorganisms, halophiles, sulfur bacteria, salt lakes, biotechnology, microbiome, Khojaipok.

Introduction

In recent years, interest has significantly increased in natural sulfur-compound lakes, particularly the compounds found in medicinal and rejuvenating mineral waters originating from underground geothermal springs. The various health benefits and unique medicinal properties of these compounds have attracted the attention of both researchers and medical professionals. Sulfur compounds play a vital role in many biological processes; this is primarily explained by their active participation in metabolic processes and their function as vital signaling molecules within the body. Khojaipok lake, located in the Khojaipok village of the Dehkanabad district in the Kashkadarya region, is famous for its richness in minerals; its water contains sulfur (sulfides) and 42 types of microelements. The water and medicinal mud of this lake are widely used in the treatment of rheumatoid diseases, various skin diseases, and nervous system disorders. Studying the microbiota living in such a mineral-rich extreme ecosystem is highly relevant for fundamental science. The purpose of this study is to isolate pure bacterial isolates from the Khojaipok mineral lake and evaluate their phenotypic characteristics.

Materials and Methods

Water and sediment samples collected from Khojaipok lake during the winter and spring seasons were used as the object of study. The collected water samples were submitted for hydrochemical analysis. To isolate pure cultures of microorganisms, the samples were inoculated on various selective nutrient media (Halophilic agar, Marine agar, Starkey, HS, etc.) with a salt concentration ranging from 5% to 25%. The samples were incubated at a temperature of 25-37°C for 2-5 days. After incubation, isolates were separated from the samples using the serial dilution method. The morpho-cultural characteristics (colony color, shape, surface) and susceptibility to the Gram reaction of the isolates were tested. The cell shape, motility, and size of the isolates were evaluated using phase-contrast microscopy (ZEISS universal microscope).

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Results and Discussion

According to the results of the hydrochemical analysis, the pH of the water environment in Khojaipok lake was found to be 7.5, and the dry residue mass was 7.3 g/l. It was confirmed that this reservoir, which has a high amount of sulfate ions (4938 mg/l), is a calcium-magnesium-sulfate type lake with a salinity of up to 7%. As a result of the microbiological enrichment and inoculation processes, a total of 25 pure bacterial isolates were obtained from Khojaipok lake. Morpho-cultural analyses showed that the isolated cultures exhibit phenotypic diversity. Under the microscope, the cell shape of all 25 isolates was observed to be rod-shaped. The color of the formed colonies was highly diverse, displaying white, cream, light blue, dark cream, light brown, pink, and yellow pigments. It was determined that the surface of the colonies had a solid or mucous structure depending on the type of isolate. The occurrence of mucous colonies may be associated with the survival strategy of bacteria (secretion of exopolysaccharides) to protect themselves from dehydration in a mineral-sulfate environment. Gram staining analysis confirmed the active presence of both Gram-negative and Gram-positive bacterial isolates (e.g., X.T.10(1), X.T.10(2)) in the Khojaipok ecosystem.

Conclusion

The conducted research shows that Khojaipok lake, which possesses medicinal mineral properties, contains a highly rich and phenotypically diverse community of microorganisms. The distinct pigmentation and structural characteristics of the 25 pure isolates obtained indicate their strong adaptation to these specific extreme conditions. These local halotolerant bacteria will serve as a valuable raw material source for the development of new biologically active substances and biotechnological preparations in the future.

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FERULA SAMARKANDICA DORIVOR O‘SIMLIGI ENDOFIT BAKTERIYALARIDA ANTIMIKROB FAOLLIGINI BAHOLASH

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Annotatsiya: Ushbu tadqiqotning maqsadi *Ferula samarkandica* dorivor o‘simligidan ajratib olingan bakteriya shtammlarining antimikrob faolligini baholashdan iborat. O‘simlik tarkibidan 21 dan ortiq bakteriya shtammlari ajratib olindi. Ularning antimikrob faolligi quyidagi mikroorganizmlar: *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans* va *Bacillus subtilis*ga nisbatan blokli agar usuli orqali baholandi. Natijada 6 ta izolyat *S. aureus*ga qarshi faollik ko‘rsatdi. O‘sishni ingibitsiya qilish zonasi 12-18 mm ni tashkil etdi. Qolgan izolyatlarda test-mikroorganizmlarga qarshi faollik kuzatilmadi.

Kalit so‘zlar: *F. samarkandica*, endofit bakteriyalar, dorivor o‘simlik, antimikrob faollik, bakterial izolyatlar, biologik faollik, fitopatogen mikroorganizmlar, biotexnologiya.

Kirish

O‘simliklar tarkibida turli xildagi bakteriyalar uchraydi, ayniqsa dorivor o‘simliklar tarkibida uchraydigan bakteriyalarning sanoatda, farmasevtika va qishloq xo‘jaligida o‘rni beqiyosdir. O‘simlik va bakteriyalar birgalikda yashashi bir-biriga qulay sharoit yaratib berishi simbioz holda yashashi o‘zaro foyda keltiradi. Ba’zi o‘simliklar tarkibida umuman mikroorganizmlar faoliyat ko‘rsatmaydi. Bunday bakteriyalarni aniqlash hamda ularning biologik faolligini o‘rganish mikroorganizmlarning biotexnologik imkoniyatlarini baholashda muhim ahamiyatga ega. Ayniqsa, bakteriya izolyatlarining patogen mikroorganizmlarga qarshi antagonistik faolligini aniqlash ularning keyingi tadqiqotlar uchun istiqbolliligini baholashga imkon beradi.

Material va metodlar

Bakteriya shtammlarining antimikrob faolligi blokli agar usuli yordamida baholandi. Dastlab, tuproqdan ajratilgan bakteriya shtammlari Nutrient Agar (NA) muhitida 28 °C haroratda 48 soat davomida o‘stirildi. Test-patogen mikroorganizmlar esa 37 °C haroratda 24 soat davomida o‘stirildi. Ular quyidagilar: *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans* va *Bacillus subtilis.* Shundan so‘ng, shtammlarimiz o‘stirilgan chashkalardan agarli o‘yiqchalar tayyorlanib, oldindan o‘stirilgan test mikroorganizmlar o‘stirilgan chashkalarga joylashtirildi. Inkubatsiyadan so‘ng patogenlarning o‘sishi to‘xtagan zonalar diametri millimetrda o‘lchanib, shtammlarning antagonistik faolligi baholandi.

Natija va muhokama

Tadqiqot natijalariga ko‘ra, tekshirilayotgan 21 ta bakteriya izolyatining 6 tasi (Ar P2, Ar I14, Ar I12, Ar I12, Ar I1, Ar I4) *S. aureus*ga qarshi antagonistik faollik namoyon etdi. Faol izolyatlarda o‘sishni to‘xtatish zonasi 12-18mm oralig‘idagi o‘lchamlarga ega bo‘ldi. Eng yuqori o‘lchamdagi ko‘rsatkich Ar I12 izolyatida 18 mm ni, eng past ko‘rsatkich esa Ar I1 izolyatida 12 mm ni namoyon etdi. Alohida izolyatlar bo‘yicha *S. aureus*ga qarshi o‘sishni ingibitsiya qilish zonalari quyidagicha

IQTIBOS UCHUN
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bo‘ldi: Ar I1 12 mm, Ar I4 18mm, Ar I12 18mm, Ar I12 16 mm, Ar I14 12 mm, Ar P 2 17mm. Shuningdek, *C. albicans, P. aeruginosa, E. coli* va *B. subtilis*ga qarshi faollik kuzatilmadi. Olingan natijalar F. *samarkandica* dorivor o‘simligidan ajratib olingan bakteriya shtammlarining ayrimlari *S. aureus*ning o‘sishini cheklash xususiyatiga ega ekanligini ko‘rsatdi.

Xulosa

Tekshirilgan izolyatlarning antagonistik faolligi o‘rganilganligi ushbu bakteriyalarni keyingi tadqiqotlar uchun tanlab olish mumkinligini ko‘rsatadi. Ammo mazkur natijalar bakteriyalarning turini, faol moddaning tabiatini aniqlamaydi. *F. samarkandica* dorivor o‘simligining turli qismlaridan ajratib olingan endofit bakterial izolyatlarning ayrimlari *S. aureus*ga qarshi antagonistik faollik namoyon etishini ko‘rsatdi. Kuzatilgan o‘sishni ingibitsiya qilish zonalari 12-18mm oralig‘ida bo‘lib, ushbu izolyatlarni keyingi tadqiqotlar uchun istiqbolli nomzodlar sifatida tanlab olish imkonini beradi. Biroq mazkur natijalar bakteriyalarning turini va antagonistik faollikni yuzaga keltiruvchi biologik faol moddalar tabiatini aniqlash uchun yetarli emas. Shu sababli istiqbolli izolyatlarni taksonomik identifikatsiya qilish va ularning biologik vazifalarini batafsil o‘rganish, antimikrob faolligini qo‘shimcha tajribalar yordamida baholash lozim.

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IDENTIFICATION OF GUT BACTERIA IN WORKER AND SOLDIER CASTES OF THE TERMITE *ANACANTHOTERMES AHNGERIANUS*

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Abstract: Cultivable gut bacteria from worker and soldier castes of *Anacanthotermes ahngerianus* were isolated and analysed using MALDI-TOF MS and Gram staining. Fifteen pure isolates were obtained: seven from workers and eight from soldiers. Worker isolates were assigned to *Enterobacter* (57.1%) and *Bacillus* (28.6%); one isolate (14.3%) remained unidentified. All soldier isolates were assigned to *Acinetobacter*. The results indicate differences in the taxonomic composition of cultivable gut bacteria between the two castes under the experimental conditions.

Keywords: *Anacanthotermes ahngerianus*; gut bacteria; worker caste; soldier caste; MALDI-TOF MS; Gram staining.

Introduction

Gut microorganisms play an important role in the digestion of cellulose-rich food by termites [1]. Studying the gut microbiota of *Anacanthotermes ahngerianus* is therefore relevant to understanding its feeding biology, identifying cellulose-degrading microorganisms and developing the biological basis of termite control. Termite guts harbour complex microbial communities involved in lignocellulose degradation. Because worker and soldier castes differ in colony functions and feeding characteristics, their cultivable gut bacterial communities may also differ. This study aimed to identify bacterial isolates from the guts of both castes using MALDI-TOF MS and to compare their taxonomic composition.

Materials and methods

Termite specimens were collected from Beruniy District, Republic of Karakalpakstan, in collaboration with the Republican Scientific and Production Center for Termite Control. Ten termites from each caste were used. Guts were dissected under aseptic conditions and homogenised in sterile phosphate buffer. The homogenates were diluted in sterile 0.9% NaCl solution and plated on meat-peptone agar. Cultures were incubated at 30 °C for 72 h. Morphologically distinct colonies were repeatedly subcultured to obtain pure cultures. Isolates were characterised using conventional methods, including Gram staining, and identified by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS) [2].

Results

Fifteen pure bacterial isolates were obtained: seven from workers (WG-1, WG-2, WG-4, WG-6, WG-5/1, WG-5/2 and WG-5/3) and eight from soldiers (SG-1 to SG-8). Worker isolates WG-5/2 and WG-5/3 were Gram-positive; the remaining worker isolates and all soldier isolates

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were Gram-negative. These reactions were consistent with the general phenotypic characteristics of the bacterial taxa assigned by MALDI-TOF MS (Table 1).

Table 1. MALDI-TOF MS results for gut bacterial isolates from worker and soldier castes of *Anacanthotermes ahngerianus*

Caste	Isolate code	MALDI-TOF MS identification	Identification score
Worker	WG-5/1	Unidentified	1.47
Worker	WG-5/2	*Bacillus megaterium*	2.42
Worker	WG-5/3	*Bacillus subtilis*	2.04
Worker	WG-4	*Enterobacter cloacae*	2.05
Worker	WG-6	*Enterobacter cloacae*	2.26
Worker	WG-1	*Enterobacter asburiae*	1.95
Worker	WG-2	*Enterobacter cloacae*	2.21
Soldier	SG-1	*Acinetobacter junii*	1.98
Soldier	SG-2	*Acinetobacter parvus*	1.88
Soldier	SG-3	*Acinetobacter junii*	1.94
Soldier	SG-4	*Acinetobacter junii*	1.99
Soldier	SG-5	*Acinetobacter parvus*	2.10
Soldier	SG-6	*Acinetobacter pittii*	1.86
Soldier	SG-7	*Acinetobacter junii*	2.31
Soldier	SG-8	*Acinetobacter parvus*	2.04

Discussion

Among worker isolates, MALDI-TOF MS assignments comprised *Enterobacter* (57.1%) and *Bacillus* (28.6%), while one isolate (14.3%) remained unidentified. All eight soldier isolates were assigned to *Acinetobacter*. These findings indicate differences in the taxonomic composition of cultivable bacteria between termite castes under the experimental conditions.

Conclusion

A total of 15 pure bacterial isolates were recovered and analysed by MALDI-TOF MS. Worker isolates included representatives of *Bacillus* and *Enterobacter*, whereas all soldier isolates were assigned to *Acinetobacter*. Assessing their cellulolytic activity and confirming species-level identifications using molecular genetic methods are necessary to establish their functional roles in termite nutrition.

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MIKROBIOLOGIYA FANINI O‘QITISHNING ZAMONAVIY HOLATI, MUAMMOLARI VA SHIFOKORLAR TAYYORLASHDAGI O‘RNI

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Annotatsiya: Ushbu tezisda tibbiy oliy ta’lim muassasalarida mikrobiologiya fanini o‘qitishning zamonaviy holati, erishilayotgan yutuqlar, ta’lim jarayonida uchrayotgan muammolar hamda fanning bo‘lajak shifokorlarni tayyorlashdagi ahamiyati tahlil qilingan. Mikrobiologiyani o‘qitishda klinik yo‘naltirilgan ta’lim, amaliy laboratoriya mashg‘ulotlari, interaktiv pedagogik texnologiyalar, raqamli ta’lim resurslari va kompetensiyaga asoslangan yondashuvning ahamiyati yoritilgan. Antibiotikorezistentlikning ortishi, gospital infeksiyalar, yangi va qayta paydo bo‘layotgan infeksiyalar hamda zamonaviy laboratoriya diagnostikasi usullarining rivojlanishi mikrobiologiya ta’limi mazmunini muntazam yangilab borishni talab etayotgani asoslangan. Mikrobiologiya ta’limini klinik fanlar bilan integratsiyalash, talabalarda laboratoriya natijalarini talqin qilish, infeksion xavfsizlik va antimikrob preparatlardan oqilona foydalanish kompetensiyalarini shakllantirish ta’lim samaradorligini oshirishning muhim sharti sifatida ko‘rsatilgan.

Kalit so‘zlar: tibbiy mikrobiologiya, tibbiy ta’lim, bo‘lajak shifokor, klinik fikrlash, laboratoriya diagnostikasi, antibiotikorezistentlik, infeksion xavfsizlik, interaktiv ta’lim, amaliy ko‘nikma.

Kirish

Mikroorganizmlar odam organizmidagi fiziologik jarayonlar, yuqumli kasalliklarning etiologiyasi va patogenezi, immun javob, mikrobiota hamda antimikrob preparatlarga rezistentlik kabi ko‘plab tibbiy jarayonlarda muhim o‘rin tutadi. Shu sababli mikrobiologiya fani bo‘lajak shifokorning fundamental va klinik tayyorgarligini bog‘lovchi muhim o‘quv fanlaridan biri hisoblanadi.

Zamonaviy tibbiyotda infeksion kasalliklarning klinik ko‘rinishi, laboratoriya diagnostikasi va davolash tamoyillari doimiy ravishda takomillashib bormoqda. Ayniqsa, antibiotikorezistentlikning global muammoga aylanishi shifokordan nafaqat infeksiya qo‘zg‘atuvchilarini bilishni, balki antimikrob preparatlardan oqilona foydalanish, laboratoriya tekshiruvlarini to‘g‘ri talqin qilish va infeksiyalarning tarqalishining oldini olish bo‘yicha kompetensiyalarni ham talab qiladi [1, 2].

2024-yilda JSST tomonidan tibbiy ta’lim dasturlarida antibiotikorezistentlik mazmunini baholash uchun maxsus vosita ishlab chiqilgan bo‘lib, uning maqsadi tibbiyot talabalarida ushbu muammoga oid kompetensiyalarni shakllantirishdagi bo‘shliqlarni aniqlashdan iborat [2].

2026-yilda chop etilgan zamonaviy mikrobiologiya ta’limi bo‘yicha tavsiyalarda ham o‘quv dasturlarini zamonaviy tibbiy amaliyot ehtiyojlariga moslashtirish zarurligi ta’kidlangan. Mualliflar tibbiy ta’limda fundamental fanlarga ajratiladigan vaqt qisqarayotgani va integratsiyalashgan ta’lim kuchayayotgani fonida mikrobiologiyaning asosiy o‘quv maqsadlarini aniq belgilash muhimligini ko‘rsatgan [3].

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Material va usullar

Ushbu tezisda tibbiy ta’lim va mikrobiologiyani o‘qitishga oid ilmiy adabiyotlar, Jahon sog‘liqni saqlash tashkilotining ta’lim va antibiotikorezistentlikka oid tavsiyalari, infeksiyalarning oldini olish va nazorat qilish bo‘yicha o‘quv dasturlari hamda 2026-yilda e’lon qilingan zamonaviy mikrobiologiya ta’limiga oid ilmiy maqola tahlil qilindi [1–5].

Natijalar va muhokama

Tahlil natijalari mikrobiologiya fanini o‘qitishda an’anaviy yondashuvlar bilan bir qatorda talabaning mustaqil fikrlashi va amaliy faoliyatini rivojlantiruvchi pedagogik texnologiyalardan foydalanish zarurligini ko‘rsatdi.

Mikrobiologiyani o‘qitishning muhim yutuqlaridan biri — fan mazmunining klinik yo‘nalishining kuchayishidir. Talaba mikroorganizmning morfologiyasi va biologik xususiyatlarini alohida yodlash bilan cheklanmasdan, uni muayyan klinik holat, infeksiya mexanizmi, laboratoriya diagnostikasi va profilaktika bilan bog‘lay olishi kerak [3].

Bunday yondashuvda «qo‘zg‘atuvchi → yuqish mexanizmi → patogenez → klinik belgilar → laboratoriya diagnostikasi → davolash → profilaktika» mantiqiy zanjiri muhim ahamiyatga ega. Bu esa mikrobiologiya fanini klinik fikrlashni shakllantiruvchi fundamental fan sifatida qarash imkonini beradi.

Mikrobiologiya ta’limida laboratoriya mashg‘ulotlarining o‘rni ham alohida ahamiyatga ega. Mikroskopiya, preparat tayyorlash va bo‘yash, oziq muhitlarga ekish, sof kultura ajratish, mikroorganizmlarni identifikatsiya qilish, antibiotiklarga sezuvchanlikni aniqlash kabi amaliy mashg‘ulotlar talabaning kasbiy kompetensiyalarini shakllantirishga xizmat qiladi.

Biroq ta’lim jarayonida qator muammolar ham mavjud.

Birinchi muammo — mikrobiologiya o‘quv materialining hajmi kattaligi va unga ajratiladigan o‘quv vaqti cheklanganligidir. 2026-yilgi zamonaviy o‘quv maqsadlarida ham tibbiy ta’limda fundamental fanlarga ajratilgan vaqtning qisqarishi fonida mikrobiologiyaning eng muhim bazaviy kompetensiyalarini belgilash zarurligi ko‘rsatilgan [3].

Ikkinchi muammo — nazariy bilimlarning klinik vaziyatlar va amaliy ko‘nikmalar bilan yetarlicha bog‘lanmasligidir. Talaba mikroorganizmlarning morfologiyasi, fiziologiyasi, patogenlik xususiyatlari va laboratoriya diagnostikasi usullarini nazariy jihatdan yaxshi o‘zlashtirgan holda ham ushbu bilimlarni real klinik vaziyatlarda qo‘llashda qiyinchilikka duch kelishi mumkin. Shuning uchun tibbiy oliy ta’lim muassasalarida zamonaviy talablarga javob beradigan mikrobiologik o‘quv laboratoriyalarini tashkil etish va ularni o‘quv jarayoniga tizimli integratsiya qilish muhim ahamiyatga ega.

Mikrobiologik o‘quv laboratoriyasi talabalarga mikroskopiya, surtma tayyorlash va bo‘yash, oziq muhitlariga ekish, sof kultura ajratish, mikroorganizmlarni identifikatsiya qilish, antibiotiklarga sezuvchanlikni aniqlash kabi amaliy ko‘nikmalarni bosqichma-bosqich egallash imkonini beradi. Bunday mashg‘ulotlar nazariy bilimlarni amaliy faoliyat bilan bog‘lash, talabalarda laboratoriya natijalarini tahlil qilish va klinik fikrlash ko‘nikmalarini shakllantirishga xizmat qiladi.

Uchinchi muhim muammo — antibiotikorezistentlik masalasini o‘qitishning dolzarbligi. 2024-yilda Jahon sog‘liqni saqlash tashkiloti tomonidan tibbiy ta’lim dasturlarida antibiotikorezistentlik bo‘yicha bilim va kompetensiyalarni baholashga mo‘ljallangan maxsus metodik vosita — “Antimicrobial Resistance Curriculum Assessment Tool for Medical Education” ishlab chiqildi. U tibbiyot universitetlaridagi o‘quv dasturlarini tahlil qilish, mavjud bo‘shliqlarni aniqlash va antibiotikorezistentlikka oid ta’lim mazmunini takomillashtirishga xizmat qiladi [2].

Bundan tashqari, infeksion xavfsizlik masalalari ham mikrobiologiya ta’limi bilan uzviy bog‘liq. 2025-yilda JSST tibbiy ta’limning turli yo‘nalishlari uchun infeksiyalarning oldini olish va nazorat qilish bo‘yicha maxsus diplomoldi o‘quv dasturini ishlab chiqdi [4].

Shuningdek, mikrobiologiya ta’limida raqamli texnologiyalardan foydalanish imkoniyatlari kengaymoqda. Virtual laboratoriyalar, raqamli mikroskopiya, interaktiv testlar, klinik keyslar va

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multimedia materiallari talabalarga murakkab mikrobiologik jarayonlarni vizual va mantiqiy ravishda o‘zlashtirish imkonini beradi.

Ta’lim samaradorligini oshirish uchun keys-stadi, muammoli ta’lim, kichik guruhlarda ishlash, «aqliy hujum», klaster, konseptual xarita va klinik vaziyatli masalalardan foydalanish maqsadga muvofiq. Bunday usullar talabaning tayyor ma’lumotni qabul qilishidan ko‘ra, uni tahlil qilish, dalillarni taqqoslash va klinik qarorga kelish faolligini oshiradi.

Mikrobiologiyaning shifokor tayyorlashdagi yana bir muhim jihati — infeksiyalarning oldini olish va nazorat qilish kompetensiyalarini shakllantirishdir. Bunda sterilizatsiya, dezinfeksiya, antiseptika, qo‘l gigienasi, tibbiy asboblarni xavfsiz qo‘llash, gospital infeksiyalarning oldini olish kabi masalalar muhim o‘rin tutadi [4, 5].

Shunday qilib, zamonaviy mikrobiologiya ta’limi uchta asosiy yo‘nalishni birlashtirishi maqsadga muvofiq: fundamental mikrobiologik bilimlar, amaliy laboratoriya ko‘nikmalari va klinik-infeksion kompetensiyalar.

Xulosa

Mikrobiologiya fani bo‘lajak shifokorlarni tayyorlashda muhim fundamental fan bo‘lib, uning mazmuni klinik tibbiyot ehtiyojlari bilan uzviy bog‘langan holda tashkil etilishi zarur.

Tahlillar shuni ko‘rsatadiki, zamonaviy mikrobiologiya ta’limida asosiy e’tibor mikroorganizmlar haqidagi ma’lumotlarni yodlashdan ko‘ra, ularni klinik vaziyatda qo‘llash, laboratoriya natijalarini talqin qilish, infeksion xavfsizlikni ta’minlash va antibiotiklardan oqilona foydalanish kompetensiyalarini shakllantirishga qaratilishi kerak [1–5]. Mikrobiologiya fanini o‘qitish samaradorligini oshirish uchun o‘quv dasturlarini muntazam yangilash, klinik fanlar bilan integratsiyani kuchaytirish, laboratoriya mashg‘ulotlarini amaliy yo‘naltirish, interaktiv va raqamli ta’lim texnologiyalaridan foydalanish hamda antibiotikorezistentlik va infeksion xavfsizlik masalalarini tizimli ravishda o‘quv jarayoniga kiritish maqsadga muvofiq.

Bu yondashuv mikrobiologiya fanini faqat nazariy bilim beruvchi fan emas, balki zamonaviy, mustaqil fikrlaydigan va infeksion kasalliklarni profilaktika qilish, diagnostika va davolashda ilmiy asoslangan qaror qabul qila oladigan shifokorni shakllantiruvchi muhim ta’limiy komponent sifatida rivojlantirishga xizmat qiladi.

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“*SALVIA OFFICINALIS*” BARGIDAN AJRATIB OLINGAN ENDOFIT ZAMBURUG‘INING MORFOLOGIK VA KULTURAL XUSUSIYATLARI

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Annotatsiya: Ushbu tadqiqotda Lamiaceae oilasiga mansub Salvia officinalis L. barglarida uchraydigan endofit zamburug‘-Alternaria izolyatining morfologik hamda kultural xususiyatlari tahlil qilindi. Ajratib olingan izolyat yorug‘lik mikroskopiyasi va mikologik ma’lumotlar bazalari orqali Alternaria alternata sifatida dastlabki identifikatsiya qilindi. Tadqiqot natijalari Salvia officinalis barglarida endofit zamburug‘lar mavjudligini ko‘rsatadi.
Kalit so‘zlar: Alternaria alternata, MycoBank, endofit zamburug‘, konidiya, Salvia officinalis

Abstract: This study investigated the isolation and morphological and cultural characteristics of an endophytic fungal isolate of Alternaria obtained from the leaves of Salvia officinalis L., a member of the Lamiaceae family. The isolated fungus was preliminarily identified as Alternaria alternata based on light microscopy and comparison with mycological databases. The results of the study demonstrated in the leaves of Salvia officinalis L.
Keywords: Alternaria alternata, MycoBank, endophytic fungi, conidium, Salvia officinalis

Kirish

Endofit zamburug‘lar o‘simlik to‘qimalarida yashab, kasallik belgilarini namoyon qilmaydigan va o‘simliklarning o‘sishi, rivojlanishi hamda tashqi stress omillariga chidamliligini oshiradigan mikroorganizmlar hisoblanadi [3,5]. Endofit zamburug‘lar o‘simliklar bilan simbiotik munosabatda bo‘lib, ularning fiziologik holatiga ijobiy ta’sir ko‘rsatadi. Shuningdek, endofit zamburug‘lar ikkilamchi metabolitlarning keng manbaini sintez qilish qobiliyatiga egaligi uchun o‘simliklarga foydali ta’sir qiladi [4]. Lamiaceae oilasiga mansub o‘simliklar — yalpiz (Mentha), tog‘ rayhoni (Origanum vulgare), lavanda (Lavandula angustifolia) va boshqa turlar — efir moylari, fenolik birikmalar va boshqa-boshqa biologik faol moddalarga boy bo‘lib, dorivor, oziq-ovqat va kosmetika sanoatida keng qo‘llaniladi. Ushbu o‘simliklarning farmakologik xususiyatlari asosan ularning ikkilamchi metabolitlari bilan bog‘liq bo‘lsa-da, so‘nggi ilmiy ma’lumotlarga ko‘ra ushbu metabolitlarning ayrimlari aynan endofit zamburug‘lar faoliyati bilan bevosita yoki bilvosita bog‘liq bo‘lishi mumkin [6,1].

Ushbu oilaga mansub Salvia turkumi vakillari ham dorivor va biologik faol xususiyatlari bilan katta qiziqish uyg‘otadi. Shuning uchun Salvia officinalis o‘simligida uchraydigan endofit zamburug‘larni o‘rganish yangi zamburug‘ izolyatlarini aniqlash va ularning biologik xususiyatlarini tadqiq etish uchun muhim yo‘nalish hisoblanadi.

Filamentli zamburug‘lar guruhiga kiradigan Alternaria turkumi vakillari ham tabiatda keng tarqalgan, shu jumladan, Alternaria alternata ham o‘simliklardan tez-tez ajratib olinadigan umumiy zamburug‘lar guruhiga kiradi. *Alternaria alternata* o‘simliklardan patogen sifatida ajratib olinishi bilan bir qatorda, ular sog‘lom o‘simlik to‘qimalaridan endofit sifatida ham ajratib olingan [2].

Ushbu tadqiqotning maqsadi Salvia officinalis bargidan zamburug‘ izolyatini ajratib olish, uning toza kulturasini olish hamda morfologik belgilar asosida identifikatsiya qilishdan iborat.

IQTIBOS UCHUN
Yo‘ldosheva S.M. “Salvia officinalis” bargidan ajratib olingan endofit zamburug‘ining morfologik va kultural xususiyatlari // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 116–118.
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Materiallar va tadqiqot metodlari

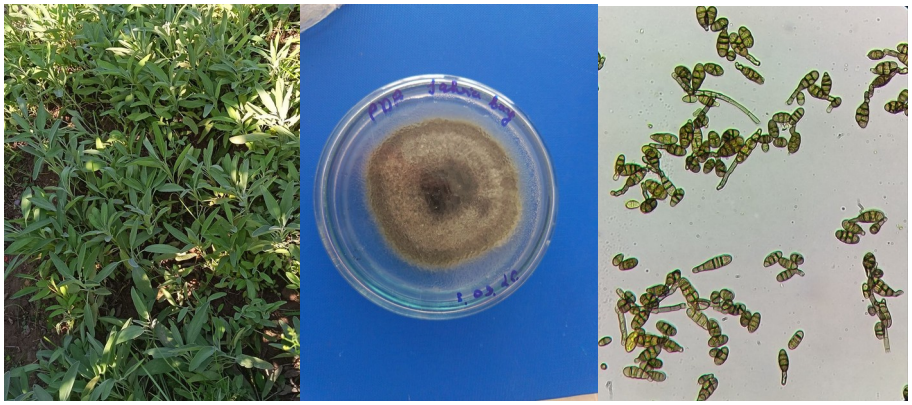
Tadqiqot materiali sifatida O‘zbekiston Respublikasi Botanika instituti huzuridagi Botanika bog‘ida joylashgan Dorivor o‘simliklar kolleksiyasidan *Salvia officinalis* L. o‘simligining sog‘lom ko‘rinishdagi barg namunalari olindi. Endofit zamburug‘larni ajratib olishda eng asosiy usullardan biri yuzaki sterilizatsiya usulidan foydalanildi. Dastlab o‘simlik to‘qimalari oqar suvda yuvildi, so‘ngra 70 % etil spirti va yuzaki sterilizatsiya qiluvchi eritmasida ma’lum vaqt davomida ushlab turildi. Keyin to‘qimalar steril distillangan suv bilan bir necha marotaba yuvildi. Ushbu usul o‘simlik ichida joylashgan endofit zamburug‘larni saqlab qolgan holda tashqi mikroflorani yo‘q qilish imkonini beradi [6].

Sterilizatsiyadan so‘ng o‘simlik to‘qimalari steril sharoitda kichik bo‘laklarga kesildi va PDA ozuqa muhitiga joylashtirildi. Kontrol sifatida oxirgi yuvilgan suvdan bir tomchi suv agar muhitga sepildi.

N-300M(HDCE-X5) modelli mikroskopida mitseliy, gifalarning tuzilishi, konidiyalarning shakli, septalarining mavjudligi hamda joylashish xususiyatlari o‘rganildi.

Tadqiqot natijalari va ularning muhokamasi

Salvia officinalis L. barglaridan endofit zamburug‘larni ajratib olish maqsadida mikrobiologik tadqiqot ishlari olib borildi. Steril qilingan o‘simlik namunalari steril ozuqa muhitiga ekildi va koloniyalarning rivojlanishi kuzatildi. Dastlab koloniya oqish mitseliy hosil qildi, keyinchalik koloniyaning rangi to‘qroq rangga kirdi. Kultura yuzasi zich mitseliy ko‘rinishida bo‘lib, vaqt o‘tishi bilan koloniyaning markaziy qismi to‘qroq rangga kirdi. Mikroskopik, morfologik xususiyatlarini o‘rganish davomida *Alternaria* turkumiga xos belgilar aniqlandi. Mikroskopik kuzatishlar davomida septali gifalar, konidiyalarning hosil bo‘lishi aniqlandi. Konidiyalar zanjirsimon yoki yakka bo‘lib uchrashi, ko‘ndalang va ba’zi hollarda bo‘ylama septalarga ega bo‘lishi bilan tavsiflanadi. Olingan morfologik va kultural xususiyatlari asosida *Alternaria alternata* turiga yaqin deb baholandi.



1-rasm. A — Salvia officinalis; B — Salvia officinalis bargidan ajratib olingan endofit zamburug‘; C — Sporalarning mikroskop ostida ko‘rinishi

Xulosa

Ilmiy tadqiqot davomida, Salvia officinalis barglaridan endofit zamburug‘ izolyati ajratib olindi va morfologik hamda kultural xususiyatlari o‘rganildi. Koloniyaning tuzilishi, rangining o‘zgarishi, konidioforalarining bo‘lishi, konidiyalarining hosil bo‘lishi va tuzilishi, mitseliy tuzilishi kabi belgilar asosida ajratib olingan izolyatning Alternaria turkumiga mansubligini ko‘rsatdi. Morfologik belgilar asosida izolyat Alternaria alternata sifatida dastlabki identifikatsiya qilindi.

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ABUNDANCE OF THE MICROBIAL COMMUNITY IN VARIOUS GUT SECTIONS OF *ANACANTHOTERMES AHNGERIANUS* WORKER TERMITES

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Termites are a vital component of terrestrial ecosystems, playing a key role in the decomposition of plant debris, the transformation of organic matter, and the cycling of biogenic elements. Microorganisms inhabiting the termite gut play a significant role in these processes. The gut microbiota comprises a diverse array of microorganisms capable of breaking down complex organic compounds including plant cell wall components and generating microbial metabolites. Notably, the abundance and composition of the microbial community vary according to the physiological and physicochemical conditions within different sections of the gut.

Studying the spatial distribution of key physiological and taxonomic microbial groups within the termite gut provides insight into the formation of the microbial community. A comparison of microbial abundance across the anterior, mid-, and posterior gut sections of *Anacanthotermes ahngerianus* workers is of particular interest. Such studies are crucial for understanding the interaction between termites and their gut microbiota and for determining the potential role of microorganisms in the transformation of organic substrates.

The aim of the study was to examine the abundance of microorganisms in various sections of the gut of *A. ahngerianus* worker termites and to identify the characteristics of their spatial distribution. The study subjects were worker termites of the species *A. ahngerianus* collected in the Beruni District of the Republic of Karakalpakstan, Uzbekistan. To study microbial abundance, the gut was divided into three sections: anterior, middle, and posterior. Ten termite individuals were selected for the analysis of each section. The guts were dissected under aseptic conditions, pooled according to section, and homogenized in sterile phosphate-buffered saline. The resulting suspensions were serially diluted with sterile 0.9% sodium chloride (NaCl) solution. Microorganisms were inoculated using the pour-plate method from serial dilutions of the gut suspension onto appropriate culture media: Czapek medium (for cultivating micromycetes), meat-peptone agar (MPA) (for determining the total count of cultivable bacteria), Hutchinson medium (for detecting aerobic cellulose-degrading microorganisms), and Omeliansky medium (for cultivating anaerobic cellulose-degrading microorganisms). The cultures were incubated at 29°C. Colony counts were performed on day 7 for micromycetes, day 3 for bacteria, and day 25 for cellulose-degrading microorganisms. The abundance of cultivable microorganisms was calculated and expressed as colony-forming units per termite (CFU/termite). The study revealed differences in the abundance of major microorganism groups depending on the gut section of *A. ahngerianus* worker termites (Table 1).

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Table 1. Abundance of cultivable microorganisms from various sections of the gut of the worker termite *Anacanthotermes ahngerianus*

No.	Section of the intestine	Microorganisms, CFU/termite				
		Bacteria	*Clostridium*	Fungi	Cellulose-degrading aerobes	Cellulose-degrading anaerobes
1.	Anterior gut	$4{,}5x10^3$	$1{,}5x10^2$	$1{,}5x10^1$	$7{,}0x10^2$	$6x10^1$
2.	Midgut	$3x10^2$	not detected	$4{,}5x10^1$	$1{,}3x10^3$	$2{,}5x10^3$
3.	Hindgut	$6x10^3$	$6x10^2$	$3x10^1$	$1{,}1x10^5$	$1{,}3x10^2$

The study established that the abundance of various microorganism groups in the gut of *A. ahngerianus* worker termites varies depending on the specific section of the intestinal tract. The most pronounced differences were observed among cellulose-degrading microorganisms.

In the anterior gut section, bacterial abundance was $4.5x10^3$ CFU/termite; *Clostridium* counts were $1.5x10^2$ CFU/termite, and micromycete counts were $1.5x10^1$ CFU/termite. The abundance of aerobic cellulose-degrading microorganisms reached $7.0x10^2$ CFU/termite, whereas anaerobic representatives of this functional group numbered $6.0x10^1$ CFU/termite. Thus, in the anterior section, the abundance of aerobic cellulose-degraders exceeded that of anaerobes by approximately 11.7-fold.

In the midgut, a decrease in total bacterial abundance to $3.0x10^2$ CFU/termite was observed. No Clostridium species were detected. However, the abundance of aerobic cellulose-degrading microorganisms increased to $1.3x10^3$ CFU/termite, and that of anaerobic ones to $2.5x10^3$ CFU/termite. In the midgut, the abundance of anaerobic cellulose-degraders exceeded that of aerobes by approximately 1.9-fold. This may indicate differences in the conditions favoring the development of the respective functional groups; however, confirming this hypothesis requires a direct assessment of oxygen levels and other characteristics of the gut environment. The highest abundance of aerobic cellulose-degrading microorganisms was recorded in the hindgut, amounting to $1.1x10^5$ CFU/termite. This figure was approximately 157 times higher than that observed in the foregut and 85 times higher than that in the midgut. In contrast, the abundance of anaerobic cellulose-degraders in the hindgut was $1.3x10^2$ CFU/termite, a value significantly lower than that found in the midgut. Consequently, a marked quantitative predominance of cultivable aerobic cellulose-degrading microorganisms was observed in the hindgut.

Bacterial abundance in the hindgut reached $6.0x10^3$ CFU/termite, while *Clostridium* counts were $6.0x10^2$ CFU/termite. Conversely, the maximum abundance of micromycetes was recorded in the midgut, at $4.5x10^1$ CFU/termite. These results indicate a heterogeneous distribution of the studied microbial groups and suggest that the population dynamics of cellulose-degrading groups do not fully mirror the dynamics of the total bacterial population.

Thus, the data demonstrate that the different gut sections of the worker termite *A. ahngerianus* are characterized by distinct ratios of cultivable microorganisms. The hindgut stands out particularly, as it harbored the highest abundance of aerobic cellulose-degrading microorganisms. The midgut is characterized by a predominance of anaerobic cellulose-degraders over aerobes. These findings are of interest for further research into the potential role of gut microbiota in the transformation of plant residues.

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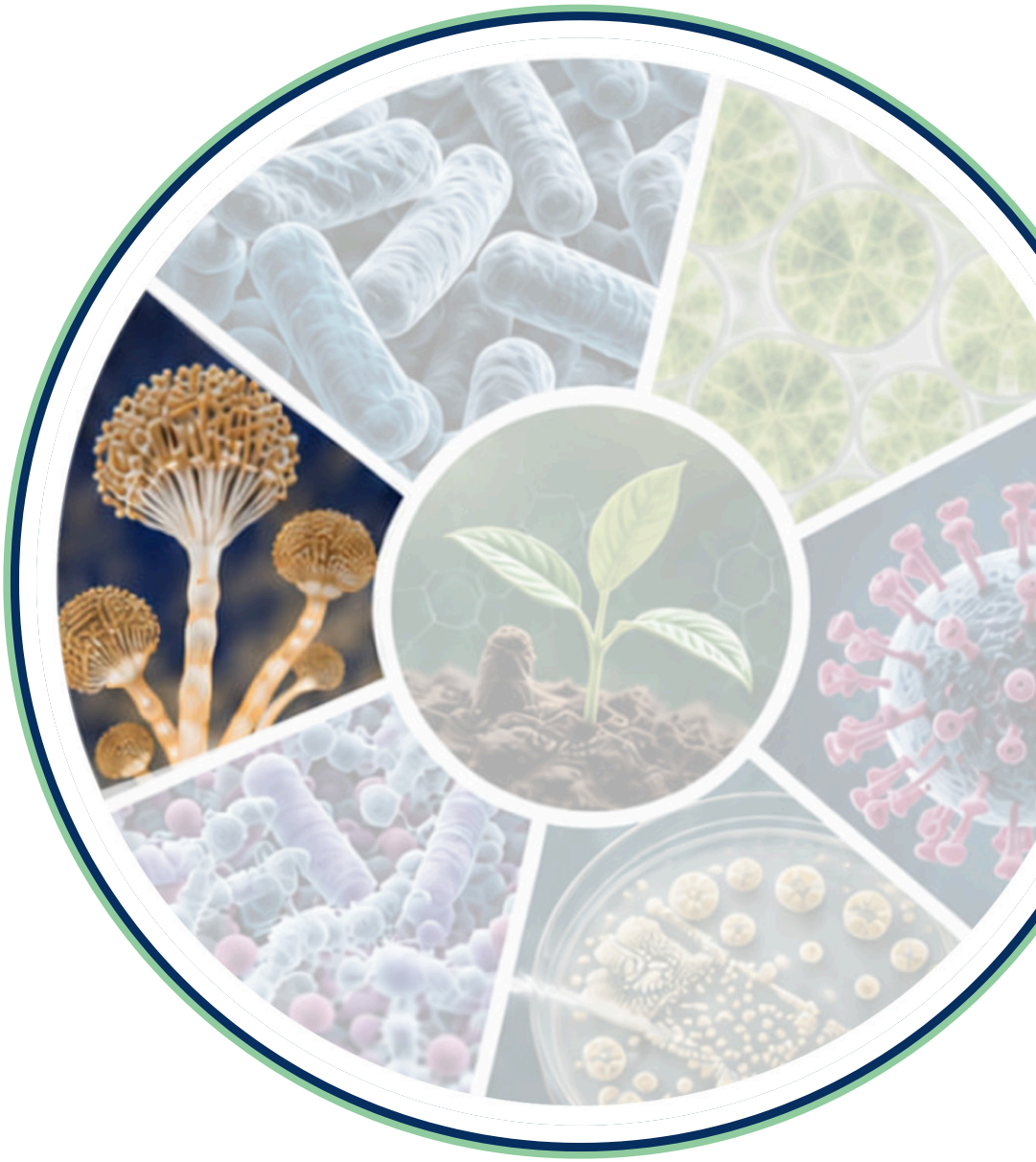
II

BO‘LIM · SECTION · СЕКЦИЯ

BIOTEXNOLOGIYA, MOLEKULYAR BIOLOGIYA VA BIOINFORMATIKA

Biotechnology, Molecular Biology and Bioinformatics

Биотехнология, молекулярная биология и биоинформатика



27
ta maqola va tezis

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KARTOSHKA NAVLARIDAGI CHIDAMLILIK GENLARINING VIRUSLARGA QARSHI HIMOYA MEXANIZMI

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Annotatsiya: Maqolada kartoshka (*Solanum tuberosum* L.) navlarida uchraydigan virusga chidamlilik genlarining ishlash mexanizmlari adabiyotlar asosida tahlil qilingan. Gipersezgirlik reaksiyasi va ekstremal chidamlilikni ta’minlovchi genlar (*Rx1*, *Rx2*, *Ny*, *Ry*), ularning virus oqsillarini tanib olishi hamda RNK-interferensiya tizimi bilan bog‘liqligi yoritilgan. Chidamlilik genlarini molekulyar markerlar yordamida aniqlashning seleksiyadagi ahamiyati ko‘rsatilgan.

Kalit so‘zlar: kartoshka, virusga chidamlilik, *Rx1*, NLR oqsillari, ekstremal chidamlilik, gipersezgirlik, RNK-interferensiya, KXV, KYV.

Аннотация: В статье на основе литературных данных проанализированы механизмы действия генов вирусоустойчивости у картофеля (*Solanum tuberosum* L.). Рассмотрены гены (*Rx1*, *Rx2*, *Ny*, *Ry*), обеспечивающие реакцию сверхчувствительности и экстремальную устойчивость, их распознавание вирусных белков и связь с системой РНК-интерференции. Показано значение молекулярных маркеров в селекции на устойчивость.

Ключевые слова: картофель, вирусоустойчивость, *Rx1*, NLR-белки, экстремальная устойчивость, сверхчувствительность, РНК-интерференция, ВКХ, ВКУ.

Abstract: The article analyzes, based on the literature, the mechanisms of virus resistance genes in potato (*Solanum tuberosum* L.). Genes (*Rx1*, *Rx2*, *Ny*, *Ry*) that provide the hypersensitive response and extreme resistance are reviewed, together with their recognition of viral proteins and their link to the RNA interference system. The importance of molecular markers in resistance breeding is shown.

Keywords: potato, virus resistance, *Rx1*, NLR proteins, extreme resistance, hypersensitive response, RNA interference, PVX, PVY.

Kirish

Kartoshka (*Solanum tuberosum* L.) dunyoning eng muhim oziq-ovqat ekinlaridan biridir. FAO ma’lumotlariga ko‘ra, rivojlanayotgan mamlakatlarning ko‘pchiligida u guruch, bug‘doy va makkajo‘xoridan keyin to‘rtinchi o‘rinda turadi, dunyo bo‘yicha ishlab chiqarish esa 2007-yilda 325 million tonnaga yetgan (FAO, 2009). Shu sababli kartoshka hosildorligini saqlash oziq-ovqat xavfsizligi uchun muhim vazifadir.

Kartoshka asosan vegetativ yo‘l bilan, ya’ni tuganaklar orqali ko‘paytiriladi. Bunday ekinlarda virus tuganak bilan keyingi yilga o‘tadi va nazorat qilinmasa, hosil miqdori va sifatini sezilarli kamaytiradi (Loebenstein va boshq., 2001; Valkonen, 2007). Toza urug‘lik material olish uchun to‘qima kulturasi usullaridan foydalanilsa-da, ko‘p mamlakatlarda virus bilan zararlanish hanuzgacha katta yo‘qotishlarga sabab bo‘lmoqda (Loebenstein va boshq., 2001).

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Ahmadjonova S.U., Jovliyeva D.T., Fayziyev V.B. Kartoshka navlaridagi chidamlilik genlarining viruslarga qarshi himoya mexanizmi // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 123–126.
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Kartoshkada eng ko‘p o‘rganilgan viruslarga kartoshka X virusi (KXV, *Potato virus X*) va kartoshka Y virusi (KYV, *Potato virus Y*) kiradi. O‘simlik virusologlari o‘rtasida o‘tkazilgan so‘rovda ilmiy va iqtisodiy ahamiyati bo‘yicha eng muhim 10 ta o‘simlik virusi aniqlanganda, KYV beshinchi, KXV esa o‘ninchi o‘rinni egalladi (Scholthof va boshq., 2011).

Virus o‘simlik hujayrasi ichida ko‘payadi, shuning uchun uni kimyoviy vositalar bilan yo‘qotish qiyin. Eng ishonchli yo‘l chidamli navlarni yaratishdir. Chidamlilik genlarining ko‘pchiligi virus oqsilini maxsus taniydigan NLR oqsillarini kodlaydi (Jones va Dangl, 2006). Genlarning ketma-ketligi ma’lum bo‘lgani sari ularni molekulyar markerlar yordamida aniqlash imkoniyati ham kengaymoqda (Ahmadvand va boshq., 2013). Shuning uchun chidamlilik genlari qanday ishlashini bilish seleksiyada to‘g‘ri gen tanlash va yangi navlarni tez baholash uchun zarur.

Maqolaning maqsadi kartoshkadagi asosiy chidamlilik genlarining viruslarga qarshi ishlash mexanizmini adabiyotlar asosida tahlil qilish va ularni aniqlash usullari bilan bog‘lashdir.

Metodlar

Ish adabiyotlar tahlili usulida bajarildi. PubMed Central, Google Scholar va NCBI ma’lumotlar bazalaridagi ilmiy maqolalar o‘rganildi. Chidamlilik genlari qaysi turdan olingani, qaysi virus oqsilini tanishi va qanday javob reaksiyasi berishi bo‘yicha solishtirildi. Natijalar 1-jadvalda jamlandi.

Natijalar

1. Chidamlilik genlarining turlari

Jones va Dangl (2006) o‘simlik immunitetini ikki bosqichga bo‘ladi: birinchisida o‘simlik patogenning umumiy belgilarini tanisa, ikkinchisida patogenning aynan o‘ziga xos oqsilini taniydi. Kartoshkadagi virusga qarshi genlar ko‘pincha ikkinchi bosqichga kiradi. Ular NLR oqsillarini (NB-LRR) kodlaydi. Bu oqsil virusning ma’lum bir oqsilini taniganda himoya javobini ishga tushiradi. Asosiy genlar 1-jadvalda berilgan.

Javob ikki xil bo‘lishi mumkin. Birinchisi gipersezgirlik reaksiyasi (GR): virus kirgan hujayralar nobud bo‘ladi va virus bargdagi kichik nekrotik dog‘ ichida qolib ketadi. Ikkinchisi ekstremal chidamlilik (EC): virus juda erta to‘xtatiladi va o‘simlikda deyarli hech qanday belgi ko‘rinmaydi. *Rx* genida ikkala javob ham mavjud. Bendahmane va boshq. (1999) ko‘rsatishicha, *Rx* hujayra nobud bo‘lishini ham boshlay oladi, lekin ekstremal chidamlilik nekrozdan alohida ishlaydi va undan ustun turadi.

1-jadval. Kartoshkadagi asosiy virusga chidamlilik genlari

Gen	Manba	Virus	Reaksiya turi	Virus omili
Rx1	*S. tuberosum* ssp. *andigena*	KXV	Ekstremal chidamlilik	Qobiq oqsili (CP)
Rx2	*S. acaule*	KXV	Ekstremal chidamlilik	Qobiq oqsili (CP)
Nb	Madaniy kartoshka navlari	KXV (ayrim shtammlari)	Gipersezgirlik	25K harakat oqsili
Ny-1, *Ny-2*, *Ny-tbr*	Madaniy kartoshka navlari	KYV (ayrim shtammlari)	Gipersezgirlik	To‘liq aniqlanmagan
Ry-adg, *Ry-sto*, *Ry-chc*	*S. tuberosum* ssp. *andigena*, *S. stoloniferum*, *S. chacoense*	KYV (ko‘p shtammlari)	Ekstremal chidamlilik	To‘liq aniqlanmagan

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2. *Rx1* va *Rx2* genlari: KXVga qarshi himoya

Rx1 geni *S. tuberosum* ssp. *andigena* shaklidan, *Rx2* geni esa yovvoyi *S. acaule* turidan olingan. *Rx1* XII xromosomada, *Rx2* esa V xromosomada joylashgan. Ikkala gen ham CC-NB-LRR oqsilini kodlaydi va KXVning qobiq oqsilini taniydi (Bendahmane va boshq., 1995, 1999, 2000). Bu ikki gen bir-biriga juda o‘xshash bo‘lgani uchun ularni ajratib aniqlash uchun alohida molekulyar markerlar ishlab chiqilgan (Ahmadvand va boshq., 2013).

Rx oqsilining qismlari bir-biri bilan o‘zaro ta’sirlashadi: CC qismi NB-LRR qismi bilan, LRR qismi esa CC-NB qismi bilan bog‘lanadi. Bu qismlarni alohida ifodalab ham ishlaydigan oqsil hosil qilish mumkin (Moffett va boshq., 2002). Tameling va Baulcombe (2007) *Rx* oqsili hujayrada RanGAP2 oqsili bilan bog‘lanishini aniqladi. RanGAP2 kamaytirilganda *Rx* orqali chidamlilik susayadi, ya’ni bu oqsil KXVga qarshi himoya uchun kerak.

3. *Nb*, *Ny* va *Ry* genlari

Nb geni ham KXVga qarshi ishlaydi, lekin gipersezgirlik orqali. U virusning 25K harakat oqsilini taniydi, bunda oqsilning 6-o‘rnidagi izoleysin aminokislotasi muhim (Malcuit va boshq., 1999). KYVga qarshi *Ny* genlari gipersezgirlik, *Ry* genlari esa ekstremal chidamlilik beradi. *Ry-adg* (*S. andigena*dan) XI xromosomada, *Ry-sto* (*S. stoloniferum*dan) XII xromosomada joylashgan, *Ry-chc* esa *S. chacoense* turidan olingan. Grech-Baran va boshq. (2020) *Ry-sto* geni TIR-NLR oqsilini kodlashini, uning ishlashi haroratga bog‘liq emasligini va EDS1 hamda NRG1 oqsillarini talab qilishini ko‘rsatdi.

4. RNK-interferensiya

Genlardan tashqari, o‘simlikda RNK-interferensiya tizimi ham virusga qarshi ishlaydi: u virus RNKsini parchalaydi. Viruslar bunga qarshi susaytirish supressorlarini hosil qiladi. KXVda bu p25 oqsili, KYVda HC-Pro oqsilidir.

Muhokama

Ekstremal chidamlilik beradigan genlar (*Rx1*, *Rx2*, *Ry*) seleksiya uchun qulayroq, chunki ular virusni nekroz hosil qilmasdan erta to‘xtatadi. Lekin bu genlarning hammasi virus oqsilini tanishga asoslangan. Agar virus oqsili o‘zgarsa, gen uni tanimay qo‘yishi mumkin. Bendahmane va boshq. (1995) qobiq oqsilini KXV shtammlariga xos elitsitor deb ko‘rsatgan, ya’ni shtammlar orasida farq bor.

Shu sababli bitta genga tayanish xavfli. Bitta navda turli mexanizmli genlarni birlashtirish (piramidalash) va virus shtammlarini kuzatib borish maqsadga muvofiq.

Genlarning ketma-ketligi ma’lum bo‘lgani uchun ularni PCR markerlari bilan aniqlash mumkin. *Rx1* geni kartoshka sista nematodasiga (*Globodera pallida*) qarshi *Gpa2* geniga juda o‘xshash. Ikkala gen XII xromosomada bir-biridan atigi 0,02 cM masofada joylashgan va bitta yovvoyi shakldan (*S. tuberosum* ssp. *andigena* CPC 1673) o‘tgan (Rouppe van der Voort va boshq., 1999; Van der Vossen va boshq., 2000). Shuning uchun praymerlar *Rx1*ga xos bo‘lishi va *Gpa2* bilan chalkashmasligi kerak. Buni dastlab kompyuterda (Primer-BLAST, *in silico* PCR) tekshirish vaqt va mablag‘ni tejaydi.

Bu ishning cheklovi shuki, mexanizmlar asosan xorijiy navlar va model o‘simliklarda o‘rganilgan. Mahalliy navlarda genlarning bor-yo‘qligini alohida tekshirish kerak.

Xulosa

1. Kartoshkadagi virusga chidamlilik genlarining ko‘pchiligi NLR oqsillarini kodlaydi va virus oqsilini tanib, gipersezgirlik yoki ekstremal chidamlilikni ishga tushiradi.

2. *Rx1* va *Rx2* KXV qobiq oqsilini taniydi, *Nb* esa 25K harakat oqsilini taniydi. *Ry* genlari KYVga qarshi ekstremal chidamlilik beradi.

3. Viruslar o‘zgarib chidamlilikni yengib o‘tishi mumkin, shuning uchun turli genlarni birlashtirish zarur.

4. Gen-spetsifik praymerlar chidamli navlarni tez va aniq tanlash imkonini beradi.

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A BRIEF COMPARATIVE BIOINFORMATICS ANALYSIS OF A KatB-LIKE CATALASE PROTEIN CANDIDATE FROM *BACILLUS THURINGIENSIS Bt26* AND REFERENCE KatB PROTEINS FROM OTHER *B. THURINGIENSIS* STRAINS

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Abstract: This study comparatively analyzed the catalase protein candidate corresponding to the *JEEBFNLG_01767* locus in the genome of *Bacillus thuringiensis* 26 against reference KatB protein sequences from 50 other *B. thuringiensis* strains. BLASTP analysis revealed amino acid sequence identity ranging from 94.672% to 100%, with 27 reference proteins showing 100% identity. BLASTN analysis identified 26 reference sequences with 100% nucleotide identity. Multiple sequence alignment revealed 40 variable amino acid positions and a total of 125 recorded differences, with the most frequent differences occurring at positions 254, 169, and 291. Phylogenetic analysis indicated close sequence relationships between the protein candidate and many reference proteins. However, despite being annotated as *katA_1*, the locus exhibited high similarity to reference KatB proteins. Therefore, the protein is provisionally described as a KatB-like catalase candidate, and further studies are required to clarify its functional identity.

Keywords: *Bacillus thuringiensis*, *Bt*26, catalase, KatB protein, amino acid substitutions, comparative bioinformatics.

Annotatsiya: Ushbu tadqiqotda *B. thuringiensis* 26 shtammi genomidagi *JEEBFNLG_01767* lokusiga mos katalaza oqsili nomzodi boshqa 50 ta *B. thuringiensis* larning KatB oqsillari referens ketma-ketlik bilan qiyosiy tahlil qilindi. BLASTP tahlilida aminokislota identikligi 94,672–100% oralig‘ida bo‘lib, 27 ta referens oqsil bilan 100% identiklik aniqlandi. BLASTN tahlilida 26 ta referens ketma-ketlik bilan 100% nukleotid identikligi qayd etildi. Ko‘p ketma-ketlikli tekislash natijasida 40 ta o‘zgaruvchan aminokislota pozitsiyasi va jami 125 ta farq qaydi aniqlandi; eng ko‘p farqlar 254-, 169- va 291-pozitsiyalarda kuzatildi. Filogenetik tahlil oqsil nomzodining ko‘plab referens oqsillar bilan yaqin ketma-ketlik munosabatlariga ega ekanini ko‘rsatdi. Biroq lokus *katA_1* sifatida annotatsiya qilinganiga qaramay, referens KatB oqsillari bilan yuqori o‘xshashlik namoyon etdi. Shu sababli, ushbu oqsil hozircha KatB-ga o‘xshash katalaza nomzodi sifatida tavsiflanadi; uning funksional mansubligini aniqlashtirish uchun qo‘shimcha tadqiqotlar talab etiladi.

Kalit so‘zlar: *B. thuringiensis*, *Bt*26, katalaza, KatB oqsili, aminokislota almashinishlari, qiyosiy bioinformatika.

Аннотация: В настоящем исследовании проведён сравнительный анализ белка-кандидата каталазы, соответствующего локусу JEEBFNLG_01767 в геноме *Bacillus thuringiensis* 26, с референсными аминокислотными последовательностями белков KatB из 50 других штаммов *B. thuringiensis*. Анализ BLASTP выявил идентичность аминокислотных последовательностей в диапазоне от 94,672 до 100%; при этом 27 референсных белков показали 100%-ную идентичность. В результате анализа BLASTN были выявлены 26

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референсных последовательностей со 100%-ной идентичностью нуклеотидных последовательностей. Множественное выравнивание последовательностей выявило 40 вариабельных позиций аминокислот и в общей сложности 125 зарегистрированных различий. Наиболее часто различия наблюдались в позициях 254, 169 и 291. Филогенетический анализ показал близкое родство последовательностей белка-кандидата со многими референсными белками. Однако, несмотря на аннотацию локуса как *katA_1*, он продемонстрировал высокую степень сходства с референсными белками KatB. Таким образом, данный белок предварительно охарактеризован как кандидат на KatB-подобную каталазу, а для уточнения его функциональной идентичности необходимы дальнейшие исследования.

Ключевые слова: *Bacillus thuringiensis*, штамм 26, каталаза, белок KatB, аминокислотные замены, сравнительный биоинформатический анализ.

Introduction

Catalases (EC 1.11.1.6) are enzymes that protect cells against oxidative damage by decomposing hydrogen peroxide into water and oxygen. They play an important role in the bacterial response to oxidative stress. Based on their structural and catalytic properties, catalases are classified into monofunctional catalases, catalase-peroxidases, and manganese catalases. Because proteins with similar sequences may differ in their enzymatic properties, functional classification requires the evaluation of multiple lines of evidence [1–3].

Different catalases with distinct physiological roles occur in the genus *Bacillus*. For example, in *Bacillus subtilis*, KatA is the major catalase in growing cells, whereas KatX is associated with sporulation and contributes to protection against hydrogen peroxide during spore germination [4]. The enzymatic activity and stability under acidic conditions of KatB isolated from *Bacillus altitudinis* SYBC hb4 have also been characterized experimentally [5]. More recently, the catalase-peroxidase activity of KatB from *B. thuringiensis* strain 97–27 and its involvement in Mn(II) oxidation were experimentally demonstrated [6]. These studies highlight the importance of comparing bacterial catalases in terms of both sequence characteristics and functional properties.

Studies of *B. thuringiensis* genomics have reported that genome annotations do not always fully correspond to protein expression data [7]. Comparative genomic analyses among strains also enable the investigation of genetic similarities and evolutionary relationships [8]. In our previous study, 60 genes associated with abiotic stress were identified in the genome of *B. thuringiensis* Bt-26, including several genes associated with oxidative stress [9].

The aim of this study was to compare the catalase protein candidate corresponding to the *JEEBFNLG_01767* locus in the *B. thuringiensis Bt26* genome with 50 reference sequences, identify amino acid differences, and assess phylogenetic relationships. The locus was annotated as *katA_1*; however, preliminary comparisons revealed high similarity to KatB proteins. This discrepancy was also an important aspect of the study.

Materials and Methods

The previously assembled and annotated genome sequence of *B. thuringiensis* strain *Bt26* was used in this study. Prokka v1.14.6 was used for the previous genome annotation [9, 10]. The nucleotide and amino acid sequences corresponding to the *JEEBFNLG_01767* locus were retrieved. Fifty reference sequences selected from the NCBI RefSeq database were used for comparison [11].

Protein and nucleotide sequence similarity was assessed using the BLASTP and BLASTN algorithms in BLAST+ v2.12.0+ [12]. Protein comparisons were evaluated based on sequence identity, alignment length, query coverage, E-value, and bit score, whereas nucleotide comparisons were evaluated based on sequence identity, coverage, and alignment length.

The *Bt26* protein candidate and reference proteins were subjected to multiple sequence alignment using MAFFT v7.526 [13]. Variable amino acid positions were identified from the aligned sequences. Phylogenetic analysis was performed using the maximum-likelihood method in IQ-TREE v3.1.4 [14]. The evolutionary model was selected using ModelFinder based on the Bayesian

information criterion (BIC) [15], and branch support was assessed using 1,000 ultrafast bootstrap replicates [16].

Results

Similarity of the *Bt26* Catalase Protein Candidate to Reference Proteins

The protein candidate corresponding to the *JEEBFNLG_01767* locus in the *B. thuringiensis* 26 genome consisted of 488 amino acids. BLASTP analysis identified 50 reference hits, with amino acid sequence identity ranging from 94.672% to 100%. Of these, 27 hits showed 100% identity.

One of the highest-scoring matches was the reference KatB protein with accession number WP_001069180.1, for which complete alignment across all 488 amino acids was observed. The query coverage was 100%, the E-value was 0.0, and the bit score was 1024. These results indicate a very high degree of sequence similarity between the *Bt*26 protein candidate and this reference protein.

Nucleotide Sequence Similarity.

In the BLASTN analysis, the nucleotide sequence corresponding to the *Bt26* catalase candidate was compared with 50 reference sequences. Complete nucleotide sequence identity (100%) was observed in 26 references. Two references showed identity values between 99% and 100%, 21 showed values between 95% and 99%, and one reference exhibited identity below 95%.

The lowest sequence identity was 92.371%. Although query coverage was reported as 100% for all hits, one alignment had a length of 1,468 nucleotides, whereas the query sequence was 1,467 nucleotides long.

Evaluating sequence identity at both the nucleotide and protein levels is important. Nucleotide substitutions may occur without changing the encoded amino acid because of the properties of the genetic code. Therefore, nucleotide sequence identity and amino acid sequence identity were considered distinct measures.

Variable Positions in the Amino Acid Sequence

Multiple sequence alignment of the *Bt26* KatB protein candidate and 50 reference proteins identified 40 variable amino acid positions. A total of 125 reference-specific differences were recorded across these positions. This value represents the cumulative number of differences observed across the reference sequences rather than 125 distinct variable positions.

The most frequent difference occurred at position 254: the *Bt26* protein contained tyrosine (Y), whereas histidine (H) was present in 22 reference sequences. At position 169, serine (S) in *Bt26* was replaced by threonine (T) in 16 references. At position 291, isoleucine (I) was observed in 12 references instead of methionine (M) in the *Bt26* protein.

Additionally, proline (P) was observed in nine references at position 73, where the *Bt26* protein contained glutamine (Q). At position 221, serine (S) or aspartate (D) was present in eight references instead of glycine (G) in Bt-26. At position 373, methionine (M) occurred in eight references instead of valine (V). At position 395, proline (P) or serine (S) was found in seven references instead of lysine (K) in the *Bt26* protein (Table 1).

Table 1. Conservation and Variable Positions in the Protein Sequence

Amino acid position	*Bt26* residue	Amino acid residue(s) observed in reference sequences	Number of reference sequences showing a difference
254	Y	H	22
169	S	T	16
291	M	I	12
73	Q	P	9
221	G	S (7), D (1)	8
373	V	M	8
395	K	P (6), S (1)	7
338	Y	C	4

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352	Q	K	3
414	E	D	3

Conservation and Variable Positions in the Protein Sequence

These results indicate that although most of the protein sequence is conserved, differences occur at certain positions among the reference sequences. However, the effects of these substitutions on enzymatic activity, protein stability, or responses to oxidative stress cannot be determined from sequence data alone.

Phylogenetic Relationships

Phylogenetic analysis was performed using a total of 51 sequences, comprising the *Bt26* protein candidate and 50 reference proteins. The alignment contained 488 amino acid positions. IQ-TREE analysis identified 448 constant sites, 29 singleton sites, and 11 parsimony-informative sites.

Phylogenetic distances among many reference sequences were small. The terminal branch length of the *Bt26* protein candidate was zero, consistent with an exact sequence match to one or more reference proteins. The distance matrix indicated zero distance for 27 reference sequences.

The largest distance among the reference sequences was observed for GCF_025947955.1, with a value of 0.0630343. This result indicates that this protein sequence was more divergent from the *Bt26* candidate than the other reference sequences examined. The JTT+I model was selected for phylogenetic analysis, and 1,000 ultrafast bootstrap replicates were specified. During the analysis, the split-frequency correlation reached 0.990. This value reflects the convergence of the phylogenetic tree search and does not indicate that all internal nodes had support values of 99%. Therefore, the support value of each individual node should be considered when evaluating the reliability of specific groups.

Overall, the results indicate that the *Bt26* KatB protein candidate has very close sequence relationships with many reference proteins. However, the phylogenetic tree alone does not definitively establish the functional identity or biological activity of this protein.

Discussion

BLASTP analysis of the *Bt26* KatB protein candidate revealed high sequence identity, including complete matches with several reference proteins. These results indicate that the candidate is closely related to reference catalases. However, because the catalase family includes groups with distinct structural and functional properties, sequence similarity alone is insufficient to establish the definitive functional classification of the enzyme [1–3].

Mo et al. experimentally demonstrated the catalase-peroxidase activity of KatB from *B. thuringiensis* strain 97–27 and its involvement in Mn(II) oxidation [6]. The length of the *Bt26* protein candidate and its high similarity to reference KatB proteins provide a basis for comparison with these findings. Nevertheless, the present bioinformatics analysis does not confirm that the *Bt26* protein also oxidizes Mn(II) or possesses the same enzymatic activities.

An important issue is the discrepancy between the *katA_1* annotation assigned to the locus and its similarity to reference proteins annotated as *katB*. The distinct physiological roles of KatA and KatX in *B. subtilis* [4], together with the different biochemical properties reported for KatB proteins from other *Bacillus* strains [5], indicate that catalase genes should not be classified solely on the basis of their names. Therefore, the genomic context of the *JEEBFNLG_01767* locus, its conserved domains, and the annotations of the reference sequences require further examination.

The amino acid differences identified by MAFFT characterize sequence diversity among the proteins but do not directly demonstrate effects on enzymatic activity. The site-directed mutagenesis experiments reported by Mo et al. show that the functional significance of specific amino acid residues must be established experimentally [6]. Similarly, phylogenetic proximity reflects evolutionary relationships between sequences but does not prove functional equivalence [8, 14].

In our previous study, *katE*, *katA-1* and other stress-associated genes were identified in the *Bt26* genome [9]. The present study extends this work by characterizing the sequence-level properties of another catalase candidate and contributes to the investigation of catalase diversity in this strain.

However, the presence of a gene in the genome does not necessarily indicate its expression or activity under stress conditions. Such discrepancies between genomic predictions and proteomic evidence have also been reported in studies of *B. thuringiensis* [7].

Conclusion

Comparative analysis of the catalase protein candidate corresponding to the JEEBFNLG_01767 locus in the *Bacillus thuringiensis Bt26* genome revealed 94.672–100% amino acid identity across 50 reference proteins, including 27 exact matches. BLASTN analysis identified 100% nucleotide identity with 26 reference sequences. Multiple sequence alignment revealed 40 variable amino acid positions and 125 recorded differences. These findings indicate high sequence similarity between the candidate and many reference proteins. However, given the discrepancy between the *katA_1* annotation and its high similarity to KatB proteins, the protein should be described as a KatB-like catalase candidate, and its functional identity requires further investigation.

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FERMENTATSIYAGA ASOSLANGAN BIOSINTEZ YORDAMIDA PORTULACA OLERACEA ENDOFIT MIKROORGANIZMLARI TOMONIDAN KO‘P TO‘YINMAGAN YOG‘ KISLOTALARINING ISHLAB CHIQARILISHI

Normurodova Q.T., Bekmaxamatova Nargiza Voxidovna *Mirzo Ulug‘bek nomidagi O‘zbekiston Milliy universiteti*

Annotatsiya: Ushbu tadqiqotda Toshkent viloyatining Qibray va Yangiyo‘l tumanlari agroekologik zonalaridan to‘plangan dorivor *Portulaca oleracea* o‘simligi to‘qimalaridan ajratib olingan endofit mikroorganizmlarning biologik xavfsizligi va ko‘p to‘yinmagan yog‘ kislotalari (PUFA) sintez qilish salohiyati o‘rganildi. Jami ajratilgan 31 ta endofit shtammdan qat’iy skrining va seleksiya natijasida yuqori mahsuldor va patogen bo‘lmagan 4 ta yetakchi shtamm (BPRC32, RSMAB-1, MD va PP6C1) saralab olindi. Gaz xromatografiyasi (GC-FID) va molekulyar-genetik identifikatsiya natijalari *Bacillus subtilis* RSMAB-1 (NCBI: MW368768) shtammining eykozapentaen kislota (EPA, 3.20 mg/100 mg), *Saccharomyces cerevisiae* MD (DDBJ: LC528142) shtammining esa dokozageksaen kislota (DHA, 0.25 mg/100 mg) va umumiy PUFA (10.93 mg/100 mg) ishlab chiqarishda yuqori samaradorlikka ega ekanini ko‘rsatdi. Mazkur mahalliy shtammlar sanoat biotexnologiyasida import o‘rnini bosuvchi Omega-3 va Omega-6 biologik faol qo‘shimchalarini olishda ekologik va iqtisodiy jihatdan barqaror bio-platforma bo‘lib xizmat qiladi.

Kalit so‘zlar: endofitlar, *Portulaca oleracea*, EPA, DHA, PUFA, *Bacillus subtilis*, *Saccharomyces cerevisiae*, fermentatsiya, biosintez.

Аннотация: В данном исследовании изучены биологическая безопасность и потенциал синтеза полиненасыщенных жирных кислот (ПНЖК) эндофитными микроорганизмами, выделенными из тканей лекарственного растения *Portulaca oleracea*, собранного в агроэкологических зонах Кибрайского и Янгиюльского районов Ташкентской области. Из 31 выделенного эндофитного штамма путем строгого скрининга и селекции были отобраны 4 перспективных непатогенных штамма (BPRC32, RSMAB-1, MD и PP6C1). Результаты газовой хроматографии (GC-FID) и молекулярно-генетической идентификации показали, что штамм *Bacillus subtilis* RSMAB-1 (NCBI: MW368768) обладает высокой эффективностью в производстве эйкозапентаеновой кислоты (EPA, 3.20 мг/100 мг), а штамм *Saccharomyces cerevisiae* MD (DDBJ: LC528142) – докозагексаеновой кислоты (DHA, 0.25 мг/100 мг) и общих ПНЖК (10.93 мг/100 мг). Данные локальные штаммы могут служить экологически и экономически устойчивой биоплатформой для получения импортозамещающих биологически активных добавок Омега-3 и Омега-6 в промышленной биотехнологии.

Ключевые слова: эндофиты, *Portulaca oleracea*, EPA, DHA, ПНЖК, *Bacillus subtilis*, *Saccharomyces cerevisiae*, ферментация, биосинтез.

Abstract: In this study, the biological safety and polyunsaturated fatty acid (PUFA) synthesis potential of endophytic microorganisms isolated from the tissues of the medicinal plant *Portulaca oleracea*, collected from the agroecological zones of Qibray and Yangiyo‘l districts of Tashkent region, were investigated. Out of 31 isolated endophytic strains, 4 highly productive and non-pathogenic leading strains (BPRC32, RSMAB-1, MD, and PP6C1) were selected through rigorous

IQTIBOS UCHUN
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screening and selection. Gas chromatography (GC-FID) and molecular-genetic identification results revealed that *Bacillus subtilis* RSMAB-1 (NCBI: MW368768) strain exhibited high efficiency in eicosapentaenoic acid (EPA, 3.20 mg/100 mg) production, while *Saccharomyces cerevisiae* MD (DDBJ: LC528142) strain excelled in docosahexaenoic acid (DHA, 0.25 mg/100 mg) and total PUFA (10.93 mg/100 mg) production. These indigenous strains serve as an ecologically and economically sustainable bio-platform for obtaining import-substituting Omega-3 and Omega-6 biologically active supplements in industrial biotechnology.

Keywords: endophytes, *Portulaca oleracea*, EPA, DHA, PUFA, *Bacillus subtilis*, *Saccharomyces cerevisiae*, fermentation, biosynthesis.

Kirish

Zamonaviy tibbiyot, diyetologiya va farmatsevtikada inson salomatligini saqlash hamda surunkali kasalliklarning oldini olishda ko‘p to‘yinmagan yog‘ kislotalarining (PUFA — Polyunsaturated Fatty Acids) o‘rni beqiyosdir. Ayniqsa, uzun zanjirli omega-3 sinfiga mansub eykozapentaen (EPA) va dokozageksaen (DHA) kislotalari inson organizmidagi eng muhim fiziologik jarayonlarni boshqarishda, qon plazmasidagi xolesterin va past zichlikdagi lipoproteinlar (PZLP) miqdorini kamaytirishda, tomirlar elastikligini oshirishda hamda yurak-qon tomir tizimi kasalliklari xavfini keskin pasaytirishda ishtirok etadi. Evolyutsion-biologik xususiyatlar tufayli inson organizmi ushbu essensial makromolekulalarni mustaqil sintez qila olmaydi, chunki odam hujayralarida tegishli desaturaza fermentlari sintezlanmaydi. Shu sababli, inson ularni muntazam ravishda tashqi manbalar — oziq-ovqat yoki biologik faol qo‘shimchalar (BFQ) orqali qabul qilishga majbur. JSST ma’lumotlariga ko‘ra, dunyo aholisining qariyb 31 foizi PUFA yetishmovchiligidan aziyat chekmoqda.

Bugungi kunda jahon bozorida ushbu moddalarning asosiy manbasi dengiz baliqlarining moyi hisoblanadi. Ammo an’anaviy baliqchilik sanoati jiddiy ekologik va iqtisodiy muammolarga duch kelmoqda. Birinchidan, global sanoat chiqindilarining dunyo okeaniga tashlanishi oqibatida baliq moyida og‘ir metallar, mikroplastiklar va dioksidlar kabi toksik moddalar to‘planmoqda. Ikkinchidan, baliq zaxiralarining kamayishi tufayli mahsulot tannarxi yil sayin oshmoqda. O‘simlik manbalari (zig‘ir, soya) esa uzun zanjirli EPA va DHA kislotalarini to‘liq shaklda saqlamaydi, ularning o‘tmishdoshi bo‘lgan alfa-linolen kislotasining organizmda faol shaklga aylanish koeffitsiyenti o‘ta past (<5%) hisoblanadi. Ushbu muammolarni bartaraf etish maqsadida, fermentatsiyaga asoslangan mikrobiologik biosintez texnologiyasini rivojlantirishga alohida e’tibor qaratilmoqda. Mikroorganizmlar yordamida PUFA olish texnologiyasi iqlim sharoitlariga va atrof-muhitning ifloslanishiga bog‘liq bo‘lmagan holda, qisqa muddatda yuqori sifatli va ekologik toza mahsulot olish imkonini beradi.

Materiallar va tadqiqot metodlari

1. O‘simlik namunalarini tanlash va fitosanitar yig‘ish. Portulaca oleracea namunalari Toshkent viloyatining Qibray va Yangiyo‘l tumanlari agrar maydonlaridan o‘simlikning jadal o‘sish (vegetatsiya) davrida, ertalabki soatlarda, ildiz, poya va barg qismlari shikastlanmagan holda yig‘ildi. Namunalar laboratoriyaga maxsus muzlatgichli konteynerlarda 2 soat ichida yetkazildi.

2. Yuzaki (sirtqi) sterilizatsiya qilish. Epifit mikroorganizmlarni tozalash maqsadida ildiz, poya va barglar dastlab oqar suvda 15 daqiqa davomida yuvildi. So‘ngra laminar-boks ichida ketma-ket: 70% li etil spirtida (1 daqiqa), 0.1% li simob dixlorid (HgCl2) eritmasida (3–5 daqiqa) ishlov berildi va steril distillangan suvda 5 marotaba chayildi. Oxirgi chayilgan suv ozuqa muhitlariga ekilib, nazorat (kontrol) o‘tkazildi.

3. Endofit mikrob kulturalarini ajratib olish (Izolyatsiya). Sterillangan organlar chinni hovonchalarda maydalanib, 1 g porsiyasi 9 ml 0.9% li NaCl eritmasida suspenziya qilindi. Eritmalar 10^-1 dan 10^-5 gacha ketma-ket suyultirilib, universal MRS agarli ozuqa muhitiga (pH 6.5) sirtqi yoyish usuli bilan ekildi. Namunalar 37°C haroratda 48 soat davomida inkubatsiya qilindi. Birinchi bosqichda o‘sgan koloniyalar morfologik belgilari bo‘yicha guruhlanib, MRS bulyonida qayta

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ko‘paytirish orqali toza kultura holatiga keltirildi. Mikrob hujayralari konsentratsiyasi MakFarland standarti bo‘yicha 10^7 KOU/ml darajasiga keltirildi.

4. In vitro sharoitida toksiklik va gemolitik faollik tahlili. Biologik xavfsizlikni aniqlash uchun tarkibida 5% yuvilgan qo‘y qoni bo‘lgan oziqa agari tayyorlandi. Toza kulturalar nuqtali usulda ekilib, 37°C da 24 soat inkubatsiya qilindi. Koloniyalar atrofida to‘liq shaffof zona hosil qilgan alfa (α) yoki beta (β) gemolizli patogen shtammlar eksperimentdan chiqarib tashlandi. Atrofida hech qanday parchalanish zonasi hosil qilmagan, qon eritrotsitlariga nisbatan mutlaq neytral bo‘lgan gamma (γ) gemoliz ko‘rsatgan shtammlar xavfsiz deb topildi.

5. Lipid to‘planishini ekspress-skrining qilish usullari. Sudan Black B (Sudan qorasi B) bilan bo‘yash. Hujayra surtmasi tayyorlanib, Sudan Black B bo‘yog‘i bilan 10 daqiqa davomida bo‘yaldi va 0.5% li safranin bilan kontrastlandi. Immersion mikroskop ostida (100×) hujayra maydonining 50% dan ko‘pini egallagan yirik ko‘kimtir-qora rangli lipid globulalari aniqlangan shtammlar tanlandi.

TTC kolorimetrik tahlili: Suyuq kultura supernatantiga 0.1% li TTC (trifeniltetrazoliydixlorid) eritmasi qo‘shilib, 25°C da 1 soat saqlandi. Δ5-desaturaza fermenti ta’sirida rangsiz moddaning qizil rangli trifenilformazan (TF) cho‘kmasiga aylanishi kolorimetrik o‘lchandi.

Vodorod peroksid (H_2O_2) plastinka tahlili: Shtammlarning oksidlanishli (oksidativ) stressga bardoshliligini tekshirish uchun LB agar plastinkalariga mikrob suspenziyasi yoyilib, filtr qog‘oz disklari joylashtirildi va ularga turli konsentratsiyali H_2O_2 eritmasi (0.01%, 0.5%, 1.0%) tomizildi. 24 soatdan keyin o‘sishni ingibitsiya qilish zonalari o‘lchandi.

6. Lipidlarni jadal ekstraksiya qilish va FAME modifikatsiyasi. Umumiy lipidlarni ajratib olish Blay va Dayer (Bligh and Dyer) usuli asosida bajarildi. Hujayra qobig‘ini parchalash uchun pulsli elektroporatsiya texnologiyasi (20 kV/sm, 10 ta impuls) qo‘llanildi. Gomogenatga BHT (butilirlangan gidroksitoluol, 15 mg/ml) va xloroform: metanol (2:1 nisbatda) qo‘shilib aralashtirildi hamda sentrifugatsiya (5000 ayl/daqiqa, 10 daqiqa) qilindi. Lipid cho‘kmasiga 1 ml 0.5 N HCl ning metanoldagi eritmasi qo‘shilib, 4 soat davomida 40°C da transesterifikatsiya (yog‘ kislotalari metil efirlarini — FAME hosil qilish) reaksiyasi o‘tkazildi. FAME fraksiyasi 0.05 ml geksanda qayta eritildi.

7. Gaz xromatografiyasi (GC-FID) sharoitlari va miqdoriy tahlil. Tahlil Agilent GC gaz xromatografiyasi tizimida, Supelcowax 10 kapillyar kolonkasida bajarildi. Tashuvchi gaz — geliy (1.5 ml/daqiqa), injektor harorati 250°C, oqim bo‘linish (split) nisbati 50:1, kiritilgan namuna hajmi 1 µL. Termostat harorati 140°C dan 240°C gacha (minutiga 4°C tezlikda) bosqichma-bosqich ko‘tarildi. Komponentlar cho‘qqilari xalqaro standart etalon namunalar (Supelco 37 Component FAME Mix) tutilish vaqtlari (retention time) bilan solishtirilib aniqlandi.

8. Molekulyar-genetik identifikatsiya va statistik tahlil. Butun genomik DNK maxsus tijorat to‘plamlari (Sigma-Aldrich, AQSh) yordamida ajratildi. Bakteriyalar uchun 16S rDNK geni, zamburug‘ va achitqilar uchun ITS hududlari universal praymerlar yordamida amplifikatsiya qilindi (PZR), sekvenirlanib, NCBI BLAST ma’lumotlar bazasi bilan solishtirildi. Raqamli ma’lumotlar GraphPad Prism dasturida One-way ANOVA usulida statistik qayta ishlandi ($p \leq 0.05$).

Tadqiqot natijalari va ularning tahlili

Portulaca oleracea o‘simligi namunalarini mikrobiologik tahlil qilish natijasida jami 31 ta endofit mikroorganizm toza kultura holatida ajratib olindi. Ajratilgan umumiy mikrob izolyatlarining hududlar va o‘simlik organlari bo‘yicha miqdoriy taqsimoti 1-jadvalda keltirilgan.

1-jadval. *Portulaca oleracea* o‘simligi organlaridan ajratilgan endofit kulturalarning miqdoriy taqsimoti

***Portulaca oleracea* qismlari**	**Ildiz**	**Poya**	**Barglar**	**Jami**
1-hudud: Qibray	8	6	5	**19**

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2-hudud: Yangiyo‘l	6	4	2	**12**
Jami	**14**	**10**	**7**	**31**

1-jadval ma’lumotlaridan ko‘rinib turibdiki, endofit mikroorganizmlarning eng yuqori to‘planish konsentratsiyasi o‘simlikning ildiz tizimiga to‘g‘ri keladi (14 ta shtamm yoki umumiy miqdorning 45.1% qismi). Ushbu holat ildiz tizimining tuproq mikroflorasi va ildiz eksudatlari (shakar, aminokislotalar, organik kislotalar) bilan bevosita aloqada bo‘lishi hamda endofitlar kirishi uchun qulay ekologik nisha (muhit) yaratishi bilan izohlanadi. Eng kam mikrob yuklamasi esa barg qismida (7 ta shtamm) kuzatildi.

Ajratib olingan barcha 31 ta endofit shtammdan 23 tasi mutlaq γ-gemoliz ko‘rsatib, ularning biologik xavfsiz ekanligi tasdiqlandi. Qolgan 8 ta shtammda turli darajadagi gemoliz zonalari kuzatilganligi sababli tadqiqotdan chetlashtirildi. Xavfsiz deb topilgan 23 ta shtamm Sudan Black B bo‘yog‘i yordamida skrining qilinganda, ulardan 12 tasi lipid to‘plash bo‘yicha yuqori ijobiy ko‘rsatkich namoyon etdi.

Keyingi bosqichda H2O2 plastinka testi hamda TTC kolorimetrik tahlili orqali tekshirilganda, faqatgina 4 ta shtamm (BPRC32, RSMAB-1, MD va PP6C1) yuqori konsentratsiyali vodorod peroksid ta’sirida ham o‘zining metabolik yaxlitligini saqlab, yuqori fermentativ faollik ko‘rsatdi. Mazkur 4 ta yetakchi shtammning komponentli PUFA profili ko‘rsatkichlari 2-jadvalda bayon etilgan.

2-jadval. Izolyatlarning PUFA profili tahlili natijalari (mg / 100 mg FAs, M ± m, n = 3)

T/r	Kulturalar	Umumiy PUFA	DGLA	AA	EPA	NA	DHA
1	BPRC32	7.50	4.28	0.28	2.31	0.44	0.19
2	RSMAB-1	8.80	4.32	0.45	3.20	0.71	0.12
3	MD	10.93	4.94	2.69	2.63	0.42	0.25
4	PP6C1	7.69	3.70	0.05	2.28	1.55	0.11

Izoh: FAs — yog‘ kislotalari (Fatty Acids); DGLA — digomo-γ-linolen kislota; AA — araxidon kislota; EPA — eykozapentaen kislota; NA — nervon kislota; DHA — dokozageksaen kislota.

2-jadvalda keltirilgan xromatografik tahlil natijalari shuni ko‘rsatadiki, barcha 4 ta shtamm tarkibida ko‘p to‘yinmagan yog‘ kislotalarining to‘liq kompleksi mavjud. MD shtammi umumiy PUFA miqdori bo‘yicha mutlaq yetakchilikni qayd etdi (10.93 mg / 100 mg) hamda asab tizimi va miya hujayralari uchun eng qimmatli hisoblangan DHA miqdorini maksimal darajada sintez qildi (0.25 mg / 100 mg). Shuningdek, ushbu shtamm digomo-γ-linolen (4.94 mg) va araxidon (2.69 mg) kislotalariga ham boy ekanligi aniqlandi.

Bacillus subtilis RSMAB-1 shtammi esa yurak-qon tomir tizimini himoya qiluvchi va antioksidant xususiyatga ega EPA sintezi bo‘yicha eng yuqori ko‘rsatkichni namoyon etdi (3.20 mg / 100 mg).

Butun genomik DNK sekvenirlash va PZR tahlillari natijasiga ko‘ra, RSMAB-1 shtammining nukleotidlar ketma-ketligi *Bacillus subtilis* ekanligini ko‘rsatdi va u NCBI xalqaro gen bankida MW368768 kirish raqami bilan, MD shtammi esa *Saccharomyces cerevisiae* ekanligi tasdiqlanib, DDBJ xalqaro ma’lumotlar bazasida LC528142 kirish raqami bilan rasman ro‘yxatga olindi.

Muhokama

Tadqiqot davomida olingan ijobiy natijalar va yuqori lipid profili ko‘rsatkichlari o‘simliklar olami va ularning ichki to‘qimalarida simbioz yashovchi endofit mikroorganizmlar o‘rtasidagi chuqur biokimyoviy va evolyutsion aloqalarni ilmiy jihatdan asoslaydi. *Portulaca oleracea* o‘simliklar dunyosida o‘zining yuqori miqdordagi alfa-linolen, olein va linol kislotalarini sintez qilish xususiyati bilan tanilgan. Ko‘plab zamonaviy fitogenetik va molekulyar tadqiqotlar shuni isbotlaydiki, o‘simlik to‘qimalari ichida asrlar davomida birga yashash (koevolyutsiya) natijasida o‘simlik tarkibidagi ma’lum metabolik yo‘llarga javobgar bo‘lgan o‘ziga xos genlar zanjiri gorizontal transfer

mexanizmlari orqali endofitlar guruhiga o‘tishi mumkin. Aynan shu sababli, tarkibida tabiiy ravishda PUFA ko‘p bo‘lgan o‘simliklardan ajratilgan endofitlar, boshqa neytral manbalardan olingan mikroblarga qaraganda bir necha barobar yuqori lipid to‘plash salohiyatiga ega bo‘ladi.

TTC testida mikrob kulturalarining qizil rangga kirishi hujayra ichidagi Δ5-desaturaza fermentining faolligi yuqori ekanligini ko‘rsatdi. Ushbu ferment to‘yingan yog‘ kislotalari zanjirida qo‘sh bog‘lar hosil qilib, ularni yuqori molekulali PUFA shakliga o‘tkazishda asosiy katalizator hisoblanadi. H2O2 plastinka tahlilida o‘sish ingibitsiya zonalarining mutlaq kuzatilmaganligi esa ajratilgan Bacillus subtilis (MW368768) va *Saccharomyces cerevisiae* (LC528142) shtammlari hujayra membranasining tarkibiy qismi bo‘lgan lipid zanjirlari tashqi kuchli oksidlovchilar va erkin radikallar ta’siriga o‘ta yuqori strukturaviy barqarorlikka ega ekanini ko‘rsatdi. Bu xususiyat yirik bioreaktorlarda havo bilan intensiv aeralash sharoitida mikrob hujayralarining barqaror ko‘payishi uchun o‘ta muhim texnologik afzallik hisoblanadi.

Xulosa

Portulaca oleracea o‘simligining ichki to‘qimalari yuqori miqdorda lipid to‘plash va ko‘p to‘yinmagan yog‘ kislotalari (PUFA) sintez qilish qobiliyatiga ega bo‘lgan biologik xavfsiz endofit mikroorganizmlarning boy tabiiy manbai ekanligi to‘liq isbotlandi.

Ajratib olingan 31 ta shtammdan barcha skrining bosqichlaridan (gemoliz, Sudan Black B, H2O2, TTC) muvaffaqiyatli o‘tgan 4 ta eng istiqbolli shtamm aniqlandi va ularning yuqori lipid profili gaz xromatografiyasi yordamida tasdiqlandi.

Molekulyar-genetik jihatdan xarakterlangan *Bacillus subtilis* RSMAB-1 (NCBI: MW368768) shtammi yuqori miqdorda EPA (3.20 mg / 100 mg) kislotasini, *Saccharomyces cerevisiae* MD (DDBJ: LC528142) shtammi esa maksimal darajada DHA (0.25 mg / 100 mg) va umumiy PUFA (10.93 mg / 100 mg) kislotalarini sintez qilishi aniqlandi va ular xalqaro gen banklariga kiritildi.

Ajratib olingan ushbu mahalliy shtammlar patogen xususiyatga ega emasligi, inson organizmi uchun mutlaq xavfsizligi hamda mahalliy arzon ozuqa substratlarida (masalan, qishloq xo‘jaligi chiqindilari, patoka, bulyonlar) juda tez ko‘payib, yuqori ekologik toza biomassani hosil qila olish xususiyati bilan ajralib turadi.

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TURLI STRESS SHAROITIDA CHLORELLA VULGARIS SUSPENZIYASI ORQALI Buxoro-10 G‘O‘ZA NAVINING CHIDAMLILIGINI VA HOSILDORLIGINI OSHIRISH

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Annotatsiya: Buxoro viloyatining qurg‘oqchil, o‘rtacha sho‘rlangan va yuqori havo harorati kuzatiladigan agroekologik hududlarida g‘o‘za yetishtirish jarayonida suv taqchilligi, tuproq sho‘rlanishi va garmsel kabi abiotik stress omillari o‘simliklarning o‘sishi-rivojlanishiga sezilarli ta’sir ko‘rsatadi. Shu bois, ushbu hududlarda Chlorella vulgarisni MUM-S v 2 (Modified Universal Medium for Stress) muhitida ultratovush yordamida dezintegratsiyalab hujayra qobig‘ini parchalash orqali g‘o‘zaning kompleks stress omillariga nisbatan chidamliligini oshirish, suv resurslaridan samarali foydalanish, hosildorlik va tola sifatini barqarorlashtirishga yo‘naltirilgan ekologik xavfsiz biotexnologik usullarni ishlab chiqish bugungi kunning dolzarb masalalaridan biri bo‘lib, alohida ahamiyatga egadir.

Kalit so‘zlar: Chlorella vulgaris; tomchilatib sug‘orish; fertigatsiya; sho‘rlanish stressi; qurg‘oqchil dehqonchilik; fenologiya.

Аннотация: В агроэкологических условиях Бухарской области, для которых характерны засушливость, умеренное засоление почв и высокие температуры воздуха, такие абиотические стрессовые факторы, как дефицит влаги, засоление почв и жаркие сухие ветры («гармсель»), оказывают существенное влияние на рост и развитие хлопчатника. В связи с этим возникает острая необходимость в разработке экологически безопасных биотехнологических методов для данных регионов. Подобные методы, основанные на применении ультразвука для разрушения клеточных стенок Chlorella vulgaris (культивируемой в «модифицированной универсальной среде для стрессовых условий» — MUM-S v 2), направлены на повышение устойчивости хлопчатника к комплексу стрессовых факторов, обеспечение эффективного использования водных ресурсов, а также на стабилизацию урожайности и качества волокна. Решение этой задачи является актуальным и имеет особое значение.

Ключевые слова: Chlorella vulgaris; капельное орошение; фертигация; солевой стресс; земледелие в аридных зонах; фенология.

Abstract: In the agro-ecological conditions of the Bukhara region—characterized by aridity, moderate soil salinity, and high air temperatures—abiotic stressors such as moisture deficiency, soil salinity, and hot, dry winds (“garmsel”) exert a significant impact on the growth and development of cotton. Consequently, there is an urgent need to develop environmentally safe biotechnological methods tailored to these regions. Such methods, based on the use of ultrasound to disrupt the cell walls of Chlorella vulgaris (cultivated in a “modified universal medium for stress conditions”—MUM-S v 2), are aimed at enhancing the resistance of cotton plants to a complex of stress factors, ensuring the efficient use of water resources, and stabilizing both crop yield and fiber quality. Addressing this challenge is both timely and of particular importance.

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Keywords: Chlorella vulgaris; drip irrigation; fertigation; salt stress; agriculture in arid zones; phenology.

Kirish

Sug‘oriladigan qurg‘oqchil dehqonchilik suv ta’minotining cheklanishi, sho‘rlanish, yuqori bug‘lanish talabi va issiq davrlarning birgalikdagi ta’siriga tobora ko‘proq duch kelmoqda. Buxoro vohasida g‘o‘za yetishtirish suvni puxta boshqarishga ayniqsa bog‘liq, chunki tuproq namligining yo‘qolishi va tuzlarning to‘planishi vegetativ o‘sish, generativ organlarning saqlanib qolishi hamda ko‘saklarning yetilishini cheklashi mumkin. Tomchilatib sug‘orish suv yetkazib berishni makon va vaqt bo‘yicha aniqroq boshqarish imkonini beradi hamda avvalgi tadqiqotlarda O‘zbekistonda egatlab sug‘orishga nisbatan g‘o‘zaning suvdan foydalanish samaradorligini oshirgan.

O‘rtacha sho‘rlangan, o‘tloqi-allyuvial tuproqlar sharoiti uchun bir vaqtning o‘zida ham suv resurslarining tejalishiga, tuproqning sho‘rlanish darajasi va pH muhitining yaxshilanishiga hamda g‘o‘zaning o‘sish va rivojlanishiga hosil, tola va chigitning sifatining oshishiga, shuningdek, tuproq strukturasiga ijobiy ta’sir etuvchi Chlorella vulgarisni MUM-S v 2 (Modified Universal Medium for Stress) maxsus modifikatsiyalangan oziqa muhitida ultratovush yordamida dezintegratsiyalab hujayra qobig‘ini buzish orqali abiotik stresslarga qarshi uning suspenziyasini g‘o‘za navlariga ekish oldidan chigitiga ishlov berib (20 kg/ tuksizlantirilgan chigit uchun Ch. vulgaris suspenziyasidan 1 mlda 30-35mln dona bo‘lgan me’yorini, ya’ni 100 ml/kg hisobida bir xil namlangunicha ivitilib, oftobga bir oz yoyib ekish) hamda g‘o‘za vegetatsiyasining 5-6 chinbarg chiqarishida, shonalash, gullash, ko‘saklash fazalarida (1 tnlik rezervuar uchun Ch. vulgaris suspenziyasidan 2l +498 l suv (jami 500 l ishchi eritmani) tomchilatgich idishiga solib 1 ga maydon uchun mo‘ljallangan) 4 marta tomchilatib sug‘orish tizimi orqali g‘o‘za ildizi atrofiga fertigatsiyalash yo‘li bilan fermer xo‘jaliklarida qo‘llash qishloq xo‘jaligining dolzarb yo‘nalishlaridan hisoblanadi.

Metodika

Ayniqsa suv taqchil, sho‘rlangan va yuqori haroratli garmsel sharoitlarida abiotik stresslarning oldini oluvchi maxsus modifikatsiyalangan oziqa muhitida o‘stirilgan Chlorella vulgarisning samarali maqbul suspenziyasini tomchilatgichlar vositasida kompleks qo‘llash borasida 2023-2026 yillar davomida Paxta seleksiyasi, urug‘chiligi va yetishtirish agrotexnologiyalari ilmiy-tadqiqot institutining Buxoro ilmiy-tajriba stansiyasining 6,25 gektarlik dala maydonida o‘rta tolali Buxoro-10 g‘o‘za navida dissertatsiya tadqiqot ishlari olib borildi.

Shuningdek, dala maydonlarida Chlorella vulgarisni MUM-S v 2 (Modified Universal Medium for Stress) maxsus modifikatsiyalangan oziqa muhitida ultratovush yordamida dezintegratsiyalab hujayra qobig‘ini parchalash orqali abiotik stresslarga qarshi uning suspenziyasini g‘o‘za navlariga ekish oldidan chigitiga ishlov berib (20 kg/ tuksizlantirilgan chigit uchun Ch. vulgaris suspenziyasidan 1 mlda 30-35mln dona bo‘lgan me’yori, ya’ni 100 ml/kg hisobida gektariga hisoblab, bir xil namlangunicha ivitilib, g‘o‘za vegetatsiyasi davrlarida 4 marta tomchilatgichlar vositasida 1 gektar uchun har bir qo‘llanilish uchun, ya’ni 2l Ch. vulgaris va 498 l suvni obdon aralashtirib, tomchilatgich rezervuariga gektariga hisoblab qo‘llanilganligi bo‘yicha tavsiyalar ishlab chiqildi.

Shuningdek, Chlorella vulgarisni MUM-S v 2 maxsus modifikatsiyalangan oziqa muhitida ultratovush yordamida dezintegratsiyalab hujayra qobig‘ini parchalash orqali abiotik stresslarga qarshi uning suspenziyasini qo‘llashda Chlorella vulgarisning tarkibiga kiruvchi prolin; trehaloza; glitsin-betain; poliaminlar; antioksidant fermentlar (SOD, CAT, POD); fitogormonlar kabi metabolitlar o‘simliklarning abiotik stresslarga moslashuv mexanizmlarini faollashtirib, fiziologik jarayonlarning barqaror kechishini ta’minladi, ya’ni modifikatsiyalangan oziqa muhiti tarkibini optimallashtirish natijasida: kaliy va mikroelementlar hisobiga osmoregulyatorlar sintezi kuchaydi; temir, marganets va rux ta’sirida antioksidant tizim faollashdi; fosfor va magniy hisobiga hujayra bo‘linishi va fotosintetik faollik oshdi; natriy, kaliy va kalsiy nisbatining optimallashtirilishi osmotik muvozanatni yaxshilaganligi borasida ilmiy ma’lumotlar olinganligi bilan baholangan.

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Natijalar va muhokama

Ishlab chiqarish sharoitida Chlorella vulgaris suspenziyasi bilan tomchilatgichlar yordamida fertigatsiyalangan va bir mavsumda 3150 m3/ga suv sarflanib, 8 marta tomchilatib sug‘orish agrotadbiri o‘tkazilgan, tomchilatib sug‘orishda oziqlantirish gektariga N200P140K80 kg/ga me’yori qo‘llanilib, qo‘shimchasiga maxsus modifikatsiyalangan oziqa muhitida o‘stirilgan va MUM-S v 2 muhitida ultratovushli dezintegratsiya usulida xlorella hujayralari qobig‘ini parchalash yo‘li bilan bir mavsumda 5 marta oziqlantirish orqali nazorat variantiga nisbatan 3,5-5 s/gacha yuqori sifatli hosil yetishtirilib sug‘orish suvi egatlab sug‘orishga nisbatan 2 marta tejalishi, o‘g‘it, ishchi kuchi, YOMM, texnika vositalarining 30-40%ga kamayishi dala tajribalari hamda ishlab chiqarish tajribalarida o‘zining ijobiy natijalarini berganligi bilan ilmiy va amaliy ravishda baholandi.

Buxoro viloyatining sug‘oriladigan va tuprog‘i o‘rtacha sho‘rlangan, suv taqchil va yuqori haroratli garmsel shamoli esadigan yerlarida ilmiy-tadqiqot ishlari olib borilgan bo‘lib, tadqiqotlarda ekoxavfsiz bioorganik komponentlarga boy bo‘lgan Xlorella vulgaris tarkibidagi 600 dan ortiq turli xil mikro-makroelementlar, oqsil, uglevod, ferment, antioksidant, fitogormon va turli xil metabolitlarni oziqa sifatida g‘o‘za o‘simligining chigitiga va ildiziga berish yo‘li bilan abiotik stresslar va sho‘rlangan tuproqlar sharoitida morfologik, fiziologik, biokimyoviy, meliorativ va mahsuldorlik xususiyatlari bo‘yicha ilmiy yechimlar ishlab chiqishga qaratilgan.

O‘tloqi-allyuvial tuproqlar sharoitida tomchilatib sug‘orilgan g‘o‘za navlarida o‘rganilgan fiziologik, biotexnologik, agrobiologik ko‘rsatkichlar qiymati maxsus modifikatsiyalangan oziqa muhitida o‘stirilgan Xlorella vulgarisning hujayra qobig‘larini MUM-S v 2 muhitida ultratovushli dezintegratsiya usulida parchalash yo‘li bilan oziqlantirish nazorat variantiga nisbatan Xlorella vulgaris suspenziyasining maxsus modifikatsiyalangan oziqa muhitida o‘stirilganligiga va bu muhit g‘o‘zaning kompleks stresslarga nisbatan chidamliligini oshirganligiga hamda namlikning me’yor darajasida saqlanganligi natijasida g‘o‘za navlarining biologik xususiyatlariga bog‘liq holda har xil darajada o‘zgarishi ilmiy asoslangan.

Xulosa

Bu kabi tadqiqot natijalari kelgusida suv tanqisligi, kompleks abiotik stresslarning bo‘lib turishi kuzatiladigan hududlarda samarali ekoxavfsiz biostimulyatorlarni va g‘o‘za navlari hamda suv tejovchi texnologiyalarni tanlash va suv stressiga chidamlilik belgilari bo‘yicha seleksiya yo‘nalishlarini aniqlashda muhim ahamiyat kasb etadi.

O‘tloqi-allyuvial tuproqlar va abiotik stresslar sharoitida o‘rganilgan fiziologik, biotexnologik, biokimyoviy va sug‘orish usullari, mahsuldorlik ko‘rsatkichlari qiymatining suv tanqisligiga, sho‘rlanish, garmselga chidamlilik va moslashish darajasi bilan bevosita bog‘liqligi asoslangan. Natijada g‘o‘za navlarini suvtejamkor texnologiyalar asosida ekoxavfsiz maxsus modifikatsiyalangan oziqa muhitida xlorella vulgarisni o‘stirib, g‘o‘za navlarida qo‘llanilganda, tuproqdagi suv tanqisligi, sho‘rlanish, garmselga fiziologik munosabatiga asoslanib, kompleks stresslarga chidamli va abiotik stresslarni yumshatuvchi va tuproq unumdorligining tiklanishiga ijobiy ta’sir etuvchi universal ta’sir etuvchi biostimulyator deyish mumkin. Shunga asoslanib, g‘o‘za navlarini suv tanqisligi, sho‘rlanishi turlicha bo‘lgan va garmsel kuzatiladigan maydonlarga g‘o‘za navlarini joylashtirish hisobiga yuqori va sifatli hosil olish imkoniyati yaratilgan.

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IMMOBILIZATSIYALANGAN MIKROORGANIZMLAR VA FERMENTLARDAN FOYDALANIB GLUKOZA-FRUKTOZALI SIROP ISHLAB CHIQARISHNING BIOTEXNOLOGIK ASOSLARI

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Annotatsiya: Ushbu maqolada immobilizatsiyalangan mikroorganizmlar va fermentlar yordamida glukoza-fruktozali sirop (GFS) ishlab chiqarishning biotexnologik asoslari tizimli yoritildi. Tadqiqotning maqsadi kraxmalli xomashyoni fermentativ gidroliz va izomerizatsiya bosqichlari orqali yuqori fruktoza ulushiga ega siropga aylantirishda immobilizatsiya texnologiyasining samaradorligini ilmiy asoslashdan iborat. Metodologiya sifatida ferment kinetikasi, massa almashinuvi, tashuvchi matritsa tanlovi, reaktor modellashtirish va jarayon barqarorligini baholash bo‘yicha nazariy-tahliliy yondashuv qo‘llanildi. Ilmiy yangilik sifatida immobilizatsiya qilingan glukoza izomeraza hamda ko‘p fermentli tizimlar uchun optimal pH (muhitning kislotalilik yoki ishqoriylik ko‘rsatkichi), harorat, substrat konsentratsiyasi va diffuziya cheklovlarini birgalikda hisobga oluvchi konseptual model taklif etildi. Natijalar GFS sifat ko‘rsatkichlarini barqarorlashtirish, ferment sarfini kamaytirish va uzluksiz ishlab chiqarish samaradorligini oshirish imkonini ko‘rsatadi.

Kalit so‘zlar: glukoza-fruktozali sirop; immobilizatsiya; glukoza izomeraza; amilaza; massa almashinuvi; uzluksiz bioreaktor; ferment kinetikasi

Аннотация: В статье системно рассмотрены биотехнологические основы производства глюкозо-фруктозного сиропа (ГФС) с использованием иммобилизованных микроорганизмов и ферментов. Цель исследования заключается в научном обосновании эффективности иммобилизационных технологий при превращении крахмалсодержащего сырья в сироп с повышенной долей фруктозы посредством ферментативного гидролиза и стадии изомеризации. В качестве методологии применены теоретико-аналитические подходы, включающие кинетику ферментов, массообмен, выбор матриц-носителей, моделирование реакторов и оценку стабильности процесса. Научная новизна состоит в предложении концептуальной модели для иммобилизованной глюкозоизомеразы и мультиферментных систем, учитывающей совместно оптимальные значения pH, температуры, концентрации субстрата и диффузионные ограничения. Полученные выводы демонстрируют возможность стабилизации показателей качества ГФС, снижения расхода ферментов и повышения эффективности непрерывного производства.

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Ключевые слова: глюкозо-фруктозный сироп; иммобилизация; глюкозоизомераза; амилаза; массообмен; непрерывный биореактор; кинетика ферментов

Abstract: This article systematically describes the biotechnological foundations of producing glucose–fructose syrup (GFS) using immobilized microorganisms and enzymes. The study aims to scientifically justify the efficiency of immobilization technologies for converting starch-based feedstocks into syrup with an increased fructose fraction via enzymatic hydrolysis followed by isomerization. The methodology relies on a theoretical and analytical framework combining enzyme kinetics, mass-transfer analysis, carrier-matrix selection, reactor modeling, and process-stability assessment. The scientific novelty lies in proposing a conceptual model for immobilized glucose isomerase and multi-enzyme systems that jointly accounts for optimal pH, temperature, substrate concentration, and diffusion limitations. The findings indicate that immobilization can stabilize key quality attributes of GFS, reduce enzyme consumption through extended operational lifetime, and improve the performance of continuous production schemes in industrial bioprocessing.

Keywords: glucose–fructose syrup; immobilization; glucose isomerase; amylase; mass transfer; continuous bioreactor; enzyme kinetics

Kirish

Glukoza-fruktozali sirop deganda kraxmal yoki kraxmal gidrolizatlaridan olinadigan, quruq modda tarkibida glukoza va fruktoza ulushi boshqariladigan shirinlashtiruvchi mahsulot tushuniladi, uning sanoatdagi dolzarbligi shundan iboratki, u saxaroza o‘rnini bosuvchi sifatida ichimliklar, nonvoychilik va konserva mahsulotlarida reologik hamda organoleptik barqarorlikni ta’minlaydi. Mazkur mahsulotni olish mexanizmi odatda uch bosqichdan tuziladi: kraxmalni suyuqlantirish, dekstrinlarni saxarifikatsiya qilish va hosil bo‘lgan glukozani fruktozaga izomerizatsiya qilish, bunda yakuniy fruktoza ulushi 42–55 foiz oralig‘ida sozlanadi va ayrim texnologik zanjirlarda fruktoza ulushi 90 foizgacha boyitilishi mumkin. Masalan, kukun yoki don kraxmalidan olingan 96 DE (dekstroza ekvivalenti — kraxmalning gidrolizlanish darajasi ko‘rsatkichi) bo‘lgan glukoza siropi immobilizatsiyalangan glukoza izomeraza qatlamidan o‘tkazilganda ichimlik sanoati uchun keng qo‘llanadigan HFCS-42 (yuqori fruktozali makkajo‘xori siropining tarkibida taxminan 42% fruktoza bo‘lgan turi) mahsuloti hosil bo‘ladi, shuningdek, qo‘shimcha ajratish bosqichlari bilan HFCS-55 (taxminan 55% fruktozali makkajo‘xori siropi) yoki yuqori fruktozali fraksiyalar olinadi. Raqamiy baholash nuqtayi nazaridan, izomerizatsiya muvozanati sanoat sharoitida odatda 42–45 foiz fruktoza atrofida cheklanadi, uzluksiz ishlashda esa fermentning xizmat muddati haftalardan oylargacha cho‘zilishi iqtisodiy samara beradi. Ilmiy izoh sifatida bu cheklovlar termodinamik muvozanat, fermentning faol markazida Mg^{2+} (magniy ioni) kabi kofaktorlarning roli, pH va haroratga sezgirlik hamda immobilizatsiya natijasida yuzaga keladigan ichki diffuziya qarshiliklari bilan tushuntiriladi [1; 4].

Immobilizatsiyalangan fermentlar va mikroorganizmlar tushunchasi ferment yoki hujayralarni ma’lum tashuvchi matritsaga fizik adsorbsiya, kovalent bog‘lash, qamash yoki ko‘priklovchi agentlar orqali biriktirilgan holat sifatida ta’riflanadi va bu yondashuv GFS ishlab chiqarishda jarayonni uzluksizlashtirish hamda biokatalizatorni qayta ishlatish imkonini beradi. Mexanizm jihatidan immobilizatsiya ferment molekulalarining fazoviy konfiguratsiyasini nisbatan barqarorlashtiradi, reaktordan yuvilib ketishini cheklaydi va katalitik qatlamda yuqori samarali konsentratsiya hosil qiladi, biroq shu bilan birga substrat va mahsulotning matritsa ichiga kirishi hamda chiqishida diffuziya cheklovi paydo bo‘lishi mumkin. Ilmiy izoh nuqtayi nazaridan bu afzalliklar ferment denaturatsiyasining kinetik sekinlashuvi, mikro-muhit pH tamponlanishi va tashuvchi bilan o‘zaro ta’sirdan kelib chiqadigan konformatsion cheklanishlar bilan izohlanadi [2; 6].

Mavzu bo‘yicha zamonaviy ilmiy yondashuvlar fermentlar kaskadi, reaktor gidrodinamikasi va massa almashinuvi nazariyasini birlashtirgan holda integratsiyalashgan optimallashtirishga tayanadi, chunki GFS sifat ko‘rsatkichlari faqat ferment tanlovi bilan emas, balki butun jarayon zanjiridagi cheklovlar bilan belgilanadi. Mexanizmga ko‘ra, α-amilaza kraxmalni dekstrinlarga parchalashni boshlaydi, glukoamilaza dekstrinlarni glukozaga qadar gidrolizlaydi, glukoza izomeraza

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esa aldosa-ketoz izomerizatsiyasi orqali glukozani fruktozaga aylantiradi, natijada umumiy konversiya bosqichma-bosqich boshqariladi. Misol sifatida, pH 4,0–4,5 da glukoamilaza samarali bo‘lsa, glukoza izomeraza ko‘pincha pH 7,0–8,0 oralig‘ida yuqori faollik ko‘rsatadi, shu sababli amaliyotda oraliq neytrallash va ion tarkibini moslashtirish amalga oshiriladi. Raqamiy jihatdan, harorat rejimlari ham farqlanadi: suyuqlantirish bosqichi ko‘pincha 90–105 daraja atrofida, saxarifikatsiya 55–60 daraja atrofida, izomerizatsiya esa 55–65 daraja atrofida olib boriladi, bu ko‘rsatkichlar ferment termobarqarorligi bilan uyg‘unlashtiriladi. Ilmiy izoh sifatida bu yondashuvlar fermentlarning faollik profili, Arrenius tenglamasi orqali haroratning tezlikka ta’siri, hamda ion kuchi va metall kofaktorlarning kataliz mexanizmiga ta’siri bilan asoslanadi [3; 5].

Tadqiqot materiallari va metodlari

Tadqiqot materiali sifatida GFS ishlab chiqarish zanjirining nazariy modeli, ochiq ilmiy manbalardagi sanoatga xos texnologik parametrlar, hamda immobilizatsiya va bioreaktor muhandisligiga doir konseptual yondashuvlar majmuasi tanlandi. Mexanizm nuqtayi nazaridan, asosiy metodlar ferment kinetikasini Mixaelis–Menten ferment kinetikasi modeli doirasida ifodalash, immobilizatsiyada kuzatiladigan diffuziya cheklovlarini samaradorlik omili orqali tuzatish, hamda uzluksiz reaktorlarda statsionar holat modda balansi tenglamalarini qo‘llashdan iborat bo‘ldi. Misol sifatida, glukoza izomeraza uchun tezlik $v = V_{max} \cdot S/(K_m + S)$ ko‘rinishida ifodalanadi (bu yerda v — reaksiya tezligi, V_{max} — maksimal reaksiya tezligi, S — substrat konsentratsiyasi, K_m — Mixaelis doimiysi); immobilizatsiya sharoitida kuzatiladigan samarali tezlik $v_{app} = \eta \cdot v$ (v_{app} — kuzatiladigan reaksiya tezligi, η — ferment samaradorlik omili) tarzida yoziladi, bu yerda η 0 dan 1 gacha qiymat olib, tashuvchi g‘ovakligi, zarracha radiusi va diffuziya koeffitsientiga bog‘liq. Raqamiy parametrizatsiya uchun amaliyotda uchraydigan substrat konsentratsiyalari (quruq modda 40–55 foiz izomerizatsiya kirishida), harorat (55–65 daraja), pH (7,0–8,0) va Mg^{2+} miqdori kabi omillar diapazon sifatida qabul qilinib, sezgirlik tahlili mantig‘ida ularning yo‘nalishli ta’siri baholandi. Ilmiy izoh sifatida metodologik tanlov jarayonning ko‘p omilli ekanligi, ya’ni faqat kinetika bilan cheklanib qolmasdan, gidrodinamika va massa almashinuvi bilan bog‘liq cheklovlar mahsulot tarkibini belgilashini inobatga olgani bilan asoslandi [2; 5].

Immobilizatsiya tashuvchilari va bog‘lash usullarini tahlil qilish uchun kimyoviy va fizik moslik mezonlari material sifatida olindi, chunki fermentning faol markazi saqlanishi va oziq-ovqat xavfsizligi talablariga moslik sanoat uchun hal qiluvchi ahamiyatga ega. Mexanizm bo‘yicha adsorbsiya fermentni elektrostatik va gidrofob o‘zaro ta’sirlar orqali ushlab turadi, kovalent bog‘lash esa funksional guruhlar orqali mustahkam birikma hosil qiladi, qamash esa gel tarmog‘ida fizik to‘siq yaratadi va har bir mexanizmning massa almashinuvi va yuvilish xavfi bo‘yicha profili turlicha bo‘ladi. Ilmiy izoh sifatida tashuvchi tanlovida oziq-ovqat bilan kontaktda bo‘ladigan materiallarning migratsiya xavfi, ion almashinish xususiyati va mikrobiologik barqarorligi ham jarayon loyihasining ajralmas qismi sifatida qaraladi [6].

Jarayonni baholash uchun nazariy hisoblashlar bilan birga, sifat ko‘rsatkichlari va texnologik nazorat nuqtalari tizimi metod sifatida qabul qilindi, chunki GFS ishlab chiqarish amaliyotida tarkibiy barqarorlik va rang, kul miqdori, HMF (gidroksimetilfurfural — shakarni qizdirishda paydo bo‘lishi mumkin bo‘lgan birikma) kabi ko‘rsatkichlar muhim hisoblanadi. Mexanizm jihatidan, izomerizatsiya natijasida fruktoza ulushi ortishi bilan birga, yuqori harorat va uzoq turg‘un vaqt sharoitida noxush yon reaksiyalar, xususan, Maillard reaksiyalari va karamelizatsiya xavfi ortadi, shu sababli statsionar rejimni barqaror ushlab turish texnologik maqsadga aylanadi. Misol sifatida, faol ko‘mirda dekoloratsiya, ion almashinish smolalarida tuzlardan tozalash va filtrlash bosqichlari immobilizatsiyalangan izomerizatsiya blokidan oldin yoki keyin joylashtirilib, fermentni inhibitorlardan himoya qilish amaliyoti uchraydi. Raqamiy jihatdan, quruq modda 70 foizga yaqinlashganda viskozlik keskin ortib, bosim yo‘qotishi va diffuziya cheklovlari kuchayishi mumkin, shu bois ko‘plab liniyalarda izomerizatsiya nisbatan pastroq quruq modda sharoitida olib borilib, keyin bug‘latish orqali konsentratsiya oshiriladi. Ilmiy izoh sifatida nazorat nuqtalari tizimi jarayonning kritik parametrlarini pH, harorat, o‘tkazuvchanlik, rang va fruktoza ulushi bo‘yicha real

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vaqt rejimida yoki davriy nazorat usulida baholash orqali biokatalizatorning degradatsiya tezligini bilvosita kuzatish imkonini beradi [3].

Natijalar

Natija sifatida GFS ishlab chiqarishning immobilizatsiyalangan biokatalizatorlarga tayangan konseptual texnologik sxemasi tizimlashtirildi va unda har bir bosqichning maqsadi hamda cheklovchi omillari aniqlashtirildi. Mexanizm bo‘yicha sxema kraxmalni suyuqlantirishda α-amilaza, saxarifikatsiyada glukoamilaza, izomerizatsiyada immobilizatsiyalangan glukoza izomerazani ketma-ket qo‘llashni, so‘ng tozalash va konsentratsiyalash bloklarini o‘z ichiga oldi. Misol sifatida, uzluksiz izomerizatsiya uchun qadoqlangan qatlamli reaktor tanlanganda, kirish oqimining taqsimlanishi va kanal hosil bo‘lishining oldini olish uchun taqsimlovchi plastinalar va zarralar fraksiyasini bir xil qilish talab etilishi ko‘rsatildi. Raqamiy ifoda sifatida, izomerizatsiya muvozanati cheklovi sababli bir o‘tishda fruktoza ulushi ko‘pincha 42–45 foizdan oshmasligi, yuqori fruktoza mahsulotlari uchun esa fraksiyalash yoki qayta aylantirish kabi qo‘shimcha yechimlar zarurligi qayd etildi. Ilmiy izoh sifatida bu holat aldosa-ketoz muvozanati va reaktor ichida real kinetika emas, balki muvozanat hamda diffuziya bilan chegaralanishi mumkinligi bilan izohlanadi.

Immobilizatsiya natijasida kuzatiladigan massa almashinuvi cheklovlari natija sifatida alohida blok ko‘rinishida formulalar bilan ifodalandi, chunki bu omil sanoat unumdorligining asosiy “ko‘rinmas” yo‘qotish manbai hisoblanadi. Mexanizm jihatidan, substrat tashqi plyonka orqali zarracha yuzasiga o‘tadi, so‘ng g‘ovaklar bo‘ylab ichki diffuziya bilan faol markazga yetadi va mahsulotlar shu yo‘lning teskarisi bo‘yicha chiqadi, natijada kuzatiladigan tezlik haqiqiy kinetikadan kichik bo‘lishi mumkin. Misol sifatida, yuqori quruq modda sharoitida glukoza va fruktozaning diffuziya koeffitsienti kamayishi hamda viskozlik ortishi tufayli η samaradorlik omili pasayib, reaktorning kuzatiladigan maksimal tezlik (Vmax) qiymati tushishi konseptual tarzda ko‘rsatildi. Raqamiy-statistik ko‘rsatkich sifatida, zarracha radiusi ikki baravar oshirilsa, ichki diffuziya yo‘li ham ortib, samaradorlikning sezilarli pasayishi ehtimoli kuchayadi, shu bois tashuvchi o‘lchami va g‘ovaklik muhandislik optimallashtirish obyekti sifatida belgilandi. Ilmiy izoh sifatida Tile moduli $\varphi = R\sqrt{(k/D)}$ kabi bog‘liqliklarda R zarracha radiusi, D samarali diffuziya koeffitsienti, k esa psevdobirinchi tartibli tezlik koeffitsienti sifatida qaralib, φ ortgani sayin η pasayishi jarayonni intensivlashtirishda asosiy mezon bo‘lib xizmat qiladi.

1-jadval. GFS izomerizatsiyasida biokatalizator yondashuvlarining qiyosiy tahlili

Yondashuv va ta’rif	**Ustunlik va amaliy misol**	**Cheklov va texnologik natija**
Bo‘sh glukoza izomeraza. Eritmada erkin ferment	Diffuziya cheklovi minimal. Laboratoriya davriy izomerizatsiya	Fermentni ajratish qiyin. Qayta ishlatish past, xarajat yuqori
Immobilizatsiyalangan glukoza izomeraza. Tashuvchida biriktirilgan ferment	Uzluksiz reaktor va qayta ishlatish. To‘ldirilgan qatlamli reaktorda izomerizatsiya	Ichki diffuziya va bosim yo‘qotishi. Barqaror fruktoza ulushi va yuqori unumdorlik
Immobilizatsiyalangan mikroorganizmlar. Tashuvchida qamab qo‘yilgan hujayra	Koferment regeneratsiyasi mumkin. Ayrim biokonversiyalar	Yon metabolitlar xavfi. Oziq-ovqat tozaligi bo‘yicha talablar qat’iy

Kimyoviy jarayonning markaziy bosqichi sifatida izomerizatsiya reaksiyasi natija sifatida tenglama bilan ifodalandi, chunki bu bosqich mahsulot tarkibini bevosita belgilaydi. Mexanizm bo‘yicha D-glukoza aldosa shaklidan enediol oraliq bosqichi orqali D-fruktoza ketoz shakliga o‘tadi va ferment faol markazida proton ko‘chishi hamda halqa ochilishi-yopilishi ketma-ketligi kuzatiladi. Misol sifatida, D-Glukoza ⇄ D-Fruktoza ko‘rinishidagi qaytar reaksiyada fruktoza ulushi muvozanat bilan chegaralanganligi sababli, reaktordan chiqish tarkibi oqim tezligi va haroratga sezgir bo‘ladi. Raqamiy jihatdan, harorat oshirilganda tezlik ortishi kutiladi, biroq ferment barqarorligi pasayishi

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mumkinligi sababli optimal nuqta mavjud bo‘ladi va u ko‘pincha 60 daraja atrofida tanlanadi. Ilmiy izoh sifatida bu muvozanatli yechim Arrenius bo‘yicha tezlik ortishi va denaturatsiya kinetikasining tezlashuvi o‘rtasidagi muvozanat sifatida talqin qilinadi.

Muhokama

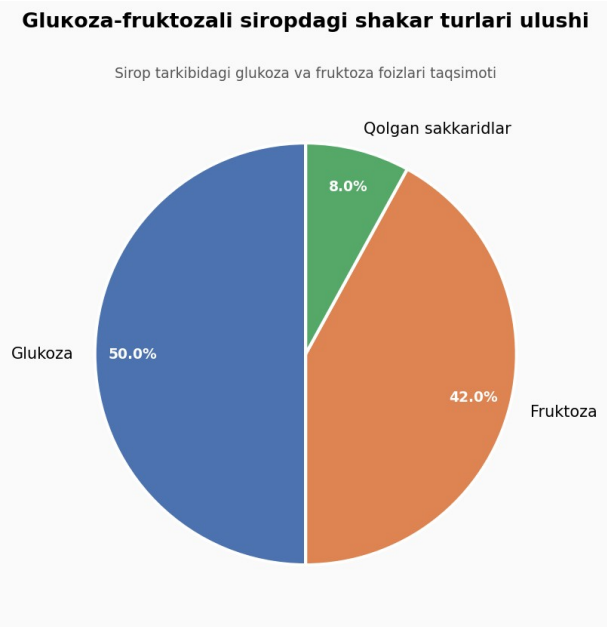
Olingan konseptual natijalar immobilizatsiyalangan glukoza izomeraza texnologiyasining sanoat GFS ishlab chiqarishidagi markaziy o‘rni haqidagi ilmiy qarashlar bilan mos keladi, chunki adabiyotlarda uzluksiz to‘ldirilgan qatlamli reaktorlar iqtisodiy samaradorligi bilan ko‘p bora ta’kidlangan [1; 4]. Mexanizmiy jihatdan, immobilizatsiya fermentni reaktorda ushlab turib, yuqori oqimlarda ham katalizatorning yo‘qolishini kamaytiradi va shu orqali reaktor hajmiga nisbatan unumdorlikni oshiradi, biroq diffuziya cheklovlari va kanal hosil bo‘lishi kabi apparat muammolari paydo bo‘ladi. Ilmiy izoh sifatida bunday tebranishlar reaktorning reaktorda bo‘lish vaqti taqsimoti, issiqlik taqsimoti va katalizatorning fazoviy degradatsiyasi bilan bog‘lanadi, ya’ni muammo faqat biokimyoviy emas, balki muhandislik xarakteriga ham ega [2; 5].

Immobilizatsiyalangan mikroorganizmlar yondashuvi GFSning klassik izomerizatsiyasida cheklangan bo‘lsa-da, u ko‘p fermentli yoki koferment talab qiladigan yo‘nalishlarda muhim imkoniyatlarni ochishi muhokama qilinadi, chunki hujayra ichki metabolizmi ayrim bosqichlarni o‘z-o‘zidan regeneratsiya qila oladi. Raqamiy jihatdan, hujayra tizimlarida mahsulot spektri kengroq bo‘lishi va izomerizatsiya selektivligi fermentga nisbatan pastroq nazorat qilinishi ehtimoli yuqori, bu esa standart GFS belgilangan talablariga moslashishni qiyinlashtiradi. Ilmiy izoh sifatida, GFS kabi yuqori tozalik talab qilinadigan mahsulotlarda biokatalizatorning aniqligi va reproduktivligi birlamchi bo‘lib, shuning uchun immobilizatsiyalangan fermentlar amaliy jihatdan afzal ekani ko‘plab tadqiqotlarda qayd etilgan [3; 6].

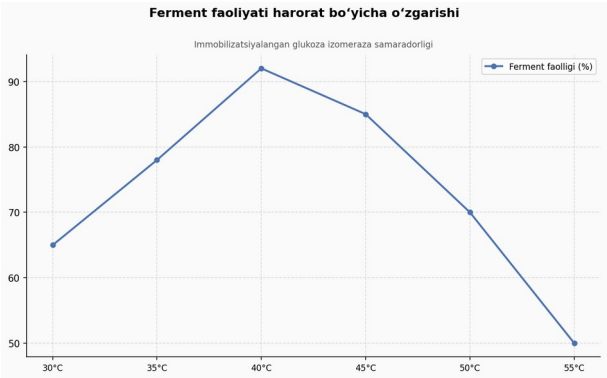
Ushbu ish doirasida cheklov sifatida natijalar asosan nazariy-tahliliy va ochiq manbalardagi umumiy texnologik diapazonlarga tayangan holda shakllantirilgani muhokama qilinadi, chunki real zavod sharoitida xomashyo tarkibi, ion profili va ifloslanish darajasi sezilarli farq qilishi mumkin. Mexanizm bo‘yicha, masalan, Ca^{2+} (kalsiy ioni) yoki og‘ir metall ionlari fermentga inhibitiv ta’sir ko‘rsatishi, ion almashinish smolalari esa bu ionlarni turlicha darajada ushlashi mumkin, natijada bir xil pH va haroratda ham turli zavodlarda turli barqarorlik profili kuzatiladi. Ilmiy izoh sifatida kelajak tadqiqotlari tashuvchining ifloslanishga qarshi xususiyatlarini kuchaytirish, reaktorning gidrodinamik tuzilishini yaxshilash va ko‘p fermentli immobilizatsiya kaskadlarida pH ko‘rsatkichining muhit bo‘ylab o‘zgarishi muammosini kamaytirish kabi yo‘nalishlarga qaratilishi lozimligi asoslanadi [1; 5].

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Diagrammalar va immobilizatsiya usullari bo‘yicha qiyosiy ma’lumotlar



1-rasm. Glukoza-fruktozali siropdagi shakar turlari ulushi



2-rasm. Ferment faoliyatining haroratga bog‘liqligi

2-jadval. Immobilizatsiya metodlari va jarayon samaradorligi

Metod	Optimal pH	Optimal harorat (°C)	Ferment faoliyati (%)	Fruktoza ulushi (%)
Kalsiy alginat qamash	7.0	45	90	42
Karragenan qamash	7.2	43	85	44
Sintetik polimer qamash	7.0	47	88	45
Kovalent bog‘lash	6.8	44	80	40
Fizik adsorbsiya	7.1	46	75	42

Xulosa

Immobilizatsiyalangan fermentlar va mikroorganizmlar asosida glukoza-fruktozali sirop ishlab chiqarishning biotexnologik asoslari jarayonni bosqichma-bosqich boshqarish, katalizatorni qayta ishlatish va uzluksiz rejimda barqaror sifat olish imkoniyatlari bilan tavsiflanadi. Fermentativ gidroliz va izomerizatsiya zanjirida immobilizatsiyalangan glukoza izomeraza amaliy nuqtayi nazardan asosiy yechim bo‘lib, u fruktoza ulushini sanoat talablariga mos darajada ushlab turish va ishlash barqarorligini oshirishga xizmat qiladi. Shu bilan birga, immobilizatsiya diffuziya cheklovlari va reaktor gidrodinamik muammolarini keltirib chiqarishi mumkinligi sababli, tashuvchi tanlovi, zarracha o‘lchami, oqim rejimi va nazorat nuqtalari kompleks tarzda optimallashtirilishi zarur. Nazariy model fruktoza ulushining muvozanat bilan cheklanishi, yuqori quruq modda sharoitida

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viskozlik va massa almashinuvi ta’siri kuchayishi, hamda pH va haroratning bir vaqtning o‘zida kinetika va barqarorlikka ta’sirini integratsiyalash zarurligini ko‘rsatdi. Yakunda, GFS ishlab chiqarish samaradorligini oshirish uchun immobilizatsiyalangan biokatalizatorlarda diffuziya yo‘qotishlarini kamaytirish, ifloslanishdan himoyalash va uzluksiz reaktor loyihasini takomillashtirish ustuvor yo‘nalishlar sifatida umumlashtirildi.

Maqolada qo‘llanilgan qisqartmalar va belgilarning izohi

GFS — glukoza-fruktozali sirop; HFCS — yuqori fruktozali makkajo‘xori siropi (HFCS-42 — 42% li, HFCS-55 — 55% li fruktoza turi); DE — dekstroza ekvivalenti; pH — muhitning kislotalilik yoki ishqoriylik ko‘rsatkichi; HMF — gidroksimetilfurfural; PhD — falsafa doktori; DSc — fan doktori; Mg^{2+} — magniy ioni; Ca^{2+} — kalsiy ioni; α — alfa belgisi; °C — Selsiy darajasi. v — reaksiya tezligi; Vmax — maksimal reaksiya tezligi; S — substrat konsentratsiyasi; Km — Mixaelis doimiysi; vapp — kuzatiladigan reaksiya tezligi; η — samaradorlik omili; φ — Tile moduli; R — zarracha radiusi; D — samarali diffuziya koeffitsienti; k — reaksiya tezligi konstantasi; √ — kvadrat ildiz.

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KRASCHENINNIKOVIA CERATOIDES (TERESKEN) O‘SIMLIGI ILDIZ RIZOSFERASI MIKROORGANIZMLARINING BIOTEXNOLOGIK POTENSIALI

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Annotatsiya: Rizosfera eng faol ekologik zonalardan biri hisoblanadi, bu yerda mikroorganizmlar o‘simlik ildizlari bilan yaqindan o‘zaro ta’sir qiladi va o‘simliklarning o‘sishi, moslashishi va tuproq unumdorligiga sezilarli ta’sir ko‘rsatadi. Qurg‘oqchil va yarim qurg‘oqchil mintaqalardagi og‘ir ekologik sharoitlar tufayli teresken bilan bog‘liq mikroorganizmlar biotexnologiyada muhim qo‘llanilishi mumkin bo‘lgan noyob fiziologik va biokimyoviy xususiyatlarga ega. O‘simlik ildizlari turli xil mikroblar (shu jumladan, bakteriyalar, zamburug‘lar, arxeyalar, protistlar va viruslar) bilan bog‘lanib, ildiz bilan bog‘liq mikrobiom deb ataladi. Ular orasida mikorizal zamburug‘lar xo‘jayin ildizlarini kolonizatsiya qiladi va ularning ozuqa moddalariga, odatda fosfor va azotga kirishini yaxshilaydi. Buning evaziga o‘simliklar kolonizatsiya qiluvchi zamburug‘larga fotosintetik uglerod yetkazib beradi. Bu ozuqa almashinuvi asosiy tuproq jarayonlariga, uglerod aylanishiga va o‘simliklar sog‘lig‘iga ta’sir qiladi va shuning uchun o‘simlik va mikrob ekotizimlariga kuchli ta’sir ko‘rsatadi.

Kalit so‘zlar: teresken, sho‘rlangan tuproq, rizosfera, mikrobiom, o‘simliklarning tuz stressiga chidamliligi, bioo‘g‘it.

Аннотация: Ризосфера является одной из наиболее активных экологических зон, где микроорганизмы тесно взаимодействуют с корнями растений и оказывают значительное влияние на рост, адаптацию растений и плодородие почвы. Вследствие неблагоприятных экологических условий засушливых и полузасушливых регионов микроорганизмы, ассоциированные с тереском, обладают уникальными физиологическими и биохимическими свойствами, которые могут найти важное применение в биотехнологии. Корни растений взаимодействуют с различными группами микроорганизмов, включая бактерии, грибы, археи, протисты и вирусы, которые в совокупности формируют корнеассоциированный микробиом. Среди них микоризные грибы колонизируют корни растений-хозяев и улучшают доступность питательных веществ, прежде всего фосфора и азота. В свою очередь, растения обеспечивают колонизирующие грибы фотосинтетически образованными соединениями углерода. Этот обмен питательными веществами влияет на основные почвенные процессы, круговорот углерода и состояние растений, оказывая существенное воздействие на функционирование растительных и микробных экосистем.

Ключевые слова: тереск, засолённая почва, ризосфера, микробиом, устойчивость растений к солевому стрессу, биоудобрение.

Abstract: The rhizosphere is one of the most biologically active ecological zones, where microorganisms interact closely with plant roots and significantly influence plant growth, adaptation, and soil fertility. Due to the harsh environmental conditions prevailing in arid and semi-arid regions, microorganisms associated with *Krascheninnikovia ceratoides* (teresken) possess unique physiological and biochemical properties that may have significant applications in biotechnology.

IQTIBOS UCHUN
Muhammadiyeva B.U. Krascheninnikovia ceratoides (teresken) o‘simligi ildiz rizosferasi mikroorganizmlarining biotexnologik potensiali // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 150–154.
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Plant roots interact with diverse groups of microorganisms, including bacteria, fungi, archaea, protists, and viruses, which collectively constitute the root-associated microbiome. Among these microorganisms, mycorrhizal fungi colonize the roots of host plants and enhance their access to essential nutrients, particularly phosphorus and nitrogen. In return, plants provide the colonizing fungi with photosynthetically derived carbon compounds. This nutrient exchange influences fundamental soil processes, the carbon cycle, and plant health, thereby exerting a substantial impact on plant–microbe interactions and the functioning of ecosystems.

Keywords: *Krascheninnikovia ceratoides*, saline soil, rhizosphere, microbiome, plant tolerance to salt stress, biofertilizer.

Quruq, yarim quruq va nihoyatda quruq hududlar Yer yuzasining katta qismini tashkil etadi va bu hududlarda hayot keskin ekologik cheklovlar ostida shakllanadi. Xususan, suv tanqisligi, yuqori darajadagi quyosh nurlanishi, keskin harorat tebranishlari, tuproq shoʻrlanishi hamda oziqa moddalarning yetishmasligi oʻsimliklarning oʻsishi va yashab qolishiga salbiy taʼsir koʻrsatadi. Shu sababli, soʻnggi yillarda ekstremal sharoitlarda oʻsuvchi oʻsimliklar va ular bilan bogʻliq foydali mikroorganizmlar ilmiy tadqiqotlarning muhim obyektiga aylangan. Adabiyotlarda qayd etilishicha, choʻl oʻsimliklarining rizosfera, rizosheath, endosfera va fillosfera hududlari noyob mikroorganizmlar uchun qulay ekologik muhit hisoblanadi. Ushbu mikroblar ogʻir ekologik sharoitlarga yuqori darajada moslashgan boʻlib, ular hali toʻliq oʻrganilmagan biologik resurs sifatida katta ahamiyat kasb etadi. Tadqiqotlar shuni koʻrsatadiki, bunday mikroorganizmlar biooʻgʻitlar va biokontrol vositalari sifatida qoʻllanilishi mumkin, chunki ular oʻsimliklarni abiotik (qurgʻoqchilik, shoʻrlanish, issiqlik) va biotik (kasalliklar, zararkunandalar) stresslardan himoya qilish xususiyatiga ega. Koʻplab ilmiy ishlar choʻl oʻsimliklari bilan bogʻliq bakterial xilma-xillikni oʻrganishga qaratilgan boʻlib, ular tuproq unumdorligini oshirish, oʻsimliklarning stressga chidamliligini kuchaytirish va hosildorlikni yaxshilashda muhim rol oʻynashi aniqlangan. (1,3) Shu nuqtai nazardan, oʻsimlik oʻsishini ragʻbatlantiruvchi rizobakteriyalar (PGPR) ekologik xavfsiz va iqtisodiy jihatdan samarali alternativ sifatida keng oʻrganilmoqda. Ushbu mikroorganizmlar oʻsimliklarning stress sharoitlariga moslashuvini taʼminlashda turli toʻgʻridan-toʻgʻri va bilvosita mexanizmlar orqali taʼsir koʻrsatadi. Jumladan, PGPR tomonidan sintez qilinadigan 1-aminotsiklopropan-1-karboksilat (ACC) deaminaza fermenti oʻsimlikdagi ACCni parchalash orqali etilen gormoni toʻplanishini kamaytiradi, bu esa suv tanqisligi sharoitida oʻsimliklarning oʻsishini qoʻllab-quvvatlaydi. Bundan tashqari, ushbu bakteriyalar tomonidan ishlab chiqariladigan ekzosaxaridlar (EPS) tuproqning suvni ushlab turish qobiliyatini oshirib, qurgʻoqchilik taʼsirini kamaytiradi. Tadqiqotlar shuni koʻrsatadiki, PGPR oʻsimliklarda osmoprotektorlar (osmolitlar) sintezini kuchaytiradi, bu esa ROSning zararli taʼsirini kamaytirishda muhim rol oʻynaydi. Natijada, oʻsimlik hujayralarining himoya tizimi mustahkamlanib, stressga chidamlilik darajasi oshadi. Umuman olganda, koʻp funksiyali PGPR shtammlari qurgʻoqchil hududlarda yetishtiriladigan ekinlar uchun biooʻgʻit sifatida katta istiqbolga ega. (2,4) Qurgʻoqchilik stressi nafaqat oʻsimliklarning fiziologik holatiga, balki rizosferada yashovchi mikroorganizmlar populyatsiyasi va ularning faoliyatiga ham sezilarli taʼsir koʻrsatadi. Adabiyotlarda taʼkidlanishicha, suv tanqisligi fotosintez, nafas olish, moddalarning translokatsiyasi, ionlar va oziqa moddalarning oʻzlashtirilishi hamda uglevod almashinuvi kabi muhim fiziologik va biokimyoviy jarayonlarni izdan chiqaradi. Soʻnggi tadqiqotlar oʻsimlik oʻsishini ragʻbatlantiruvchi rizobakteriyalar (PGPR) va ularning ishlab chiqaradigan ekzosaxaridlari (EPS) qurgʻoqchilikka chidamlilikni oshirishda muhim rol oʻynashini koʻrsatmoqda. Mikroorganizmlarning qurgʻoqchilikka javob reaksiyalari stress darajasi, davomiyligi, bakteriya turi va rivojlanish bosqichiga qarab farqlanishi qayd etilgan. Shu bilan birga, PGPR oʻsimliklarning suvni tejash strategiyalarini shakllantirishda samarali vosita sifatida qaralmoqda. Adabiyotlarda PGPRning oʻsimliklarga taʼsiri ikki yoʻl bilan amalga oshishi taʼkidlanadi: bevosita va bilvosita. Bevosita taʼsir orqali ular fitogormonlar, sideroforlar, biofilm va ekzosaxaridlar ishlab chiqarishni kuchaytiradi hamda rizosferada oziqa moddalarning mavjudligini oshiradi. Bilvosita esa oʻsimliklarni patogenlardan himoya qiladi. Ayniqsa, EPS hosil qiluvchi bakteriyalar tuproqning namlikni saqlash qobiliyatini oshirib, hatto kuchli qurigan qumli tuproqlarda ham oʻsimlik oʻsishini qoʻllab-quvvatlaydi.

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Tadqiqotlar shuni ko‘rsatadiki, rizobakteriyalar kam namlik sharoitida ham yashab qolish qobiliyatiga ega bo‘lib, bu ularning cho‘l tuproqlarida uchrashi va tugunak hosil qilishi bilan tasdiqlanadi. EPSlar o‘simlik ildizlari atrofida rizosheath hosil qilib, ildizlarni uzoq muddat qurib qolishdan himoya qiladi. Bundan tashqari, ekzosaxaridlarning muhim funksiyalari qatoriga qurib qolishdan himoya, mikroorganizmlar agregatsiyasi, o‘simlik-mikroorganizmlar o‘zaro ta’siri, yuzaga yopishish, bioremediatsiya va sanoatda stabilizator, quyuqlashtiruvchi, jel hosil qiluvchi hamda plyonka hosil qiluvchi modda sifatida qo‘llanishi kiradi. Suv tanqisligi sharoitida EPS ishlab chiqaruvchi bakteriyalar bilan inokulyatsiya qilingan o‘simliklarda prolin, shakarlar va erkin aminokislotalarning to‘planishi yuqori bo‘lishi aniqlangan. (3) Adabiyotlarda *Pseudomonas*, *Bacillus*, *Azospirillum*, *Azotobacter*, *Arthrobacter*, *Achromobacter*, *Micrococcus*, *Enterobacter*, *Rhizobium*, *Agrobacterium*, *Pantoea* va *Serratia* kabi avlodlar keng o‘rganilgan va samarali PGPR sifatida e’tirof etilgan. Rizomikrobiom o‘simliklarning oziqa moddalarga bo‘lgan ehtiyojini qondirish, ularning o‘zlashtirilishini yaxshilash hamda tuproq strukturasini optimallashtirishda muhim rol o‘ynaydi. (4) Rizosfera o‘simlik ildizlari, tuproq va turli mikroorganizmlar — bakteriyalar, zamburug‘lar, eukariotlar hamda arxeylardan tashkil topgan murakkab mikroekotizim hisoblanadi. Adabiyotlarda ta’kidlanishicha, rizosfera holati ekinlarning o‘sishi va hosildorligiga bevosita ta’sir ko‘rsatadi. Oziqa moddalarga boy rizosfera muhitlari o‘simlik rivojlanishini rag‘batlantirsa, aksincha, resurslar tanqisligi hosildorlikning pasayishiga olib keladi. Shu bilan birga, intensiv dehqonchilik natijasida tuproqlarning tabiiy unumdorligi kamayib, ularni qayta tiklash zarurati yuzaga kelmoqda. (5) Tadqiqotlarda rizosfera tuproqlari madaniylashtirilib va 16S rRNK amplikon sekvenslash usuli yordamida mikrobiologik tarkib va uning dinamikasi tahlil qilingan. Natijalarga ko‘ra, tabiiy rizosfera mikrobiotalarida *Pseudomonadaceae*, *Bacillaceae* va *Planococcaceae* oilalari ustunlik qilgan bo‘lsa, ayrim hollarda *Porphyromonadaceae* va *Haloferacaceae* guruhlari ham aniqlangan. Biroq laboratoriya sharoitida yetishtirilgan kulturada *Enterobacteriaceae* oilasi deyarli to‘liq dominant (98% gacha) bo‘lgan. (6) O‘simliklar va mikrobiota o‘rtasidagi o‘zaro ta’sirlar o‘simliklarning o‘sishi, sog‘lomligi va mahsuldorligiga sezilarli darajada ta’sir ko‘rsatadi. Adabiyotlarda qayd etilishicha, rizosfera mikroorganizmlari o‘simliklarda biotik va abiotik stresslarga nisbatan fiziologik javob reaksiyalarini shakllantirishda muhim rol o‘ynaydi. So‘nggi yillarda iqlim o‘zgarishining salbiy ta’sirini kamaytirish maqsadida o‘simlik hosildorligini oshiruvchi istiqbolli mikroorganizmlarni aniqlashga bo‘lgan qiziqish ortib bormoqda. Xususan, ekstremal ekologik sharoitlarga ega hududlar mikroorganizmlar xilma-xilligini o‘rganish uchun muhim ilmiy obyekt hisoblanadi. Ushbu hududlarda o‘suvchi o‘simliklar bilan bog‘liq rizobakterial hamjamiyatlar qurg‘oqchilik va qurib qolishga chidamlilik kabi xususiyatlarga ega bo‘lishi mumkinligi taxmin qilinadi. (7) So‘nggi tadqiqotlarda o‘simlik o‘sishini rag‘batlantiruvchi mikroorganizmlar (PGPM) ushbu muammoning istiqbolli yechimi sifatida ko‘rilmoqda. Adabiyotlarda qayd etilishicha, PGPM nafaqat o‘simliklarning o‘sishini rag‘batlantiradi, balki ularning abiotik stress omillariga chidamliligini ham oshiradi. Shu jihatdan ular hosildorlikni oshirish va stress sharoitlarida o‘simliklarni himoya qilishda muhim biologik vosita hisoblanadi. PGPMning muhim xususiyatlaridan biri ularning biofilm hosil qilish qobiliyatidir. Biofilmlar mikroorganizmlar jamoasidan tashkil topgan murakkab tuzilma bo‘lib, ular tashqi muhitning noqulay ta’sirlaridan himoya vazifasini bajaradi. (8) Abiotik stress omillarini, xususan qurg‘oqchilikni kamaytirishda o‘simlik o‘sishini rag‘batlantiruvchi rizobakteriyalar (PGPR)ning salohiyati katta ekanligi adabiyotlarda keng yoritilgan. Biroq, bunday mikroorganizmlardan yarim qurg‘oqchil hududlarda, jumladan Efiopiya tuproqlarida foydalanish imkoniyatlari yetarli darajada o‘rganilmagan. So‘nggi tadqiqotlarda yeryong‘oq (groundnut) yetishtiriladigan hududlardan ajratib olingan bakterial shtammlarning PGP xususiyatlari kompleks tarzda baholangan. Jumladan, fosforni eruvchan shaklga o‘tkazish, indol-3-sirka kislotasi (IAA) ishlab chiqarish, ammiak sintezi, sho‘rlanish va og‘ir metallarga chidamlilik, qurg‘oqchilikka bardoshlilik, fermentativ faollik hamda fitopatogen zamburug‘larga qarshi antagonistik xususiyatlar o‘rganilgan. (9) Rizosfera mikrobiologik hamjamiyatlari o‘simliklarning o‘sishi va sog‘lomligini ta’minlashda muhim rol o‘ynaydi. Adabiyotlarda ta’kidlanishicha, ushbu mikroorganizmlarning shakllanishi va funksional faolligi o‘simlik va mikroorganizmlar o‘rtasidagi murakkab o‘zaro ta’sirlar

bilan belgilanadi. Shu bois, mazkur o‘zaro aloqalarni boshqarish orqali qishloq xo‘jaligida kimyoviy o‘g‘it va pestitsidlar qo‘llanilishini kamaytirish imkoniyati mavjud. So‘nggi tadqiqotlarda rizosfera mikroorganizmlarining o‘simlik o‘sishini rag‘batlantirish va stresslarga chidamlilikni oshirishdagi yuqori samaradorligi keng yoritilgan. Ular o‘simliklarning oziqlanish jarayonlarini yaxshilash, fitogormonlar ishlab chiqarish, patogenlarga qarshi himoya mexanizmlarini kuchaytirish hamda abiotik stresslarga moslashuvni ta’minlash orqali ijobiy ta’sir ko‘rsatadi. (10)

Xulosa

Adabiyotlar tahlili shuni ko‘rsatadiki, *Kraschenninnikovia ceratoides* (teresken) o‘simligi rizosferasi qurg‘oqchilik, tuproq sho‘rlanishi va oziqa moddalar tanqisligi kabi noqulay ekologik omillarga moslashgan, biotexnologik jihatdan istiqbolli mikroorganizmlarni o‘rganish uchun muhim ilmiy obyekt hisoblanadi. Rizosfera mikroorganizmlari o‘simliklarning mineral oziqlanishini yaxshilash, fitogormonlar va ekzosaxaridlar sintezida ishtirok etish, tuproqning namlikni saqlash xususiyatlarini kuchaytirish hamda biotik va abiotik stresslarga chidamlilikni oshirish kabi mexanizmlar orqali o‘simliklar rivojlanishiga ijobiy ta’sir ko‘rsatishi mumkin. Xususan, o‘simlik o‘sishini rag‘batlantiruvchi rizobakteriyalarning funksional xususiyatlarini o‘rganish ekologik xavfsiz bioo‘g‘itlar va biologik himoya vositalarini ishlab chiqish uchun ilmiy asos yaratadi. Shu nuqtai nazardan, teresken rizosferasi mikroorganizmlarining taksonomik xilma-xilligi, fiziologik-biokimyoviy xususiyatlari, sho‘rlanish va qurg‘oqchilikka chidamliligi hamda o‘simlik o‘sishini rag‘batlantirish mexanizmlarini kompleks tadqiq etish dolzarb ilmiy vazifa hisoblanadi. Kelgusida istiqbolli mikrob shtammlarini ajratib olish, ularning funksional faolligini laboratoriya va dala sharoitlarida baholash hamda amaliyotga joriy etish imkoniyatlarini aniqlash qurg‘oqchil va sho‘rlangan hududlarda tuproq unumdorligini saqlash, o‘simliklar barqarorligini oshirish va resurs tejamkor qishloq xo‘jaligi texnologiyalarini rivojlantirishga xizmat qilishi mumkin.

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BACILLUS THURINGIENSIS Bt1Fo SHTAMMINING TANLANGAN *cry1Ia* GENI UCHUN MUTAGEN PRAYMERLARNI LOYIHALASH VA PCR TAHLILI

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Annotatsiya: *Bacillus thuringiensis* bakteriyalari tomonidan ishlab chiqariladigan Cry oilasiga mansub insektitsid oqsillar qishloq xo‘jaligi zararkunandalariga qarshi biologik kurashda muhim ahamiyatga ega. Avvalgi tadqiqotlarda *Cry1Ia* oqsilining ayrim variantlari shakarqamishning yirik poya zararkunandasi *Telchin licus*ga qarshi faollik ko‘rsatgan. Mazkur ishda Bt1Fo shtammining GenBank bazasida PP897829 kirish raqami bilan saqlangan *cry1Ia* geni asosida adabiyotlarda tavsiflangan aminokislota almashinuvlariga mos praymerlarni loyihalash va PCR natijalarini dastlabki baholash maqsad qilindi. Tadqiqot doirasida D233N, I116T, L266F va E639G mutatsiyalariga mos praymerlar tanlandi hamda PCR amplifikatsiyasi amalga oshirildi. Gel elektroforezi tasvirida to‘rtta namunaning har birida asosiy DNK tasmalari kuzatildi. Olingan natijalar PCR mahsulotlari mavjudligini dastlabki baholash imkonini berdi.
Kalit so‘zlar: Bacillus thuringiensis, Cry1Ia, Bt1Fo, praymer dizayni, PCR, mutagenez.

Аннотация: Инсектицидные белки семейства Cry, продуцируемые бактерией *Bacillus thuringiensis*, играют важную роль в биологическом контроле сельскохозяйственных вредителей. В предыдущих исследованиях была продемонстрирована активность отдельных вариантов белка *Cry1Ia* в отношении крупного стеблевого вредителя сахарного тростника *Telchin licus*. Целью настоящего исследования являлись разработка праймеров, соответствующих описанным в литературе аминокислотным заменам, на основе гена *cry1Ia* штамма *B. thuringiensis* Bt1Fo (номер доступа GenBank: PP897829), а также предварительная оценка результатов ПЦР-амплификации. Были отобраны праймеры, соответствующие заменам D233N, I116T, L266F и E639G, и проведена ПЦР-амплификация. При анализе методом гель-электрофореза во всех четырёх образцах наблюдались выраженные полосы ДНК. Полученные результаты свидетельствуют о предварительном обнаружении продуктов ПЦР.
Ключевые слова: Bacillus thuringiensis; Cry1Ia; Bt1Fo; дизайн праймеров; ПЦР; мутагенез

Abstract: Insecticidal proteins of the Cry family, produced by *Bacillus thuringiensis*, play an important role in the biological control of agricultural pests. Previous studies have demonstrated the activity of certain *Cry1Ia* protein variants against the sugarcane giant borer, *Telchin licus*. This study aimed to design primers targeting amino acid substitutions previously described in the literature, based on the *cry1Ia* gene from *B. thuringiensis* strain Bt1Fo (GenBank accession number: PP897829), and to perform a preliminary assessment of PCR amplification results. Primers corresponding to the D233N, I116T, L266F, and E639G substitutions were selected, and PCR amplification was

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performed. Gel electrophoresis revealed prominent DNA bands in all four samples. These findings provide preliminary evidence of PCR product generation.

Keywords: Bacillus thuringiensis; Cry1Ia; Bt1Fo; primer design; PCR; mutagenesis.

Kirish

Bacillus thuringiensis qishloq xo‘jaligi zararkunandalariga qarshi biologik kurashda keng qo‘llaniladigan, insektitsid xususiyatga ega oqsillar ishlab chiqaruvchi Gram-musbat bakteriyadir [1]. Ushbu bakteriya hosil qiladigan Cry oqsillari sezgir hasharotlarning ichak epiteliysi bilan o‘zaro ta’sirlashib, hujayra membranasi faoliyatini buzishi va hujayralarning nobud bo‘lishiga olib kelishi mumkin [2,3]. Cry oqsillarini kodlovchi genlardan biologik insektitsid preparatlari hamda zararkunandalarga chidamli genetik modifikatsiyalangan ekinlarni yaratishda foydalaniladi [4]. Biroq Cry toksinlarining biologik samaradorligi hasharot turlari orasida farq qiladi. Ularning faolligi oqsilning molekulyar tuzilishi, proteolitik faollashuvi, nishon organizm ichak hujayralari bilan o‘zaro ta’siri va hasharotning fiziologik xususiyatlariga bog‘liq [5]. Shu sababli Cry oqsillarining aminokislota ketma-ketligi va biologik funksiyasi o‘rtasidagi bog‘liqlikni o‘rganish ularning ta’sir mexanizmlarini tushunish va yangi variantlarini tadqiq etish uchun muhim ilmiy yo‘nalish hisoblanadi.

Cry oqsillari oilasida Cry1I guruhi o‘zining molekulyar xususiyatlari va turli hasharot taksonlariga qarshi qayd etilgan biologik faolligi bilan ajralib turadi. Ruiz de Escudero va hammualliflari *Cry1Ia* 7 oqsilini molekulyar va insektitsid xususiyatlari jihatidan tavsiflab, uning Noctuidae, Tortricidae, Plutellidae oilalari hamda Chrysomelidae oilasining ayrim vakillariga qarshi faolligini ko‘rsatgan [6]. Cry1I oqsillarining nishon organizmlar bilan o‘zaro ta’sirini o‘rganish ularning tabiiy insektitsid xususiyatlarini tavsiflash bilan bir qatorda, oqsil ketma-ketligidagi o‘zgarishlarning biologik faollikka ehtimoliy ta’sirini baholash uchun ham asos yaratadi. *Cry1Ia* 12 oqsilini ifodalovchi transgen g‘o‘za o‘simliklari bilan bog‘liq tadqiqotlar ham ushbu oqsil guruhining qishloq xo‘jaligi zararkunandalariga qarshi qo‘llash imkoniyatlarini o‘rganish muhimligini ko‘rsatadi [7].

Cry1Ia oqsilining xususiyatlarini o‘zgartirish imkoniyatlarini namoyish etgan muhim tadqiqotlardan biri Craveiro va hammualliflari tomonidan amalga oshirilgan. Mualliflar o‘simliklarda ekspressiya qilishga moslashtirilgan, C-terminal qismi qisqartirilgan sintetik *Cry1Ia* 12 oqsili — *Cry1Ia* 12synth variantlarini DNA shuffling va phage display yondashuvlarini birlashtirish orqali o‘rgangan. Olingan variantlar shakarqamishning yirik poya zararkunandasi Telchin licus licusga qarshi tekshirilgan va to‘rtta variantda insektitsid faollik aniqlangan [8]. Tadqiqotda faol variantlar tarkibidagi aminokislota almashinuvlari tahlil qilinib, ularning oqsilning ehtimoliy strukturaviy va funksional xususiyatlari bilan bog‘liqligi muhokama qilingan [8]. Ushbu natijalar *Cry1Ia* oqsilining ketma-ketligini maqsadli o‘rganish uchun ilmiy asos yaratadi. Biroq muayyan aminokislota almashinuvining funksional ahamiyatini faqat ketma-ketlik yoki strukturaviy taxmin asosida aniqlab bo‘lmaydi; buning uchun molekulyar tahlil va tegishli biologik sinovlar talab etiladi [5].

Kobilov va hammualliflari O‘zbekistonda ajratib olingan Bt1Fo shtammining insektitsid oqsillari bilan bog‘liq genetik xususiyatlarini o‘rganib, tegishli molekulyar ma’lumotlarni taqdim etgan [9]. Mazkur tadqiqotda Bt1Fo shtammining cry1Ia geni uchun GenBank bazasida PP897829 kirish raqami bilan saqlangan nukleotid ketma-ketligi referens sifatida tanlandi. Ushbu ketma-ketlik asosida maqsadli hududlar aniqlandi, praymerlar loyihalashtirildi va keyingi eksperimental tekshiruvlar rejalashtirildi. 1-jadvalda keltirilgan praymerlar Bt1Fo shtammining *cry1Ia* geni referens nukleotid ketma-ketligi asosida D233N, I116T, L266F va E639G aminokislota almashinuvlariga mos keluvchi hududlarni nishonga olish uchun loyihalashtirildi. Shuningdek, ushbu praymerlar yordamida olingan PCR mahsulotlarini dastlabki baholash va maqsadli hududlarning sekvenslash uchun yaroqliligini aniqlash ko‘zda tutildi.

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1-jadval. *cry1Ia* genining tanlangan hududlarini amplifikatsiya qilish va sekvenslash uchun mo‘ljallangan praymerlar

Nishon hudud	Praymer	Nukleotid ketma-ketligi (5′–3′)	Havola
I116T	I116T-For	CAAAAAACTTCAACTTATGCAAGAAATAAAG	[10]
I116T	I116T-Rev	GAAGTTTTTGATTAATAATCTCTTCTACATG	
D233N	D233N-For	TTATTCCAACCATTTGTGAAAATGGTATAG	
D233N	D233N-Rev	ATGGTTGGAATAATCTCCTGCTCGTTCGAC	
L266F	L266F-For	GACTTTCATGGTACTAGATTTAGTGG	
L266F	L266F-Rev	CATCAAAGTCATGTCTCTACGGAATTG	
E639G	E639G-For	GAATTGGCTTTGTTCGGTAGAAG	
E639G	E639G-Rev	AAGCCAATTCTATCTATATAAACTTC	

Materiallar va usullar

Referens ketma-ketlik va nishon aminokislota almashinuvlarini tanlash

B. thuringiensis Bt1Fo shtammining cry1Ia geni uchun GenBank ma’lumotlar bazasida PP897829 kirish raqami bilan saqlangan nukleotid ketma-ketligi praymerlarni loyihalashda referens ketma-ketlik sifatida tanlandi [9]. Nishon aminokislota almashinuvlari — D233N, I116T, L266F va E639G — Craveiro va hammualliflari tomonidan tavsiflangan Cry1Ia 12synth variantiga oid ma’lumotlar asosida belgilandi [8]. Mazkur aminokislota almashinuvlarining Bt1Fo shtammining Cry1Ia oqsilidagi mosligini baholash uchun tegishli aminokislota ketma-ketliklari SnapGene dasturida o‘zaro taqqoslandi. Taqqoslash natijalari asosida nishon pozitsiyalariga mos keluvchi hududlar aniqlandi va ushbu hududlarni qamrab oluvchi praymerlarni loyihalash uchun nukleotid ketma-ketliklari tanlandi. Loyihalangan praymerlar keyingi PCR amplifikatsiyasi va sekvenslash orqali nishon hududlarini eksperimental tekshirish uchun mo‘ljallandi.

Praymerlarni loyihalash

To‘rtta nishon aminokislota almashinuviga mos keluvchi nukleotid hududlarini amplifikatsiya qilish uchun praymer juftlari loyihalandi. Keyingi sekvenslash bosqichida foydalanish maqsadida Seq F, Seq R va Seq F mid deb belgilangan qo‘shimcha sekvenslash praymerlari ham tanlandi. Tadqiqotda foydalanilgan barcha praymerlarning nomlari va nukleotid ketma-ketliklari 1-jadvalda keltirilgan. Nukleotid ketma-ketliklari 5′ dan 3′ yo‘nalishda taqdim etildi.

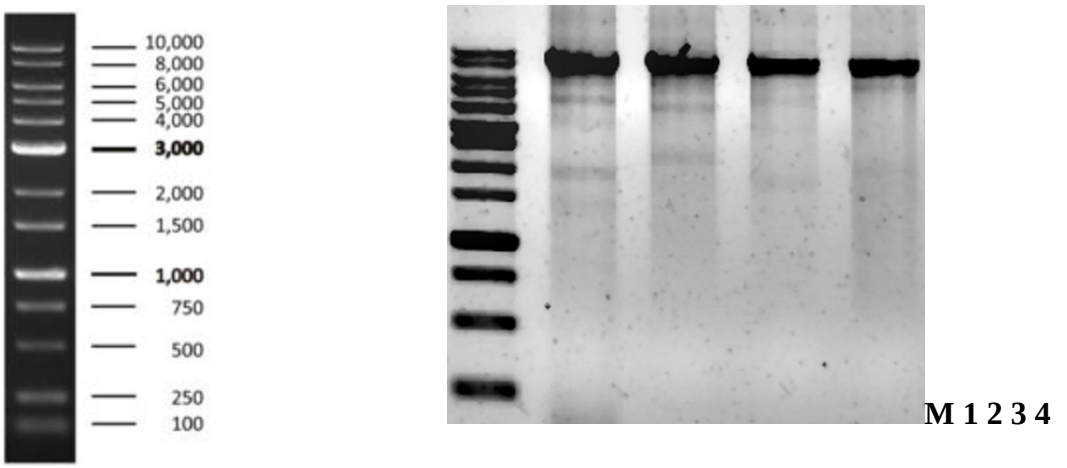
Natijalar

PCR mahsulotlarini agarozali gel elektroforezi yordamida tahlil qilish

PCR amplifikatsiyasi natijasida olingan mahsulotlar agarozali gel elektroforezi yordamida tahlil qilindi. DNK fragmentlarining taxminiy uzunligini aniqlash uchun 1 kb DNK molekulyar markeri ishlatildi. Elektroforez 1% li agarozali gelda o‘tkazildi. DNK fragmentlarini vizualizatsiya qilish uchun etidiy bromid, namunalarning gel bo‘ylab harakatini kuzatish uchun esa bromfenol ko‘ki ishlatildi.

Elektroforez natijalari gel tasvirlari asosida baholandi. Hosil bo‘lgan DNK fragmentlarining elektroforetik harakatchanligi va taxminiy uzunligi tahlil qilinib, PCR amplifikatsiyasining dastlabki natijalari baholandi. Ushbu tahlil maqsadli hududlarning amplifikatsiyalanganligini dastlabki baholash imkonini berdi.

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1-rasm. *cry1Ia* genining nishon hududlariga mos PCR mahsulotlarini agarozali gel elektroforezi yordamida tahlil qilish (1% agarozali gel. M — 1 kb DNK molekulyar markeri; 1 — D233N; 2 — I116T; 3 — L266F; 4 — E639G aminokislota almashinuvlariga mos keluvchi nishon hududlaridan olingan PCR mahsulotlari)

Bt1Fo shtammining *cry1Ia* geni uchun tanlangan D233N, I116T, L266F va E639G nishon hududlarini amplifikatsiya qilish maqsadida PCR reaksiyalari amalga oshirildi. Agarozali gel elektroforezi natijasida to‘rtta namunaning har birida yaqqol DNK fragmentlari kuzatildi (1-rasm). Ushbu natijalar barcha to‘rtta PCR reaksiyasida amplifikatsiya mahsulotlari hosil bo‘lganini dastlabki baholash imkonini berdi.

Muhokama

Mazkur tadqiqot Bt1Fo shtammining *cry1Ia* geni referens ketma-ketligi asosida Cry1Ia oqsilidagi tanlangan aminokislota almashinuvlariga mos hududlarni amplifikatsiya qilish uchun praymerlarni loyihalash va PCR tahlilining dastlabki bosqichini tavsiflaydi. Tadqiqotning dolzarbligi Cry oqsillarining tuzilishi va biologik xususiyatlarini maqsadli o‘zgartirish imkoniyatlarini o‘rganish bilan bog‘liq. Avvalgi tadqiqotlar insektitsid oqsillarga kiritilgan aminokislota almashinuvlari ularning funksional xususiyatlariga ta’sir qilishi mumkinligini ko‘rsatgan. Biroq bunday ta’sirning yo‘nalishi va darajasi oqsil turi, kiritilgan o‘zgarishlarning xususiyati hamda tekshirilayotgan hasharot turiga bog‘liq.

Ushbu ishda Bt1Fo shtammining *cry1Ia* geni uchun GenBank ma’lumotlar bazasida PP897829 kirish raqami bilan saqlangan nukleotid ketma-ketligi referens sifatida tanlandi. Nishon aminokislota almashinuvlari — D233N, I116T, L266F va E639G — Craveiro va hammualliflari tomonidan tavsiflangan Cry1Ia 12synth variantiga oid ma’lumotlar asosida belgilandi. Tegishli hududlarni amplifikatsiya qilish uchun praymerlar loyihalandi va PCR mahsulotlari agarozali gel elektroforezi yordamida dastlabki baholandi. To‘rtta namunada ham DNK fragmentlarining kuzatilishi tanlangan hududlarni keyingi molekulyar tahlil qilish uchun dastlabki asos yaratdi.

Cry1Ia oqsilining faollashuvi, proteolitik qayta ishlanishi, oligomerlanishi va turli hasharotlarga nisbatan biologik faolligi bilan bog‘liq mexanizmlarni o‘rganish Cry oqsillarining funksional xususiyatlarini tushunishda muhim ahamiyatga ega. Shu nuqtayi nazardan, tanlangan aminokislota almashinuvlariga mos hududlarni molekulyar tahlil qilish keyingi tadqiqotlar uchun dastlabki bosqich hisoblanadi. Biroq hozirgi natijalar faqat PCR mahsulotlari hosil bo‘lganini ko‘rsatadi; ular nishon ketma-ketliklarning to‘g‘riligini yoki aminokislota almashinuvlarining mavjudligini o‘z-o‘zidan tasdiqlamaydi.

Keyingi bosqichda PCR mahsulotlarini sekvenslash va olingan ketma-ketliklarni referens *cry1Ia* geni bilan taqqoslash rejalashtiriladi. Bu nishon hududlarning identifikatsiyasini tekshirish va tegishli nukleotid o‘zgarishlarini aniqlash imkonini beradi. Shundan so‘nggina ushbu o‘zgarishlarning Cry1Ia oqsilining xususiyatlariga ehtimoliy ta’siri haqida asoslangan xulosalar chiqarish mumkin.

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SARS-CoV-2 S1 OQSILINI SACCHAROMYCES CEREVISIAE HUJAYRALARIDA REKOMBINANT EKSPRESSIYA QILISHNI BAHOLASH

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Annotatsiya: Ushbu tadqiqotda SARS-CoV-2 S1 oqsilining Saccharomyces cerevisiae hujayralarida rekombinant ekspressiyasini baholashga qaratilgan texnologik yondashuv tahlil qilindi. Tadqiqotda S. cerevisiae kulturasi va pYES2-S1-Zeo konstruksiyasi asosidagi ekspressiya tizimi ko‘rib chiqilgan. Rekombinant oqsilni aniqlash uchun SDS-PAGE va Western blot usullaridan foydalanish nazarda tutilgan. S1 oqsilining 61 kDa molekulyar massasi elektroforetik identifikatsiya uchun asosiy mezon sifatida ko‘rsatilgan. Tadqiqot rekombinant antigen ishlab chiqarish platformasini baholashga qaratilgan bo‘lib, yakuniy vaksina samaradorligini aniqlashni qamrab olishi keyingi bosqichda amalga oshiriladi.

Kalit so‘zlar: S1 oqsili; SARS-CoV-2; S. cerevisiae; rekombinant ekspressiya; SDS-PAGE; Western blot.

Аннотация: В данном исследовании проанализирован технологический подход, направленный на оценку рекомбинантной экспрессии белка S1 SARS-CoV-2 в клетках *Saccharomyces cerevisiae*. В исследовании рассмотрены культура *S. cerevisiae* и система экспрессии на основе конструкции pYES2-S1-Zeo. Для выявления рекомбинантного белка предусмотрено использование методов SDS-PAGE и вестерн-блоттинга. Молекулярная масса белка S1, составляющая 61 кДа, указана в качестве основного критерия для электрофоретической идентификации. Исследование направлено на оценку платформы производства рекомбинантного антигена, а определение конечной эффективности вакцины будет осуществляться на последующем этапе.

Ключевые слова: белок S1; SARS-CoV-2; *S. cerevisiae*; рекомбинантная экспрессия; SDS-PAGE; вестерн-блоттинг.

Abstract: This study analyzed a technological approach aimed at evaluating the recombinant expression of the SARS-CoV-2 S1 protein in *Saccharomyces cerevisiae* cells. The study considered an *S. cerevisiae* culture and an expression system based on the pYES2-S1-Zeo construct. SDS-PAGE and Western blot methods were intended for the detection of the recombinant protein. The molecular mass of the S1 protein, 61 kDa, was indicated as the main criterion for electrophoretic identification. The study focused on evaluating a recombinant antigen production platform, while the determination of final vaccine efficacy is to be carried out at a subsequent stage.

Keywords: S1 protein; SARS-CoV-2; *S. cerevisiae*; recombinant expression; SDS-PAGE; Western blot.

Kirish

SARS-CoV-2 S oqsili virusning mezbon hujayra retseptori bilan o‘zaro ta’sirida muhim rol o‘ynaydi va vaksina tadqiqotlarida asosiy antigenlardan biri sifatida qaraladi. S oqsili S1 va S2

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subbirliklaridan tashkil topgan bo‘lib, S1 subbirligi tarkibida N-terminal domen hamda retseptor bilan bog‘lanishda muhim ahamiyatga ega bo‘lgan receptor-binding domain (RBD) mavjud. RBD inson hujayralaridagi angiotenzin-konvertlovchi ferment 2 (ACE2) retseptori bilan o‘zaro ta’sirlashadi. Shu sababli S oqsilining S1 qismi va uning tarkibidagi RBD SARS-CoV-2 ga qarshi vaksina tadqiqotlarida muhim antigenik yo‘nalishlardan biri hisoblanadi [1].

Rekombinant S1 oqsilini ekspressiya qilish virusning o‘zini ishlatmasdan antigen ishlab chiqarish imkoniyatini o‘rganishga yordam beradi. Rekombinant oqsilga asoslangan vaksina yondashuvida virusning butun zarrachasi o‘rniga ma’lum antigenik oqsil yoki uning bir qismidan foydalaniladi. Shu jihatdan S1 oqsilini rekombinant shaklda olish va uning mavjudligini tasdiqlash SARS-CoV-2 antigenlarini ishlab chiqarish texnologiyasini o‘rganishda muhim bosqichlardan biridir. Rekombinant spike oqsilini olish bo‘yicha tadqiqotlarda turli ekspressiya tizimlari, jumladan, xamirturush, bakterial, hasharot va sutemizuvchi hujayra tizimlaridan foydalanilgan [2].

Saccharomyces cerevisiae rekombinant oqsillarni ishlab chiqarishda qo‘llanadigan eukariot ekspressiya tizimlaridan biridir. Ushbu mikroorganizm rekombinant oqsillarni ishlab chiqaruvchi hujayra fabrikasi sifatida keng o‘rganilgan bo‘lib, uning genetik jihatdan boshqarilishi va oqsil ekspressiyasini tashkil etish imkoniyatlari mavjud. Xamirturush tizimlarining yana bir muhim jihati shundaki, ular ayrim rekombinant oqsillarning yig‘ilishi va posttranslyatsion modifikatsiyalarida eukariot hujayralarga xos jarayonlarni ta’minlay oladi [3].

SARS-CoV-2 antigenlarini xamirturush tizimida ishlab chiqarish yo‘nalishi ham alohida ilmiy qiziqish uyg‘otadi. Xususan, *S. cerevisiae* asosida SARS-CoV-2 spike oqsilining RBD qismiga yo‘naltirilgan rekombinant oqsil vaksina texnologiyalari o‘rganilgan. Bu esa xamirturush hujayralaridan SARS-CoV-2 antigenlarini rekombinant shaklda olish uchun foydalanish mumkinligini ko‘rsatadi. Shu bilan birga, S1 oqsilini ekspressiya qilishni o‘rganish ushbu yondashuvni kengaytirish va S oqsilining immunologik jihatdan muhim qismlarini rekombinant antigen sifatida tavsiflash imkonini beradi [4].

Rekombinant S1 oqsilini olishda ekspressiya konstruksiyasi muhim ahamiyatga ega. Tadqiqotda pYES2-S1-Zeo konstruksiyasi asosidagi ekspressiya tizimidan foydalanish ko‘rib chiqilgan. Ushbu yondashuv S1 oqsilini *S. cerevisiae* hujayralarida rekombinant shaklda ifodalash va keyinchalik hosil bo‘lgan oqsilni tahlil qilishga qaratilgan. Rekombinant oqsilning mavjudligini baholash uchun SDS-PAGE va Western blot kabi oqsilni aniqlash usullaridan foydalanish mumkin. Bunday tahlillar maqsadli oqsilning mavjudligi va uning kutiladigan molekulyar massasiga mosligini baholash uchun qo‘llanadi.

S1 oqsilining rekombinant ekspressiyasini o‘rganishda oqsilning molekulyar xususiyatlarini aniqlash ham muhim hisoblanadi. Tadqiqot materiallarida S1 oqsili uchun 61 kDa molekulyar massa kutiladigan mezon sifatida ko‘rsatilgan. Shu asosda elektroforetik tahlil natijalarini baholashda maqsadli oqsilning kutiladigan molekulyar massasiga mosligi e’tiborga olinadi.

Umuman olganda, SARS-CoV-2 S1 oqsilini *S. cerevisiae* asosidagi ekspressiya tizimida olish rekombinant antigen ishlab chiqarish texnologiyasini o‘rganish uchun istiqbolli yo‘nalishlardan biridir. Bunda asosiy e’tibor rekombinant konstruksiyadan foydalanish, maqsadli oqsil ekspressiyasini amalga oshirish va hosil bo‘lgan oqsilni tegishli laboratoriya usullari yordamida aniqlashga qaratiladi. Shu bilan birga, rekombinant antigenning vaksina sifatidagi samaradorligini baholash ekspressiya va oqsilni aniqlash bosqichlaridan keyingi alohida tadqiqotlarni talab qiladi.

Mazkur ishning maqsadi *S. cerevisiae* asosidagi ekspressiya tizimida SARS-CoV-2 S1 oqsilini aniqlashga mo‘ljallangan texnologik yondashuvni tahlil qilish, rekombinant konstruksiya asosidagi oqsil ekspressiyasini ko‘rib chiqish hamda S1 oqsilini SDS-PAGE va Western blot usullari orqali aniqlash imkoniyatlarini baholashdan iborat.

Materiallar va usullar

Tadqiqot materiali sifatida *Saccharomyces cerevisiae* non achitqisidan ajratilgan kulturadan foydalanildi. Dastlab achitqi kulturasidan alohida koloniyalar ajratib olindi va ularning morfologik

xususiyatlari mikroskopik tekshiruv orqali baholandi. Ushbu bosqich kulturani dastlabki tavsiflash hamda keyingi rekombinant ekspressiya tadqiqotlari uchun foydalaniladigan materialni aniqlashga xizmat qildi.

Tadqiqotda SARS-CoV-2 ning genomik va oqsil tuzilishiga oid ma’lumotlarni o‘rganish uchun NCBI hamda GISAID ma’lumotlar bazalaridan foydalanildi. Mazkur ma’lumotlar S oqsili va uning S1 qismiga oid ketma-ketliklarni o‘rganish, shuningdek, rekombinant antigen bilan bog‘liq tadqiqot yondashuvini shakllantirish uchun manba sifatida ko‘rib chiqildi.

Rekombinant konstruksiya va ekspressiya tizimi

SARS-CoV-2 S1 oqsilining rekombinant ekspressiyasini o‘rganish uchun pYES2-S1-Zeo konstruksiyasidan foydalanildi. Ushbu konstruksiya S1 oqsilini *S. cerevisiae* hujayralarida rekombinant shaklda ekspressiya qilishga mo‘ljallangan tizim sifatida tadqiqotning asosiy komponentlaridan biri bo‘ldi.

Rekombinant konstruksiya asosida maqsadli S1 oqsilining ekspressiyasini baholash uchun *S. cerevisiae* kulturasi bilan bog‘liq ekspressiya tizimi ko‘rib chiqildi. Rekombinant oqsil ekspressiyasi induksion tizim bilan bog‘langan bo‘lib, tadqiqotning keyingi bosqichida hujayra materialidan oqsilni aniqlash uchun foydalanildi.

Mazkur yondashuvda asosiy e’tibor SARS-CoV-2 ning to‘liq virusi bilan emas, balki uning antigenik jihatdan muhim bo‘lgan S1 oqsili bilan ishlashga qaratildi. Rekombinant oqsil ekspressiyasi SARS-CoV-2 antigenini alohida oqsil shaklida o‘rganish imkonini beruvchi texnologik yondashuv sifatida ko‘rib chiqildi. Xamirturush tizimlarida SARS-CoV-2 spike oqsili yoki uning qismlarini rekombinant shaklda ekspressiya qilish bo‘yicha tadqiqotlar ham mavjud.

Oqsil ekspressiyasini baholash

Rekombinant oqsil ekspressiyasini baholashda olingan hujayra materiali oqsil tahliliga tayyorlandi. Ekspressiya natijasida hosil bo‘lishi kutilayotgan maqsadli oqsilni boshqa hujayra oqsillaridan ajratib ko‘rish uchun SDS-PAGE usulidan foydalanildi.

SDS-PAGE oqsillarni molekulyar massasiga ko‘ra elektroforetik ajratish imkonini beruvchi usul bo‘lib, rekombinant oqsilning kutiladigan molekulyar massa diapazonida mavjudligini baholash uchun qo‘llanildi. Rekombinant SARS-CoV-2 oqsillarini tadqiq qilishda ushbu usul oqsil ekspressiyasini dastlabki baholash uchun keng qo‘llanadi.

Tadqiqot materiallarida S1 oqsili uchun 61 kDa molekulyar massa kutiladigan mezon sifatida qayd etilgan. Shu sababli SDS-PAGE natijalarini baholashda oqsilning elektroforetik harakatchanligi va kutiladigan molekulyar massasiga mosligi asosiy ko‘rsatkichlardan biri sifatida qaraldi.

Western blot orqali S1 oqsilini aniqlash

SDS-PAGE orqali oqsillar ajratilgandan keyin S1 oqsilini immunologik jihatdan aniqlash uchun Western blot yondashuvi qo‘llanildi. Ushbu usul maqsadli oqsilning mavjudligini immunologik aniqlash imkonini berishi sababli rekombinant oqsil ekspressiyasini tasdiqlashda muhim bosqich sifatida qaraldi.

Western blot natijalarini baholashda maqsadli S1 oqsiliga mos keluvchi immunologik signalning mavjudligi hamda uning kutiladigan molekulyar massa bilan mosligi e’tiborga olindi. Rekombinant spike oqsillari bilan olib borilgan tadqiqotlarda ham SDS-PAGE orqali oqsilni ajratish va keyinchalik Western blot yordamida maqsadli oqsilni aniqlash yondashuvi qo‘llangan.

Shunday qilib, tadqiqotning metodik yondashuvi *S. cerevisiae* kulturasini olish va baholash, pYES2-S1-Zeo rekombinant konstruksiyasidan foydalanish, S1 oqsilining ekspressiyasini o‘rganish hamda hosil bo‘lgan oqsilni SDS-PAGE va Western blot usullari orqali aniqlash bosqichlarini qamrab oldi.

Tadqiqot natijasi va muhokama

Manba materiallarida S. cerevisiae ga pYES2-S1-Zeo konstruksiyasi asosida rekombinant ekspressiya tizimi qo‘llanganligi qayd etilgan. Oqsilni baholashda SDS-PAGE va Western blotning

tanlanishi molekulyar massa hamda antigen-spetsifik signalni birgalikda tahlil qilish imkonini beradi.

Tadqiqotning mazmuni S1 antigenini rekombinant shaklda olish va keyingi vaksina tadqiqotlari uchun boshlang‘ich material sifatida baholashga qaratilgan. Biroq mavjud dissertatsiya matnida Western blot tasvirining miqdoriy tahlili, signal intensivligi, oqsil chiqimi yoki immunogenlik bo‘yicha raqamli natijalar keltirilmagan. Shuning uchun natijalar faqat manbada tasdiqlangan texnologik ma’lumotlar asosida talqin qilindi.

Xulosa

S. cerevisiae asosidagi pYES2-S1-Zeo ekspressiya tizimi SARS-CoV-2 S1 rekombinant oqsilini o‘rganish uchun texnologik platforma sifatida qo‘llanishi mumkin. SDS-PAGE va Western blot S1 oqsilini tavsiflash uchun asosiy analitik usullar sifatida belgilangan. Kelgusida oqsilning miqdoriy chiqimi, tozaligi, antigenligi va immunogenligini eksperimental baholash ushbu platformaning vaksina nomzodi sifatidagi istiqbolini chuqurroq aniqlash imkonini beradi.

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SACCHAROMYCES CEREVISIAE ASOSIDA SARS-CoV-2 S1 REKOMBINANT OQSILINI OLISH TEXNOLOGIYASINI O‘RGANISH

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Annotatsiya: Ushbu maqolada SARS-CoV-2 ga qarshi subbirlik vaksina platformasini yaratishda Saccharomyces cerevisiae achitqisidan rekombinant oqsil ekspressiyasi tizimi sifatida foydalanish imkoniyati yoritiladi. Tadqiqotning asosiy yo‘nalishi SARS-CoV-2 ning immunologik jihatdan muhim S1 oqsilini achitqi hujayralarida ekspressiya qilishga mo‘ljallangan pYES2-S1-Zeo konstruksiyasi bilan bog‘liq texnologik yondashuvlarni tahlil qilishdan iborat. Dissertatsiya materiallarida S. cerevisiae non achitqisidan ajratilgan, uning tozaligi mikroskopik nazorat qilingan va rekombinant konstruksiyani hujayraga kiritish yondashuvi qo‘llangan. Rekombinant oqsil ekspressiyasini baholash uchun SDS-PAGE va Western blot usullaridan foydalanish ko‘rsatilgan; S1 oqsili uchun kutiladigan molekulyar massa 61 kDa sifatida berilgan. Mavjud materiallar S. cerevisiae asosidagi tizimni SARS-CoV-2 rekombinant antigenlarini olish platformasi sifatida o‘rganish uchun asos beradi.

Kalit so‘zlar: SARS-CoV-2; Saccharomyces cerevisiae; S1 oqsili; rekombinant oqsil; pYES2-S1-Zeo; subbirlik vaksina; SDS-PAGE; Western blot.

Аннотация: В статье рассматривается возможность использования Saccharomyces cerevisiae в качестве экспрессионной системы для получения рекомбинантного антигена SARS-CoV-2 в рамках разработки субъединичной вакцинной платформы. Основное внимание уделено конструкции pYES2-S1-Zeo, предназначенной для экспрессии S1-белка SARS-CoV-2 в дрожжевых клетках. Согласно материалам диссертации, S. cerevisiae был выделен из хлебопекарных дрожжей, чистота культуры контролировалась микроскопически, а рекомбинантная конструкция использовалась для экспрессии антигена. Для оценки белка предусмотрены SDS-PAGE и Western blot; расчетная молекулярная масса S1 указана как 61 кДа. Полученные материалы позволяют рассматривать S. cerevisiae как технологическую платформу для рекомбинантного получения антигена SARS-CoV-2.

Ключевые слова: SARS-CoV-2; *Saccharomyces cerevisiae*; белок S1; рекомбинантный белок; pYES2-S1-Zeo; субъединичная вакцина; SDS-PAGE; вестерн-блот.

Abstract: This article examines the use of Saccharomyces cerevisiae as an expression system for producing a recombinant SARS-CoV-2 antigen within a subunit vaccine development platform. The study focuses on the pYES2-S1-Zeo construct intended for expression of the SARS-CoV-2 S1 protein in yeast cells. According to the dissertation materials, S. cerevisiae was isolated from baker’s yeast, culture purity was checked microscopically, and a recombinant expression approach was applied. SDS-PAGE and Western blotting were selected for evaluation of recombinant protein expression, with a predicted molecular mass of 61 kDa for S1. The available materials support the study of S. cerevisiae as a recombinant antigen expression platform.

Keywords: SARS-CoV-2; *Saccharomyces cerevisiae*; S1 protein; recombinant protein; pYES2-S1-Zeo; subunit vaccine; SDS-PAGE; Western blot.

IQTIBOS UCHUN
Toshboyeva F.N., Ayubov M.S., Ravshanov H.T. Saccharomyces cerevisiae asosida SARS-CoV-2 S1 rekombinant oqsilini olish texnologiyasini o‘rganish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 164–166.
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Kirish

SARS-CoV-2 pandemiyasi vaksina texnologiyalarini tezkor rivojlantirish zaruratini yuzaga keltirdi. Zamonaviy platformalar orasida mRNK, virusli vektor, inaktivatsiyalangan virus, rekombinant oqsil va virusga o‘xshash zarracha asosidagi yondashuvlar shakllangan. Rekombinant oqsil vaksinalari antigenni tayyor oqsil shaklida taqdim etishi bilan muhim ilmiy yo‘nalishlardan biridir [1].

SARS-CoV-2 ning S oqsili virusning mezbon hujayraga kirishida asosiy rol o‘ynaydi va ko‘plab vaksina platformalarida muhim antigen sifatida qo‘llanadi. S oqsilining S1 qismi immunologik jihatdan muhim domenlarni o‘z ichiga oladi. Shu sababli S1 oqsilini rekombinant ekspressiya tizimida olish va tavsiflash SARS-CoV-2 antigenlarini ishlab chiqarish texnologiyasini o‘rganishda dolzarbdir [2].

Rekombinant oqsil olish texnologiyasida antigenni tegishli ekspressiya tizimida ishlab chiqarish muhim bosqichlardan biri hisoblanadi. Bunday yondashuvda maqsadli oqsilni kodlovchi gen ekspressiya konstruksiyasi tarkibiga kiritilib, undan kerakli rekombinant oqsilni olish imkoniyati o‘rganiladi. SARS-CoV-2 S1 oqsilini rekombinant shaklda olish ushbu antigenning keyingi biologik va immunologik xususiyatlarini baholash uchun asos yaratadi.

Saccharomyces cerevisiae rekombinant oqsillarni ekspressiya qilishda foydalaniladigan achitqi tizimlaridan biri sifatida mazkur yo‘nalishda qiziqish uyg‘otadi. Ushbu tizimdan foydalanish SARS-CoV-2 ga tegishli maqsadli antigenni rekombinant shaklda olish texnologiyasini o‘rganish imkonini beradi. Shu nuqtai nazardan, *S. cerevisiae* hujayralarida SARS-CoV-2 S1 oqsilining ekspressiyasini o‘rganish rekombinant antigen olish jarayonining muhim qismi hisoblanadi.

S1 oqsilini olish jarayonida rekombinant konstruksiyaning mavjudligi va maqsadli oqsilning hosil bo‘lishini tasdiqlash muhim ahamiyatga ega. Bunda pYES2-S1-Zeo kabi rekombinant konstruksiyalardan foydalanish S1 oqsilining *S. cerevisiae* hujayralarida ekspressiyasini o‘rganishga imkon beradi. Olingan oqsilning mavjudligi va molekulyar xususiyatlarini baholashda SDS-PAGE hamda Western blot kabi oqsilni tahlil qilish usullaridan foydalanish mumkin.

SARS-CoV-2 ga qarshi subbirlik vaksina yondashuvida virusning to‘liq zarrachasi o‘rniga uning ma’lum antigenik komponentlaridan foydalanish ko‘zda tutiladi. Shu sababli S1 oqsilini rekombinant shaklda olish va uning ekspressiyasini tasdiqlash subbirlik vaksina platformasini tadqiq qilishning muhim bosqichlaridan biri sifatida qaraladi. Bunday tadqiqotlar rekombinant antigenlarni olish, ularni laboratoriya sharoitida aniqlash va keyingi tadqiqotlar uchun tavsiflash imkoniyatlarini o‘rganishga xizmat qiladi.

Mazkur ishning maqsadi Saccharomyces cerevisiae yordamida SARS-CoV-2 S1 rekombinant oqsilini olishga qaratilgan texnologik yondashuvni tahlil qilish va uning subbirlik vaksina platformasidagi imkoniyatlarini muhokama qilishdan iborat.

Materiallar va usullar

Tadqiqotda S. cerevisiae non achitqisidan ajratilgan kulturadan foydalanilgan. Alohida koloniyalar ajratilib, mikroskopik nazorat orqali kulturaga baho berilgan. SARS-CoV-2 genomik ma’lumotlarini tahlil qilishda NCBI va GISAID ma’lumotlar bazalaridan foydalanilgan.

Rekombinant konstruksiya va ekspressiya. Tadqiqot materiallarida pYES2-S1-Zeo konstruksiyasidan foydalanilganligi va S. cerevisiae ga rekombinant konstruksiyani kiritish yondashuvi qayd etilgan. Rekombinant oqsil ekspressiyasi GAL1 promoteri asosidagi induksiya tizimi bilan bog‘langan. Rekombinant konstruksiya asosida maqsadli S1 oqsilining ekspressiyasini baholash tadqiqotning muhim bosqichlaridan biri bo‘lgan. Bunda *S. cerevisiae* hujayralari rekombinant konstruksiya bilan bog‘liq holda o‘rganilib, keyingi oqsil tahlili uchun material sifatida foydalanilgan.

Oqsilni aniqlash. Rekombinant oqsil ekspressiyasini baholashda SDS-PAGE va Western blot usullari ko‘rsatilgan. S1 oqsili uchun 61 kDa molekulyar massa kutiladigan mezon sifatida berilgan.

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SDS-PAGE yordamida oqsil namunalari tarkibidagi oqsil fraksiyalarini molekulyar massasiga ko‘ra ajratish, Western blot orqali esa maqsadli S1 oqsilining mavjudligini aniqlash ko‘zda tutilgan.

Olingan oqsil profilini kutiladigan molekulyar massa bilan taqqoslash S1 rekombinant oqsilining ekspressiyasini baholash uchun asosiy mezonlardan biri sifatida qaralgan. Shu bilan birga, tadqiqot materiallarida S1 oqsilining kutiladigan molekulyar massasi 61 kDa sifatida ko‘rsatilgan.

Ma’lumotlarni tahlil qilish

Tadqiqot davomida olingan ma’lumotlarni baholashda rekombinant konstruksiyaning mavjudligi, S1 oqsilining ekspressiyasi va uning kutiladigan molekulyar massasiga mosligi asosiy yo‘nalishlar sifatida ko‘rib chiqilgan. SARS-CoV-2 ga oid genomik ma’lumotlar NCBI va GISAID ma’lumotlar bazalari asosida tahlil qilingan [3].

Shunday qilib, tadqiqotning metodik yondashuvi *S. cerevisiae* kulturasidan foydalanish, pYES2-S1-Zeo rekombinant konstruksiyasi asosida S1 oqsili ekspressiyasini o‘rganish hamda hosil bo‘lgan oqsilni SDS-PAGE va Western blot usullari orqali baholash bosqichlarini qamrab olgan.

Tadqiqot natijasi va muhokama

Dissertatsiya materiallarida S. cerevisiae kulturasi non achitqisidan ajratilganligi va mikroskopik nazoratdan o‘tkazilganligi qayd etilgan. Shundan so‘ng pYES2-S1-Zeo konstruksiyasi asosida rekombinant antigen ekspressiyasi uchun platforma shakllantirilgan. Bu yondashuv SARS-CoV-2 antigenini virusning o‘zidan emas, balki rekombinant ekspressiya tizimi orqali olish konsepsiyasiga mos keladi.

Tadqiqotning muhim jihati S1 oqsilini ekspressiya qilishni baholash uchun SDS-PAGE va Western blot usullarining tanlanganidir. 61 kDa kutiladigan molekulyar massa rekombinant S1 oqsilini elektroforez va immunodeteksiya asosida identifikatsiya qilish uchun mezon bo‘lib xizmat qiladi. Adabiyotlar rekombinant oqsil va epitopga asoslangan SARS-CoV-2 vaksinalarida S. cerevisiae kabi ekspressiya tizimlaridan foydalanish mumkinligini ko‘rsatadi. Biroq rekombinant antigenni olishning o‘zi vaksinaning himoya samaradorligini anglatmaydi. Keyingi bosqichlarda oqsilning tozaligi, strukturaviy xususiyatlari, antigenligi va immunogenligi alohida baholanadi.

Xulosa

Saccharomyces cerevisiae SARS-CoV-2 S1 rekombinant oqsilini olish uchun ekspressiya platformasi sifatida o‘rganildi. Tadqiqot materiallarida S. cerevisiae kulturasi, pYES2-S1-Zeo konstruksiyasi hamda SDS-PAGE va Western blot asosidagi oqsil identifikatsiyasi yondashuvlari keltirilgan. S1 oqsili uchun 61 kDa molekulyar massa mezon sifatida ko‘rsatilgan. Mavjud materiallar S. cerevisiae asosidagi rekombinant antigen olish texnologiyasini o‘rganish uchun asos beradi, biroq vaksina immunogenligi yoki klinik samaradorligi bo‘yicha yakuniy xulosa chiqarish uchun qo‘shimcha eksperimental ma’lumotlar talab etiladi. Bu esa keyingi tajribalarda qo‘llanishi ko‘zda tutilgan.

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BUG‘DOYNING QURG‘OQCHILIKKA CHIDAMLILIGINI *IN VITRO* SHAROITIDA BAHOLASH

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Andijon davlat universiteti [1, 3], *O‘zRFA Genetika va O‘EB instituti* [2]

Annotatsiya: Ushbu ishda qurg‘oqchilik stressiga chidamli bug‘doy navlarini saralashda *in vitro* sharoitidagi laboratoriya usullari hamda to‘qima kulturasidan foydalanishning samaradorligi yoritilgan. Tadqiqot davomida bug‘doyning yetilmagan embrionlari eksplant sifatida olinib, MS oziqa muhitida 2,4-D ta’sirida embriogen kallus hosil bo‘lishi va regeneratsiya jarayonlari baholandi. Qurg‘oqchilik stressini modellashtirish uchun selektiv muhitda osmotik agentlar sifatida PEG (10%, 20%) hamda Mannitol (10%) birikmalaridan foydalanildi. Natijalar genotiplarning osmotik bosimga chidamliligini tezkor aniqlashda hujayra va to‘qima kulturalari metodining yuqori samaradorlikka ega ekanligini ko‘rsatadi.

Kalit so‘zlar: Bug‘doy, *in vitro*, eksplant, yetilmagan embrion, kallusogenez, qurg‘oqchilik stressi.

Аннотация: В данной статье освещается эффективность использования лабораторных методов *in vitro* и тканевых культур при отборе сортов пшеницы, устойчивых к засуховому стрессу. В ходе исследования в качестве эксплантов были взяты незрелые зародыши пшеницы, оценивались процессы образования эмбриогенного каллуса под действием 2,4-Д на питательной среде MS и его регенерация. Для моделирования стресса засухи в селективной среде в качестве осмотических агентов использовались соединения ПЭГ (10%, 20%) и маннитол (10%). Результаты показывают высокую эффективность метода клеточных и тканевых культур для быстрой оценки устойчивости генотипов к осмотическому давлению.

Ключевые слова: Пшеница, in vitro, эксплант, незрелый зародыш, каллусогенез, стресс засухи.

Abstract: This article highlights the effectiveness of using *in vitro* laboratory methods and tissue cultures for selecting wheat varieties resistant to drought stress. In this study, immature wheat embryos were used as explants, and the processes of embryogenic callus formation under the influence of 2,4-D on MS nutrient medium and its subsequent regeneration were evaluated. To simulate drought stress in the selective medium, PEG compounds (10%, 20%) and mannitol (10%) were used as osmotic agents. The results demonstrate the high efficiency of the cell and tissue culture method for rapidly assessing the resistance of genotypes to osmotic stress.

Keywords: Wheat, in vitro, explant, immature embryo, callusogenesis, drought stress.

Kirish

Qurg‘oqchilik tez-tez kuzatiladigan, ekinlarning hosildorligiga salbiy ta’sir ko‘rsatuvchi omildir. Navlarning qurg‘oqchilikka chidamliligini baholash uchun laboratoriya usulidan foydalanish tez va samaraliroq usul hisoblanadi. Hozirgi kunda o‘simliklarning qurg‘oqchilik kabi tashqi omillarga chidamliligini baholash bo‘yicha ko‘plab tadqiqotlar olib borilgan. Bunday tadqiqotlarda selektiv muhitda hujayra va to‘qima kulturalaridan foydalanib stress agent sifatida Polietilen glikol (PEG), Mannitol, Sorbitol kabi moddalar ishlatilmoqda [1]. Bunda genotiplarning stressga qarshiligini aniqlash, o‘sishining susayishiga yoki kuchli osmotik bosim ostida baholangan

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Umarova G.A., Babayeva S.S., Kimsanova G.A. Bug‘doyning qurg‘oqchilikka chidamliligini in vitro sharoitida baholash // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 167–170.
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namunalarning omon qolish ko‘rsatkichi aniqlangan [2]. Kalluslar embriogen va noembriogen turlarga bo‘linadi, noembriogen kalluslarning tashqi ko‘rinishi suvsimon yumshoq tuzilishga ega bo‘lib, o‘simlik hosil qilmaydi [4].

Olib borilgan tadqiqotlardan ma‘lumki, bug‘doy to‘qima kulturasida fitogormonlar konsentratsiyasini optimallashtirish turli xil bug‘doy navlarida va eksplant turlarida, masalan, yetilgan yoki yetilmagan embrionlarda, hosil qiluvchi to‘qimalarida va barg bo‘g‘imlaridan ko‘paytirishda regeneratsiyasi hamda o‘sib rivojlanishi uchun turli xil gormon rejimlari talab qilinadi. Kallus hosil bo‘lishi uchun auksinlar guruhiga kiruvchi 2.4-D gormoni (2.4-dixlorfenoksiatsetat kislota) hujayra bo‘linishi va differensiallashmagan hujayralarning ko‘payishini, kallus massasini hosil qiladi. Normal holatda 2.4-D 2.0-mg/l hisoblanadi, 4.0-mg/l yuqori konsentratsiya bo‘lib, kallus hosil bo‘lishini tezlashtiradi. Gormonning past konsentratsiyasi (0.5-1.0 mg/l) kallusogenez jarayonining sekinlashuviga olib keladi, bu esa massasiga ham ta‘sir ko‘rsatadi [3].

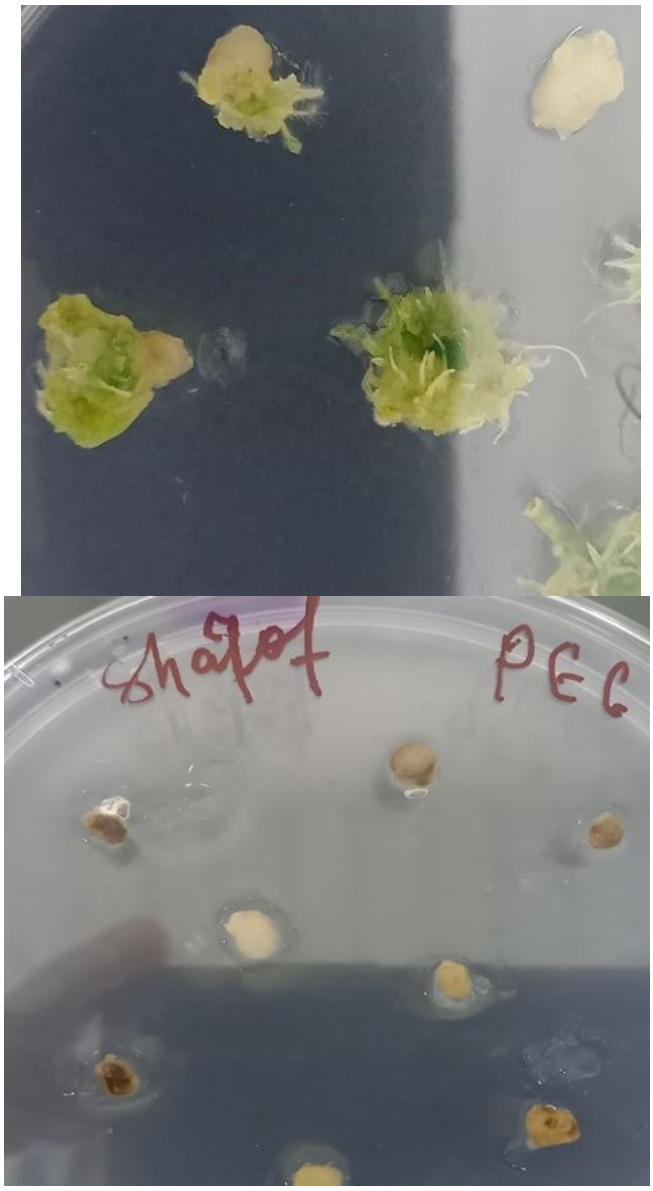
Ushbu tadqiqotda *in vitro* sharoitida navlarning embriogen kallus hosil bo‘lishi va undan o‘simlikning qayta tiklanish qobiliyati baholandi. Bug‘doyning yetilmagan embrionlari eksplant sifatida ishlatildi. Yetilmagan embrionlar qorong‘uda 23 ± 1°C da Murashige-Skoog muhitida 7gr agar, 30gr saxaroza va 2 mg/l 2,4-D (boshlang‘ich muhit) o‘z ichiga olgan makro- va mikrotuzlarning to‘liq to‘plami bilan yetishtirildi. Aziz genotipida 30% i noembriogen kallus hosil qildi. Qurg‘oqchilikni keltirib chiqarish uchun, PEG ning 10%, 20% li hamda Mannitolning 10%li konsentratsiyadagi eritmalaridan foydalanildi.

1-jadval. Genotiplarning stressga chidamliligining ko‘rsatkichlari

№	Genotip	Nazorat		PEG 10%		PEG 20%		Mannitol 10%	
		O‘rtacha (sm)	V	O‘rtacha (sm)	V	O‘rtacha (sm)	V	O‘rtacha (sm)	V
1	Sharof	156,7±37	23,6	123,3 ±40,4	32,8	36,2± 7,15	19,7	64,5± 2,23	15,4
2	Alekseyevich	159,9±0,76	2,12	69,8± 0,72	4,61	27,7± 0,84	13,5	61,8± 2,40	17,3
3	Aziz	136,2±10,7	7,9	111,6 ±38,7	31,8	34,2± 10,5	30,7	90,1± 2,09	10,3

Natijalar shuni ko‘rsatdiki, embriogen kallus hosil bo‘lishining eng yuqori chastotasi Sharof navida (156,7±37) sm ni hamda Alekseyevich genotipida (159,9±0,76) sm ni tashkil qildi. Aziz genotipida suvsimon tuzilishga ega, ya’ni noembriogen kalluslar (136,2±10,7) sm ekanligi aniqlandi.

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A - nazorat B - 20%li PEG

1-rasm. Kalluslarga stress ta’siri

Stressdan so‘ng yangi kallus massasining hosil bo‘lishi va kalluslarning eng yuqori omon qolishi Sharof genotipida (36,2±7,15) va eng pasti Alekseyevich genotipida (27,7±0,84) sm qayd etilgan. Shunda stressni keltirib chiqaruvchi Mannitolning 10% li eritmasida Alekseyevich genotipida PEG ning 10% li eritmasiga nisbatan kalluslarning nekrozga uchragani aniqlandi. Xuddi shunday ko‘rsatkich Aziz navida PEG ning 20%li eritmasida kuzatildi.

Morfogenezni qo‘zg‘atish maqsadida 60 kundan so‘ng bir xil minerallar va vitaminlar tarkibiga ega bo‘lgan differensialovchi 0.5mg/l gormon bilan to‘ldirilgan muhitda o‘tkazildi va 22-24°C da yorug‘likda, 16 soatlik fotoperiod bilan o‘stirildi. Eng yaxshi regeneratsiya qobiliyati Sharof genotipida, nazoratda hamda 10%li variantlarida kuzatildi. 20%li PEG berilganda 40% kalluslar nekrozga uchradi. Aziz genotipi stressga chidamsiz bo‘lib, shunda 30% kalluslarning nekrozga uchragani qayd etildi.

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BACILLUS SUBTILISDA REKOMBINANT OQSIL SEKRETSIYASINI OPTIMALLASHTIRISH

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Annotatsiya: *Bacillus subtilis*da rekombinant oqsillar sekretsiyasini oshirish usullari tahlil qilindi. Signal peptidlar, promotorlar, ribosoma bog‘lanish saytlari va xo‘jayin shtamm xususiyatlari o‘rtasidagi bog‘liqlik ko‘rib chiqildi. Adabiyotlar tahlili yuqori mahsuldorlikka erishish uchun oqsil sintezi, folding va membrana orqali tashilishini o‘zaro muvofiqlashtirish zarurligini ko‘rsatadi.
Kalit so‘zlar: *Bacillus subtilis*, oqsil sekretsiyasi, signal peptid, promotor, RBS, hujayra muhandisligi.

Аннотация: Рассмотрены подходы к улучшению секреции рекомбинантных белков в *Bacillus subtilis*. Проанализировано взаимодействие сигнального пептида, промотора, сайта связывания рибосомы и характеристик штамма-хозяина. Анализ литературы показывает необходимость согласования синтеза, сворачивания и мембранного транспорта белка для повышения продуктивности.
Ключевые слова: *Bacillus subtilis*, секреция белка, сигнальный пептид, промотор, RBS, инженерия клетки.

Abstract: Approaches to improving recombinant protein secretion in *Bacillus subtilis* are reviewed. Interactions between signal peptides, promoters, ribosome binding sites and host strain properties are examined. The literature highlights the need to coordinate protein synthesis, folding and membrane translocation to improve productivity.
Keywords: *Bacillus subtilis*, protein secretion, signal peptide, promoter, RBS, host chassis engineering.

Kirish

Bacillus subtilis rekombinant ekspression hujayralari hozir ham rekombinant oqsillarni ishlab chiqarishda keng foydalanilmoqda. Jumladan, butun dunyo ferment bozorida ishlab chiqarilgan 17% rekombinant fermentlar aynan ushbu xo‘jayin hujayrasiga tegishli [1]. Rekombinant fermentlarning hujayradan tashqariga sekretsiyalanishi mahsulotni ajratib olish va tozalashni soddalashtiradi. Gram-musbat *B. subtilis* bakteriya hujayralari amilaza, proteaza va lipaza kabi ko‘plab oqsillarni tabiiy ravishda oziqa muhitiga sekretsiya qobiliyati tufayli biotexnologiyada model organizm sifatida juda keng qo‘llanilib kelinmoqda. Biroq gen ekspressiyasining kuchayishi har doim ham faol oqsil sekretsiyasi ortishiga olib kelmaydi. Oqsilning noto‘g‘ri folding bo‘lishi, tashish tizimining ortiqcha yuklanishi va proteolitik parchalanish olinadigan mahsulot miqdorini cheklaydi [2]. Ishning maqsadi sekretsiyaga ta’sir qiluvchi asosiy omillarni umumlashtirish hamda ularni birgalikda optimallashtirishning ilmiy asoslarini yoritishdir.

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Materiallar va usullar

Ish so‘nggi yillarda chop qilingan maqolalar asosida tayyorlandi. Unda keltirilgan tadqiqotlar signal peptidlarni (SP) tanlash, transkripsiya va translyatsiyani boshqarish, xo‘jayin shtammni takomillashtirish hamda sun’iy intellektni (SI) ushbu sohada qo‘llash yo‘nalishlari bo‘yicha qiyosiy tahlillar olib borildi. Miqdoriy natijalar tegishli adabiyotlardan olindi; yangi laboratoriya tajribalari o‘tkazilmadi.

Natijalar

*B. subtilis*da oqsillarni hujayradan tashqariga tashishning asosiy yo‘li Sec tizimidir. SecA motor oqsili ATP energiyasidan foydalanib, odatda hali to‘liq folding bo‘lmagan polipeptidni SecYEG kanali orqali tashishda ishtirok etadi. Tat tizimi esa buklangan oqsillarni proton harakatlantiruvchi kuch hisobiga tashiydi. Shu sababli sekretsiya yo‘lini tanlashda maqsadli oqsilning folding bo‘lishi va kofaktor biriktirish xususiyatlari hisobga olinadi. Sec tizimi ko‘plab rekombinant fermentlar uchun dastlabki tanlov bo‘lsa, Tat tizimi ayrim maxsus substratlarni tashishda keng qo‘llaniladi [2].

Signal peptidning N-sohasidagi musbat zaryad, H-sohasidagi gidrofoblik va C-sohasidagi kesilish joyi oqsilning membranaga yo‘naltirilishi hamda funksional holga o‘tishiga ta’sir qiladi. Ba’zi bir ko‘p o‘rganilgan AmyQ, AprE, LipA va YoaW kabi signal peptidlar biotexnologiyada juda keng qo‘llaniladi, ammo ularning samaradorligi maqsadli oqsilga bog‘liq. Brockmeier va hammualliflar SPlar kutubxonasini yaratish va skrining qilishning ahamiyati muhim ekanligini tajriba orqali ko‘rsatishgan [3]. Shuning uchun, tabiiy SPni tanlash yoki uning ketma-ketligini o‘zgartirish natijasida ferment sekretsiyasini baholashda faqatgina tajribada tekshirish orqali aniqlash mumkin.

Promotor va ribosoma bog‘lanuvchi saytni (RBS) muvofiqlashtirish va uning sekretsiyaga ta’siri ham so‘nggi yillarda chuqur tadqiq qilinmoqda. Jumladan P43 va Pveg kabi konstitutiv promotorlar uzluksiz ekspressiyani ta’minlaydi. Induksiyalanuvchi tizimlar esa mahsulot sintezi boshlanadigan vaqtni boshqarish imkonini beradi. Haddan tashqari kuchli promotor hujayraning translyatsiya va sekretsiya imkoniyatlariga ortiqcha yuk tushirishi mumkin va bu xo‘jayin hujayra uchun stress hisoblanadi. Shu bilan birga, RBS ham juda muhim ahamiyatga ega bo‘lib, ribosoma va iRNKning bog‘lanishida muhim ahamiyatga ega. U oqsil sintezi (translatsiya) tezligiga ta’sir qiladi [4].

Yuqorida sanab o‘tilgan genetik elementlar, SP, RBS, promotor sinergetik optimallashtirish juda muhim. Misol uchun, Li va hammualliflar mini-sistron kassetasini qo‘llash, shaperon ekspressiyasini kuchaytirish va signal peptidlarni skrining qilishni uyg‘unlashtirib, inson FGF21 oqsilining eruvchan shakldagi sekretsiyasini taxminan 9 marta oshirgan [5]. RBS va signal peptidlarni tizimli ravishda kombinatsiyalashga asoslangan SCORES yondashuvida ferment ishlab chiqarish 7.5 martagacha ortgan [6]. Bu misollar oqsil sintezi va sekretsiyasini muvofiqlashtiruvchi genetik elementlar birikmalarini tanlash samarali bo‘lishi mumkinligini ko‘rsatadi.

Bundan tashqari, yaratilgan genetik konstruktni xo‘jayin hujayrasiga moslashtirish va kuchli sekretsiya natijasida yuzaga keladigan stressni kamaytirish juda muhim hisoblanadi. *B. subtilis* hujayralarida rekombinant oqsillarni ekspressiya qilishda yuzaga keladigan eng asosiy muammo bu hujayra tashqi proteazalardir. Ushbu proteazalar sekretsiya qilinayotgan rekombinant fermentni parchalaydi va mahsuldorlikni kamaytiradi. Hozirgi vaqtda ushbu muammoni yechish uchun proteaza genlari nokaut qilingan *B. subtilis* WB600, *B. subtilis* WB800 kabi sanoat shtammlar ishlab chiqilmoqda [7].

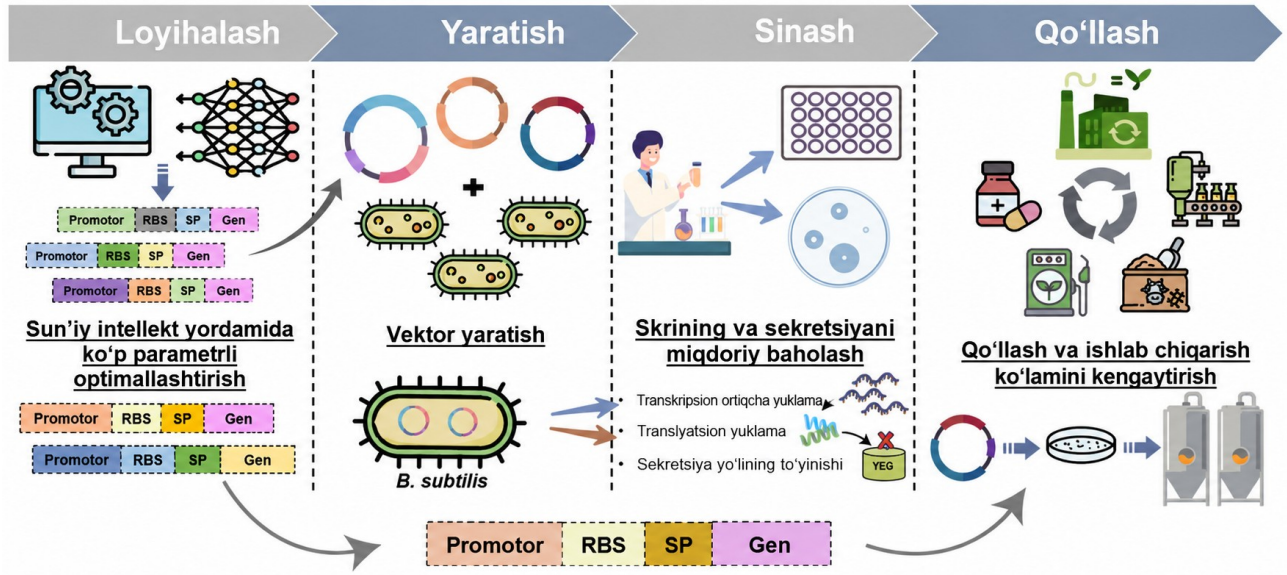
So‘nggi yillarda SI rivojlanishi gen muhandisligi sohasiga ham o‘z ta’sirini o‘tkazdi. Ko‘plab tadqiqotchilar SI qo‘llagan holda yangi sintetik promotor va SP sekvenslarini yaratishmoqda va ularni laboratoriyada sinovdan o‘tkazib yaxshi natijalar olishmoqda. Keyinchalik olingan ushbu tajriba ma’lumotlarini SI yordamida umumlashtirib, ma’lum bir shtamm uchun xos kompyuter modellari yaratiladi va bu modellar sekretsiya qilmoqchi bo‘lgan oqsil uchun istiqbolli genetik element variantlarni saralashga yordam beradi [8, 9]. Natijada juda ko‘plab mablag‘ va vaqt tejab qolinadi.

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Muhokama

Ko‘plab adabiyotlar tahlili sekretsiyani o‘zaro bog‘liq bosqichlar majmui sifatida baholash zarurligini ko‘rsatadi. Dastlab maqsadli oqsilga mos sekretsiya yo‘li va SPlar tanlanadi, so‘ngra promotor-RBS-SP kombinatsiyalari tanlanadi. *B. subtilis* xo‘jayin hujayrasi sekretsiya chekloviga qarab mos vektor konstrukt kombinatsiyasi tanlanadi, bu rekombinant oqsilning to‘g‘ri folding bo‘lishi va sekretsiyasi yaxshilanishiga yordam beradi. Loyihalash, yaratish, sinash va olingan natijalardan o‘rganish sikli navbatdagi konstruksiyalarni avvalgi tajribalar asosida tanlash imkonini beradi.

Samaradorlikni baholash faqat oziqa muhitidagi rekombinant ferment faolligi bilan cheklanmasligi kerak. Oqsil miqdori, solishtirma faollik, biomassa va hujayra o‘sish tezligini ham hisobga olish zarur. Bundan tashqari, kichik hajmli tajribalarda tanlangan konstruksiyaning bioreaktordagi samaradorligi alohida tasdiqlanishi lozim. Ushbu yondashuvning asosiy cheklovlari — genetik elementlar samaradorligining maqsadli oqsil va xo‘jayin shtammga bog‘liqligi hamda hisoblash modellarining tajriba ma’lumotlari sifati va hajmiga qaramligidir. Yuqorida keltirilgan misollar 1-rasmda sxematik tarzda umumlashtirilgan.



1-rasm. *B. subtilis*da rekombinant oqsil sekretsiyasini ko‘p parametrli optimallashtirish: loyihalash, vektor yaratish, sekretsiyani baholash va ishlab chiqarish ko‘lamini kengaytirish

Xulosa

*B. subtilis*da rekombinant oqsil sekretsiyasini oshirish uchun SP, promotor, RBS va xo‘jayin shtamm xususiyatlarini birgalikda optimallashtirish zarur. Yuqori mahsuldorlik oqsil sintezi, folding va sekretsiyasi o‘rtasidagi muvozanat bilan ta’minlanadi. SI usullari tajribada tekshiriladigan variantlarni saralashni tezlashtiradi. Yakuniy tanlov esa rekombinant oqsil sekretsiyasi miqdori va xo‘jayin hujayra barqarorligi asosida amalga oshiriladi.

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MENTHA LONGIFOLIA (L.) L. O‘SIMLIGINING ENDOFIT ZAMBURUG‘LARINI AJRATISH, SOF KULTURAGA OLISH VA ULARNING MORFOKULTURAL XUSUSIYATLARINI O‘RGANISH

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Annotatsiya: Mazkur tadqiqot *Mentha longifolia (L.) L.* o‘simligidan endofit zamburug‘larni ajratish, sof kulturaga olish va ularning morfokultural xususiyatlarini o‘rganishga bag‘ishlangan. Tadqiqotda o‘simlik namunalarini sirt sterilizatsiya qilish, oziqa muhitiga ekish va koloniyalarni qayta ekish usullari qo‘llanildi. Izolyatlarning koloniya rangi, shakli, yuzasi va mitseliy rivojlanishi kuzatildi. Natijalar endofit zamburug‘larni dastlabki tavsiflash va keyingi biologik hamda biotexnologik tadqiqotlar uchun asos bo‘lib xizmat qiladi.

Kalit so‘zlar: *Mentha longifolia (L.) L.*, endofit zamburug‘lar, izolyat, sof kultura, sirt sterilizatsiya, PDA, morfokultural xususiyatlar.

Аннотация: Данное исследование посвящено выделению эндофитных грибов из растения *Mentha longifolia (L.) L.*, получению чистых культур и изучению их морфокультуральных характеристик. В ходе исследования проводили поверхностную стерилизацию образцов растения, посев на питательные среды и повторный пересев грибных колоний. Изучали цвет, форму и поверхность колоний, а также развитие мицелия. Полученные результаты служат основой для предварительной характеристики эндофитных грибов и дальнейших биологических и биотехнологических исследований.

Ключевые слова: *Mentha longifolia (L.) L.*, эндофитные грибы, изолят, чистая культура, поверхностная стерилизация, PDA, морфокультуральные характеристики.

Abstract: This study focuses on the isolation of endophytic fungi from *Mentha longifolia (L.) L.*, obtaining pure cultures, and examining their morphocultural characteristics. The study involved surface sterilization of plant samples, inoculation onto culture media, and repeated subculturing of fungal colonies. Colony color, shape, surface, and mycelial development were observed. The results provide a basis for the preliminary characterization of endophytic fungi and further biological and biotechnological research.

Keywords: *Mentha longifolia (L.) L.*, endophytic fungi, isolate, pure culture, surface sterilization, PDA, morphocultural characteristics.

Kirish

Endofit mikroorganizmlar o‘simliklarning ichki to‘qimalarida yashovchi va mezbon o‘simlik bilan turli biologik munosabatlarga kirishuvchi mikroorganizmlardir. Ular orasida bakteriyalar, aktinomitsetlar va zamburug‘lar mavjud. Endofit zamburug‘larning biologik faol ikkilamchi metabolitlar hosil qilish xususiyati mikrobiologiya, biotexnologiya va farmatsevtika sohalarida muhim ahamiyatga ega [1]. Jumladan, Taxus baccata o‘simligidan ajratilgan Gliocladium sp. zamburug‘ining metabolit hosil qilish xususiyati o‘rganilgan [1]. *Mentha longifolia (L.) L.* Lamiaceae oilasiga mansub ko‘p yillik dorivor va aromatik o‘simlik bo‘lib, uning ildiz to‘qimalaridan Fusarium sp. endofit zamburug‘i ajratilgani va biologik faol birikmalari o‘rganilgani haqida ma’lumotlar

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Aminova M.E., Fayziyev V.B. Mentha longifolia (L.) L. o‘simligining endofit zamburug‘larini ajratish, sof kulturaga olish va ularning morfokultural xususiyatlarini o‘rganish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 175–176.
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mavjud [2]. Shu sababli mazkur o‘simlik endofit zamburug‘larini ajratish va morfokultural xususiyatlarini o‘rganish dolzarb hisoblanadi. *M. longifolia* o‘simligi to‘qimalaridan endofit zamburug‘larni ajratish, sof kulturaga olish va ularning dastlabki morfokultural xususiyatlarini tavsiflash.

Tadqiqot materiallari va usullari

Tadqiqot materiali sifatida *M. longifolia* o‘simligining sog‘lom barg, poya va ildiz to‘qimalaridan foydalanildi. Namunalar mexanik iflosliklardan tozalanib, sirt sterilizatsiyasidan o‘tkazildi va steril suv bilan yuvildi [3]. So‘ngra to‘qima bo‘laklari aseptik sharoitda PDA va Chapek oziqa muhitlariga joylashtirildi. Rivojlangan koloniyalar alohida raqamlanib, yangi oziqa muhitlariga uch marta qayta ekildi [1, 4]. Izolyatlarning morfokultural xususiyatlari koloniya rangi, shakli, yuzasi, chetki qismining tuzilishi, mitseliy zichligi va o‘sish xarakteriga ko‘ra kuzatildi.

Natijalar va muhokama

Tadqiqot davomida *M. longifolia* o‘simligining bargidan 6 ta, poyasidan 4 ta va ildizidan 11 ta, jami 21 ta zamburug‘ izolyati ajratildi. Ulardan 10 tasi PDA, 11 tasi Chapek oziqa muhitiga ekildi. Morfokultural kuzatuvlarda koloniyalarning rangi, yuzasi, chetki qismlari va mitseliy zichligi bo‘yicha farqlar aniqlandi. Ayrim koloniyalar zich va paxtasimon, boshqalari esa yupqa, tukli yoki g‘adir-budir ko‘rinishda rivojlandi. Koloniya chetlari tekis, notekis yoki radial shaklda bo‘lishi kuzatildi. Uch marta qayta ekishga qaramay, sof kultura olingani hali tasdiqlanmagan. Shu sababli izolyatlar dastlabki morfokultural belgilari asosida tavsiflandi. Ularni tur darajasida aniqlash uchun keyingi bosqichlarda mikroskopik tekshiruvlar va zarur hollarda molekulyar identifikatsiya usullarini qo‘llash talab etiladi.

Xulosa

Mentha longifolia (L.) L. o‘simligining barg, poya va ildiz qismlaridan 21 ta zamburug‘ izolyati ajratilib, PDA va Chapek oziqa muhitlarida kuzatildi. Koloniyalarning morfokultural belgilarida farqlar aniqlandi. Olingan natijalar izolyatlarni keyingi bosqichlarda sof kulturaga olish, mikroskopik o‘rganish va identifikatsiya qilish uchun dastlabki ilmiy asos bo‘lib xizmat qiladi.

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gyrA AND *rpoB* AS ALTERNATIVE MARKERS FOR BACTERIAL IDENTIFICATION

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Abstract: We evaluated the effectiveness of gyrA and rpoB as alternative markers for species-level bacterial identification when the 16S rRNA gene is insufficient, using *in silico* analysis and molecular genetic methods.

Keywords: 16S rRNA, gyrA, rpoB, nucleotide diversity

Annotatsiya: Bakteriyalarni tur darajasida identifikatsiya qilishda 16S rRNA geni yetarli bo‘lmagan holatlar uchun muqobil *gyrA* va *rpoB* markerlarining samaradorligi in silico tahlil va molekulyar-genetik usullar yordamida o‘rganildi.

Kalit so‘zlar: 16S rRNA, gyrA, rpoB, nukleotid diversligi

Аннотация: Эффективность альтернативных маркеров *gyrA* и *rpoB* для идентификации бактерий на видовом уровне в случаях, когда ген 16S рРНК недостаточен, оценивалась с помощью *in silico* анализа и молекулярно-генетических методов.

Ключевые слова: 16S рРНК, gyrA, rpoB, нуклеотидное разнообразие

The 16S rRNA gene is the most widely used marker for bacterial identification and phylogenetic analysis. However, because it is highly conserved, present in multiple copies per genome, and divergent among those copies, the 16S rRNA gene may be insufficient to reliably discriminate closely related species. Consequently, single-copy, protein-coding genes that evolve faster than 16S rRNA are being considered as alternative markers, notably *gyrA*, which encodes the DNA *gyra*se A subunit, and *rpoB*, which encodes the RNA polymerase β subunit.

For the *in silico* analysis, complete genomes of *Bacillus* representatives were retrieved from the NCBI GenBank database, and the 16S rRNA, *gyrA*, and *rpoB* sequences were extracted from them. Intraspecific variability was assessed in a total of 230 genomes of *B. subtilis* (93), *B. cereus* (79), and *B. safensis* (58). Interspecific variability was examined in a dataset of 283 genomes representing 17 species. Sequences were aligned with MUSCLE, nucleotide diversity (π) was calculated in DnaSP using a 10-bp sliding window, and the distribution of SNPs along the genes was analyzed. In the interspecific comparison, *gyrA* exhibited the highest nucleotide diversity ($\pi \approx 0.15$–0.28), *rpoB* showed intermediate values ($\pi \approx 0.06$–0.27), and the 16S rRNA gene was characterized by very low diversity ($\pi \approx 0.01$–0.03, reaching ≈ 0.11 only in isolated variable regions). Within species, the 16S rRNA gene was nearly invariant ($\pi \approx 0$), π in *rpoB* did not exceed 0.03, and π in *gyrA* rose to ≈ 0.09, with the highest value observed in *B. cereus*.

Five bacterial isolates (N1, N2, N3, N4, and N5) were used in this study. Genomic DNA was extracted from the isolates by the Marmur method. The 16S rRNA gene was amplified by PCR with the universal primers 27F and 1492R under the following conditions: initial denaturation at 95 °C for

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3 min; 30 cycles of denaturation at 95 °C for 40 s, annealing at 56 °C for 40 s, and extension at 72 °C for 1.5 min; and a final extension at 72 °C for 7 min. Amplification products were verified by electrophoresis on a 0.8% agarose gel and sequenced on a Sanger sequencer. The resulting sequences were compared against the NCBI BLAST database, and the isolates were identified to the genus level.

A fragment of the *gyrA* gene was amplified by PCR with the degenerate primers:

*gyrA*3-F (5′-GCDGCHGCNATGCGTTAYAC-3′)

*gyrA*3-R (5′-ACAAGMTCWGCKATTTTTTC-3′)

PCR was initially performed under the following conditions: initial denaturation at 95 °C for 3 min; 30 cycles of denaturation at 95 °C for 40 s, annealing at 56 °C for 40 s, and extension at 72 °C for 40 s; and a final extension at 72 °C for 7 min. However, owing to the high degeneracy of the primers and the low Tm of the reverse primer, these conditions yielded nonspecific products. A stepwise annealing program was therefore applied, consisting of 2 cycles each at 50, 51, 52, 53, and 54 °C (10 cycles in total), followed by 10 cycles at 55 °C and 10 cycles at 56 °C (30 cycles in total). The denaturation and extension steps were left unchanged. Amplification products were verified by electrophoresis on a 0.8% agarose gel.

A fragment of the *rpoB* gene was amplified by PCR with the degenerate primers:

rpoB_F (5′-GGYTWYGAAGTNCGHGACGTDCA-3′)

rpoB_R (5′-TGACGYTGCATGTTBGMRCCCATMA-3′)

PCR was performed under the following conditions: initial denaturation at 95 °C for 3 min; 30 cycles of denaturation at 95 °C for 40 s, annealing at 56 °C for 40 s, and extension at 72 °C for 40 s; and a final extension at 72 °C for 7 min. Amplification products were verified by electrophoresis on a 0.8% agarose gel.

The *in silico* analysis showed that, in the genus *Bacillus*, *gyrA* and *rpoB* have higher nucleotide diversity than the 16S rRNA gene (π: *gyrA* ≈ 0.15–0.28, *rpoB* ≈ 0.06–0.27, 16S rRNA ≈ 0.01–0.03). Whereas the 16S rRNA gene was nearly invariant within species, variability was detected in both *gyrA* and *rpoB*. These genes are therefore promising supplementary markers to 16S rRNA for discriminating closely related species. The conditions for amplifying *gyrA* and *rpoB* fragments were optimized. *gyrA* and *rpoB* can serve as effective supplementary markers for identifying closely related species that 16S rRNA cannot resolve.

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METILOTROF BAKTERIYALAR BIOMASSASINING VITAMIN TARKIBI VA VITAMINLI-OQSILLI OZUQA QO‘SHIMCHALARI OLISHDAGI AHAMIYATI

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Annotatsiya: Ikki metilotrof bakteriya shtammi biomassasida B1, B2, B3, B6, B9 va C vitaminlari miqdori qiyoslandi. Oltita vitaminning ko‘rsatkichlari yig‘indisi *M. dankookense* 3HXI da 64,68 mkg/g, *M. fujisawaense* 1HXI da 47,71 mkg/g ni tashkil etdi. Natijalar birinchi shtamm biomassasining vitamin tarkibi bo‘yicha ustunligini ko‘rsatdi.

Kalit so‘zlar: metilotrof bakteriyalar, *Methylobacterium*, biomassa, vitaminlar, ozuqa qo‘shimchasi.

Аннотация: Проведено сравнительное изучение содержания витаминов B1, B2, B3, B6, B9 и C в биомассе двух штаммов метилотрофных бактерий. Суммарные показатели шести витаминов составили 64,68 мкг/г для *M. dankookense* 3HXI и 47,71 мкг/г для *M. fujisawaense* 1HXI. Первый штамм характеризовался более высокими показателями.

Ключевые слова: метилотрофные бактерии, *Methylobacterium*, биомасса, витамины, кормовая добавка.

Abstract: The contents of vitamins B1, B2, B3, B6, B9 and C were compared in biomass from two methylotrophic bacterial strains. The sum of six reported vitamin values was 64.68 µg/g for *M. dankookense* 3HXI and 47.71 µg/g for *M. fujisawaense* 1HXI. The first strain showed higher values overall.

Keywords: methylotrophic bacteria, *Methylobacterium*, biomass, vitamins, feed supplement.

Kirish

Chorvachilik va parrandachilikda ozuqa ratsionini oqsil, vitamin va boshqa biologik faol birikmalar bilan boyitish hayvonlar organizmida moddalar almashinuvining me’yorida kechishi uchun muhim hisoblanadi. An’anaviy oqsil manbalariga bo‘lgan talab ortib borayotgan sharoitda mikroorganizmlardan biomassa olish muqobil biotexnologik yo‘nalish sifatida e’tibor qozonmoqda. Metilotrof bakteriyalar bir uglerodli organik birikmalar, jumladan metanoldan uglerod va energiya manbai sifatida foydalanishi bilan ajralib turadi. Ular qisqa muddatda biomassa to‘plashi, oqsil va ayrim biologik faol metabolitlarni saqlashi sababli bir hujayrali oqsil texnologiyalari uchun istiqbolli hisoblanadi [1–3]. Vitaminlar biomassaning biologik qiymatini belgilovchi muhim tarkibiy qismlardir. Xususan, B guruhi vitaminlari fermentativ reaksiyalarda kofermentlar tarkibiga kirib, energiya almashinuvi, aminokislotalar metabolizmi va hujayra faoliyatini ta’minlashda qatnashadi. Shu sababli metilotrof bakteriyalar biomassasining vitamin tarkibini baholash vitaminli-oqsilli ozuqa qo‘shimchalarini ishlab chiqishda amaliy ahamiyatga ega.

Tadqiqotning maqsadi *M. dankookense* 3HXI va *M. fujisawaense* 1HXI shtammlari biomassasida suvda eruvchi vitaminlar miqdorini qiyosiy baholash hamda ularning ozuqa qo‘shimchasi olishdagi istiqbolini tahlil qilishdan iborat.

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Materiallar va metodlar

Tadqiqot obyekti sifatida ikkita metilotrof bakteriya shtammi — *Methylobacterium dankookense* 3HXI va *Methylobacterium fujisawaense* 1HXI larning liofil usulda quritilgan biomassasi o‘rganildi. Oldingi tadqiqotlarimizda ushbu bakteriya shtammlari molekulyar-genetik usulda identifikatsiya qilingan, mos ravishda PX924540.1 va PX924362.1 raqamlari bilan NCBI bazasiga kiritilgan. Bakteriyalar tarkibi (g/l) KH_2PO_4 – 2,0; $(NH_4)_2SO_4$ – 2,0; $MgSO_4 \cdot 7H_2O$ – 0,025; NaCl – 0,5 va $FeSO_4 \cdot 7H_2O$ – 0,002 bo‘lgan «K» mineral oziqa muhitida o‘stirildi. Muhitga 1% metanol qo‘shildi, boshlang‘ich pH 7,0 etib belgilandi. Olingan biomassa namunalari tarkibidagi suvda eruvchi B1, B2, B3, B6, B9 va C vitaminlari miqdori yuqori samarali suyuqlik xromatografiyasi usulida o‘rganildi.

Natijalar

O‘rganilgan har ikkala shtamm biomassasida oltita suvda eruvchi vitamin bo‘yicha miqdoriy ko‘rsatkichlar qayd etildi (1-jadval). Birinchi shtammda B1 va C vitaminlari bir xil — 14,68 mkg/g, B6 — 11,86 mkg/g, B9 — 11,49 mkg/g, B3 — 10,30 mkg/g hamda B2 — 1,67 mkg/g qiymatlarda kuzatildi. Ikkinchi shtammda B1 vitamini 15,60 mkg/g bilan nisbatan yuqori, B2 vitamini esa 1,50 mkg/g bilan eng past qiymatni ko‘rsatdi. Boshqa vitaminlar uchun ushbu shtammda B3 — 6,55 mkg/g, B6 — 8,98 mkg/g, B9 — 4,78 mkg/g va C — 10,30 mkg/g natijalar qayd etildi.

1-jadval. Metilotrof bakteriyalar biomassasidagi suvda eruvchi vitaminlar (mkg/g)

Vitamin	***M. dankookense* 3HXI**	***M. fujisawaense* 1HXI**
B1 (tiamin)	14,68	15,60
B2 (riboflavin)	1,67	1,50
B3 (niatsin)	10,30	6,55
B6 (piridoksin guruhi)	11,86	8,98
B9 (folat guruhi)	11,49	4,78
C (askorbin kislota)	14,68	10,30
Oltita vitamin yig‘indisi	**64,68**	**47,71**

Muhokama

Oltita vitaminning ko‘rsatkichlari yig‘indisi *M. dankookense* 3HXI biomassasida 64,68 mkg/g, *M. fujisawaense* 1HXI biomassasida esa 47,71 mkg/g ni tashkil etdi. Demak, birinchi shtammda umumiy ko‘rsatkich 16,97 mkg/g yoki 35,6% yuqori bo‘ldi. Birinchi shtamm B2, B3, B6, B9 va C vitaminlari bo‘yicha, ikkinchi shtamm esa B1 vitamini bo‘yicha ustunlik qildi. Eng sezilarli farq B9 vitamini miqdorida kuzatildi: birinchi shtammdagi qiymat ikkinchisiga nisbatan qariyb 2,4 baravar yuqori edi. Vitaminlarning fiziologik vazifalari ham ozuqa qo‘shimchasi uchun muhimdir: B1 uglevodlardan energiya hosil bo‘lishida, B2 va B3 oksidlanish-qaytarilish jarayonlarida, B6 aminokislotalar almashinuvida, B9 esa nuklein kislotalar hosil bo‘lishi va hujayralarning bo‘linishida qatnashadi. C vitamini antioksidant xususiyati bilan ahamiyatlidir. Adabiyotlarda metilotrof mikroorganizmlardan oqsil, vitamin va boshqa qimmatli metabolitlar olish imkoniyatlari ko‘rsatilgan [1–3]. Olingan natijalar vitamin ko‘rsatkichlarining shtammga bog‘liqligini namoyon qiladi va biotexnologik maqsad uchun shtamm tanlashda biomassa tarkibini hisobga olish zarurligini ko‘rsatadi.

Xulosa

M. dankookense 3HXI va *M. fujisawaense* 1HXI shtammlari biomassasi suvda eruvchi vitaminlarning miqdoriy ko‘rsatkichlari bilan farq qilishi aniqlandi. B1 vitamini bo‘yicha ikkinchi shtamm ustun bo‘lsa-da, oltita vitamin yig‘indisi va B9, B6, B3 hamda C vitaminlari bo‘yicha birinchi shtamm yuqori ko‘rsatkichlarga ega bo‘ldi. Bu holat *M. dankookense* 3HXI shtammini vitaminlarga boy biomassa olish yo‘nalishida keyingi izlanishlar uchun istiqbolli deb baholash imkonini beradi.

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MIS NANOZARRALARINING FITOVIRUSLARGA QARSHI QO‘LLASH ISTIQBOLLARI

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Annotatsiya: Mazkur tadqiqot mis nanozarralarining (CuNPs, CuO-NPs, Cu_2O-NPs) fitoviruslarga qarshi antivirus xususiyatlari, ta’sir mexanizmlari va qishloq xo‘jaligidagi istiqbollarini o‘rganishga bag‘ishlangan. Fitoviruslarga qarshi to‘g‘ridan-to‘g‘ri kimyoviy vositalar deyarli yo‘q. Mis nanozarralari virionlarni parchalash va tizimli olingan chidamlilik (SAR) mexanizmini faollashtirish orqali samarali ta’sir ko‘rsatadi. TMV, AMV va ZYMV ga qarshi 80–100 ppm konsentrasiyada virus to‘planishini sezilarli kamaytirishi, himoya genlarini faollashtirishi va o‘simlik o‘sishini rag‘batlantirishi aniqlangan. Ushbu yondashuv ekologik toza antivirus vositalar ishlab chiqish uchun ilmiy asos yaratadi.

Kalit so‘zlar: mis nanozarralari, CuO-NPs, Cu_2O-NPs, fitoviruslar, TMV, AMV, ZYMV, SAR, antivirus faollik, nanotexnologiya.

Аннотация: Исследование посвящено антивирусным свойствам медных наночастиц (CuNPs, CuO-NPs, Cu_2O-NPs) против фитовирусов, механизмам их действия и перспективам применения в сельском хозяйстве. Прямые химические средства борьбы с фитовирусами практически отсутствуют. Медные наночастицы эффективно подавляют инфекции за счёт разрушения вирионов и индукции системной приобретённой устойчивости (SAR). При концентрации 80–100 ppm они существенно снижают накопление вируса (TMV, AMV, ZYMV), активируют защитные гены и стимулируют рост растений. Подход создаёт основу для разработки экологически безопасных средств.

Ключевые слова: медные наночастицы, CuO-NPs, Cu_2O-NPs, фитовирусы, TMV, AMV, ZYMV, SAR, антивирусная активность, нанотехнологии.

Abstract: This study examines the antiviral properties of copper nanoparticles (CuNPs, CuO-NPs, Cu_2O-NPs) against phytoviruses, their mechanisms of action and agricultural prospects. Direct chemical control agents against phytoviruses are almost unavailable. Copper nanoparticles effectively suppress infections by disrupting virions and inducing systemic acquired resistance (SAR). At 80–100 ppm they significantly reduce viral accumulation (TMV, AMV, ZYMV), activate defense genes and promote plant growth. The approach provides a scientific basis for developing environmentally friendly antiviral agents.

Keywords: copper nanoparticles, CuO-NPs, Cu_2O-NPs, phytoviruses, TMV, AMV, ZYMV, SAR, antiviral activity, nanotechnology.

Kirish

Fitoviruslar qishloq xo‘jaligi ekinlariga eng katta iqtisodiy zarar yetkazuvchi patogenlar guruhiga kiradi. Jahon miqyosida o‘simlik kasalliklari sababli yo‘qotilayotgan hosilning qariyb 47 foizi virusli infeksiyalar hissasiga to‘g‘ri keladi. Hozirgi vaqtda fitoviruslarga qarshi to‘g‘ridan-to‘g‘ri samarali kimyoviy preparatlar deyarli mavjud emas. So‘nggi o‘n yillikda nanotexnologiya

IQTIBOS UCHUN
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asosida yangi yechimlar izlanmoqda. Ayniqsa, mis nanozarralari (CuNPs, CuO-NPs, Cu_2O-NPs) kuchli antivirus xususiyatlari, o‘simlik o‘sishini rag‘batlantirish qobiliyati va nisbatan past toksikligi bilan e’tiborni tortmoqda. Tadqiqotning maqsadi – mis nanozarralarining fitoviruslarga qarshi ta’sir mexanizmlari va qishloq xo‘jaligidagi istiqbollarini tahlil qilish.

Materiallar va metodlar

Tadqiqot adabiyot tahlili usulida olib borildi. So‘nggi yillarda nashr etilgan ilmiy maqolalar (2021–2025) asosida mis nanozarralarining TMV, AMV va ZYMV ga qarshi antivirus faolligi, ta’sir mexanizmlari (virionlarni bevosita parchalash va SAR induksiyasi) hamda yashil sintez usullari tahlil qilindi. Asosiy manbalar sifatida Phytopathology Research, BMC Plant Biology, Pest Management Science va boshqa nufuzli jurnallardagi maqolalar tanlandi.

Natijalar

Mis nanozarralari 80–100 ppm konsentrasiyada TMV, AMV va ZYMV ga qarshi yuqori samara ko‘rsatgan. CuO-NPs 100 mg/L da TMV zarrachalarini fragmentatsiyaga uchratgan, AMV virus to‘planishini 97 % gacha kamaytirgan. ZYMV ga qarshi mis oksidi nanostrukturalari kasallik og‘irligini pasaytirgan. Barcha holatlarda PR1, PR2, ERF1, CHI, POD kabi himoya genlari faollashgan, salitsil va jasmonat kislotalari signal yo‘llari kuchaygan. Profilaktik va davolovchi qo‘llashning ikkalasi ham samarali ekanligi aniqlangan.

Muhokama

Mis nanozarralari ikki asosiy mexanizm orqali ta’sir qiladi: virionlarni bevosita denaturatsiya qilish va o‘simlikning o‘z himoya tizimini (SAR) faollashtirish. Yashil sintez usullari ekologik toza va arzon ishlab chiqarish imkonini beradi. Shu bilan birga, yuqori konsentrasiyalarda fitotoksiklik xavfi, tuproq va suvga uzoq muddatli ta’siri hali to‘liq o‘rganilmaganligi, ochiq dala sharoitida keng ko‘lamli sinovlar yetarli emasligi asosiy cheklovlardir. Standartlashgan doza va qo‘llash usullari ishlab chiqilishi zarur.

Xulosa

Mis nanozarralari fitoviruslarga qarshi kurashda yuqori istiqbolga ega. Ular virus zarrachalarini to‘g‘ridan-to‘g‘ri yo‘q qilish bilan birga o‘simlikning o‘z himoya mexanizmlarini ham kuchaytiradi. Hozirgi tadqiqotlar TMV, AMV, ZYMV kabi muhim fitoviruslarga qarshi yuqori samaradorligini isbotlagan. Kelajakda yashil sintez usullarini takomillashtirish, xavfsiz dozalarni aniqlash va ochiq dala sinovlarini o‘tkazish orqali ular amaliy va ekologik toza vositaga aylanishi mumkin.

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CATHARANTHUS ROSEUS DAN AJRATILGAN ENDOFIT ZAMBURUG‘LAR METABOLITLARINING SITOTOKSIK XUSUSIYATLARI

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Annotatsiya: Tadqiqotda *Catharanthus roseus* (L.) G. Don o‘simligidan ajratilgan *Aspergillus terreus* VR177L va *Aspergillus sp.* VR176L endofit zamburug‘lari ekstraktlarining sitotoksik faolligi o‘rganildi. Ekstraktlarning 100 mkg/ml konsentratsiyadagi faolligi SRB usuli yordamida baholandi. Eng yuqori faollik *Aspergillus sp.* VR176L ekstraktida kuzatilib, HeLa hujayralari o‘sishini bostirish 70,6 ± 2,5% ni tashkil etdi. Natijalar ushbu ekstraktning biologik faol birikmalar manbai sifatidagi istiqbolini ko‘rsatadi.

Kalit so‘zlar: *Catharanthus roseus*, endofit zamburug‘lar, *Aspergillus sp.* VR176L, *Aspergillus terreus* VR177L, sitotoksiklik, vinka alkaloidlari, HeLa, SRB usuli.

Аннотация: В исследовании изучена цитотоксическая активность экстрактов эндофитных грибов *Aspergillus terreus* VR177L и *Aspergillus sp.* VR176L, выделенных из растения *Catharanthus roseus* (L.) G. Don. Цитотоксическую активность экстрактов в концентрации 100 мкг/мл оценивали с использованием метода SRB. Наибольшая активность выявлена у экстракта Aspergillus sp. VR176L, который подавлял рост клеток HeLa на 70,6 ± 2,5%. Полученные результаты свидетельствуют о перспективности дальнейшего изучения данного экстракта как источника биологически активных соединений.

Ключевые слова: *Catharanthus roseus*, эндофитные грибы, *Aspergillus sp.* VR176L, *Aspergillus terreus* VR177L, цитотоксичность, алкалоиды винка, HeLa, метод SRB.

Abstract: This study investigated the cytotoxic activity of extracts from the endophytic fungi *Aspergillus terreus* VR177L and *Aspergillus* sp. VR176L isolated from *Catharanthus roseus* (L.) G. Don. The cytotoxic activity of the extracts at a concentration of 100 μg/mL was evaluated using the SRB assay. The highest activity was observed for the *Aspergillus* sp. VR176L extract, which inhibited HeLa cell growth by 70.6 ± 2.5%. These results indicate the potential of this extract as a source of biologically active compounds and support further investigation.

Keywords: *Catharanthus roseus*, endophytic fungi, *Aspergillus sp.* VR176L, *Aspergillus terreus* VR177L, cytotoxicity, Vinca alkaloids, HeLa, SRB assay.

Kirish

O‘simliklardan olinadigan biologik faol birikmalar orasida *Catharanthus roseus* (L.) G. Don alohida ahamiyatga ega bo‘lib, ushbu o‘simlik saratonga qarshi preparatlar — vinkristin va vinblastinning tabiiy manbai hisoblanadi [1]. Vinkristin va vinblastin klinik amaliyotda, jumladan, ayrim leykemiya, limfoma va boshqa o‘sma kasalliklarini davolashda qo‘llaniladi [2]. Biroq ushbu alkaloidlarning o‘simlik tarkibida juda kam miqdorda to‘planishi (taxminan 0,0002–0,0005%) ularni tabiiy xomashyodan ajratib olish va ishlab chiqarish jarayonini murakkablashtiradi [3]. Turli dorivor o‘simliklardan ajratilgan endofit zamburug‘lar biologik faol birikmalar manbai sifatida ham katta qiziqish uyg‘otmoqda. Jumladan, Kuriakose va hammualliflar *Taxus brevifolia* bilan bog‘liq *Fusarium solani* endofit zamburug‘idan ajratilgan paklitakselning biologik faolligini o‘rgangan.

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Otayeva Z., Nasmetova S., Norqo‘ziyeva O. Catharanthus roseus dan ajratilgan endofit zamburug‘lar metabolitlarining sitotoksik xususiyatlari // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 184–186.
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Tadqiqotda ushbu birikmaning o‘pka saratoni hujayralariga sitotoksik ta’siri, hujayra sikliga ta’siri hamda apoptozni induksiya qilish xususiyatlari baholangan [4]. Shu munosabat bilan, mahalliy *C. roseus* o‘simligidan ajratilgan endofit zamburug‘larning ikkilamchi metabolitlarini o‘rganish hamda ularning vinka alkaloidlarini ishlab chiqarish imkoniyatlarini baholash va sitotoksik faolligini o‘rganish muhim biotexnologik yo‘nalish hisoblanadi.

Materiallar va metodlar

Tadqiqotlar *C. roseus* o‘simligi barglaridan ajratib olingan *Aspergillus terreus* VR177L va *Aspergillus* sp. VR176L endofit zamburug‘lari makkajo‘xori asosidagi suyuq oziqa muhitida 28 °C haroratda, 140 ayl/min tezlikda 7 kun davomida o‘stirildi. Kultivatsiya yakunida zamburug‘ biomassasi ajratib olinib, uning miqdori aniqlandi. Umumiy alkaloidlarni ajratib olish uchun biomassa 1:5 nisbatda 70% li etil spirti yordamida ekstraksiyalandi va umumiy alkaloidlar kislota-ishqor ekstraksiyasi usuli yordamida ajratib olindi. Olingan alkaloidlar dimetilsulfoksidda (DMSO) eritilib, 0,22 mkm li filtrdan o‘tkazildi. Ekstraktlarining sitotoksik faolligi 100 mkg/ml konsentratsiyada HeLa, HEp-2 va A549 o‘sma hujayralari hamda HEK sog‘lom hujayralar liniyasida SRB usuli yordamida baholandi.

Natijalar

Zamburug‘ ekstraktlarining 100 mkg/ml konsentratsiyadagi sitotoksik faolligi hujayra liniyalarida turlicha namoyon bo‘ldi. *Aspergillus* sp. VR176L ekstrakti HeLa hujayralari o‘sishini 70,6 ± 2,5%, A549 hujayralarini 42,1 ± 1,5% va HEp-2 hujayralarini 17,7 ± 3,0% ga bostirdi. Sog‘lom HEK hujayralarida bu ko‘rsatkich 30,9 ± 1,6% ni tashkil etdi. *Aspergillus terreus* VR177L ekstrakti uchun esa tegishli ko‘rsatkichlar mos ravishda 52,5 ± 4,0%, 25,2 ± 3,0%, 18,5 ± 2,8% va 25,7 ± 1,8% bo‘ldi. Selektivlik indeksi birinchi ekstrakt uchun 2,3, ikkinchisi uchun 2,0 ni tashkil etdi.

Muhokama

Olingan natijalar ikkala zamburug‘ ekstrakti ham HeLa hujayralariga nisbatan yuqoriroq sitotoksik faollik namoyon etganini ko‘rsatdi. Eng yuqori faollik *Aspergillus* sp. VR176L ekstraktida kuzatilib, uning HeLa hujayralaridagi bostirish ko‘rsatkichi sisplatinning 64,2 ± 1,5% ko‘rsatkichidan yuqori bo‘ldi. Biroq, ekstraktning sog‘lom HEK hujayralariga ham ta’sir ko‘rsatishi uning selektivligi cheklanganligini anglatadi.

Xulosa

Aspergillus sp. VR176L zamburug‘i ekstrakti 100 mkg/ml konsentratsiyada HeLa hujayralariga nisbatan eng yuqori sitotoksik faollikni namoyon etdi. Olingan natijalar ushbu ekstraktni biologik faol birikmalar manbai sifatida keyingi tadqiqotlarda o‘rganish istiqbolli ekanligini ko‘rsatadi. Biroq, uning saraton hujayralariga selektiv ta’sirini baholash va faol komponentlarini aniqlash uchun qo‘shimcha tadqiqotlar talab etiladi.

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STREPTOMYCES ROCHEI IMB/AN RUz SHTAMMI KULTURA SUYUQLIGI VA BIOMASSASI METANOLLI EKSTRAKTLARINING DASTLABKI FITOKIMYOVIY SKRININGI

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Annotatsiya: *Streptomyces rochei* IMB/AN RUz shtammi kultura suyuqligi va biomassasining metanolli ekstraktlarida ikkilamchi metabolitlarning asosiy guruhlari (fenollar, flavonoidlar, alkaloidlar, steroidlar, taninlar, terpenoidlar va saponinlar) dastlabki fitokimyoviy skrining usulida o‘rganildi.
Kalit so‘zlar: *Streptomyces rochei*, metanolli ekstrakt, fitokimyoviy skrining, ikkilamchi metabolitlar.

Аннотация: Методом предварительного фитохимического скрининга изучены основные группы вторичных метаболитов (фенолы, флавоноиды, алкалоиды, стероиды, дубильные вещества, терпеноиды и сапонины) в метанольных экстрактах культуральной жидкости и биомассы штамма *Streptomyces rochei* IMB/AN RUz.
Ключевые слова: *Streptomyces rochei*, метанольный экстракт, фитохимический скрининг, вторичные метаболиты.

Abstract: The main groups of secondary metabolites (phenols, flavonoids, alkaloids, steroids, tannins, terpenoids and saponins) in methanolic extracts of the culture broth and biomass of *Streptomyces rochei* IMB/AN RUz were examined by preliminary phytochemical screening.
Keywords: *Streptomyces rochei*, methanolic extract, phytochemical screening, secondary metabolites.

Kirish

Streptomyces avlodi ikkilamchi metabolitlarning muhim manbalaridan biri hisoblanadi [1]. Ushbu avlod vakillari, jumladan *S. rochei*, o‘simlik kasalliklariga qarshi biologik nazorat va zamburug‘larga qarshi faol birikmalarni o‘rganishga oid tadqiqotlarda ko‘rib chiqilgan [2, 3]. Shu sababli yangi ajratilgan shtammlarning ikkilamchi metabolitlari tarkibini aniqlash ilmiy va amaliy ahamiyatga ega. Metabolitlarning asosiy guruhlarini aniqlashda dastlabki fitokimyoviy skrining qo‘llaniladi; sifat reaksiyalariga asoslangan bu usul keyingi miqdoriy va strukturaviy tahlillar yo‘nalishini belgilashga imkon beradi [4, 5]. Tadqiqotning maqsadi *S. rochei* IMB/AN RUz shtammi kultura suyuqligi va biomassasining metanolli ekstraktlarida fenollar, flavonoidlar, alkaloidlar, steroidlar, taninlar, terpenoidlar va saponinlar mavjudligini sifat reaksiyalari yordamida dastlabki baholashdan iborat.

Material va metodlar

Tadqiqot obyekti – tuproqdan ajratilgan *S. rochei* IMB/AN RUz shtammi. Shtamm oat meal broth (suli bulyoni) muhitida 28 °C da, 150 ayl./daq. tezlikda sheyker-inkubatorda 7 kun davomida o‘stirildi. Kultura sentrifugalash yo‘li bilan kultura suyuqligi va biomassaga ajratildi; ularning har biri alohida metanol bilan ekstraksiya qilindi; ekstraktlar rotor-bug‘latgichda vakuum ostida 40 °C da quyuqlashtirildi va sifat reaksiyalari standart usullar orqali o‘tkazildi [4, 5].

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Fenol: ekstrakt namunasiga 1 ml steril distillangan suv va 1 ml 5% li $FeCl_3$ eritmasi qo‘shildi; to‘q yashil rang ijobiy natija hisoblandi.

Tanin: 30 mg ekstrakt 2 ml metanolda eritilib, 4000 ayl./daq. tezlikda 10 daqiqa sentrifugalandi; supernatantning 1 ml ga 15% li $FeCl_3$ qo‘shildi. Qoramtir-yashil yoki ko‘k-qora rang ijobiy natija hisoblandi.

Flavonoid: ekstraktning 2 ml (70–80%) eritmasiga NaOH qo‘shilib, sentrifugalandi (4000 ayl./daq., 10 daq.); supernatantga 1% li HCl qo‘shilganda sariq rangning asta-sekin yo‘qolishi ijobiy natija hisoblandi.

Alkaloid: 15 mg ekstrakt 1 ml (80%) erituvchida eritilib sentrifugalandi; supernatantga 1 ml 1% li HCl va 2 tomchi Vagner reaktivi qo‘shildi; qizg‘ish-jigarrang cho‘kma ijobiy natija hisoblandi.

Steroid (Salkovskiy reaksiyasi): 10 mg/ml ekstraktning 1 ml ga 500 mkl xloroform va 1 ml konsentrlangan H_2SO_4 qo‘shildi; qizg‘ish-jigarrang rang ijobiy natija hisoblandi.

Terpenoid: 50 mg ekstrakt 1 ml xloroformda eritilib quritildi, 1 ml 96% li H_2SO_4 qo‘shilib, 75 °C da 2 daqiqa isitildi; kulrang hosila ijobiy natija hisoblandi.

Saponin: ekstrakt namunasiga 2 ml distillangan suv qo‘shilib, 25 °C da vorteksda 30 soniya intensiv chayqatildi; barqaror ko‘pik hosil bo‘lishi ijobiy natija hisoblandi.

Natijalar va muhokama

O‘tkazilgan dastlabki fitokimyoviy skrining natijalari *S. rochei* IMB/AN RUz shtammining kultura suyuqligi va biomassa metanolli ekstraktlarida ikkilamchi metabolitlarning tarqalishi o‘ziga xos xarakterga ega ekanligini ko‘rsatdi. Kultura suyuqligi ekstraktida fenollar, flavonoidlar, alkaloidlar, steroidlar, taninlar va terpenoidlar mavjudligi qayd etildi. Biomassa ekstraktida esa flavonoidlar, alkaloidlar, steroidlar, taninlar va terpenoidlar aniqlangan bo‘lsa-da, fenollar va saponinlar guruhi qayd etilmadi (1-jadval).

1-jadval. *S. rochei* IMB/AN RUz shtammi metanolli ekstraktlarining fitokimyoviy skrining natijalari

Birikma guruhi	Test (reagent)	Kultura suyuqligi ekstrakti	Biomassa ekstrakti
Fenollar	$FeCl_3$	+	–
Flavonoidlar	NaOH, HCl	+	+
Alkaloidlar	Vagner reaktivi	+	+
Steroidlar	Salkovskiy (xloroform + H_2SO_4)	+	+
Taninlar	$FeCl_3$	+	+
Terpenoidlar	Xloroform + H_2SO_4	+	+
Saponinlar	Distillangan suv (ko‘pik testi)	–	–

Izoh: (+) – aniqlandi; (−) – aniqlanmadi.

Fenolli birikmalarning faqat kultura suyuqligida aniqlanishi *S. rochei* IMB/AN RUz shtammi ushbu metabolitlarni hujayra tashqarisiga (ekstrasellyulyar) ajratishini ko‘rsatadi. Ekstraktlarda flavonoidlar, alkaloidlar, steroidlar va terpenoidlarning mavjudligi shtammning antimikrob, sitotoksik va antifungal faollikka ega birikmalar manbasi bo‘lishi mumkinligidan dalolat beradi [1, 3]. Keyingi bosqichlarda ushbu birikmalarning kimyoviy tuzilishi va miqdorini aniqlash uchun YSSX hamda mass-spektrometrik tahlillarni o‘tkazish rejalashtirilgan.

Xulosa

Streptomyces rochei IMB/AN RUz shtammining kultura suyuqligi va biomassa ekstraktida flavonoidlar, alkaloidlar, steroidlar, taninlar va terpenoidlar guruhlari aniqlandi. Fenolli birikmalar

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faqat kultura suyuqligi ekstraktida aniqlangan bo‘lib, biomassa tarkibida ularning yo‘qligi shtammning ekstrasellyulyar ajratish xususiyatini ko‘rsatadi. Saponinlar guruhi esa o‘rganilgan har ikkala ekstraktda ham aniqlanmadi.

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METHYLOBACILLUS FLAGELLATUS БАКТЕРИЯ БИОМАССАСИДАГИ УМУМИЙ ОҚСИЛ МИҚДОРИНИ АНИҚЛАШ

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Аннотация: Ушбу тадқиқотда метилотроф бактерия *Methylobacillus flagellatus* Shd-N1 биомассасидаги умумий оқсил миқдорини Кьельдаль усули ёрдамида аниқлаш натижалари келтирилган. Таҳлил учун 1 г қуруқ биомасса олиниб, намунадаги азот миқдори ва азотни оқсилга айлантириш коэффициенти асосида умумий оқсил миқдори баҳоланди. Олинган натижалар мазкур бактерия биомассасининг оқсил манбаи сифатидаги истиқболини ўрганиш учун муҳим аҳамиятга эга.

Калит сўзлар: *Methylobacillus flagellatus*, метилотроф бактерия, микробиал биомасса, умумий оқсил, азот, Кьельдаль усули.

Аннотация: В настоящем исследовании представлены результаты определения общего содержания сырого белка в биомассе метилотрофной бактерии *Methylobacillus flagellatus* Shd-N1 методом Кьельдаля. Для анализа использовали 1 г сухой биомассы. Содержание общего сырого белка оценивали на основании количества азота в образце с применением коэффициента пересчёта азота на белок. Полученные результаты имеют важное значение для дальнейшего изучения перспектив использования биомассы данной бактерии в качестве источника белка.

Ключевые слова: *Methylobacillus flagellatus*, метилотрофные бактерии, микробная биомасса, общий белок, азот, метод Кьельдаля.

Abstract: This study presents the results of determining the total crude protein content in the biomass of the methylotrophic bacterium *Methylobacillus flagellatus* Shd-N1 using the Kjeldahl method. A 1 g sample of dry biomass was used for the analysis. The total crude protein content was estimated based on the nitrogen content of the sample using a nitrogen-to-protein conversion factor. The results are important for further investigation of the potential use of this bacterial biomass as a protein source.

Keywords: *Methylobacillus flagellatus*, methylotrophic bacteria, microbial biomass, total protein, nitrogen, Kjeldahl method.

Кириш

Бугунги кунда аҳолини оқсилга бой озиқ-овқат маҳсулотлари билан таъминлаш ва муқобил оқсил манбаларини яратиш биотехнологиянинг муҳим йўналишларидан бири ҳисобланади. Шу муносабат билан микроорганизмлар биомассасидан бир ҳужайрали оқсил олишга бўлган қизиқиш ортиб бормоқда. Бактериялар тез ўсиши, турли углерод манбаларидан фойдаланиш имконияти ва биомассада оқсилнинг юқори миқдорда тўпланиши билан аҳамиятлидир [1, 2]. Метилотроф бактериялар, жумладан, *Methylobacillus flagellatus*, метанолни углерод ва энергия манбаи сифатида ўзлаштира олиши билан ажралиб туради. Ушбу бактериянинг биомассаси таркиби ва озуқавий-технологик хусусиятлари замонавий

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тадқиқотларда ўрганилмоқда. Jia ва ҳаммуаллифлар [1] томонидан ўтказилган тадқиқотда *M. flagellatus* биомассасининг оқсил миқдори юқори эканлиги ва уни муқобил оқсил манбаи сифатида қўллаш имкониятлари кўрсатилган. Биомасса таркибидаги оқсил миқдорини аниқлаш штаммнинг биотехнологик салоҳиятини баҳолашда муҳим кўрсаткич ҳисобланади. Кьельдаль усули намунанинг умумий азот миқдорини аниқлашга асосланган бўлиб, олинган натижани тегишли коэффициентга кўпайтириш орқали умумий оқсил миқдори ҳисобланади [3].

Материаллар ва тадқиқот усуллари

Тадқиқот объекти сифатида *Methylobacillus flagellatus* Shd-N1 бактерия биомассасидан фойдаланилди. Таҳлил учун 1 г қуруқ биомасса олинди. Намунадаги умумий азот миқдори Кьельдаль усули ёрдамида аниқланган лаборатория натижаси асосида баҳоланди. Умумий оқсил миқдори азот миқдорини 6,25 коэффициентига кўпайтириш орқали ҳисобланади [4].

Умумий оқсил миқдори (%) = Азот миқдори (%) × 6,25.

Мазкур коэффициент оқсил таркибидаги азотнинг ўртача улушига асосланган бўлиб, Кьельдаль усулида аниқланган азот миқдорини хом оқсил кўрсаткичига айлантиришда қўлланилади. Шу билан бирга, ушбу усул оқсилга кирмайдиган азотли бирикмаларни ҳам ҳисобга олиши мумкин. Шу сабабли олинган натижа ҳақиқий оқсил миқдоридан фарқ қилиши эҳтимоли мавжуд [3].

Тадқиқот натижалари

Кьельдаль усулида олинган лаборатория маълумотларига кўра, *Methylobacillus flagellatus* Shd-N1 бактериясида умумий азот миқдори 11,96 % ни, умумий хом оқсил миқдори эса лаборатория натижасида 74,77 % ни ташкил этди (1-жадвал).

1-жадвал. *Methylobacillus flagellatus* биомассасидаги азот ва умумий оқсил миқдори

№	Намуналар	Азот миқдори (%)	Умумий оқсил миқдори (%)
1.	**Shd-N1**	11,96	74,77

Олинган натижа *Methylobacillus flagellatus* Shd-N1 бактерия қуруқ биомассасида умумий оқсил миқдори юқори эканлигини кўрсатади. Бу кўрсаткични *M. flagellatus* биомассаси бўйича олиб борилган замонавий тадқиқот натижалари билан таққослаш мумкин. Хусусан, Jia ва ҳаммуаллифлар [1] қайта ишланмаган *M. flagellatus* биомассасида оқсил миқдорини 73 % деб қайд этганлар. Ушбу натижа мазкур бактерия биомассасининг оқсил манбаи сифатидаги салоҳиятини қўллаб-қувватлайди.

Хулоса

Кьельдаль усулида олинган лаборатория натижалари асосида *Methylobacillus flagellatus* Shd-N1 бактериясининг азот миқдори 11,96 % эканлиги аниқланди. Лаборатория маълумотида умумий оқсил миқдори 74,77 % деб қайд этилган. Мазкур натижалар бактерия биомассасининг оқсил манбаи сифатидаги салоҳиятини кўрсатади.

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MORPHOLOGICAL, MICROSCOPIC, ENZYMATIC AND BIOCHEMICAL CHARACTERISTICS OF XANTHOMONAS ISOLATES ISOLATED FROM BRASSICA L

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Abstract: In this study, bacterial isolates belonging to the genus Xanthomonas were obtained from infected cabbage (Brassica L.) leaves and comparatively evaluated according to their morphological, microscopic, enzymatic and selected biochemical characteristics. YDC medium was used for isolation. The obtained X1, X2 and X3 isolates formed yellowish, convex, smooth-edged and mucoid colonies and showed a Gram-negative reaction. Enzymatic tests included starch and gelatin hydrolysis, proteolytic and lecithinase activities, citrate utilization and lipolytic activity. The results demonstrated differences in the level of enzymatic activity among the isolates and provided a basis for comparative selection of promising variants for subsequent biotechnological studies.

Keywords: Xanthomonas, Brassica L., bacterial isolate, morphology, enzymatic activity, biochemical characteristics, exopolysaccharide.

Introduction

Members of the genus Xanthomonas are Gram-negative bacteria closely associated with plants. In addition to causing diseases in agricultural crops, some representatives are of considerable biotechnological interest because of their ability to synthesize biologically active metabolites and extracellular polysaccharides, particularly xanthan gum. Xanthan produced by X. campestris is widely used in food, pharmaceutical, cosmetic and technical formulations because of its high viscosity, pseudoplastic behavior and stability over a broad range of pH and ionic conditions [1,2]. Therefore, isolation of local Xanthomonas strains, characterization of their phenotypic and enzymatic properties, and selection of promising variants for further biotechnological studies remain relevant. The aim of this work was to comparatively characterize the morphological, microscopic, enzymatic and biochemical properties of Xanthomonas isolates obtained from Brassica L. leaves.

Materials and methods

The objects of the study were bacterial isolates X1, X2 and X3 obtained from cabbage (Brassica L.) leaves showing signs of infection. YDC nutrient medium was used for isolation and colony characterization and contained, g/L: yeast extract, 10.0; sucrose, 20.0; $CaCO_3$, 20.0; and agar, 20.0. Colony color, elevation, margin, growth intensity and mucoid consistency were recorded. Microscopic characterization included Gram staining. Enzymatic and biochemical properties were assessed by tests for starch hydrolysis, gelatin hydrolysis, proteolytic activity, lecithinase activity, lipase activity and citrate utilization. Activity was evaluated according to the diameter of the reaction zones. Numerical values reported in the source experimental data are presented as mean ± deviation.

Results

The isolated X1, X2 and X3 cultures formed yellowish, convex, smooth-edged, profusely growing and mucoid colonies on YDC medium. Colony diameter was approximately 1–2 mm, and

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all isolates showed a Gram-negative reaction. The mucoid phenotype may be associated with extracellular polysaccharide production and is an important diagnostic feature of representatives of the genus Xanthomonas [1]. According to the source table, all three isolates were assigned to the phylum Pseudomonadota.

In enzymatic tests, all three isolates demonstrated the ability to hydrolyze starch, with an average hydrolysis zone of 6±1.0 mm. Gelatin hydrolysis produced an average zone of 5±1.0 mm in all isolates. In tests associated with proteolytic and lecithinase activities, isolate X2 produced a zone of up to 8±1.0 mm, whereas X1 and X3 formed relatively smaller zones. In the citrate-utilization test, values of 1 mm for X1, 7±1.0 mm for X2 and 11±1.0 mm for X3 were recorded. No detectable activity zone was observed for any of the three isolates in the lipase test.

Table 1. Morphological characteristics of the isolated bacterial strains

Strains	Colour	Texture	Margins of colony	Degree of growth	Nature	Gram staining	Size
X1	yellow	raised	smooth	profuse	viscous	-ve	Pseudomonadota
X2	yellow	raised	smooth	profuse	viscous	-ve	Pseudomonadota
X3	yellow	raised	smooth	profuse	viscous	-ve	Pseudomonadota

Discussion

The obtained results show that isolates X1, X2 and X3 were similar in their principal morphological characteristics but differed in several enzymatic properties. In particular, the relatively larger zone observed for X2 in the proteolytic/lecithinase tests and the stronger citrate-associated reaction of X3 indicate differences in the metabolic potential of the isolates. Such phenotypic variation may reflect strain-level physiological diversity. Enzymatic systems of Xanthomonas species are important both for interactions with plant tissues and for utilization of available nutrient sources [3]. At the same time, morphological and biochemical tests alone are insufficient for definitive species-level identification; therefore, promising isolates should subsequently be confirmed by molecular or proteomic methods such as MALDI-TOF MS or 16S rRNA gene sequencing. The present preliminary screening provides a basis for selecting isolates with promising potential for subsequent studies of xanthan production.

Conclusion

The bacterial isolates X1, X2 and X3 obtained from Brassica L. leaves were similar in forming yellowish, mucoid, convex colonies with smooth margins and in showing a Gram-negative reaction. Starch- and gelatin-degrading activities were detected in all isolates, whereas lipase activity was not observed. Differences among the isolates were recorded for selected enzymatic and biochemical parameters. The obtained data make it possible to comparatively evaluate Xanthomonas isolates and to select promising strains for further biotechnological investigation.

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ВЫДЕЛЕНИЕ И СКРИНИНГ ПРИРОДНЫХ ИЗОЛЯТОВ ДРОЖЖЕЙ ПО СПОСОБНОСТИ К ПРОДУКЦИИ L-АСПАРАГИНАЗЫ

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Аннотация: В данном исследовании из различных природных образцов Республики Узбекистан было выделено 146 изолятов дрожжевых культур, из которых 70 относились к пигментообразующим (красным) дрожжам, а 76 к непигментообразующим. Первичный скрининг бромтимолом синим показал, что среди пигментообразующих дрожжей наиболее высокой L-аспарагиназной способностью обладал 31 штамм, среди непигментообразующих дрожжей наиболее высокой L-аспарагиназной активностью отличались 4 штамма.
Ключевые слова: дрожжи, красные дрожжи, скрининг, L-аспарагиназа

Abstract: In this study, 146 yeast isolates were obtained from various natural samples collected in the Republic of Uzbekistan. Of these, 70 isolates belonged to pigment-producing (red) yeasts, while 76 were non-pigment-producing yeasts. Primary screening using bromothymol blue revealed that 31 strains of pigment-producing yeasts exhibited the highest L-asparaginase-producing potential, whereas 4 strains of non-pigment-producing yeasts demonstrated the highest L-asparaginase activity.
Keywords: yeasts, red yeasts, screening, L-asparaginase.

L-аспарагиназа (АС) применяется в качестве терапевтического средства при лечении некоторых гематологических злокачественных заболеваний, в частности острого лимфобластного лейкоза (ОЛЛ) [1]. Пролиферация лейкозных клеток при ОЛЛ в значительной степени зависит от доступности L-аспарагина (LA), циркулирующего в крови и поступающего в организм с пищей либо синтезируемого нормальными клетками [2]. Зависимость опухолевых клеток от внеклеточного LA обусловлена тем, что некоторые из них не экспрессируют аспарагинсинтетазу — фермент, катализирующий синтез LA из аспартата и глутамина, либо продуцируют его в недостаточном количестве для обеспечения потребностей клетки за счёт эндогенного синтеза LA [3, 4-6]. В связи с этим включение АС в клинические протоколы химиотерапии, особенно при лечении детского ОЛЛ, стало важным достижением в онкогематологии [3, 5, 7]. L-аспарагиназа катализирует гидролиз LA с образованием L-аспартата и аммиака, что приводит к снижению концентрации LA в сыворотке крови [4, 8, 9]. Поскольку LA необходим для синтеза белков и участвует в поддержании метаболических процессов, обеспечивающих рост и деление клеток, его дефицит ограничивает пролиферацию чувствительных лейкозных клеток и может индуцировать апоптоз [7, 9]. В пищевой промышленности АС используется для снижения содержания акриламида, образующегося при высокотемпературной обработке пищевых продуктов, а также может способствовать сохранению их органолептических характеристик и пищевой ценности [10]. В последние годы микробная АС привлекает значительное внимание исследователей благодаря широким возможностям её биотехнологического применения и перспективам промышленного производства. В настоящее время основными

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источниками АС, применяемой в медицинской практике, являются бактерии *Escherichia coli* и *Erwinia* spp. Однако использование ферментных препаратов бактериального происхождения может сопровождаться развитием нежелательных иммунологических реакций, включая гиперчувствительность, а также другими побочными эффектами, ограничивающими возможности длительной терапии [11]. В связи с этим актуальным направлением исследований является поиск альтернативных источников АС, в том числе среди эукариотических микроорганизмов.

Целью исследования является поиск, выделение и первичный скрининг природных изолятов дрожжей по способности к продукции L-аспарагиназы. Источником выделения дрожжевых культур являлись овощи, плоды, субстанция из бумажного цеха, пищевые продукты (сыр, кислое молоко, кимиз, сметана). Первичный скрининг бромтимолом синим показал, что среди пигментообразующих дрожжей наиболее высокой L-аспарагиназной способностью обладал 31 штамм, среди непигментообразующих дрожжей наиболее высокой L-аспарагиназной активностью отличались 4 штамма. На основании результатов идентификации методом MALDI-TOF MS установлено, что некоторые штаммы пигментообразующих дрожжей были отнесены к видам *Rhodotorula mucilaginosa*, *Geotrichum candidum*, *Candida lipolytica*, *Hanseniaspora uvarum*, *Kluyveromyces marxianus.* В результате исследования сформирована коллекция из 146 дрожжевых изолятов, выделенных из различных природных и пищевых субстратов, включающая 70 пигментообразующих (красных) и 76 непигментообразующих дрожжевых культур.

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ITS-BASED IDENTIFICATION AND PHYLOGENETIC CHARACTERIZATION OF ENDOPHYTIC *ALTERNARIA SP.* H8 ISOLATED FROM *HELICHRYSUM MUSSAE*

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Abstract: An endophytic fungal isolate, H8, recovered from *Helichrysum mussae*, was investigated using internal transcribed spacer (ITS) sequence analysis to clarify its taxonomic placement. A quality-trimmed, 544-bp reverse-strand ITS read was compared with reference sequences of five *Alternaria* type strains. Phylogenetic analysis placed H8 within the genus *Alternaria*. The isolate matched the *A. destruens* type strain across 521 aligned positions and shared 99.4–99.8% sequence identity with four additional species. Because the ITS region showed limited variation among the reference taxa, these findings support identification at the genus level but do not establish a definitive species assignment. Additional multilocus sequencing is required for species-level resolution.

Keywords: endophytic fungi; *Helichrysum mussae*; *Alternaria*; ITS sequencing; fungal identification; phylogenetic analysis.

Introduction

Endophytic fungi colonize internal tissues of apparently healthy plants and represent a valuable resource for exploring fungal diversity and specialized metabolism. Accurate taxonomic characterization is essential before assessing their biological activities or biotechnological applications. Although the internal transcribed spacer (ITS) region is widely used as a fungal DNA barcode, closely related species may share highly similar ITS sequences. This study aimed to determine the phylogenetic position of fungal isolate H8 obtained from *Helichrysum mussae* and to evaluate the taxonomic resolution provided by its ITS sequence.

Materials and Methods

A single reverse-strand ITS sequence of 544 bp was obtained from isolate H8 after quality trimming (mean Phred score: 34). The sequence was aligned with ITS reference sequences from five *Alternaria* type strains: *A. destruens* (NR_137143.1), *A. alstroemeriae* (NR_163686.1), *A. doliconidium* (NR_158361.1), *A. tectorum* (NR_187081.1), and *A. eichhorniae* (NR_111832.1). Pseudophaeosphaeria rubi (NR_154351.1) served as the outgroup. Four ambiguous nucleotide calls were treated as compatible with their corresponding aligned reference bases. Sequence similarity and phylogenetic placement were evaluated using the aligned ITS region.

Results

The ITS-based phylogenetic analysis positioned isolate H8 within *Alternaria* (Figure 1). The sequence was identical to that of the *A. destruens* type strain across 521 aligned positions. Comparisons with *A. alstroemeriae* and *A. doliconidium* each revealed one difference (99.8%

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identity), whereas *A. tectorum* and *A. eichhorniae* differed at two (99.6%) and three (99.4%) positions, respectively. The outgroup showed 17.9% sequence divergence.

Discussion

The close ITS similarity between H8 and multiple *Alternaria* type strains indicates that this marker alone cannot reliably discriminate among the examined species. Differences relative to *A. alstroemeriae*, *A. doliconidium*, and *A. tectorum* involved single-base length variants in adenine-rich regions, while *A. eichhorniae* showed two additional substitutions. Consequently, the proximity of H8 to *A. destruens* in the phylogenetic tree should not be interpreted as conclusive evidence of species identity. Analysis of additional loci, including GAPDH, RPB2, and TEF1, would provide greater taxonomic resolution.

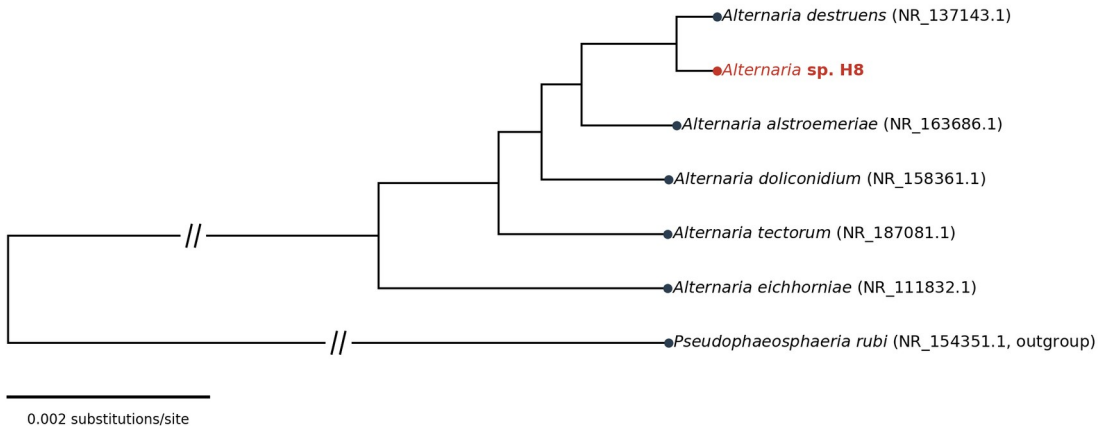


Figure 1. ITS-based phylogenetic tree showing the placement of *Alternaria sp.* H8 (red) among *Alternaria* type strains, with *Pseudophaeosphaeria rubi* as the outgroup. Truncated basal branches are indicated by //. Scale bar: 0.002 substitutions per site

Conclusion

ITS sequence comparisons support assignment of the endophytic isolate H8 to the genus *Alternaria*. However, the limited sequence divergence among closely related reference species prevents confident species-level identification. The isolate should therefore be designated *Alternaria sp.* H8 pending multilocus confirmation.

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ВЛИЯНИЕ ЭПИГЕНЕТИЧЕСКИХ МОДИФИКАТОРОВ НА ВТОРИЧНЫЙ МЕТАБОЛИЗМ И УРЕАЗОИНГИБИРУЮЩУЮ АКТИВНОСТЬ ЭНДОФИТНЫХ ГРИБОВ *ASPERGILLUS SYDOWII* AV5L И *PENICILLIUM VERRUCOSUM* AV6L

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Аннотация: В данном исследовании изучено влияние эпигенетических модификаторов на индукцию биосинтетических путей вторичных метаболитов эндофитных грибов *Aspergillus sydowii* AV5L и *Penicillium verrucosum* AV6L. В работе были использованы такие модификаторы, как вальпроат натрия, 5-азацитидин и кверцетин. При обработке эндофитных грибов данными модификаторами наблюдались увеличение выхода биомассы, изменение цвета культур и синтез метаболитов с умеренной уреазоингибирующей активностью. Наблюдаемые изменения зависели от концентрации модификатора и штамма.
Ключевые слова: эпигенетические модификаторы, вальпроат натрия, 5-азацитидин, кверцетин

Annotatsiya: Ushbu tadqiqotda epigenetik modifikatorlarning endofit zamburug‘lari *Aspergillus sydowii* AV5L va *Penicillium verrucosum* AV6L ikkilamchi metabolitlari biosintetik yo‘llari induksiyasiga ta’siri o‘rganildi. Tadqiqotda natriy valproat, 5-Azatsitidin va kversetin kabi modifikatorlardan foydalanildi. Endofit zamburug‘lariga ushbu modifikatorlar bilan ishlov berilganda biomassa unumining ortishi, kulturalar rangining o‘zgarishi hamda antiureaza faolligiga ega bo‘lgan yangi metabolitlar sintezi kuzatildi. Kuzatilgan o‘zgarishlar modifikator konsentratsiyasiga va shtammga bog‘liq ekanligi aniqlandi.
Kalit so‘zlar: epigenetik modifikatorlar, natriy valproat, 5-Azatsitidin, kversetin

Abstract: This study examined the effect of epigenetic modifiers on the induction of biosynthetic pathways of secondary metabolites in the endophytic fungi *Aspergillus sydowii* AV5L and *Penicillium verrucosum* AV6L. Sodium valproate, 5-Azacitidine and quercetin were used as modifiers. Treatment of the endophytic fungi with these modifiers resulted in increased biomass yield, changes in culture color and the synthesis of new metabolites with moderate anti-urease activity. The observed changes depended on the concentration of modifiers and on the strain.
Keywords: epigenetic modifiers, sodium valproate, 5-Azacitidine, quercetin

Введение

Эндофитные грибы, бессимптомно колонизирующие ткани растений, способны синтезировать широкий спектр вторичных метаболитов, которые обладают противовоспалительными, антиоксидантными, противоопухолевыми, а также фермент-ингибирующими свойствами. В связи с этим эндофитные грибы все чаще рассматриваются как перспективный источник биологически активных природных соединений для разработки лекарственных препаратов. [1] Актуальным направлением является поиск вторичных метаболитов, ингибирующих уреазу, повышенная активность которой связана с патогенезом язвенной болезни желудка, мочекаменной болезни, а также инфекцией мочевыводящих путей.

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Вахабова Н., Рузиева Д., Йулдошева М. Влияние эпигенетических модификаторов на вторичный метаболизм и уреазоингибирующую активность эндофитных грибов Aspergillus sydowii AV5L и Penicillium verrucosum AV6L // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 200–202.
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[2] Эндофитные грибы, как продуценты биоактивных соединений, обладают рядом преимуществ перед лекарственными средствами растительного происхождения. Они быстро растут, культивируются в контролируемых условиях и подходят для крупномасштабной ферментации, что позволяет осуществлять непрерывное производство. [3] Однако эндофитные грибы не всегда способны реализовать свой биосинтетический потенциал в аксенических культурах, поскольку отсутствие естественных биотических взаимодействий и сигналов растения-хозяина может приводить к снижению продукции некоторых вторичных метаболитов, так как часть биосинтетических генных кластеров в условиях in vitro остаются неактивными, скрытыми и слабоэкспрессируемыми. Эти слабоактивные генные кластеры могут быть экспрессированы с помощью культивационных и молекулярных методов, среди которых особое место занимает эпигенетическая регуляция, воздействующая на структуру хроматина с помощью ингибиторов HDAC (ингибиторы гистондеацетилазы) и ингибиторов DNMT (ингибиторы ДНК-метилтрансферазы). [4]

Материалы и методы

Объектами наших исследований были эндофитные грибы *Aspergillus sydowii strain* AV5L и *Penicillium verrucosum* AV6L, выделенные из листьев и корней растения *Aloe vera*, произрастающего в условиях защищенного грунта в г. Ташкенте. Культивирование выделенных эндофитов проводили методом глубинной ферментации на картофельно-декстрозной среде. Для изучения влияния эпигенетических модификаторов на биосинтез вторичных метаболитов эндофитных грибов использовали вальпроат натрия, 5-Азацитидин и кверцетин в различных концентрациях. Исследования проводили согласно Magotra et al. с некоторыми модификациями. [5] Ингибирование уреазы измеряли по методу Weatherburn, 1967.[6]

Результаты и обсуждение

Результаты исследования показали, что воздействие вальпроата натрия, 5-Азацитидина и кверцетина сопровождалось изменениями роста биомассы, изменением цвета питательной среды, продукцией вторичных метаболитов с уреазоингибирующей активностью эндофитных грибов *A. sydowii strain* AV5L и *P. verrucosum* AV6L. Однако характер экспрессии существенно зависел как от природы модификатора, так и от особенностей исследуемого штамма. Так, при добавлении 5-Азацитидина наблюдалось увеличение выхода вторичных метаболитов у *A. sydowii strain* AV5L, тогда как аналогичный эффект наблюдался у *P. verrucosum* AV6L при обработке вальпроатом натрия. В обоих случаях вторичные метаболиты проявляли умеренную уреазоингибирующую активность по сравнению с контролем. При добавлении кверцетина в питательную среду наблюдалось незначительное повышение продукции вторичных метаболитов, уреазоингибирующая активность которых также была ниже по сравнению с контролем.

Выводы

Обработка эндофитных грибов такими эпигенетическими модификаторами, как ингибиторы гистондеацетилазы и ингибиторы ДНК-метилтрансферазы может быть перспективным подходом для запуска биосинтетических путей биоактивных метаболитов эндофитных грибов, находящихся в состоянии покоя в лабораторных условиях.

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IDENTIFICATION AND PHYLOGENETIC PLACEMENT OF AN ENDOPHYTIC *ALTERNARIA* ISOLATE D15 FROM *FERULA KHUSTANICA*

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Abstract: An endophytic fungal isolate, D15, recovered from *Ferula khustanica* (Apiaceae), was investigated to establish its taxonomic placement using internal transcribed spacer (ITS) sequencing. A 582-base reverse-strand Sanger read was compared with reference sequences from five Alternaria type strains, and a UPGMA phylogenetic tree was constructed. The isolate clustered within Alternaria and showed 99.2–99.8% sequence identity to the examined type strains. However, the low ITS divergence among these reference species prevents a reliable species-level assignment. The isolate is therefore designated Alternaria sp. D15 pending multilocus characterization.

Keywords: *Alternaria*; *Ferula khustanica*; endophytic fungi; ITS sequencing; molecular identification; phylogenetic analysis.

Introduction

Endophytic fungi colonize internal plant tissues and may represent valuable sources of structurally diverse secondary metabolites. Accurate taxonomic identification is essential before their biological and biosynthetic potential can be evaluated. The internal transcribed spacer (ITS) region is widely used as a fungal DNA barcode, although its resolution varies among taxonomic groups. This study aimed to determine the phylogenetic position of fungal isolate D15 obtained from Ferula khustanica and to assess whether the available ITS sequence supports identification at the species level.

Materials and Methods

The ITS region of isolate D15 was analyzed using a 582-base reverse-strand Sanger sequencing read spanning the ITS4–ITS5 region. The sequence was compared by semi-global alignment with ITS sequences of five *Alternaria* type strains retrieved from the NCBI RefSeq targeted-loci database: *A. destruens* (NR_137143.1), *A. alstroemeriae* (NR_163686.1), *A. doliconidium* (NR_158361.1), *A. tectorum* (NR_187081.1), and *A. eichhorniae* (NR_111832.1). *Pseudophaeosphaeria rubi* (NR_154351.1) was used as an outgroup. A UPGMA tree was reconstructed using pairwise p-distances.

Results

Phylogenetic analysis placed isolate D15 within the genus *Alternaria* (Figure 1). Its ITS sequence differed from *A. destruens* at 1 of 521 aligned positions (99.8% identity), from *A. alstroemeriae* and *A. doliconidium* at 2 of 530 and 2 of 529 positions, respectively (99.6%), from *A. tectorum* at 3 of 520 positions (99.4%), and from *A. eichhorniae* at 4 of 521 positions (99.2%). The outgroup exhibited 17.6% sequence divergence. The five *Alternaria* type strains differed from one another by only 0.2–0.8% in the analyzed region.

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Discussion

The close similarity of the examined ITS sequences supports assignment of D15 to *Alternaria* but does not allow confident discrimination among the reference species. Although *A. destruens* showed the highest sequence identity, this observation alone is insufficient to identify D15 as that species. Additional sequence data from more informative loci, such as GAPDH, RPB2, and TEF1, are needed for a robust species-level determination.

Conclusion

ITS sequencing and phylogenetic analysis identified D15 as a member of the genus *Alternaria*. Given the limited discriminatory power of the available ITS region, the isolate should be reported as *Alternaria* sp. D15 until multilocus analysis provides a more precise taxonomic assignment.

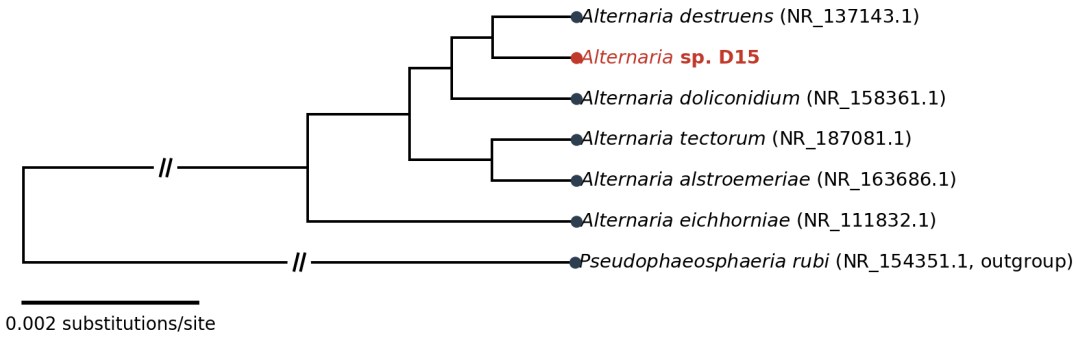


Figure 1. UPGMA tree based on ITS sequences showing the placement of *Alternaria sp*. D15 (red) relative to five *Alternaria* type strains, with *Pseudophaeosphaeria rubi* as the outgroup. Basal branches are truncated (//)

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IDENTIFICATION AND PHYLOGENETIC PLACEMENT OF THE FUNGAL ISOLATE S14 FROM *SILYBUM MARIANUM* WITHIN *ASPERGILLUS* SECTION *NIGRI*

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Abstract: Endophytic fungal isolate S14 from *Silybum marianum* was examined using a 340-bp ITS sequence and compared with reference sequences of *Aspergillus* section Nigri type strains. Phylogenetic analysis placed S14 within section *Nigri*, with 98.5% sequence identity to five closely related type strains. Because the analyzed ITS region did not discriminate among these species, the isolate was designated *Aspergillus sp*. (section Nigri) S14 pending confirmatory sequencing and analysis of additional loci.

Keywords: *Silybum marianum*; endophytic fungi; *Aspergillus* section Nigri; ITS sequencing; phylogenetic analysis; fungal identification.

Introduction

Endophytic fungi inhabit healthy plant tissues without causing visible symptoms and are an established source of structurally diverse secondary metabolites. Medicinal plants such as *Silybum marianum* (milk thistle), known for silymarin, are attractive hosts for bioprospecting. Reliable isolate identification is a prerequisite for such investigations. The internal transcribed spacer (ITS) region is the standard first-line fungal DNA barcode. This study aimed to identify isolate S14 recovered from *S. marianum* using ITS sequence analysis and to assess whether the available barcode supports species-level identification.

Materials and Methods

A single ITS4-primed sequence read of 340 bp, spanning the 5.8S rRNA gene and adjacent ITS regions, was obtained from isolate S14. The sequence was compared with six *Aspergillus* section *Nigri* type-strain sequences from the NCBI RefSeq targeted-loci database: *A. niger* (NR_111348.1), *A. tubingensis* (NR_131293.1), *A. luchuensis* (NR_135449.1), *A. costaricensis* (NR_103604.1), *A. foetidus* (NR_163668.1), and *A. hubkae* (NR_200571.1). *Aspergillus flavus* (NR_111041.1; section Flavi) served as an outgroup. Phylogenetic relationships were visualized using a UPGMA tree.

Results

Isolate S14 clustered within *Aspergillus* section *Nigri* (Figure 1). It differed from the type strains of *A. niger*, *A. tubingensis*, *A. luchuensis*, *A. costaricensis*, and *A. foetidus* at five of 341 alignment positions (98.5% identity), and from *A. hubkae* at ten of 343 positions (97.1% identity). Divergence from the *A. flavus* outgroup was 7.5%. The five closest reference sequences were identical throughout the analyzed window, whereas *A. hubkae* differed from them at five positions.

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Discussion

The short ITS window cannot distinguish the five closest species. All five observed differences between S14 and its nearest references occurred in G/C-rich tracts, consisting of three single-nucleotide insertions or deletions and one adjacent GC/CG exchange. These differences may arise from base-calling uncertainty in a single sequence read and should not be interpreted as species-specific markers without sequencing the opposite strand. Further analysis of calmodulin and β-tubulin loci is needed to resolve the isolate at species level.

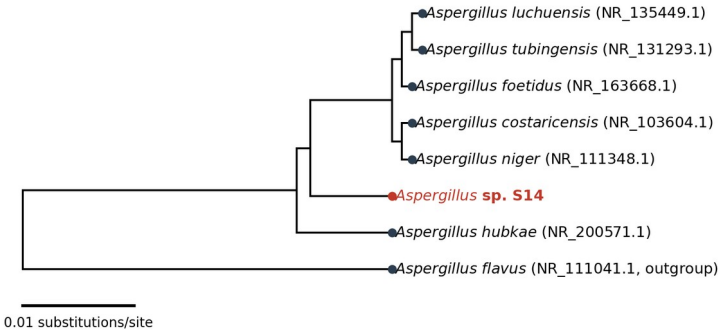


Figure 1. UPGMA tree of the ITS region (340-bp window) placing *Aspergillus sp*. S14 (red) among *Aspergillus* section *Nigri* type strains; *A. flavus* (section Flavi) is the outgroup. Scale bar: 0.01 substitutions per site

Conclusion

The available ITS sequence supports assignment of isolate S14 to *Aspergillus* section *Nigri* but does not permit reliable species-level identification. Until complementary sequence data and additional genetic markers become available, the isolate should be designated *Aspergillus sp*. (section Nigri) S14.

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LAMINARIA QO‘NG‘IR SUV O‘TI ASOSIDA GIDROGEL BIOBOG‘LAM YARATISH

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Annotatsiya: Ushbu tezisda Laminaria qo‘ng‘ir suv o‘ti tarkibidagi natriy alginat polisaxaridi va kalsiy xlorid (CaCl2) o‘zaro ta’siri asosida gidrogel biobog‘lamlar olish texnologiyasi o‘rganilgan. Tadqiqotda gidrogelning struktura hosil qilish sharoitlari, fizik-kimyoviy parametrlari, suv yutish hamda uzoq muddat namlik saqlash xususiyatlari tahlil qilingan. Olingan gidrogellarning jarohat bitishini tezlashtirish va dori vositalarining yaxshi so‘rilish samaradorligi baholangan. Eksperiment natijalari ushbu biomaterialning regenerativ tibbiyot va farmatsevtikada ekologik xavfsiz va yuqori samarali biobog‘lam sifatida qo‘llanilish istiqbollarini asoslab bergan.

Kalit so‘zlar: alginat, gidrogel, kalsiy xlorid, biomaterial, tashuvchi, farmatsevtik texnologiya, regenerativ tibbiyot, nanobiotexnologiya.

Kirish

Bugungi kunda tibbiyot va farmatsevtika sohalarida qo‘llaniladigan, biologik xavfsiz, atrof-muhitga zarar yetkazmaydigan ekologik toza biomateriallarga bo‘lgan ehtiyoj ortib bormoqda. Ayniqsa, yaralarning bitishini tezlashtirish va dori moddalarini samarali yetkazib berish muammolari zamonaviy biotexnologiyaning dolzarb yo‘nalishlaridan biri hisoblanadi. Ko‘pgina hollarda an’anaviy bog‘lov materiallari jarohat yuzasiga yopishib qolishi hamda o‘zida yetarli darajada namlikni saqlay olmasligi sababli yaraning bitishini qiyinlashtiradi va ushbu jarayon ko‘p vaqt talab etadi. Shu sababli, zamon talablariga javob beradigan, farmatsevtika va tibbiyotda qo‘llaniladigan antibakterial biotashuvchi bog‘lamlarni yaratish bo‘yicha ilmiy izlanishlar olib borish dolzarb masala hisoblanadi. Ta’kidlash joizki, hozirda turli polimerlar asosida biobog‘lamlar yaratilgan bo‘lib, ular orasida suv o‘tlari asosida xorijiy mamlakatlarda ishlab chiqilgan biobog‘lamlar alohida o‘rin egallaydi. Ushbu biobog‘lamlar biologik xavfsizligi va tez parchalanib, ekologiyaga zarar yetkazmasligi bilan ajralib turadi. Shu sababli, ushbu ishda asosiy e’tibor Laminaria suv o‘tiga qaratildi. Laminaria suv o‘tining asosiy strukturaviy komponenti natriy alginat bo‘lib, ushbu modda tabiiy polisaxarid hisoblanadi va mustahkam gidrogel hosil qilishda polimer karkas vazifasini bajaradi. Shu sababli, Laminaria asosida alginatli polimer to‘r tashuvchilarni yaratish muhim ahamiyatga ega.

Tadqiqot metodlari

Laminaria qo‘ng‘ir suv o‘tidan olingan natriy alginat asosida gidrogel polimer to‘rini sintez qilish va uning xususiyatlarini baholashda quyidagi zamonaviy farmatsevtik va fizik-kimyoviy metodikalardan foydalanildi:

Gidrogel sintezi va ionli tikilish (Cross-linking). Alginatli polimer to‘r hosil qilish Flory P.J. klassik polimer tarmoqlari nazariyasi hamda Grant G.T. tomonidan tavsiya etilgan “Egg-box” modeli asosida amalga oshirildi. Bunda natriy alginatning suvli eritmasiga ionli bog‘lovchi agent sifatida kalsiy xlorid (CaCl2) eritmasi diffuzion usulda kiritildi.

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Gidrofob va gidrofil xususiyatlarni baholash. Gidrogelning suv yutish kinetikasi va shishish darajasi Peppas N.A. uslubiyati bo‘yicha, og‘irlik (gravimetrik) o‘lchov analizi yordamida 37°C haroratda fosfat bufer eritmasida (pH=7.4) aniqlandi.

G‘ovaklilik va morfologik tahlil. Gidrogelning ichki mikrotuzilishi, g‘ovak o‘lchamlari va karkas tuzilishi skanerlovchi elektron mikroskopiya (SEM) va struktura tahlili metodlari yordamida o‘rganildi.

Statistik tahlil. Tajriba natijalarini statistik qayta ishlash va dispersion tahlil qilish Student t-kriteriysi hamda Fisher (ANOVA) usullari yordamida, $p < 0.05$ ishonchlilik darajasida amalga oshirildi.

Olingan natijalar va ularning tahlili

Olib borilgan laboratoriya tajribalarida tibbiyot uchun qo‘llash mumkin bo‘lgan biobog‘lam yaratishning optimal sharoitlari o‘rganildi. Bunda dastlab suv o‘tining quruq ekstrakti sochuluvchan kukuni tayyorlandi. So‘ngra alginatli kukun eritmasining turli miqdordagi (1,0%, 1,5%, 2,0%, 2,5%, 3,0%) eritmalari tayyorlandi. Shu bilan birga biobog‘lam hosil qilishda biobog‘lovchi vazifasini o‘ynaydigan komponent CaCl2 ning optimal konsentratsiyasi ham aniqlandi. Ushbu tadqiqotda biobog‘lam hosil qilishda muhim ahamiyatga ega komponentlardan biri bo‘lganligi uchun, bog‘lovchi vosita sifatida ishlatilayotgan CaCl2 ning ham turli konsentratsiyalari, jumladan 0,5%, 1,0%, 1,5%, 2,0% eritmalari tayyorlandi. Ushbu komponentlar asosida sintez jarayoni amalga oshirilib, gidrogel ko‘rinishidagi biobog‘lam olindi. Bu jarayon 2,5% alginat eritmasida va bog‘lovchi vazifasini bajaruvchi CaCl2 ning 1,0% eritmasi qo‘llanilganda muvaffaqiyatli amalga oshdi. Tadqiqot natijalariga ko‘ra, olingan gidrogellar eng yuqori mexanik barqarorlik va elastiklik ko‘rsatkichlarini ham namoyon etdi.

Gidrogelning shishish darajasini tahlil qilish natijalari shuni ko‘rsatdiki, optimal tarkibli biobog‘lam o‘z quruq vazniga nisbatan 600–850% gacha suvli muhitni yutish va uni 48 soat davomida barqaror saqlash qobiliyatiga ega. Bu ko‘rsatkich jarohat yuzasidagi ortiqcha ekssudatni so‘rib olish va jarohat bitishi uchun zarur bo‘lgan nam mikromuhitni barqaror ushlab turish imkonini beradi.

Laminaria tarkibidagi tabiiy kollagen, aminokislotalar va vitaminlar majmuasi gidrogel tarkibida saqlanib qolganligi sababli, biomaterial teri fibroblastlari regeneratsiyasini va hujayralar proliferatsiyasini an’anaviy bog‘lamlarga qaraganda 1.5–2.0 barobargacha tezlashtirishi aniqlandi. Bu xususiyat jarohat ustida patogen mikroorganizmlardan himoya qiluvchi to‘siq hosil qiladi.

Xulosa

Olib borilgan tadqiqotlar natijasida Laminaria qo‘ng‘ir suv o‘ti natriy alginati asosida yuqori elastiklik va biomexanik barqarorlikka ega bo‘lgan gidrogel biobog‘lamlar muvaffaqiyatli sintez qilindi. Aniq dalillar shuni ko‘rsatdiki, biobog‘lam o‘zining yuqori ekssudat yutish xususiyati tufayli yaralarni davolashda mukammal muhit yaratadi. Ushbu ekologik xavfsiz va biologik parchalanuvchan gidrogellar kelgusida jarrohlik, regenerativ tibbiyot va nanobiotexnologiyada dori yetkazib beruvchi intellektual tizimlar sifatida qo‘llanilishi uchun mustahkam ilmiy asos bo‘lib xizmat qiladi.

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ГЕНОМНЫЕ И МОЛЕКУЛЯРНО-БИОТЕХНОЛОГИЧЕСКИЕ ПЕРСПЕКТИВЫ ИЗУЧЕНИЯ LAGOCHILUS INEBRIANS BUNGE

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Аннотация: На основе литературных данных рассмотрены перспективы геномного и молекулярно-биотехнологического изучения Lagochilus inebrians Bunge. Приоритетными задачами являются поиск генов биосинтеза лагохилина, разработка молекулярных маркеров и оценка генетического разнообразия природных популяций.
Ключевые слова: Lagochilus inebrians, геном, лагохилин, молекулярные маркеры, дитерпеноиды, биотехнология.

Annotatsiya: Adabiyot ma’lumotlari asosida Lagochilus inebrians Bunge turini genomik va molekulyar-biotexnologik o‘rganish istiqbollari ko‘rib chiqildi. Lagochilin biosintezi genlarini aniqlash, molekulyar markerlar yaratish va tabiiy populyatsiyalarning genetik xilma-xilligini baholash ustuvor yo‘nalishlar sifatida belgilandi.
Kalit so‘zlar: Lagochilus inebrians, genom, lagochilin, molekulyar markerlar, diterpenoidlar, biotexnologiya.

Abstract: Literature data were analyzed to assess genomic and molecular-biotechnological prospects for Lagochilus inebrians Bunge. Priority tasks include identification of genes involved in lagochilin biosynthesis, development of molecular markers, and assessment of genetic diversity in natural populations.
Keywords: Lagochilus inebrians, genome, lagochilin, molecular markers, diterpenoids, biotechnology.

Введение

L. inebrians - лекарственное растение семейства Lamiaceae, распространённое в Центральной Азии. Его фармакологическая ценность связана с комплексом вторичных метаболитов, среди которых особое место занимает дитерпеноид лагохилин [1]. При этом молекулярно-генетические механизмы формирования ценных метаболитов изучены значительно слабее их химического и фармакологического профиля.

Материалы и методы

В качестве материала использовали опубликованные сведения о L. inebrians, относящиеся к его химическому составу, культивированию in vitro и перспективам молекулярного исследования. Источники анализировали по трём взаимосвязанным блокам: характеристика вторичных метаболитов, изучение ферментативных звеньев биосинтеза дитерпеноидов и применение ДНК-маркеров для характеристики растительного материала [1-3].

ДЛЯ ЦИТИРОВАНИЯ
Бакеев Р.С. Геномные и молекулярно-биотехнологические перспективы изучения Lagochilus inebrians Bunge // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 210–211.
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Результаты

Сопоставление публикаций позволяет выделить последовательную схему дальнейших исследований вида. На первом этапе целесообразно получить геномные и транскриптомные данные, после чего проводить поиск генов-кандидатов, связанных с формированием дитерпеноидного профиля. Особый интерес представляют ферменты, участвующие в циклизации и последующей модификации терпеновых предшественников [2]. Параллельно ДНК-маркеры могут применяться для различения генотипов и оценки разнообразия природного материала. Культура in vitro, уже апробированная для L. inebrians, создаёт удобную контролируемую систему для последующего сопоставления генотипа, морфогенетического ответа и биохимических признаков [3, 4].

Обсуждение

Научная ценность такого подхода состоит не в отдельном применении каждого метода, а в объединении результатов. Связь генетических различий с химическим профилем и поведением эксплантов in vitro может дать более содержательную характеристику перспективных форм L. inebrians и одновременно повысить обоснованность мероприятий по сохранению его генетических ресурсов.

Заключение

Таким образом, для L. inebrians целесообразна комплексная стратегия, объединяющая получение геномных данных, исследование генов, потенциально связанных с образованием лагохилина, маркерную характеристику растительного материала и культуру in vitro. Такая последовательность работ позволит одновременно решать задачи идентификации, изучения биосинтеза и сохранения ценного лекарственного вида.

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БИОЛОГИЧЕСКИ АКТИВНЫЕ СОЕДИНЕНИЯ LAGOCHILUS INEBRIANS BUNGE КАК ОСНОВА ФАРМАЦЕВТИЧЕСКОЙ БИОТЕХНОЛОГИИ

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Аннотация: Проведён анализ данных о биологически активных соединениях Lagochilus inebrians Bunge и возможностях их использования в фармацевтической биотехнологии. Особое внимание уделено лагохилину, полифенольным соединениям и перспективе получения стандартизированного растительного материала в культуре in vitro.
Ключевые слова: Lagochilus inebrians, лагохилин, биологически активные соединения, фармацевтическая биотехнология, in vitro.

Annotatsiya: Lagochilus inebrians Bunge tarkibidagi biologik faol birikmalar va ularni farmatsevtik biotexnologiyada qo‘llash imkoniyatlari tahlil qilindi. Lagochilin, polifenol birikmalar hamda in vitro kulturada standartlashtirilgan o‘simlik materialini olish istiqbollariga alohida e’tibor qaratildi.
Kalit so‘zlar: Lagochilus inebrians, lagochilin, biologik faol birikmalar, farmatsevtik biotexnologiya, in vitro.

Abstract: Data on biologically active compounds of Lagochilus inebrians Bunge and their potential use in pharmaceutical biotechnology were analyzed. Particular attention was paid to lagochilin, polyphenolic compounds, and prospects for obtaining standardized plant material through in vitro culture.
Keywords: Lagochilus inebrians, lagochilin, biologically active compounds, pharmaceutical biotechnology, in vitro.

Введение

L. inebrians традиционно рассматривается как ценное лекарственное растение Центральной Азии. Фитохимические исследования выявили дитерпеноиды, флавоноиды, фенольные соединения и другие метаболиты, определяющие интерес к виду [1, 2]. Ограниченность природных ресурсов усиливает необходимость контролируемого получения и стандартизации растительного материала.

Материалы и методы

Для анализа отобраны публикации, характеризующие химический состав L. inebrians, действие отдельных групп его метаболитов и возможности получения растительного материала в условиях in vitro. Сведения систематизировали по трём позициям: состав целевых соединений, подтверждённые виды биологической активности и перспективы биотехнологического получения воспроизводимой растительной биомассы [1-5].

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Бакеев Р.С. Биологически активные соединения Lagochilus inebrians Bunge как основа фармацевтической биотехнологии // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 212–213.
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Результаты

Систематизация данных подтверждает особую роль лагохилина в фитохимической характеристике L. inebrians [1, 2]. Вместе с ним значение имеют полифенольные и другие соединения, формирующие совокупный биологический профиль растения. В литературе представлены данные о гемостатическом действии препаратов вида [3] и антиоксидантной активности полифенольной фракции [4]. Отдельное практическое значение имеет возможность размножения L. inebrians в культуре in vitro [5]: контролируемое получение регенерантов создаёт исходную платформу для последующего сравнения биомассы по содержанию целевых метаболитов.

Обсуждение

С точки зрения фармацевтической биотехнологии одной только высокой скорости размножения недостаточно. Биомассу, полученную in vitro, необходимо оценивать одновременно по морфогенетическим и фитохимическим показателям. Сравнение содержания лагохилина и сопутствующих соединений между вариантами культивирования позволит определить, сохраняет ли регенерированный материал требуемые химические характеристики и какие условия наиболее перспективны для дальнейшей стандартизации.

Заключение

Следовательно, практическая перспектива L. inebrians связана с объединением микроклонального размножения и контроля вторичных метаболитов. Такой подход позволит оценивать качество получаемого растительного материала не только по росту и регенерации, но и по сохранению фармакологически значимого химического профиля, одновременно уменьшая потребность в заготовке сырья из природных популяций.

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III

BO‘LIM · SECTION · СЕКЦИЯ

PROBIOTIKLAR, OZIQ-OVQAT VA FARMATSEVTIK MIKROBIOLOGIYA

Probiotics, Food and Pharmaceutical Microbiology

Пробиотики, пищевая и фармацевтическая микробиология



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СОВРЕМЕННЫЕ ПРЕДСТАВЛЕНИЯ ОБ АНТАГОНИСТИЧЕСКОЙ АКТИВНОСТИ LACTIPLANTIBACILLUS PLANTARUM ПРОТИВ ПАТОГЕННЫХ МИКРООРГАНИЗМОВ

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Аннотация: Обзор посвящен анализу механизмов антагонистической активности штаммов *Lactiplantibacillus plantarum* и их метаболитов против пищевых патогенов *Vibrio parahaemolyticus* и *Listeria monocytogenes*. В работе описаны методы прямого клеточного вытеснения, влияние на поверхностные свойства, подвижность и блокирование системы Quorum Sensing (AI-2). Рассмотрены процессы разрушения биопленок, подавление экспрессии генов вирулентности, а также влияние метаболитов на проницаемость мембран и метаболизм патогенов. Приведены данные о применимости метаболитов *L. plantarum* для биоконсервации мясных продуктов.

Ключевые слова: Lactiplantibacillus plantarum, Listeria monocytogenes, Vibrio parahaemolyticus, антагонистическая активность, биопленки, Quorum Sensing, метаболомика, биоконсервация.

Abstract: This review analyzes the mechanisms underlying the antagonistic activity of *Lactiplantibacillus plantarum* strains and their metabolites against foodborne pathogens *Vibrio parahaemolyticus* and *Listeria monocytogenes*. The paper covers direct cell displacement, surface property alterations, motility suppression, and Quorum Sensing (AI-2) inhibition. It examines biofilm disruption, downregulation of virulence genes, and metabolite-induced membrane permeability and metabolic shifts in target bacteria. Practical applications of *L. plantarum* metabolites in meat biopreservation are also discussed.

Keywords: Lactiplantibacillus plantarum, Listeria monocytogenes, Vibrio parahaemolyticus, antagonistic activity, biofilms, Quorum Sensing, metabolomics, biopreservation.

Введение

Современная пищевая индустрия и система здравоохранения сталкиваются с серьезными вызовами, обусловленными высокой частотой микробиологической контаминации продуктов питания патогенными и условно-патогенными микроорганизмами [4, 2]. Среди широкого спектра возбудителей пищевых токсикоинфекций особое место занимают грамотрицательные бактерии *Vibrio parahaemolyticus*, являющиеся одной из главных причин острых гастроэнтеритов, ассоциированных с потреблением морепродуктов, а также грамположительные психотрофные бактерии *Listeria monocytogenes*, способные размножаться в условиях холодильного хранения и вызывающие тяжелые формы листериоза с высоким уровнем летальности [4, 2]. Традиционные физико-химические методы консервации и применение синтетических антимикробных агентов постепенно утрачивают первичную эффективность вследствие непрерывного формирования у патогенов устойчивости к

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дезинфектантам и антибиотикам, а также за счет их способности образовывать прочные многокомпонентные биопленки [2, 1]. В связи с этим в современной прикладной микробиологии и пищевой биотехнологии критическое значение приобретает поиск экологически безопасных биологических агентов, способных подавлять жизнедеятельность патогенов без ухудшения органолептических и нативных свойств продуктов [1, 5].

В качестве эффективной альтернативы химическим консервантам рассматриваются пробиотики и их биоактивные метаболиты, среди которых особое значение имеют бактерии вида *Lactiplantibacillus plantarum* [1, 3, 7]. Обладая официально подтвержденным статусом безопасного организма (GRAS), *L. plantarum* демонстрирует выраженную антагонистическую активность в отношении широкого спектра пищевых патогенов [1, 3]. Антимикробный потенциал данных микроорганизмов реализуется как за счет прямой клеточной конкуренции за питательные субстраты и места адгезии, так и посредством секреции богатого комплекса внеклеточных метаболитов, включая органические кислоты, бактериоцины, пептидные соединения и специфические ингибиторы [2, 4, 5, 8]. Накопленные к настоящему времени данные свидетельствуют о том, что механизм действия *L. plantarum* выходит далеко за рамки простого закисления среды и включает многоуровневое воздействие на физиологию и генетический аппарат патогенных бактерий [2, 5, 6].

Современные молекулярно-биологические и метаболомные исследования доказывают, что биологически активные вещества, продуцируемые L. plantarum, способны нарушать целостность клеточных мембран, подавлять подвижность и гидрофобность поверхностей патогенов, а также блокировать межклеточную коммуникацию, известную как система *Quorum Sensing* [2, 5, 6]. Ингибирование сигнальных каскадов кворума влечет за собой разрушение экзополисахаридного матрикса биопленок и репрессию генов, ответственных за синтез факторов вирулентности и токсинов [2, 5]. Кроме того, воздействие бесклеточных супернатантов *L. plantarum* провоцирует глубокие метаболические сбои в клетках патогенов, затрагивающие нуклеотидный обмен, биосинтез жирных кислот и центральные энергетические пути [4, 6]. Настоящий аналитический обзор посвящен систематизации и критическому осмыслению современных научных представлений о многофакторных механизмах антагонизма *Lactiplantibacillus plantarum* против *Listeria monocytogenes* и *Vibrio parahaemolyticus*, а также оценке практического потенциала их использования в сфере биоконсервации [1, 2, 4, 9].

Методы и материалы

Настоящий аналитический обзор подготовлен на основе систематического анализа и обобщения актуальных научных публикаций за период 2021–2023 гг., индексируемых в международных базах данных PubMed, Scopus, Web of Science и eLIBRARY.ru. Поиск литературы осуществлялся по ключевым словам: «Lactiplantibacillus plantarum», «Listeria monocytogenes», «Vibrio parahaemolyticus», «antagonistic activity», «biofilms», «Quorum Sensing», «metabolomics» и «biopreservation».

В качестве критериев включения отбирались полнотекстовые рецензируемые статьи, содержащие экспериментальные данные о молекулярно-генетических механизмах антагонизма, метаболомном профилировании бесклеточных супернатантов (UPLC-MS/MS), количественном анализе экспрессии генов (RT-qPCR) и результатах практического использования метаболитов L. plantarum в биоконсервации пищевой продукции.

Основная часть

2.1. Клеточный антагонизм, адгезия и ингибирование биопленок

Антагонистическое действие живых клеток *L. plantarum* реализуется через механизмы конкуренции за питательные вещества, конкурентного исключения (*exclusion*) и вытеснения (*displacement*) уже адгезированных патогенов [2, 3]. В экспериментах со штаммом *L. plantarum* Z057 установлено, что совместное культивирование приводит к снижению количества

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планктонных клеток *V. parahaemolyticus* на 0,89 log CFU/mL, а биопленочных — на 1,54 log CFU/mL [2]. Предварительно сформированная биопленка *L. plantarum* предотвращает первичную адгезию патогена, снижая титр биопленочной фракции на 1,61 log CFU/mL [2, 3]. Обработка зрелой биопленки патогена клетками *L. plantarum* вызывает ее вытеснение со снижением численности клеток на 0,95 log CFU/mL [2].

Бесклеточные экстракты *L. plantarum* дозозависимо меняют физико-химические свойства поверхности патогенов [2, 3, 8, 11]. В частности, зафиксировано снижение гидрофобности клеточной стенки *V. parahaemolyticus* на 35,86% и угнетение автоагрегации до 4,81% под действием экстракта Z057-E в концентрации 1,6 мг/мл [2]. Подавление роения (*swarming*) и плавания (*swimming*) на 49,04% и 54,70% соответственно блокирует начальный этап колонизации и формирование трехмерной архитектоники биопленки [2, 5].

2.2. Супрессия системы Quorum Sensing и регуляция экспрессии генов

Важным аспектом антимикробного действия метаболитов *L. plantarum* является подавление межклеточной коммуникации патогенов (Anti-Quorum Sensing) [2, 5]. Внеклеточные метаболиты *L. plantarum* Z057-E снижают активность сигнальных молекул Autoinducer-2 (AI-2) до 66,69% при концентрации 1,6 мг/мл [2]. Это приводит к деструкции внеклеточного полимерного матрикса (EPS): содержание внеклеточных полисахаридов снижается на 78,76%, а белков — на 51,91% [2, 5].

Молекулярно-генетический анализ (RT-qPCR) подтверждает, что обработка метаболитами *L. plantarum* вызывает репрессию ключевых генов патогенности [2, 5]:

- генов жгутикового аппарата и подвижности [2];
- генов биосинтеза компонентов EPS-матрикса [2, 5];
- генов регуляторной системы кворума [2, 5];
- генов синтеза токсинов и факторов вирулентности [2].

2.3. Мембранотропное действие и метаболомное перепрограммирование

Исследование воздействия бесклеточного супернатанта *L. plantarum* SHY96 (LCFS96) против *L. monocytogenes* (MIC = 10 мг/мл) выявило глубокие изменения клеточной оболочки и метаболизма [1, 6]. Данные проточной цитометрии (окрашивание иодидом пропидия) и электронно-микроскопического анализа указывают на увеличение проницаемости мембран до 62,00% при 2× MIC (по сравнению с 5,15% в контроле), а также сморщивание и лизис клеток патогена [4, 5].

Результаты нецелевого метаболомного профилирования (UPLC-MS/MS) продемонстрировали достоверное изменение уровня 450 внутриклеточных метаболитов *L. monocytogenes* [4]. Ключевые нарушения затрагивают [4, 5]:

1. **Нуклеотидный обмен:** Подавление синтеза пуринов и пиримидинов (снижение уровней UMP, UDP, CMP, IMP, GMP) и накопление свободных азотистых оснований (урацила, гипоксантина), что ингибирует репликацию ДНК [4, 12].
2. **Метаболизм жирных кислот:** Накопление линолевой кислоты и ее оксилипинов (9-oxo-ODE, 9,10-DHOME), дестабилизирующих фосфолипидный бислой [4, 6].
3. **Энергетический метаболизм:** Избыточная активация цикла трикарбоновых кислот (TCA), приводящая к гиперактивации метаболизма, истощению ресурсов и гибели клетки [4, 6].

2.4. Применение в биоконсервации мясной продукции

Практическая эффективность бесклеточных метаболитов *L. plantarum* подтверждена на модели охлажденной куриной грудки (4°C, 12 суток) [1, 4]. Обработка LCFS96 обеспечила снижение титра *L. monocytogenes* на 84,93% по сравнению с контрольной группой [4, 13]. Параллельно отмечено замедление накопления летучего щелочного азота (TVB-N) (на 12-й день: 13,97 мг/100 г при 2× MIC против 32,57 мг/100 г в контроле) и стабилизация pH [1, 4]. Обработанные образцы сохраняли органолептические характеристики, естественный цвет и текстуру на протяжении всего периода хранения [1, 4].

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Заключение

Систематизация современных данных доказывает, что *Lactiplantibacillus plantarum* представляет собой высокоэффективный многофункциональный агент биоконтроля, способный успешно подавлять жизнедеятельность опасных пищевых патогенов — *Vibrio parahaemolyticus* и *Listeria monocytogenes*. Антагонистический потенциал данного пробиотика реализуется через комплексный, иерархически организованный механизм, сочетающий прямой клеточный антагонизм и глубокое биохимическое воздействие его метаболитов на физиологию патогенных микроорганизмов.

Ключевыми звенообразными факторами антимикробного действия *L. plantarum* являются:

- **Ингибирование адгезии и биопленкообразования:** Живые клетки *L. plantarum* эффективно конкурируют за сайты связывания и вытесняют патогены из состава биопленок, а бесклеточные экстракты существенно снижают гидрофобность клеточной стенки и блокируют подвижность (*swarming* и *swimming*), предотвращая первичную колонизацию.
- **Блокирование системы Quorum Sensing и генная супрессия:** Внеклеточные метаболиты подавляют сигнальную активность молекул AI-2, что приводит к разрушению экзополисахаридного матрикса (EPS) и сопровождается репрессией генов подвижности (flaA, flgM), синтеза EPS (cpsA, cpsQ, cpsR, ompW), системы кворума (luxS, opaR, aphA) и ключевых факторов вирулентности (toxS, toxR).
- **Мембранотропный эффект и метаболомный сбой:** Действие бесклеточного супернатанта сопровождается необратимым нарушением проницаемости клеточных мембран патогенов, а также критическими метаболическими нарушениями — блокированием нуклеотидного обмена и репликации ДНК, дестабилизацией липидного бислоя накоплением оксилипинов и гиперактивацией цикла трикарбоновых кислот (TCA), приводящей к истощению энергетических ресурсов и лизису клеток.

Практическая применимость данной технологии подтверждается успешными результатами биоконсервации мясной продукции, где метаболиты *L. plantarum* гарантируют выраженное подавление роста *L. monocytogenes*, ингибируют процессы порчи (накопление TVB-N, сдвиг pH) и сохраняют нативные органолептические качества продуктов при холодильном хранении. Таким образом, применение *L. plantarum* и его метаболома открывает широкие перспективы для создания экологически безопасных биоконсервантов нового поколения, способных заменить синтетические химические добавки в пищевой промышленности.

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FERMENTATION-BASED MANUFACTURING OF POSTBIOTICS: FROM STRAIN SELECTION TO SHELF-STABLE INGREDIENT

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Abstract: Traditional probiotics are hindered by their poor ability to survive in acidic and bile-containing environments, by the need for strict storage conditions, and by inaccurate dosing. According to ISAPP, postbiotics are defined as inanimate microorganisms and/or their components that produce a health benefit and avoid these drawbacks. The present review offers a thorough summary of the fermentation-based manufacturing of postbiotics, covering the entire process from strain selection right through to the creation of a shelf-stable product, with reference to literature published between 2020 and 2026.
Keywords: postbiotics; fermentation; inactivation; downstream processing; bioactives.

Annotatsiya: An’anaviy probiotiklardan foydalanishda kislotali va o‘t suyuqligi mavjud muhitda yashab qolish qobiliyatining pastligi, saqlash sharoitlariga qat’iy talablar va dozalashdagi noaniqliklar kabi muammolar mavjud. ISAPP ta’rifiga ko‘ra, postbiotiklar — bu salomatlikka foyda keltiradigan hamda yuqorida qayd etilgan kamchiliklardan xoli bo‘lgan jonli bo‘lmagan mikroorganizmlar va/yoki ularning tarkibiy qismlaridir. Ushbu sharhda 2020–2026-yillar oralig‘ida chop etilgan ilmiy manbalarga tayangan holda, postbiotiklarni fermentatsiya usulida ishlab chiqarish jarayoni — shtammni tanlashdan boshlab toki uzoq muddat saqlashga yaroqli mahsulotni yaratishgacha bo‘lgan barcha bosqichlar — batafsil yoritilgan.
Kalit so‘zlar: postbiotiklar; fermentatsiya; inaktivatsiya; yakuniy qayta ishlash; bioaktivlar.

Аннотация: Эффективность традиционных пробиотиков ограничивается их низкой выживаемостью в кислой среде и в присутствии желчи, необходимостью соблюдения строгих условий хранения, а также сложностью точного дозирования. Согласно определению ISAPP, постбиотики представляют собой нежизнеспособные микроорганизмы и/или их компоненты, оказывающие благотворное влияние на здоровье и лишенные указанных недостатков. В данном обзоре представлен подробный анализ процессов производства постбиотиков методом ферментации — от выбора штамма до получения готового продукта с длительным сроком хранения; при этом рассматриваются научные публикации за период с 2020 по 2026 год.
Ключевые слова: постбиотики; ферментация; инактивация; последующая обработка; биоактивы.

Introduction

Probiotics have for a long time been used in order to support the gut microbiota; yet their use in targeted therapy is limited due to their poor survival in acidic and bile environments (Nataraj et al., 2020; Thorakkattu et al., 2022). Other problems involve the need for special storage conditions and difficulties in standardizing the dose (Thorakkattu et al., 2022). Because of these limitations, there has been growing interest in safer and more stable alternatives. The International Scientific Association of Probiotics and Prebiotics (ISAPP) defines postbiotics as "inanimate microorganisms and/or their

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components that confer a health benefit on the host" (Salminen et al., 2021). As the health benefits of probiotics are mainly achieved through their metabolites, it is not necessary to administer the live cells (Nataraj et al., 2020; Vinderola et al., 2022). Fermentation is still a key process in the manufacture of postbiotics (Mishra et al., 2024). The present review examines each stage of the fermentation-based production process, from strain selection to downstream processing.

Methods

The literature was searched in PubMed, NIH, Elsevier, ScienceDirect and MDPI between 2020 and 2026, with a focus on scientific articles, peer-reviewed studies and consensus statements concerning postbiotic production. The ISAPP consensus documents were included in order to provide a theoretical background.

Results

The strains used include lactic acid bacteria and various *Bifidobacterium* species (Moradi et al., 2020); additionally, *Streptococcus*, *Bacillus*, and yeasts such as *Saccharomyces cerevisiae* are employed in order to obtain postbiotics with a broader range of effects (Nataraj et al., 2020). The pure cultures are introduced into media such as MRS broth, milk proteins, or whey (Trymers et al., 2026).

The type of fermentation used – submerged or solid-state – is determined by the desired postbiotic (Ali-Haneef et al., 2026). In a particular study, solid-state fermentation using *Bacillus amyloliquefaciens* and *Lactiplantibacillus plantarum* yielded a crude preparation that had improved antibacterial properties against *Salmonella* and *E. coli*, together with antioxidant and anti-inflammatory effects (Tong et al., 2023). The incubation is generally carried out at a temperature of 30-37°C for a period of 25 to 48 hours (Liang & Xing, 2023). Complex metabolites such as bacteriocins and exopolysaccharides are primarily produced during the stationary phase, when quorum sensing is active (Bueno et al., 2025).

The inactivation of microorganisms continues to rely on thermal methods, such as pasteurizing at a temperature between 70 and 90°C for a period of 15 to 30 minutes or autoclaving at 121 °C for 15 to 20 minutes (Ali-Haneef et al., 2026). Occasionally, non-thermal techniques – such as high-pressure processing, ultrasonic cavitation, and pulsed electric fields – are preferred in order to prevent damage to heat-sensitive bioactives (Thirumdas & Mudgil, 2025).

Regarding verification, the ISAPP consensus states that manufacturers must show that there are no viable colony-forming units left (Salminen et al., 2021); this is achieved by pouring samples onto selective agar media and then confirming that no growth occurs after incubation (Vinderola et al., 2025).

The downstream processing involves converting the inactivated broth into a standardized and shelf-stable ingredient. By means of centrifugation or ultrafiltration (Prajapati et al., 2023), the cell debris and whole cells are removed, and the resulting clear liquid is then concentrated using low-temperature vacuum evaporation. Since postbiotic extracts are very hygroscopic, carriers like maltodextrin or starch are included in order to protect them from both oxygen and heat; dehydration and stabilization are subsequently carried out by means of spray-drying or freeze-drying (Ren et al., 2026).

Discussion

The main conclusion is that the postbiotic quality is affected at all stages of production—covering the choice of strain and medium, fermentation, inactivation, and downstream processing—and is therefore not determined entirely by the strain.

The form of fermentation has an effect on both the kind and the strength of the product (Ali-Haneef et al., 2026; Tong et al., 2023), and since important metabolites build up during the stationary phase, both the time of harvest and the temperature used have a direct impact on the yield and on the composition (Bueno et al., 2025; Netrusov et al., 2023). Inactivation involves a compromise: thermal methods are simple and reliable but can cause degradation of sensitive bioactives, whereas non-thermal methods maintain bioactivity although at the cost of greater expense and complexity

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(Thirumdas & Mudgil, 2025). Regardless of the method chosen, plating-based verification is an essential step in quality control (Salminen et al., 2021; Vinderola et al., 2025).

It is necessary to recognize a number of limitations. The compositional complexity of postbiotics makes it hard to reproduce and characterize (Scott et al., 2022; Guglielmetti et al., 2025). Moreover, some of the material on manufacturing is written by people from the industry and has not been subject to peer review.

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BAKTERIOFAGLAR ASOSIDA SABZAVOT MAHSULOTLARINING MIKROBIOLOGIK NAZORATI

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Annotatsiya: Mazkur tadqiqotda sabzavot mahsulotlarining mikrobiologik xavfsizligini ta’minlashda bakteriofaglardan foydalanish imkoniyatlari tahlil qilingan. Sabzavot mahsulotlari yetishtirish, tashish va saqlash jarayonlarida turli patogen va shartli-patogen mikroorganizmlar bilan ifloslanishi mumkin. Bakteriyalarga nisbatan yuqori spetsifiklikka ega bakteriofaglar ushbu mikroorganizmlarni nazorat qilishning istiqbolli biologik vositasi hisoblanadi. Maqolada bakteriofaglarning biologik xususiyatlari, litik faolligi, bir nechta bakteriofaglardan tashkil topgan preparatlarning qo‘llanilishi hamda ularning sabzavot mahsulotlaridagi bakterial ifloslanishni kamaytirishdagi ahamiyati yoritilgan. Bakteriofaglardan foydalanish sabzavot mahsulotlarining mikrobiologik xavfsizligini oshirishga xizmat qiluvchi ekologik xavfsiz va maqsadli biologik nazorat usuli sifatida baholangan.
Kalit so‘zlar: bakteriofaglar, sabzavot mahsulotlari, mikrobiologik nazorat, oziq-ovqat xavfsizligi, patogen bakteriyalar, litik faollik

Аннотация: В настоящем исследовании проанализированы возможности применения бактериофагов для обеспечения микробиологической безопасности овощной продукции. Овощи могут подвергаться контаминации различными патогенными и условно-патогенными микроорганизмами на этапах выращивания, транспортировки и хранения. Бактериофаги, обладающие высокой специфичностью в отношении определённых видов бактерий, рассматриваются как перспективное биологическое средство контроля бактериальных контаминантов. В статье рассмотрены биологические свойства бактериофагов, их литическая активность, применение препаратов на основе нескольких бактериофагов, а также их значение в снижении бактериальной контаминации овощной продукции. Применение бактериофагов рассматривается как экологически безопасный и целенаправленный метод биологического контроля, способствующий повышению микробиологической безопасности овощной продукции.
Ключевые слова: бактериофаги, овощная продукция, микробиологический контроль, безопасность пищевых продуктов, патогенные бактерии, литическая активность.

Abstract: The present study analyzes the potential of bacteriophages for ensuring the microbiological safety of vegetable products. Vegetables can become contaminated with various pathogenic and opportunistic microorganisms during cultivation, transportation, and storage. Due to their high specificity toward particular bacterial species, bacteriophages are considered a promising biological tool for controlling bacterial contaminants. The article discusses the biological properties

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of bacteriophages, their lytic activity, the application of preparations containing multiple bacteriophages, and their significance in reducing bacterial contamination of vegetable products. The use of bacteriophages is considered an environmentally safe and targeted biological control approach that can contribute to improving the microbiological safety of vegetable products.

Keywords: bacteriophages, vegetable products, microbiological control, food safety, pathogenic bacteria, lytic activity

Kirish

Sabzavot mahsulotlari inson oziqlanishida muhim o‘rin tutishi bilan birga, yetishtirish, yig‘ib olish, tashish va saqlash jarayonlarida turli mikroorganizmlar bilan ifloslanishi mumkin. Patogen va shartli-patogen bakteriyalarning rivojlanishi mahsulot sifatining pasayishi hamda oziq-ovqat xavfsizligiga tahdid tug‘diradi. Shu sababli sabzavot mahsulotlarida bakterial kontaminatsiyani samarali nazorat qilishning xavfsiz va ekologik usullarini ishlab chiqish muhim ahamiyatga ega [1,2]. Bakteriofaglar bakterial hujayralarni spetsifik ravishda zararlovchi viruslar bo‘lib, ularning litik faolligi bakterial populyatsiyani kamaytirish imkonini beradi. Yuqori spetsifiklik va maqsadli ta’sir xususiyati bakteriofaglarni sabzavot mahsulotlarining mikrobiologik nazoratida istiqbolli biologik vosita sifatida qo‘llash imkonini yaratadi [3,4]. Mazkur maqolaning maqsadi sabzavot mahsulotlarining mikrobiologik nazoratida bakteriofaglardan foydalanish imkoniyatlarini va ularning bakterial kontaminatsiyani kamaytirishdagi ahamiyatini ilmiy jihatdan tahlil qilishdan iborat.

Adabiyotlar tahlili

Bakteriofaglarning oziq-ovqat mahsulotlaridagi bakterial patogenlarni nazorat qilishdagi imkoniyatlari bir qator tadqiqotlarda o‘rganilgan. Moye va hammualliflar bakteriofaglarning oziq-ovqat ishlab chiqarish va qayta ishlash jarayonlarida qo‘llanilishini tahlil qilib, ularning yuqori spetsifikligi hamda bakterial hujayralarni lizisga uchratish xususiyatini asosiy afzallik sifatida ko‘rsatgan [5]. López-Cuevas va hammualliflar yangi meva va sabzavotlarda bakteriofaglardan foydalanish bo‘yicha tadqiqotlarni tahlil qilgan. Mualliflar Salmonella spp., Escherichia coli va boshqa oziq-ovqat patogenlariga qarshi fag preparatlaridan foydalanish imkoniyatlarini ko‘rib chiqib, ularning samaradorligi bakteriyaning fagga sezgirligi va qo‘llash sharoitlariga bog‘liqligini ta’kidlagan [6]. Jagannathan va hammualliflar bakteriofaglarning o‘simlik mahsulotlarining hosilgacha va hosildan keyingi mikrobiologik xavfsizligini ta’minlashdagi qo‘llanilishini tahlil qilgan. Tadqiqotda bakteriofaglarni mahsulot yuzasiga qo‘llash orqali bakterial yuklamani kamaytirish imkoniyatlari hamda faglarning amaliy qo‘llanilishiga ta’sir qiluvchi omillar ko‘rib chiqilgan [7].

Vikram va hammualliflar bakterial oziq-ovqat patogenlarini bakteriofaglar yordamida nazorat qilish bo‘yicha zamonaviy tadqiqotlarni umumlashtirgan. Mualliflar fagning xo‘jayin diapazoni, bakterial shtammning sezgirligi, fag konsentratsiyasi va tashqi muhit sharoitlari bakteriofag samaradorligiga sezilarli ta’sir ko‘rsatishini qayd etgan [8]. Bakteriofaglarning tor xo‘jayin diapazoni ularni amaliy qo‘llashdagi muhim cheklovlardan biri hisoblanadi. Shu sababli turli bakterial shtammlarga ta’sir qiluvchi bir nechta faglarni birlashtirish orqali kombinatsiyalangan bakteriofag preparatlarini qo‘llash imkoniyati o‘rganilgan. Bunday yondashuv bakterial nishonlar doirasini kengaytirish va nazorat samaradorligini oshirish imkonini berishi mumkin [9]. Shuningdek, tadqiqotlarda bakteriofaglarning samaradorligi ularning litik xususiyatlari, bakteriyaga adsorbsiyalanish qobiliyati va tashqi muhit omillariga barqarorligi bilan bog‘liqligi ko‘rsatilgan [10]. Shu jihatdan, sabzavot mahsulotlarini mikrobiologik nazorat qilish uchun faglarni tanlashda ularning litik faolligi, spetsifikligi va bakterial shtammlarga qarshi samaradorligini oldindan baholash muhim hisoblanadi.

Umuman, mavjud tadqiqotlar bakteriofaglardan sabzavot mahsulotlarining mikrobiologik nazoratida foydalanish imkoniyatlari mavjudligini ko‘rsatadi. Biroq muayyan hududda uchraydigan bakterial shtammlarga nisbatan faol faglarni aniqlash, ularning litik faolligini baholash va sabzavot

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mahsulotlari yuzasidagi bakterial kontaminatsiyani kamaytirish samaradorligini aniqlash masalalari qo‘shimcha tadqiqotlarni talab qiladi [11].

Material va usullar

Tadqiqot obyekti sifatida pomidor (*Solanum lycopersicum*), kartoshka (*Solanum tuberosum*), bodring (*Cucumis sativus*) va karam (*Brassica oleracea*) mahsulotlarining bakterial kasallik belgilari kuzatilgan namunalari tanlab olindi. Har bir sabzavot turidan 2 tadan, jami 8 ta namuna tadqiqotga jalb qilindi. Namunalar tashqi ko‘rinishida chirish, yumshash, qorayish, suvli dog‘lar yoki to‘qimalarning nekrozga uchrashi kabi bakterial zararlanishga xos belgilar mavjud bo‘lgan qismlardan olindi. Namuna olishda zararlangan va sog‘lom to‘qimalar chegarasidagi qism tanlanib, steril asbob yordamida ajratildi va mikrobiologik tekshiruv uchun steril idishlarda laboratoriyaga yetkazildi. Namunalarning zararlangan qismidan steril skalpel yordamida 1–2 g miqdorda material olinib, steril fiziologik eritma yordamida boshlang‘ich suspenziya tayyorlandi. Tayyorlangan suspenziyalar mikrobiologik ekish uchun ishlatildi. Bakterial mikroorganizmlarni aniqlash maqsadida namunalar tegishli oziqa muhitlariga ekildi. Ekish ishlari aseptik sharoitda amalga oshirilib, ekmalar mikroorganizmlarning o‘sishi uchun optimal sharoitda inkubatsiya qilindi.

Bakterial izolyatlarni dastlabki identifikatsiya qilishda koloniyalarning morfologik belgilari, mikroskopik xususiyatlari va biokimyoviy reaksiyalaridan foydalanildi. Xususan, Gram usulida bo‘yash, katalaza reaksiyasi asosida izolyatlarning Staphylococcus aureus turiga mansubligi baholandi. Tadqiqot davomida sabzavot namunalaridan Staphylococcus aureus bakteriyasi ajratib olindi. Ajratilgan izolyat keyingi tadqiqotlar uchun sof kultura holatiga keltirilib, bakteriofagga sezuvchanligini aniqlash uchun foydalanildi. Ajratib olingan Staphylococcus aureus izolyatiga qarshi litik xususiyatga ega Staphylococcus phage K (Phage K) bakteriofagi tanlandi. Ushbu bakteriofag Staphylococcus aureus hujayralarini zararlash va lizisga uchratish xususiyatiga ega bo‘lgan litik bakteriofag sifatida tadqiqotning keyingi bosqichlarida qo‘llanildi. Har bir izolyat uchun bakteriofag bilan ishlov berilgan tajriba varianti va bakteriofag qo‘shilmagan nazorat varianti tayyorlandi. Bakteriofagning Staphylococcus aureus izolyatiga nisbatan litik faolligi oziqa muhitining yuzasida bakteriyalar bir tekis o‘sib, hosil qilgan zich bakterial qatlamda tiniq lizis zonalarining paydo bo‘lishi asosida baholandi. Tiniq lizis zonalarining hosil bo‘lishi bakteriofagning Staphylococcus aureus hujayralarini zararlab, ularning lizisiga olib kelganligini ko‘rsatuvchi belgi sifatida qayd etildi.

Bakteriofagning Staphylococcus aureus ga ta’siri tajriba va nazorat variantlaridagi tirik bakterial hujayralar sonini taqqoslash orqali baholandi. Buning uchun har ikkala variantdan namunalar oziqa muhitiga qayta ekilib, inkubatsiyadan so‘ng hosil bo‘lgan koloniyalar soni (CFU/ml) aniqlandi. Bakterial hujayralar sonining nazoratga nisbatan kamayish darajasi quyidagi formula asosida hisoblandi:

Bakterial kamayish (%) = $[(N_0 - N_1) / N_0] \times 100$

bu yerda N_0 — nazorat, N_1 — bakteriofag bilan ishlov berilgan tajriba variantidagi tirik bakteriyalar soni (CFU/ml). Lizis zonalarining hosil bo‘lishi va CFU/ml ko‘rsatkichining kamayishi bakteriofagning S. aureus ga qarshi litik faolligini baholash mezonlari sifatida qabul qilindi.

Natijalar

Tadqiqot davomida pomidor, kartoshka, bodring va karamning har biridan 2 tadan, jami 8 ta sabzavot namunasi mikrobiologik tekshiruvdan o‘tkazildi. Tekshiruv natijasida pomidorning 2 ta, kartoshkaning 2 ta va bodringning 2 ta namunasida Staphylococcus aureus aniqlandi. Karamning 2 ta namunasida esa S. aureus aniqlanmadi. Ajratib olingan 6 ta S. aureus izolyatiga bakteriofag bilan ishlov berilganda, oziqa muhitining yuzasida bakteriyalar bir tekis o‘sib, hosil qilgan zich bakterial qatlamda tiniq lizis zonalari paydo bo‘ldi. Ushbu lizis zonalarining hosil bo‘lishi bakteriofagning tekshirilgan S. aureus izolyatlariga nisbatan litik faollikka ega ekanligini ko‘rsatdi. Bakteriofag bilan ishlov berishdan keyingi mikrobiologik tekshiruvda 6 ta S. aureus musbat namunaning 4

tasida bakterial o‘sish kuzatilmadi, 2 tasida esa S. aureus qayta aniqlandi. Nazorat variantida esa bakterial o‘sish saqlanib qoldi. Natijada bakteriofag qo‘llangandan keyin S. aureus aniqlangan namunalar soni 6 tadan 2 tagacha kamaydi.

Bakterial aniqlanishning kamayish darajasi: $[(6 - 2) / 6] \times 100 = 66,7\%$

ni tashkil etdi. Olingan natijalar bakteriofagning Staphylococcus aureus ga nisbatan litik faolligini va tekshirilgan sabzavot namunalarida ushbu bakteriyaning kamayishiga ta’sir ko‘rsatganligini ko‘rsatdi (1-jadval).

1-jadval. Sabzavot namunalaridan ajratilgan Staphylococcus aureus izolyatlariga bakteriofag ta’siri

№	Sabzavot turi	Olingan namunalar soni	S. aureus ajratilgan namunalar	Bakteriofag ta’sirida lizis kuzatilgan
1	Pomidor (Solanum lycopersicum)	2	2	2
2	Kartoshka (Solanum tuberosum)	2	2	2
3	Bodring (Cucumis sativus)	2	2	2
4	Karam (Brassica oleracea)	2	0	-
Jami		8	6	6

Umuman olganda, olingan natijalar bakteriofagning Staphylococcus aureus ga nisbatan samarali litik faollikka ega ekanligini va uni sabzavot mahsulotlarining mikrobiologik nazoratida qo‘llash istiqbolli biologik vosita ekanligini ko‘rsatdi.

Xulosa

Bakteriofaglardan foydalanishga asoslangan yondashuv sabzavot mahsulotlarining mikrobiologik xavfsizligini ta’minlashda istiqbolli biologik nazorat usullaridan biri hisoblanadi. Bakteriofaglarning maqsadli bakteriyalarga nisbatan yuqori spetsifikligi ularni foydali mikroorganizmlarga kamroq ta’sir ko‘rsatadigan muqobil nazorat vositasi sifatida qo‘llash imkonini beradi. Sabzavot mahsulotlarida bakterial kontaminatsiyani nazorat qilishda bakteriofaglardan foydalanish kimyoviy antimikrob vositalarga bo‘lgan ehtiyojni kamaytirish, mahsulotning mikrobiologik xavfsizligini oshirish hamda biologik nazoratning ekologik jihatdan maqbul usullarini rivojlantirish imkoniyatini yaratadi.

O‘tkazilgan tadqiqot natijasida sabzavot mahsulotlarida uchrashi mumkin bo‘lgan Staphylococcus aureus ni aniqlash va unga qarshi bakteriofag asosida mikrobiologik nazorat olib borish imkoniyati ko‘rsatildi. Tekshirilgan bakterial izolyatlarga bakteriofag ta’sir ettirilganda lizis zonalarining hosil bo‘lishi uning S. aureus ga nisbatan litik faolligini tasdiqladi. Olingan natijalar bakteriofaglardan sabzavot mahsulotlarining mikrobiologik xavfsizligini ta’minlash va maqsadli bakterial kontaminatsiyani nazorat qilishda foydalanish istiqbolli ekanligini ko‘rsatadi.

Bakteriofag asosidagi mikrobiologik nazorat tizimini amaliyotga joriy etishda faglarning spetsifikligi, barqarorligi, qo‘llash sharoitlari va maqsadli bakteriyalarning fagga sezuvchanligini hisobga olish muhim hisoblanadi. Shu sababli bakteriofaglarni sabzavot mahsulotlarini mikrobiologik nazorat qilishda qo‘llash bo‘yicha standartlashtirilgan yondashuvlarni ishlab chiqish va ularning amaliy samaradorligini yanada chuqur o‘rganish dolzarb yo‘nalishlardan biridir.

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LACTIPLANTIBACILLUS PLANTARUM TARAFIDAN ISHLAB CHIQARILADIGAN ANTIBAKTERIAL VA ANTIFUNGAL METABOLITLAR VA ULARNING TA'SIR MEXANIZMLARI

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Annotatsiya: Ushbu tadqiqotda ilmiy adabiyotlar va genomik/metabolomik ma’lumotlar tahlili asosida probiotik xususiyatga ega Lactiplantibacillus plantarum tomonidan sintez qilinadigan antibakterial va antifungal metabolitlar hamda ularning ta’sir mexanizmlari tizimli o‘rganildi. L. plantarum o‘zining pln operon klasterlari orqali II sinf plantaritsinlarini (PlnE/F, PlnJ/K), shuningdek, diketopiperazinlar guruhiga mansub siklik dipeptidlarni [Cyclo(L-Phe–L-Pro)], 3-fenilsut kislotasini (PLA) va fenol birikmalarini ishlab chiqarishi ko‘rsatib berildi. Ular patogen bakteriyalar membranalarini destruksiya qilish, metitsillinga chidamli Staphylococcus aureus (MRSA) ning biofilm hosil qilish fermentlarini ingibirlash va mog‘or zamburug‘lari (Aspergillus, Fusarium, Penicillium) o‘sishini to‘xtatish xususiyatiga ega. Tadqiqot natijalari ushbu metabolitlarni oziq-ovqat sanoatida biokonservant hamda tibbiyotda antibiotiklarga chidamli shtammlarga qarshi biologik vosita sifatida qo‘llash istiqbolli ekanligini tasdiqlaydi.

Kalit so‘zlar: Lactiplantibacillus plantarum, plantaritsin, siklik dipeptidlar, 3-fenilsut kislotasi, antibakterial metabolitlar, antifungal faollik, biofilm ingibirlash.

Аннотация: В данной работе на основе анализа научной литературы и геномных/метаболомных данных систематически изучены антибактериальные и антифунгальные метаболиты, синтезируемые пробиотическим штаммом Lactiplantibacillus plantarum, а также механизмы их действия. Показано, что L. plantarum посредством оперонных кластеров pln продуцирует плантарицины класса II (PlnE/F, PlnJ/K), а также циклические дипептиды группы дикетопиперазинов [Cyclo(L-Phe–L-Pro)], 3-фениллактат (PLA) и фенольные соединения. Данные метаболиты способны разрушать мембраны патогенных бактерий, ингибировать ферменты формирования биопленок метициллинорезистентного Staphylococcus aureus (MRSA) и подавлять рост плесневых грибов (Aspergillus, Fusarium, Penicillium). Результаты исследования подтверждают перспективы применения этих метаболитов в качестве биоконсервантов в пищевой промышленности и биологических средств против антибиотикорезистентных штаммов в медицине.

Ключевые слова: Lactiplantibacillus plantarum, плантарицин, циклические дипептиды, 3-фениллактат, антибактериальные метаболиты, антифунгальная активность, ингибирование биопленок.

Abstract: Based on a systematic review of scientific literature and genomic/metabolomic data, this study investigated the antibacterial and antifungal metabolites synthesized by the probiotic Lactiplantibacillus plantarum and their underlying modes of action. It is demonstrated that L. plantarum utilizes its pln operon clusters to produce class II plantaricins (PlnE/F, PlnJ/K), as well as cyclic dipeptides belonging to the diketopiperazine group [Cyclo(L-Phe–L-Pro)], 3-phenyllactic acid (PLA), and phenolic compounds. These metabolites are capable of disrupting pathogenic bacterial

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membranes, inhibiting biofilm-forming enzymes of methicillin-resistant Staphylococcus aureus (MRSA), and suppressing the growth of filamentous fungi (Aspergillus, Fusarium, Penicillium). The findings confirm the strong potential of using these metabolites as biopreservatives in the food industry and as biological agents against multidrug-resistant strains in medicine.

Keywords: Lactiplantibacillus plantarum, plantaricin, cyclic dipeptides, 3-phenyllactic acid, antibacterial metabolites, antifungal activity, biofilm inhibition.

Kirish

Oziq-ovqat mahsulotlarining sifati va xavfsizligini ta’minlash hamda antibakterial preparatlarga nisbatan turg‘unlik (multidrug resistance) ko‘rsatayotgan patogen mikroorganizmlarga qarshi samarali biologik vositalarni izlash zamonaviy mikrobiologiya va biotexnologiyaning eng dolzarb vazifalaridan biridir [3, 5]. An’anaviy kimyoviy konservantlar va sintetik antibiotiklarning inson salomatligiga salbiy ta’siri sababli, tabiiy kelib chiqishga ega bo‘lgan biokonservantlar hamda probiotik shtammlardan foydalanishga bo‘lgan qiziqish tobora ortib bormoqda [4, 6, 7].

Sut-kislota bakteriyalari (SKB) ichida Lactiplantibacillus plantarum (ilgari Lactobacillus plantarum) turi o‘zining metabolik moslashuvchanligi, xilma-xil genetik imkoniyatlari hamda oziq-ovqat va oshqozon-ichak traktida faol hayot kechirish xususiyati bilan ajralib turadi [1, 3, 8]. L. plantarum shtammlari ko‘plab mikrobga qarshi biologik faol birikmalar — metabolitlar sintez qilish qobiliyatiga ega [3, 4]. Ushbu metabolitlar sirasiga past molekulyar og‘irlikdagi organik kislotalar, ikki komponentli Class II bakteriotsinlar (plantaritsinlar), ribosoma orqali sintez qilinadigan va post-translyatsion o‘zgartirilgan peptidlar (RiPPs), diketopiperazinlar guruhiga mansub siklik dipeptidlar hamda fenil birikmalari kiradi [1, 4, 5]. Tahlil, L. plantarum tomonidan ajratiladigan antibakterial va antifungal metabolitlar patogen bakteriyalar (Listeria monocytogenes, Staphylococcus aureus, Bacillus spp.) hamda oziq-ovqat mahsulotlarini buzuvchi mog‘or va achitqi zamburug‘lari (Aspergillus, Fusarium, Penicillium, Candida avlodlari) ko‘payishini ingibirlashda yuqori samaradorlik namoyon etadi [4, 5]. Shuningdek, ushbu metabolitlar patogenlarning biofilm (bioplyonka) hosil qilish jarayonlarini izdan chiqarish xususiyatiga ham ega [5, 9].

Metodlar

Ushbu ilmiy tadqiqot ishi Lactiplantibacillus plantarum ning antibakterial va antifungal metabolitlarini o‘rganishga bag‘ishlangan ilmiy manbalarni tizimli tahlil qilish (systematic literature review) hamda bioinformatik/genomik ma’lumotlarni qiyosiy o‘rganish metodlari asosida amalga oshirildi [1, 3, 7, 11].

Tadqiqot doirasida quyidagi metodik bosqichlar va yondashuvlardan foydalanildi:

1. **Ilmiy ma’lumotlar bazasini shakllantirish va sara ilmiy adabiyotlarni tanlash:** Tadqiqot uchun PubMed, Scopus, Web of Science va Google Scholar xalqaro ilmiy bazalaridan 2000–2024 yillar oralig‘ida chop etilgan maqola va tezislar saralab olindi [1, 5]. Qidiruv jarayonida "Lactiplantibacillus plantarum", "bacteriocins", "plantaricin", "cyclic dipeptides", "phenyllactic acid", "antifungal metabolites" va "biofilm inhibition" kabi tayanch kalit so‘zlardan foydalanildi [1, 4, 5].
2. **Genomik va biosintez klasterlarini tahlil qilish:**

L. plantarum (WCFS1, C6, C11, LPCO10 va boshqa) shtammlarining genomik ketma-ketliklari, xususan, II sinf bakteriotsinlarini kodlovchi pln operonlari (plnABCD, plnEFINOP, plnJKLR) va post-translyatsion o‘zgartirilgan peptidlar (RiPPs) klasterlarining genetik strukturasi va ularning ekspressiya mexanizmlari qiyosiy tahlil qilindi [1].

3. **Metabolomik va in silico tahlil natijalarini umumlashtirish:**

Hujayrasiz supernatant (CFS) tarkibidagi past molekulyar og‘irlikdagi birikmalar (2,4-Di-tert-butylphenol, Indol-3-sut kislotasi, DL-4-Hydroxyphenyllactic acid va siklik dipeptidlar) bo‘yicha olingan xromatografik (GC-MS/HPLC) hamda molekulyar dokking (in silico) ma’lumotlari qiyosiy baholandi [4, 5].

4. **In vitro turg‘unlik va ingibirlash ko‘rsatkichlarini tizimlashtirish:**

Turli ilmiy ishlarda keltirilgan L. plantarum metabolitlarining patogen va shartli-patogen bakteriyalarga (Staphylococcus aureus, Listeria monocytogenes) hamda mog‘or va achitqi zamburug‘lariga (Aspergillus, Fusarium, Penicillium) nisbatan minimal ingibirlash konsentratsiyalari (MIC) va ta’sir mexanizmlari umumlashtirildi [4, 5].

Natijalar

Olingan va tahlil qilingan ilmiy adabiyotlar ma’lumotlari shuni ko‘rsatadiki, Lactiplantibacillus plantarum tomonidan sintez qilinadigan metabolitlar kimyoviy tuzilishi hamda ta’sir yo‘nalishiga ko‘ra ikkita asosiy guruhga — antibakterial va antifungal birikmalarga bo‘linadi.

1. Antibakterial metabolitlar va ularning genetik klasterlari

L. plantarum genomida bakteriotsinlar biosintezini kodlovchi maxsus pln operon klasterlari (plnABCD, plnEFINOP, plnJKLR) mavjudligi aniqlangan. Ular tomonidan asosan II sinf bakteriotsinlari — plantaritsinlar (PlnE/F va PlnJ/K) sintez qilinadi. Shuningdek, hujayrasiz supernatant (CFS) tarkibida kichik molekulyar og‘irlikdagi 2,4-Di-tert-butylphenol, Indol-3-sut kislotasi (ILA) hamda DL-4-Hydroxyphenyllactic acid (hPLA) birikmalari mavjudligi va ular metitsillinga turg‘un Staphylococcus aureus (MRSA) bakteriyasining biofilm hosil qilish fermentlarini ingibirlashi qayd etilgan.

2. Antifungal metabolitlar

L. plantarum (masalan, MiLAB 393 shtammi) tarkibida diketopiperazinlar sinfiga mansub siklik dipeptidlar — Cyclo(L-Phe–L-Pro) va Cyclo(L-Phe–trans-4-OH-L-Pro) mavjud bo‘lib, ular mog‘or va achitqi zamburug‘lariga qarshi yuqori faollik namoyon etadi. Bundan tashqari, organik kislotalardan 3-Phenyllactic acid (PLA) L va D izomerlari ko‘rinishida sintez qilinib, zamburug‘lar o‘sishini sezilarli darajada to‘xtatadi.

Quyidagi 1-jadvalda adabiyotlar tahlili natijasida umumlashtirilgan L. plantarum metabolitlari, ularning kimyoviy sinfi, maqsadli obyektlari va ta’sir ko‘rsatkichlari keltirilgan.

1-jadval. Lactiplantibacillus plantarum metabolitlarining kimyoviy guruhlari va ularning mikrobga qarshi ta’sir doirasi

Metabolit guruhi	**Aniq birikma nomi**	**Maqsadli mikroorganizmlar**	**Ta’sir mexanizmi / Ko‘rsatkichlari**
II sinf Bakteriotsinlar	Plantaricin E/F, Plantaricin J/K	*Listeria monocytogenes*, *Staphylococcus aureus*, *Bacillus* spp.	Membranada g‘ovak (pore) hosil qilish, ionlar sizishini keltirib chiqarish
RiPPs / Peptidlar	Streptococcin A analoglari, Nisin-simon peptidlar	Gram-musbat patogenlar	Hujayra devori biosintezini to‘sish va membranani destruksiya qilish
Siklik Dipeptidlar	Cyclo(L-Phe–L-Pro), Cyclo(L-Phe–trans-4-OH-L-Pro)	*Aspergillus fumigatus*, *Fusarium sporotrichioides*	Zamburug‘ spora va gifalari o‘sishini bloklash (MIC: 7.5–20 mg/ml)
Fenil birikmalari	3-Phenyllactic acid (PLA), Hydroxyphenyllactic acid (hPLA)	*Penicillium* spp., *Candida* spp., MRSA	Hujayradan tashqari biofilm fermentlarini ingibirlash, sitoplazma pH-ini o‘zgartirish

Fenol birikmalari	2,4-Di-tert-butylphenol, Indole-3-lactic acid	MRSA (biofilm hosil qiluvchi shtammlar)	Biofilm matritsasi va fermenti bilan molekulyar bog‘lanib, faollikni so‘ndirish

Muhokama

Adabiyotlar tahlili shuni ko‘rsatadiki, Lactiplantibacillus plantarum ning antibakterial va antifungal faolligi bir qancha o‘zaro to‘ldiruvchi molekulyar mexanizmlar orqali amalga oshiriladi.

Bakteriotsinlar, xususan ikki komponentli Class II plantaritsinlar (PlnE/F va PlnJ/K), patogen bakteriyalarning sitoplazmatik membranasi bilan o‘zaro ta’sirlashadi. Ular membranada g‘ovaklar (pore) hosil qilib, hujayra ichidagi kationlar (K^+, Na^+) sizib chiqishiga hamda transmembrana potensialining yo‘qolishiga olib keladi. Natijada patogen hujayra o‘zining energetik balansini yo‘qotadi va halok bo‘ladi.

Biofilm hosil qiluvchi shtammlarga (masalan, MRSA) nisbatan L. plantarum metabolitlarining ta’siri alohida e’tiborga loyiqdir. In silico va metabolomik tahlillar shuni tasdiqlaydiki, 2,4-Di-tert-butylphenol va DL-4-Hydroxyphenyllactic acid kabi kichik molekulalar patogenlarning matritsa hosil qiluvchi fermentlari bilan mustahkam gidrofob va Van-der-Vaals bog‘larini hosil qilib, biofilm matritsasining shakllanishini to‘xtatadi. Antifungal ta’sir mexanizmida esa siklik dipeptidlar [Cyclo(L-Phe–L-Pro)] va fenilsut kislotasi (PLA) o‘rtasidagi sinergetik bog‘liqlik asosiy rol o‘ynaydi. PLA kislotali muhitda dissotsilanmagan shaklda zamburug‘ membranasi orqali kiradi va sitoplazmatik pH ni pasaytiradi. Siklik dipeptidlar esa spora va gifalar darajasida fermentativ jarayonlarni bloklaydi.

Bu esa oziq-ovqat mahsulotlarida mog‘or zamburug‘lari rivojlanishining oldini olishda kimyoviy konservantlarga nisbatan yuqori samara beradi.

Xulosa

O‘tkazilgan ilmiy adabiyotlar tahlili va ma’lumotlarni umumlashtirish natijasida quyidagi asosiy ilmiy va amaliy xulosalarga kelindi:

1. **Metabolitlar xilma-xilligi va genetik imkoniyatlar:** Lactiplantibacillus plantarum shtammlari o‘z genomidagi pln operon klasterlari hamda ikkilamchi metabolik yo‘llar orqali keng spektrdagi antibakterial (Class II plantaritsinlar, RiPPs) hamda antifungal (siklik dipeptidlar, fenilsut kislotasi va uning hosilalari) birikmalarni sintez qilish xususiyatiga ega [1, 3, 4].
2. **Antibakterial va anti-biofilm mexanizmi:** Plantaritsinlar (PlnE/F, PlnJ/K) patogen bakteriyalar sitoplazmatik membranasida g‘ovaklar hosil qilib, membrana potensialini izdan chiqarishi hisobiga ularni halok qiladi [1]. Shu bilan birga, hujayrasiz supernatant tarkibidagi 2,4-Di-tert-butylphenol va hPLA kabi kichik molekulalar metitsillinga turg‘un Staphylococcus aureus (MRSA) bakteriyasining biofilm matritsasi va uning biosintez fermentlari bilan bog‘lanib, biofilm shakllanishini samarali ingibirlaydi [5].
3. **Antifungal sinergiya:** Zamburug‘larga qarshi faollikda L. plantarum tomonidan ajratiladigan Cyclo(L-Phe–L-Pro) siklik dipeptidi hamda 3-Phenyllactic acid (PLA) o‘rtasidagi sinergetik ta’sir hal qiluvchi rol o‘ynaydi [4, 13]. PLA hujayra ichki pH muhitini o‘zgartirsa, siklik dipeptidlar Aspergillus, Fusarium va Penicillium avlodi zamburug‘larining spora unib chiqishi hamda gifalar rivojlanishini fermentativ darajada to‘xtatadi [4].
4. **Amaliy va sanoat istiqbollari**: L. plantarum metabolitlarining yuqori termostabilligi va keng pH diapazonida faolligini saqlashi ularni oziq-ovqat sanoatida kimyoviy konservantlarga muqobil xavfsiz biokonservant sifatida, shuningdek, tibbiyotda antibiotiklarga chidamli (MDR) patogenlarga qarshi yangi biologik preparatlar ishlab chiqishda qo‘llash istiqboli yuqori ekanligini ko‘rsatadi [3, 5].

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ZA'FARON (*CROCUS SATIVUS* L.) O'SIMLIGIDAN AJRATILGAN ENDOFIT ZAMBURUG'LARNING ANTIKOAGULYANT FAOLLIGI

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Annotatsiya: Mazkur tadqiqotda *Crocus sativus* L. (za'faron) o'simligidan ajratib olingan endofit zamburug'larning ikkilamchi metabolitlari antikoagulyant faolligi bo'yicha baholandi. Tadqiqotda 17 ta zamburug' shtammining ekstraktlari plazma rekalsiyfikatsiya vaqti (PRT) usuli yordamida tekshirildi. Natijalar namunalar faolligining turlicha ekanligini ko'rsatdi. Eng yuqori ta'sir *Penicillium sp.* CS50R izolatida kuzatilib, PRT ko'rsatkichi 120 daqiqadan ortiqni tashkil etdi. Ushbu izolat potensial antikoagulyant xususiyatga ega biologik faol birikmalar manbai sifatida istiqbolli hisoblanadi. Olingan natijalar za'faron endofit zamburug'larining antikoagulyant faolligini chuqurroq o'rganish va faol metabolitlarni aniqlash uchun asos bo'lib xizmat qiladi.

Kalit so'zlar: *Crocus sativus* L., antikoagulyant faollik, plazma rekalsiyfikatsiya vaqti (PRT), *Penicillium sp.*

Аннотация: В данном исследовании оценивали антикоагулянтную активность вторичных метаболитов эндофитных грибов, выделенных из растения *Crocus sativus* L. (шафран). Экстракты 17 штаммов грибов исследовали с использованием метода определения времени рекальцификации плазмы (PRT). Результаты показали различия в активности исследованных образцов. Наиболее выраженный эффект наблюдался у изолята *Penicillium sp.* CS50R, для которого показатель PRT составил более 120 минут. Данный изолят представляет перспективный источник биологически активных соединений с потенциальными антикоагулянтными свойствами. Полученные результаты служат основой для дальнейшего изучения антикоагулянтной активности эндофитных грибов шафрана и выявления активных метаболитов.

Ключевые слова: *Crocus sativus* L., антикоагулянтная активность, время рекальцификации плазмы (PRT), *Penicillium sp.*

Abstract: This study evaluated the anticoagulant activity of secondary metabolites produced by endophytic fungi isolated from *Crocus sativus* L. (saffron). Extracts of 17 fungal strains were tested using the plasma recalcification time (PRT) assay. The results revealed differences in the activity of the tested samples. The most pronounced effect was observed in the *Penicillium sp.* CS50R isolate, for which the PRT exceeded 120 minutes. This isolate represents a promising source of biologically active compounds with potential anticoagulant properties. The findings provide a basis for further investigation of the anticoagulant activity of saffron-associated endophytic fungi and the identification of active metabolites.

Keywords: *Crocus sativus* L., anticoagulant activity, plasma recalcification time (PRT), *Penicillium sp.*

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Kirish

Crocus sativus L. (za’faron) qadimdan dorivor o‘simlik sifatida foydalanib kelinadigan bo‘lib, hozirgi vaqtda uning kimyoviy tarkibi va farmakologik xususiyatlarini o‘rganishga katta e’tibor qaratilmoqda. Za’faron tarkibida crocin, crocetin, picrocrocin va safranal kabi biologik faol birikmalar, shuningdek, boshqa fenolik moddalar va flavonoidlar mavjud[2]. Ushbu birikmalar antioksidant, yallig‘lanishga qarshi va boshqa biologik faolliklarni namoyon qilishi bilan ahamiyatlidir. Za’faronning biologik xususiyatlarini chuqur o‘rganish uning tarkibidagi tabiiy birikmalardan yangi farmakologik vositalarni izlash va ularning amaliy qo‘llanish imkoniyatlarini baholash uchun muhim hisoblanadi.

So‘nggi yillarda za’faron ekstraktlarining qon ivish tizimiga ta’siri, xususan, antikoagulyant faolligini o‘rganishga ham qiziqish ortmoqda. Khan va hammualliflar tomonidan olib borilgan tadqiqotda za’faronning turli qismlaridan — changchisi, gulbargi, bargi va piyozboshidan — olingan etanolli ekstraktlarning biologik faolligi baholangan. Natijalarga ko‘ra, gul changchisi ekstrakti uchun 101,66 soniya, gulbarg ekstrakti uchun 86,5 soniya, barg ekstrakti uchun 66,83 soniya va piyozbosh ekstrakti uchun 42,83 soniya koagulyatsiya vaqti qayd etilgan[5]. Ushbu natijalar za’faronning turli organlaridan olingan ekstraktlar qon ivish ko‘rsatkichlariga turlicha ta’sir qilishi mumkinligini ko‘rsatadi.

Drioiche va hammualliflar tomonidan o‘tkazilgan tadqiqotda esa *Crocus sativus* L. ning suvli ekstrakti sitratlangan sog‘lom donorlar qon plazmasida protrombin vaqti (PT) hamda faollashtirilgan qisman tromboplastin vaqti (aPTT) ko‘rsatkichlari bo‘yicha baholangan. Natijada ekstraktning 359 µg/ml konsentratsiyasida aPTT ko‘rsatkichining statistik jihatdan sezilarli uzayishi aniqlangan ($p <$ 0,001), PT ko‘rsatkichida esa sezilarli o‘zgarish kuzatilmagan[2]. Ushbu natijalar za’faronning suvli ekstrakti qon ivish tizimining ayrim ko‘rsatkichlariga ta’sir qilishi mumkinligini ko‘rsatadi.

Za’faronning farmakologik xususiyatlariga bag‘ishlangan ilmiy sharhlarda ham uning ko‘p komponentli kimyoviy tarkibi va turli biologik faolliklari ta’kidlangan. Biroq mavjud ma’lumotlar za’faron ekstraktlarining antikoagulyant ta’sir mexanizmlarini, faol metabolitlarning o‘zaro ta’sirini va ularning samarali konsentratsiyalarini yanada chuqurroq o‘rganish zarurligini ko‘rsatadi. Shu nuqtayi nazardan, nafaqat o‘simlikning o‘zi, balki u bilan bog‘liq mikroorganizmlar tomonidan ishlab chiqariladigan ikkilamchi metabolitlarni ham tadqiq etish muhim ilmiy yo‘nalish hisoblanadi.

O‘simliklarning to‘qimalarida yashovchi endofit zamburug‘lar mezbon o‘simlik bilan yaqin biologik munosabatda bo‘lib, turli xil ikkilamchi metabolitlarni sintez qilish qobiliyatiga ega. Ushbu metabolitlar antibakterial, antioksidant va boshqa biologik faolliklarni namoyon qilishi mumkin. Endofit zamburug‘lar tomonidan ishlab chiqariladigan birikmalar tarkibi va faolligi zamburug‘ turiga, mezbon o‘simlikka hamda o‘stirish sharoitlariga bog‘liq bo‘lishi mumkin. Shu sababli, dorivor o‘simliklardan ajratib olingan endofit zamburug‘lar yangi biologik faol moddalarni izlashda istiqbolli manba sifatida qaraladi.

Chamkhi va hammualliflar Marokashning Taliouine hududida o‘sadigan *Crocus sativus* L. ildizlaridan 60 ta endofit zamburug‘ izolatini ajratib olib, ularning biologik xususiyatlarini o‘rgangan. Tadqiqot natijasida *Rhizopus oryzae*, *Aspergillus fumigatiaffinis* va *Aspergillus niger* turlari identifikatsiya qilingan. Ushbu zamburug‘lardan olingan ekstraktlarning antibakterial va antioksidant faolligi baholangan[1],[4]. Shunga qaramay, yuqorida keltirilgan za’faron endofitlariga oid tadqiqotlarda zamburug‘ ekstraktlarining antikoagulyant faolligi bevosita baholanmagan. Demak, *Crocus sativus* endofitlarining qon ivish jarayoniga ta’siri va ular sintez qiladigan metabolitlarning potensial antikoagulyant xususiyatlari yetarlicha o‘rganilmagan ilmiy yo‘nalishlardan biri bo‘lib qolmoqda.

Endofit zamburug‘larni ajratish, ularni identifikatsiya qilish, ekstraktlarining biologik faolligini baholash va faol metabolitlarni aniqlash ushbu bo‘shliqni to‘ldirishga xizmat qilishi mumkin. Shu munosabat bilan, mazkur tadqiqotning dolzarbligi *Crocus sativus* L. bilan bog‘liq endofit zamburug‘larning biologik faol metabolitlarini o‘rganish va ularning antikoagulyant xususiyatlarini baholash zarurati bilan belgilanadi.

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Material va metodlar

Endofit zamburug‘larning biomassasidan ikkilamchi metabolitlarni ajratib olishda Hazalin va boshqalar uslubidan biroz modifikatsiya bilan foydalanildi [3]. Bunda -40° C da muzlatilgan 1g biomassa maydalangan kvarts bilan chinni xovonchada yaxshilab ezilib gomogenizat holiga kelgandan so‘ng sirka kislotaning etil efiri (etilatsetat)dan 5 ml solindi va kolbaga o‘tkazilib, xona temperaturasida 24 soatga tebratgichda qoldirildi. Keyin massa filtr (Vattman №1) qog‘ozdan filtrlab o‘tkazildi va suvli qatlamni yo‘qotish maqsadida 40 mkg/ml natriy sulfat solindi. Shundan keyin aralashmalarni rotorli bug‘latgichda bug‘latildi. Quruq ikkilamchi metabolitlari 1,0 ml etil spirtida qayta suspenziya qilindi va +4° C da saqlandi.

Ekstraksiyalar plazma rekalsiyfikatsiya vaqti (PRT) testiga quyidagi metod orqali tekshirildi. Venoz qon 3,8% natriy sitratini o‘z ichiga olgan probirkalarga olindi. Ushbu probirkalar qonning antikoagulyantga nisbatini 9:1 darajasida ushlab turdi. Qonni qayta kalsiyfikatsiya qilish vaqti odatda namuna olinganidan keyin yarim soat ichida o‘lchandi. 0,2 ml sitratlangan qon namunasi 12 x 75 mm idishga o‘tkazildi. Shisha probirka va suv hammomda 37 ° C da 2 daqiqa davomida inkubatsiya qilindi. Bunga 0,2 ml 0,025 M kalsiy xlorid qo‘shildi va bir vaqtning o‘zida taymerni (sekundomer) yoqildi. Ingredientlar aralashtirildi va trubka fibrin iplarining ko‘rinishini kuzatish uchun taxminan 20 soniya oralig‘ida yengil aylanish harakati bilan oldinga va orqaga sekin egildi. Kalsiy xlorid qo‘shilishi va eng birinchi kuzatilgan fibrin iplari hosil bo‘lishi o‘rtasidagi vaqt qonni qayta kalsiyfikatsiya qilish vaqti sifatida qayd etildi[6].

Natijalar va ularning muhokamasi

Tadqiqot uchun foydalanilgan endofit zamburug‘lar *Crocus sativus* o‘simligidan ajratilgan bo‘lib, o‘simlik Toshkent viloyatining Chatqol qo‘riqxonasi tog‘oldi hududidan (dengiz sathidan 1000 m balandlikda) keltirildi. Za’faronning poyasi, ildizi va bargidan ajratib olingan zamburug‘ izolatlarining tarkibi xilma-xil, ya’ni o‘simlikning turli organlaridan *Aspergillus, Penicillium, Fusarium, Alternaria* kabi avlodlarga mansub endofit zamburug‘lar ajratilgan. Tadqiqotda *Crocus sativus* o‘simligidan ajratilgan 17 ta shtammini umumiy ekstraktlarining ikkilamchi metabolitlari rekalsiyfikatsiya usuli bo‘yicha tekshirildi.

1-jadval. Endofit zamburug‘lar ekstraktlarining plazma rekalsiyfikatsiya vaqtiga (PRT) ta’siri

№	Namunalar	PRT (soniya)
	Nazorat	1,48 ± 0,02
	Etanol	1,43 ± 0,01
	Varfarin	>120
	Geparin	>120
1	*Aspergillus terreus CS16S*	2,45±0,04
2	*Aspergillus terricola CS17S*	3,16±0,04
3	*Penicillium sp. CS18S*	2,18±0,03
4	*Fusarium sp. CS23S*	1,49±0,02
5	*Penicillium rubrum CS51S*	2,34±0,03
6	*Alternaria sp. CS53S*	2,51±0,04
7	*Gliocladium sp. CS54S*	3,07±0,05
8	*Aspergillus niger CS14R*	2,18±0,03
9	*Aspergillus terreus CS15R*	2,10±0,03
10	*Penicillium sp. CS19R*	4,09±0,06
11	*Penicillium sp. CS20R*	2,24±0,03
12	*Penicillium sp. CS21R*	1,53±0,02
13	*Fusarium sp. CS22R*	1,58±0,02
14	*Acremonium sp. CS24R*	2,28±0,03

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15	*Cunninghamella sp. CS25R*	2,13±0,03
16	*Penicillium sp. CS50R*	>120,0
17	*Alternaria sp. CS52L*	4,49±0,07

Jadval natijalariga ko‘ra, endofit zamburug‘lar ekstraktlarining PRT ko‘rsatkichiga ta’siri turlicha bo‘lgan. Eng qisqa vaqt *Fusarium sp.* CS23S namunasida (1,49 ± 0,02 daqiqa), eng uzoq vaqt esa *Penicillium sp.* CS50R namunasida (>120 daqiqa) kuzatilgan. CS50R namunasida PRTning keskin uzayishi potensial antikoagulyant faollik mavjudligini taxmin qiladi. Biroq ushbu xulosani tasdiqlash uchun qo‘shimcha tajribalar va statistik tahlil talab etiladi.

Xulosa

Tadqiqot natijalariga ko‘ra, za’faron (*Crocus sativus* L.) endofit zamburug‘lari ekstraktlarining plazmani rekalsiyfikatsiya vaqtiga ta’siri turlicha bo‘ldi. Ayniqsa, *Penicillium sp.* CS50R izolatida PRT ko‘rsatkichining 120 daqiqadan ortishi uning potensial antikoagulyant faolligini ko‘rsatadi. Ushbu izolat kelgusida antikoagulyant xususiyatga ega biologik faol birikmalarni aniqlash uchun istiqbolli manba sifatida chuqurroq o‘rganilishi lozim.

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EKSPERIMENTAL SEMIRISHDA SINBIOTIK TERAPIYANING LIPID ALMASHINUVI BIOMARKERLARIGA TA’SIRI

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Annotatsiya: Ushbu tadqiqotda yuqori yog‘li ratsion (HFD) yordamida induksiyalangan eksperimental semirish modelida mahalliy sut kislotasi bakteriyalari shtammlari va inulin asosida yaratilgan sinbiotik kompozitsiyaning tana vazni, lipid almashinuvi biomarkerlari hamda enteroendokrin gormonlar darajasiga ta’siri baholandi. Tajribalar olti guruhga ajratilgan 36 ta laboratoriya kalamushida o‘tkazildi. Sinbiotik vosita 30 kun davomida qo‘llanildi. Tadqiqot natijalariga ko‘ra, sinbiotik qabul qilgan hayvonlarda tana vazni, jigar va yog‘ to‘qimasi massasi HFD nazorat guruhiga nisbatan kamaydi. Qon zardobida triglitseridlar va past zichlikdagi lipoproteinlar miqdori pasayib, yuqori zichlikdagi lipoproteinlar darajasi oshdi. Shuningdek, GLP-1, GLP-2 va PYY enteroendokrin gormonlari darajasining ortishi aniqlandi. Olingan natijalar mahalliy probiotik shtammlar va inulin asosidagi sinbiotik kompozitsiyaning eksperimental semirish sharoitida lipid almashinuvini yaxshilash va metabolik buzilishlarni modulyatsiya qilish salohiyatiga ega ekanligini ko‘rsatadi.

Kalit so‘zlar: eksperimental semirish, sinbiotik, probiotik bakteriyalar, inulin, lipid almashinuvi, triglitseridlar, lipoproteinlar, GLP-1, GLP-2, PYY.

Аннотация: В работе изучено влияние синбиотической композиции на основе местных штаммов молочнокислых бактерий и инулина на массу тела, биомаркеры липидного обмена и уровень энтероэндокринных гормонов при экспериментальном ожирении, индуцированном высокожировой диетой (HFD). Исследование проведено на 36 лабораторных крысах, распределённых на шесть экспериментальных групп. Синбиотическую композицию применяли в течение 30 дней. Установлено, что введение синбиотика сопровождалось снижением массы тела, печени и жировой ткани по сравнению с контрольной группой, получавшей высокожировую диету. Выявлено снижение концентрации триглицеридов и липопротеинов низкой плотности при одновременном повышении уровня липопротеинов высокой плотности. Кроме того, отмечено увеличение концентрации энтероэндокринных гормонов GLP-1, GLP-2 и PYY. Полученные результаты свидетельствуют о потенциальной эффективности синбиотической композиции на основе местных пробиотических штаммов и инулина в коррекции нарушений липидного обмена и модуляции метаболических процессов при экспериментальном ожирении.

Ключевые слова: экспериментальное ожирение, синбиотик, пробиотические бактерии, инулин, липидный обмен, триглицериды, липопротеины, GLP-1, GLP-2, PYY.

Abstract: This study evaluated the effects of a synbiotic formulation containing indigenous lactic acid bacterial strains and inulin on body weight, lipid metabolism biomarkers, and enteroendocrine hormone levels in a high-fat diet (HFD)-induced experimental model of obesity. The experiment was conducted on 36 laboratory rats randomly assigned to six groups. The synbiotic formulation was administered for 30 days. The results demonstrated that synbiotic supplementation was associated with reductions in body weight, liver weight, and adipose tissue mass compared with the untreated HFD group. Furthermore, serum triglyceride and low-density lipoprotein cholesterol

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levels decreased, while high-density lipoprotein cholesterol levels increased. Elevated levels of the enteroendocrine hormones GLP-1, GLP-2, and PYY were also observed. These findings suggest that a synbiotic formulation comprising indigenous probiotic strains and inulin may improve lipid metabolism and modulate metabolic disturbances associated with diet-induced obesity.

Keywords: experimental obesity, synbiotic, probiotic bacteria, inulin, lipid metabolism, triglycerides, lipoproteins, GLP-1, GLP-2, PYY.

Kirish

Hozirgi kunda semizlik butun dunyo miqyosida keng tarqalib borayotgan, inson salomatligi va hayot sifatiga jiddiy ta’sir ko‘rsatuvchi surunkali metabolik buzilishlardan biri hisoblanadi. Semizlikning rivojlanishi energiya almashinuvi muvozanatining buzilishi bilan bir qatorda, glyukoza va lipid almashinuvi, ichak mikrobiotasi tarkibi, immun va gormonal jarayonlarning o‘zgarishi bilan chambarchas bog‘liq. So‘nggi yillarda semizlikning rivojlanish mexanizmlarida ichak mikrobiotasining tarkibiy va funksional o‘zgarishlari muhim omil sifatida qaralmoqda. Ichak disbiozi metabolik jarayonlarning yanada izdan chiqishiga, yallig‘lanish mediatorlari ishlab chiqarilishining ortishiga va insulin rezistentligining kuchayishiga olib keladi. Shu nuqtai nazardan, organizmga yumshoq ta’sir ko‘rsatuvchi, metabolik jarayonlarni kompleks ravishda modulyatsiya qila oladigan va xavfsizlik profili yuqori bo‘lgan biologik vositalarni, xususan probiotik mikroorganizmlar va prebiotik komponentlarning (inulin) sinergik birikmasidan iborat sinbiotik kompozitsiyalarni o‘rganish va yaratish zamonaviy mikrobiologiya hamda biotexnologiyaning dolzarb vazifalaridan biridir [1, 2].

Tadqiqot maqsadi. Yuqori yog‘li ozuqa ratsioni (High-Fat Diet, HFD) bilan induksiyalangan kalamushlardagi semirish eksperimental modelida mahalliy sut kislotasi bakteriyalari shtammlari aralashmasi hamda inulin asosida tayyorlangan sinbiotik vositaning hayvonlar tana vazni, ichki organ ko‘rsatkichlari, lipid profili hamda enteroendokrin gormonlar darajasiga ta’sirini in vivo sharoitda qiyosiy baholash.

Materiallar va uslublar

Tadqiqotlar massasi 140–160 g bo‘lgan laboratoriya oq kalamushlarida o‘tkazildi. Semirishning eksperimental modeli laboratoriya kalamushlarini 2 oy davomida yog‘lar hisobiga ratsion kaloriyasining 60% ini ta’minlaydigan yuqori yog‘li dieta (HFD) bilan oziqlantirish orqali yaratildi. Hayvonlar har bir guruhda 6 tadan bo‘lgan 6 ta guruhga randomizatsiya qilindi: A guruh — nazorat guruhi (standart ratsion); B guruh — semirish modeli (HFD, davolash davrida suv berildi); C guruh — HFD + «Laktobakteriyalar» shtammlari aralashmasi (L. plantarum FC-2, E. faecium 1, P. acidilactici AK 1.2, P. acidilactici AK 1.5, L. paracasei G/S 4.2); D guruh — HFD + sinbiotik vosita («Laktobakteriyalar» + 1% inulin); E guruh — HFD + inulin (5 mg/kg); F guruh — HFD + Lacto Fit Probiotics Slim (Janubiy Koreya, taqqoslash preparati). Tadqiq etilayotgan namunalar 30 kun davomida har kuni 1×10^8 KHB dozada og‘iz orqali yuborildi. Hayvonlarning tana vazni dinamikasi muntazam qayd etildi. Eksperiment yakunida qon zardobida lipid almashinuvi ko‘rsatkichlari (umumiy xolesterin, triglitseridlar (TG), YuZLP va PZLP xolesterini) hamda ichak gormonlari (GLP-1, GLP-2, PYY) konsentratsiyasi immunoferment tahlili (IFA) usuli yordamida aniqlandi. Evtanaziyadan so‘ng jigar, yurak va aorta massasi o‘lchandi. Natijalar GraphPad Prism 8.0.0 dasturida ANOVA usuli bilan tahlil qilindi ($p=0,05$).

Tadqiqot natijalari va ularning muhokamasi

Tadqiq qilinayotgan namunalarni qo‘llash boshlanguniga qadar (60-kun) barcha HFD guruhlaridagi hayvonlarning tana massasi izchil ortib, guruhlararo farqsiz bo‘ldi. Biroq, 90-kunlik tajriba yakunida korreksiya qo‘llanilmagan B guruhida (HFD) tana massasi eng yuqori darajaga — 352,33±8,41 g ga yetdi, bu semirishning yaqqol rivojlanganligini ko‘rsatadi. C guruhida (HFD + «Laktobakteriyalar») hayvonlar massasi 333,00±7,92 g ni tashkil etib, B guruhiga nisbatan statistik jihatdan ishonchli darajada past bo‘ldi ($p\leq0,01$). Eng sezilarli antiobezogen samara D guruhida (HFD + «Laktobakteriyalar» + inulin) qayd etildi, unda hayvonlar massasi 320,83±6,08 g bo‘lib, B guruhiga

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nisbatan eng keskin kamayishni namoyon qildi (p≤0,001). Taqqoslash guruhi F da esa vazn 318,67±6,35 g bo‘ldi (p≤0,001).

Ichki organlar massasi tahlili shuni ko‘rsatdiki, B guruhida jigar massasi intakt guruhga nisbatan keskin ortib, 8,107±0,976 g ni tashkil etdi, bu esa jigarning yog‘li infiltratsiyasi (steatoz) bilan bog‘liq. Sinbiotik vosita qo‘llanilgan D guruhida jigar massasi 6,535±0,242 g gacha ishonchli ravishda kamaydi (p≤0,001), bu ko‘rsatkich F guruhida 6,583±0,801 g ni tashkil etdi (p≤0,001). B guruhida yog‘ to‘qimasi massasi 3,229±0,522 g ga yetgan bo‘lsa, D guruhida u 2,627±0,461 g gacha, F guruhida esa 2,583±0,496 g gacha kamaydi. Yurak va aorta massasida guruhlararo keskin farqlar aniqlanmadi.

Lipid almashinuvi tahlili shuni ko‘rsatdiki, HFD (B guruh) xolesterin (1,515±0,260 mmol/l) va TG (266,17±18,81 mkg/ml) hamda PZLP (1,372±0,066 mmol/l) darajasining oshishi, shuningdek YuZLP (0,818±0,071 mmol/l) darajasining pasayishi bilan kechdi. Sinbiotik kompozitsiyani qo‘llash (D guruhi) TG miqdorini 193,01±48,13 mkg/ml gacha (p≤0,01), PZLP darajasini 1,028±0,062 mmol/l gacha (p≤0,001) pasaytirdi va antiaterogen YuZLP xolesterinini 1,070±0,088 mmol/l gacha (p≤0,001) oshirdi, bu taqqoslash preparati (F guruhi) ko‘rsatkichlariga juda yaqin bo‘ldi.

Energetik almashinuv va ishtahani boshqarishda ishtirok etuvchi ichak gormonlarini o‘rganish natijasida, B guruhida to‘qlik hissini beruvchi GLP-1 va PYY gormonlarining ishlab chiqarilishi susayganligi aniqlandi. Sinbiotik vosita (D guruhi) yuborilishi qon zardobida GLP-1 darajasini 146,31±25,08 pg/ml gacha (p≤0,05; B guruhida 108,77±10,51 pg/ml), GLP-2 darajasini 134,64±22,06 pg/ml gacha (p≤0,05; B guruhida 86,59±15,67 pg/ml) va PYY miqdorini 105,36±5,25 pg/ml gacha (B guruhida 71,84±32,00 pg/ml) sezilarli darajada ko‘tardi. Ushbu gormonal rag‘batlantirish sinbiotikning ishtahani markaziy boshqarish va tana vaznini tormozlash qobiliyatining asosiy mexanizmi hisoblanadi [3].

Xulosalar

- Yuqori yog‘li parhez ta’sirida rivojlanadigan semirish sharoitida mahalliy probiotik laktobakteriyalar shtammlari va inulin asosidagi sinbiotik vositani qo‘llash hayvonlar tana vazni ortishini samarali tormozlaydi, jigar va adipoz to‘qimalarda ortiqcha lipidlar to‘planishini ishonchli darajada cheklaydi.
- Sinbiotik vosita lipid profilining aterogen fraksiyalari (TG, PZLP) miqdorini pasaytirib, yuqori zichlikdagi lipoproteinlar (YuZLP) darajasini oshirish orqali tizimli gipolipidemik va gepatoprotektiv ta’sir ko‘rsatadi.
- Mahalliy sinbiotik kompozitsiyaning antiobezogen ta’sir mexanizmi ichak enteroendokrin L-hujayralari faoliyatini modulyatsiya qilish, to‘qlik gormonlari (GLP-1, GLP-2 va PYY) sekretsiyasini rag‘batlantirish hamda shu orqali organizmda metabolik homeostazni tiklash qobiliyati bilan chambarchas bog‘liqdir.

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STREPTOMYCES SPECTABILIS IMB Uz-1 ҚУРУҚ БИОМАССАСИ ВА ПРОДИГИОЗИННИНГ *IN VIVO* ШАРОИТДА ЎТКИР ТОКСИКЛИГИНИ БАҲОЛАШ

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Республика тиббиёт ва фармацевтика ходимларининг малакасини ошириш ва ихтисослаштириш маркази Наманган филиали ўқитувчиси.

Кириш

Микроорганизмлар томонидан синтез қилинадиган биологик фаол бирикмалар фармацевтика ва биотехнология соҳалари учун истиқболли манбалардан бири ҳисобланади. Хусусан, *Streptomyces* авлоди вакиллари турли иккиламчи метаболитларни ишлаб чиқариши билан ажралиб туради. Ушбу бирикмаларнинг биологик фаоллигини ўрганиш билан бир қаторда, уларнинг хавфсизлигини баҳолаш ҳам амалий қўллаш имкониятларини аниқлашда муҳим аҳамиятга эга. Продигиозин — айрим бактериялар, жумладан *Serratia* авлоди вакиллари ҳамда бошқа микроорганизмлар томонидан ишлаб чиқариладиган қизил рангли, пиррол тузилишига эга иккиламчи метаболитдир. Адабиётларда унинг антибактериал, цитотоксик ва иммуномодулятор хусусиятлари ёритилган. Бироқ продигиозиннинг биологик фаоллиги унинг хавфсизлигини тўлиқ ифодаламайди. Шу сабабли унинг токсикологик хусусиятларини экспериментал баҳолаш зарур. Микробиологик маҳсулотлар хавфсизлигини ўрганишда мақсадли метаболит билан бир қаторда, уни ишлаб чиқарувчи микроорганизм биомассасини ҳам баҳолаш муҳимдир. Қуруқ биомасса ҳужайра компонентлари ва турли метаболитларни сақлаши мумкин. Шу сабабли *Streptomyces spectabilis IMB_Uz-1* қуруқ биомассаси ва ундан ажратилган продигиозиннинг токсикологик таъсирини алоҳида ўрганиш уларнинг хавфсизлик хусусиятларини фарқлаш имконини беради. Ўткир токсикликни in vivo шароитида баҳолаш текширилаётган модданинг қисқа муддатли таъсири билан боғлиқ ножўя оқибатларни аниқлашга хизмат қилади. Иқтисодий ҳамкорлик ва тараққиёт ташкилоти (OECD) томонидан ишлаб чиқилган 423 ва 425-сонли тест қўлланмалари оғиз орқали юбориладиган моддаларнинг ўткир токсиклигини баҳолаш бўйича халқаро методологик тавсияларни белгилайди. Бунда олинган натижалар қўлланилган доза, юбориш йўли, кузатув даври ва тажрибада қайд этилган кўрсаткичлар ҳисобга олинган ҳолда талқин қилиниши лозим.

Шу муносабат билан, мазкур тадқиқотнинг мақсади *Streptomyces spectabilis IMB_Uz-1* штаммининг қуруқ биомассаси ва ундан ажратилган продигиозиннинг in vivo шароитидаги ўткир токсиклигини баҳолаш ҳамда тажрибада кузатилган токсикологик кўрсаткичларни тавсифлашдан иборат.

ИҚТИБОС УЧУН
Абдуназаров Н., Мамарасулов Б., Бойматова М. Streptomyces spectabilis IMB Uz-1 қуруқ биомассаси ва продигиозиннинг in vivo шароитда ўткир токсиклигини баҳолаш // Фундаментал ва амалий микробиологиянинг бугунги ҳолати ва ривожланиш истиқболлари: ёш олимлар нигоҳи: Республика илмий-амалий анжумани материаллари. – Тошкент, 2026. – Б. 241–244.
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Тадқиқот методологияси

Streptomyces spectabilis IMB_Uz-1 штаммининг қуритилган биомассаси ҳамда ундан ажратиб олинган тозаланган продигиозиннинг in vivo шароитдаги ўткир токсиклик хусусиятлари лаборатория ҳайвонларида баҳоланди. Тадқиқот лаборатория ҳайвонларида биомедицин тадқиқотлар ўтказишнинг халқаро биоэтик меъёрлари ҳамда OECD Guideline 423 (Acute Oral Toxicity - Acute Toxic Class Method) талабларига мувофиқ амалга оширилди. Тажриба учун соғлом вояга етган эркак оқ сичқонлар (20–25 g) танланди. Ҳайвонлар тажриба бошланишидан олдин стандарт виварий шароитида сақланди (22±2°C ҳарорат, 50–60% нисбий намлик, 12 соат ёруғлик/12 соат қоронғилик режими), озуқа ва сув билан эркин таъминланди. Тажриба олдидан ҳайвонлар 12 соат давомида оч қолдирилди, сув эса эркин берилди. Ҳайвонлар тасодифий равишда тажриба ва назорат гуруҳларига ажратилди. Ҳар бир гуруҳда 5 тадан ҳайвон бўлди. Қуруқ биомасса 2000 mg/kg дозада, тозаланган продигиозин эса 800, 1500 ва 2000 mg/kg дозаларда бир марта перорал усулда юборилди. Назорат гуруҳига шу ҳажмда физиологик эритма (ёки препаратни эритишда ишлатилган эритувчи) берилди. Препарат юборилгандан кейин ҳайвонлар дастлабки 4 соат давомида узлуксиз кузатилди, кейин эса 14 кун мобайнида ҳар куни мониторинг қилинди. Кузатувлар давомида ўлим ҳолати, умумий хулқ-атвор, ҳаракат фаоллиги, нафас олиш, овқат ва сув истеъмоли, жун қопламининг ҳолати, тана вазнининг ўзгариши ҳамда интоксикациянинг бошқа клиник белгилари баҳоланди. Тана вазни тажрибанинг 1-, 7- ва 14-кунларида ўлчанди. Кузатув даври тугагач, ҳар бир доза учун ўлим кўрсаткичлари таҳлил қилиниб, препаратларнинг ўртача летал дозаси (LD_{50}) OECD тавсиялари асосида баҳоланди. Шунингдек, қуруқ биомасса ва продигиозиннинг хавфсизлик даражаси уларнинг клиник белгилари, тирик қолиш кўрсаткичлари ҳамда тана вазни динамикаси асосида баҳоланди.

Натижа

Streptomyces spectabilis IMB Uz-1 штамми ҳамда ундан ажратиб олинган продигиозиннинг ўткир токсиклиги OECD TG 420 (Fixed Dose Procedure) халқаро қўлланмаси асосида лаборатория сичқонларида баҳоланди (2-жадвал). Тадқиқот давомида ҳайвонларнинг умумий ҳолати, клиник белгилари, тана массасидаги ўзгаришлар, тирик қолиш даражаси ҳамда летал ҳолатлар мунтазам кузатиб борилди. *Streptomyces spectabilis IMB Uz-1* штамми 2000 mg/kg дозада интрагастрал юборилганда ҳайвонларда дастлабки 10 дақиқа ичида нафас олиш тезлашиши ва қисқа муддатли ҳаракат фаолиятининг пасайиши кузатилди. Бироқ ушбу функционал ўзгаришлар 50–55 дақиқа давом этиб, 4-5 соатдан кейин ҳайвонларнинг умумий ҳолати тўлиқ меъёрлашди. Кейинги 14 кунлик кузатув давомида ўлим ҳолатлари қайд этилмади (5/5 тирик), кечиккан интоксикация белгилари ҳам аниқланмади. Шунингдек, тана массасида статистик жиҳатдан аҳамиятли салбий ўзгаришлар кузатилмади. Продигиозин 2000 mg/kg дозада юборилганда ҳайвонларда нафас олиш тезлашиши, ҳаракат фаоллигининг пасайиши ҳамда бир жойда тўпланиб қолиш каби клиник белгилар кузатилди. Ушбу ҳолатлар тахминан 1-1,5 соат сақланди.

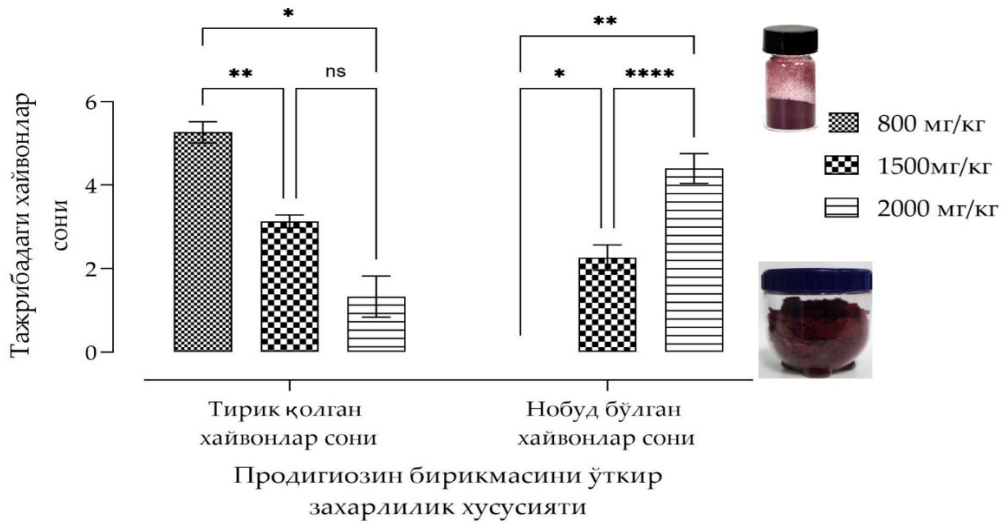
1-жадвал. *S. spectabilis IMB_ Uz-1* штамми биомассаси ва продигиозин бирикмасининг ўткир заҳарлилик хусусияти

Гуруҳлар	Ҳайвон тури ва жинси	Доза мг/кг	Гуруҳдаги нобуд бўлган ҳайвон сони	ҳайвон массаси (г)			LD_{50}
				1	7	14	
Биомасса	Оқ эркак сичқонлар	2000	5/0	22	24	25	>2000 мг/кг
Продигиозин		2000	5/4	22	20	18	

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		1500	5/2	21	20	20	800 - 2000 мг/кг
		800	5/0	21	22	23	
Назорат		0,4 мл	5/0	21	22	24	

Кейинги кузатувларда тажрибанинг иккинчи кунида ҳайвонларнинг 60 % ида, учинчи кунида эса 80 % ида ўлим ҳолати қайд этилди (4/5). Тирик қолган ҳайвонларда эса тана массасининг камайиши ва ўткир интоксикацияга хос функционал ўзгаришлар сақланиб қолди. Токсиклик даражасини аниқроқ баҳолаш мақсадида продигиозиннинг 1500 ва 800 mg/kg дозалари ҳам синовдан ўтказилди. 1500 mg/kg дозада умумий ҳолатнинг сусайиши, ҳаракат фаоллигининг пасайиши, нафас олиш тезлашиши ҳамда ташқи таъсирларга реакциянинг камайиши қайд этилди. Ушбу гуруҳда 14 кунлик кузатув давомида ҳайвонларнинг 40 % ида (2/5) ўлим ҳолати кузатилди. Тирик қолган ҳайвонларда тана массасининг бироз пасайиши ҳамда енгил функционал ўзгаришлар сақланди (1-расм).



1-расм. Турли дозаларда продигиозиннинг лаборатория сичқонларида ўткир токсиклиги (OECD TG 420) бўйича тирик қолган ва нобуд бўлган ҳайвонлар сони

(Изоҳ: Қийматлар ҳар бир гуруҳдаги ҳайвонлар сони (n = 5) бўйича келтирилган. *p < 0.05; **p < 0.01; ***p < 0.0001; ns – статистик аҳамиятга эга эмас)

Продигиозиннинг 800 mg/kg дозасида эса аҳамиятли токсик таъсир кузатилмади. Айрим ҳайвонларда ҳаракат фаоллигининг вақтинчалик пасайиши қайд этилган бўлса-да, улар қисқа вақт ичида меъёрий ҳолатга қайтди. Кузатув давомида ўлим ҳолатлари қайд этилмади (5/5 тирик), тана массасида ҳам статистик жиҳатдан аҳамиятли салбий ўзгаришлар аниқланмади. Олинган натижаларга асосан *Streptomyces spectabilis IMB Uz-1* штамми учун ўртача ўлим дозаси (LD_{50}) 2000 mg/kg дан юқори экани аниқланди. Бу кўрсаткич мазкур штаммнинг ўткир токсиклиги жуда паст эканлигини кўрсатади. Продигиозин учун эса LD_{50} 800–2000 mg/kg диапазонида бўлиб, у GHS таснифи бўйича IV синф (кам заҳарли модда)га мансуб эканлиги аниқланди. Ўткир токсиклик синовлари *Streptomyces spectabilis IMB Uz-1* штамминг лаборатория ҳайвонлари учун хавфсизлигини кўрсатди, чунки унинг LD_{50} қиймати 2000 mg/kg дан юқори бўлди. Продигиозин юқори дозаларда дозага боғлиқ токсик таъсир намоён қилган бўлса-да, 800 mg/kg дозада аҳамиятли токсик таъсир кузатилмади. LD_{50} қийматининг 800–2000 mg/kg оралиғида бўлиши продигиозиннинг GHS таснифи бўйича IV синфга мансублигини кўрсатади ва унинг келгусида фармакологик ҳамда биотехнологик тадқиқотларда эҳтиёткорлик билан қўлланилиши мумкинлигини тасдиқлайди.

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Муҳокама

Қуруқ биомасса ва ажратилган продигиозин натижаларининг фарқланиши уларнинг таркиби ва биологик таъсир хусусиятлари билан боғлиқ бўлиши мумкин. Бироқ бу фарқнинг аниқ механизмларини белгилаш учун қўшимча токсикологик ва биокимёвий тадқиқотлар талаб этилади. Натижаларни талқин қилишда тажриба гуруҳларининг кичик ҳажми (n=5) ҳам ҳисобга олиниши лозим. Умуман, олинган маълумотлар *S. spectabilis IMB_Uz-1* қуруқ биомассаси ва продигиозиннинг ўткир токсикологик хусусиятлари бир хил эмаслигини кўрсатди. Бироқ продигиозин учун LD_{50} қийматини ва GHS бўйича хавф синфини ишончли белгилаш мақсадида қўлланилган дозалар, ўлим кўрсаткичлари ва тегишли баҳолаш методикаси ўзаро мувофиқ бўлиши керак. Шу сабабли мазкур натижаларни дастлабки токсикологик баҳолаш сифатида кўриб чиқиш ва келгусида хавфсизлик кўрсаткичларини кенгайтирилган тадқиқотлар орқали аниқлаш мақсадга мувофиқ.

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МИКРОБИОЛОГИЧЕСКИЕ АСПЕКТЫ РАЗРАБОТКИ И ПРОИЗВОДСТВА ЖЕЛЕЗОСОДЕРЖАЩИХ ТАБЛЕТОК «АФЕРОЛ»

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Аннотация: В статье представлены результаты анализа микробиологических рисков при разработке технологии нестерильных железосодержащих таблеток на основе фумарата железа (препарат «Аферол»). В ходе отработки технологического процесса определены критические точки, установлены практические числовые ориентиры по остаточной влаге и биозагрузке, проведен микробиологический контроль вспомогательных веществ и готовой продукции, а также сформулированы меры по обеспечению микробиологической чистоты в соответствии с требованиями GMP.

Ключевые слова: микробиологические риски, железосодержащие таблетки, фумарат железа, «Аферол», GMP, остаточная влага, биозагрузка, ТАМС, ТУМС.

Annotatsiya: Maqolada temir fumarat asosidagi steril bo‘lmagan temir saqlovchi tabletkalar texnologiyasini ishlab chiqishda mikrobiologik xavflarni tahlil qilish natijalari keltirilgan («Aferol» preparati). Texnologik jarayonni ishlab chiqish davomida kritik nuqtalar aniqlangan, qoldiq namlik va bioburden bo‘yicha amaliy raqamli yo‘naltiruvchi qiymatlar belgilangan, yordamchi moddalar va tayyor mahsulotning mikrobiologik nazorati o‘tkazilgan hamda GMP talablariga muvofiq tozalikni ta’minlash choralari shakllantirilgan.

Kalit so‘zlar: mikrobiologik xavflar, temir saqlovchi tabletkalar, temir fumarat, Aferol, GMP, qoldiq namlik, bioyuklama, TAMC, TYMC.

Abstract: The article presents the results of the analysis of microbiological risks during the development of the technology of non-sterile iron-containing tablets based on ferrous fumarate (drug «Aferol»). During the process development, critical points were identified, practical numerical guidelines for residual moisture and bioburden were established, microbiological control of excipients and finished product was performed, and measures to ensure microbiological purity in accordance with GMP requirements were formulated.

Keywords: microbiological risks, iron-containing tablets, ferrous fumarate, Aferol, GMP, residual moisture, bioburden, TAMC, TYMC.

Введение

Железосодержащие таблетки, предназначенные для коррекции железодефицитных состояний, относятся к категории нестерильных лекарственных средств для приёма внутрь. Согласно требованиям Государственной фармакопеи РУз для твёрдых (неводных) препаратов данной группы установлены следующие критерии микробиологической чистоты: общее число аэробных микроорганизмов (ТАМС) — не более 10^3 КОЕ/г, общее число дрожжевых и плесневых грибов (ТУМС) — не более 10^2 КОЕ/г, отсутствие Escherichia coli в 1 г [1, 2].

ДЛЯ ЦИТИРОВАНИЯ
Юнусова Х.М., Илхамова Н.Б., Касимова Ш.А., Анварова М.Ж. Микробиологические аспекты разработки и производства железосодержащих таблеток «Аферол» // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 245–248.
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В процессе разработки технологии таблеток «Аферол» (на основе фумарата железа) особое внимание уделялось микробиологическим рискам, связанным с влажной грануляцией, составом вспомогательных веществ и условиями хранения.

Цель работы — выявить критические точки процесса, провести контроль микробиологической чистоты используемых материалов и установить практические числовые ориентиры, обеспечивающие соответствие готовой продукции фармакопейным требованиям.

Материалы и методы

Исследования проводились в ходе разработки и апробации технологии получения таблеток «Аферол». Анализировались критические точки процесса: сырьё и вспомогательные вещества, стадии влажной грануляции и сушки, производственная среда, а также условия хранения готовой продукции.

В процессе отработки технологии проводился входной микробиологический контроль вспомогательных веществ, определялись фактические значения остаточной влаги гранулята и результаты контроля готовых таблеток. Оценка рисков проводилась с учётом вероятности контаминации и влияния влаги на рост микроорганизмов. Установленные ориентиры использовались для корректировки параметров процесса и формирования спецификаций.

Результаты

В ходе разработки технологии таблеток «Аферол» выделены основные микробиологические риски. Критерии приёмки для готовой продукции приведены в таблице 1.

Таблица 1. Критерии микробиологической чистоты нестерильных лекарственных препаратов для приёма внутрь

Категория препарата	ТАМС, КОЕ/г	ТУМС, КОЕ/г	E. coli
Твёрдые для приёма внутрь	≤ 10^3	≤ 10^2	Отсутствие в 1 г
Жидкие для приёма внутрь	≤ 10^2	≤ 10^1	Отсутствие в 1 мл

Примечание. Лимит «≤ 10^3» интерпретируется как максимально допустимое количество 2000 КОЕ/г при учёте результатов (ГФ РУз. 5.1.4).

Требования к вспомогательным веществам, использованным при разработке технологии, представлены в таблице 2. Результаты проведённого микробиологического контроля партий вспомогательных веществ приведены в таблице 3.

Таблица 2. Микробиологические требования к вспомогательным веществам, использованным в технологии «Аферол»

Вспомогательное вещество	ТАМС, КОЕ/г	ТУМС, КОЕ/г	Дополнительные требования
Микрокристаллическая целлюлоза	≤ 1000	≤ 100	Отсутствие E. coli, Salmonella и др.
Магния стеарат	≤ 1000	≤ 500	Отсутствие E. coli, Salmonella
Лактозы моногидрат	≤ 100	≤ 50	Отсутствие E. coli
Крахмал кукурузный	≤ 1000	≤ 100	Отсутствие E. coli, Salmonella

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Таблица 3. Результаты микробиологического контроля вспомогательных веществ, использованных при разработке технологии «Аферол»

Вспомогательное вещество	ТАМС, КОЕ/г	ТУМС, КОЕ/г	Указанные микроорганизмы
Микрокристаллическая целлюлоза	120–280	< 10	Не обнаружены
Магния стеарат	40–150	< 10	Не обнаружены
Лактозы моногидрат	< 10–40	< 10	Не обнаружены
Крахмал (натрия гликолат)	80–220	< 10	Не обнаружены
Повидон	< 10	< 10	Не обнаружены

Примечание. Результаты получены при входном контроле партий, использованных в ходе отработки технологии. Все значения значительно ниже установленных требований.

Лимиты микробиологического мониторинга производственной среды, принятые при отработке процесса, приведены в таблице 4.

Таблица 4. Лимиты микробиологического мониторинга производственной среды для класса D

Класс чистоты	Активный отбор воздуха, КОЕ/м³	Седиментационные чашки (90 мм), КОЕ/4 ч	Контактные чашки (55 мм), КОЕ/чашка
D	200	100	50

Примечание. Пределы тревоги и действия устанавливались ниже рекомендуемых на основании полученных трендов.

В ходе разработки и апробации технологии таблеток «Аферол» определены практические числовые ориентиры по остаточной влаге и биозагрузке, которые использовались для корректировки параметров процесса (таблица 5).

Таблица 5. Практические числовые ориентиры, установленные при разработке технологии таблеток «Аферол»

Параметр	Установленное значение / диапазон	Применение в технологии
Остаточная влага гранулята после сушки	1,0–2,5 %	Использовано как целевой диапазон для контроля сушки
ТАМС готовых таблеток	< 10–100 КОЕ/г	Достигнуто на опытных сериях
Мониторинг воздуха (класс D)	10–80 КОЕ/м³	Поддерживалось в ходе отработки процесса

Примечание. Значения установлены в ходе отработки технологии и использованы для формирования внутренних спецификаций и параметров процесса.

Наиболее критичными точками оказались стадии влажной грануляции и сушки. Контроль остаточной влаги в установленном диапазоне 1,0–2,5 % в сочетании с входным контролем биозагрузки вспомогательных веществ (таблица 3) позволил стабильно получать таблетки с низкими значениями ТАМС.

Полученные ориентиры и результаты контроля были заложены в технологическую документацию и использованы при масштабировании процесса.

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Обсуждение

Результаты, полученные при разработке технологии «Аферол», подтверждают, что основные микробиологические риски связаны с наличием свободной влаги на стадиях грануляции и сушки, а также с биозагрузкой отдельных вспомогательных веществ. Проведённый микробиологический контроль (таблица 3) показал, что фактические значения ТАМС и ТУМС используемых партий значительно ниже установленных требований. Установленные числовые ориентиры (таблица 5) позволили формализовать контроль и обеспечить соответствие готовой продукции фармакопейным лимитам.

Практика показала, что поддержание остаточной влаги в диапазоне 1,0–2,5 % и контроль биозагрузки критичных эксципиентов являются эффективными мерами. Мониторинг производственной среды классов C и D служил дополнительным индикатором стабильности процесса. Полученные данные использовались для корректировки параметров сушки, выбора поставщиков и формирования внутренних спецификаций.

Интеграция микробиологического контроля в систему качества на этапе разработки технологии позволила снизить риски на последующих стадиях производства и хранения.

Заключение

В ходе разработки технологии таблеток «Аферол» определены основные микробиологические риски, проведён контроль микробиологической чистоты вспомогательных веществ и установлены практические числовые ориентиры по остаточной влаге и биозагрузке. Соблюдение этих ориентиров в сочетании с контролем критических точек обеспечивает соответствие готовой продукции фармакопейным требованиям по микробиологической чистоте.

Полученные результаты использованы при формировании технологической документации и могут быть применены при масштабировании производства антианемических таблеток. Дальнейшая работа направлена на накопление статистических данных по производственным сериям и уточнение внутренних спецификаций.

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PARRANDA MAHSULOTLARIDAGI *E. COLI*: ANTIBIOTIK REZISTENTLIGI VA MDR

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Annotatsiya: Mahalliy bozorlarda sotiladigan tovuq go‘shti va shaurma namunalaridan ajratib olingan bakterial izolyatlarning antibiotiklarga sezgirligi baholandi. Izolyatlarning streptomitsin, sefotaksim, siprofloksatsin, tetratsiklin va ampitsillinga sezgirligi disk-diffuzion usulda aniqlandi. Tovuq go‘shti namunalaridan 34 ta, shaurma namunalaridan esa 14 ta bakterial izolyat ajratib olindi. Ulardan 8 tasida ko‘p dori vositalariga chidamlilik (MDR) belgilari aniqlandi. Rezistent izolyatlarning tur darajasidagi identifikatsiyasi MALDI-TOF usuli yordamida amalga oshirilib, ularning *Escherichia coli* turiga mansubligi tasdiqlandi. Olingan natijalar tekshirilgan oziq-ovqat mahsulotlarida antibiotiklarga rezistent, jumladan MDR xususiyatiga ega *E. coli* shtammlari mavjudligini ko‘rsatdi hamda ularning mikrobiologik xavfsizligini muntazam monitoring qilish zarurligini asoslaydi.

Kalit so‘zlar: *Escherichia coli*, antibiotiklarga chidamlilik, AMR, MDR, parranda go‘shti, shaurma, MALDI-TOF.

Аннотация: Проведена оценка антибиотикочувствительности бактериальных изолятов, выделенных из куриного мяса и шаурмы, реализуемых на местных рынках. Чувствительность изолятов к стрептомицину, цефотаксиму, ципрофлоксацину, тетрациклину и ампициллину определяли диско-диффузионным методом. Из образцов куриного мяса было выделено 34 бактериальных изолята, из образцов шаурмы – 14 изолятов. У 8 изолятов выявлены признаки множественной лекарственной устойчивости (MDR). Видовая идентификация резистентных изолятов методом MALDI-TOF подтвердила их принадлежность к *Escherichia coli*. Полученные результаты свидетельствуют о наличии антибиотикорезистентных, в том числе MDR, штаммов *E. coli* в исследованных пищевых продуктах и подчёркивают необходимость микробиологического мониторинга их безопасности.

Ключевые слова: *Escherichia coli*, антибиотикорезистентность, AMR, MDR, мясо птицы, шаурма, MALDI-TOF.

Abstract: The antibiotic susceptibility of bacterial isolates obtained from chicken meat and shawarma samples sold in local markets was evaluated. The susceptibility of the isolates to streptomycin, cefotaxime, ciprofloxacin, tetracycline, and ampicillin was determined using the disk diffusion method. A total of 34 bacterial isolates were recovered from chicken meat samples and 14 isolates from shawarma samples. Among them, 8 isolates showed signs of multidrug resistance (MDR). Species-level identification of the resistant isolates by MALDI-TOF confirmed their affiliation with *Escherichia coli*. The obtained results indicate the presence of antibiotic-resistant, including MDR, *E. coli* strains in the investigated food products and highlight the need for regular microbiological monitoring of their safety.

Keywords: *Escherichia coli*, antimicrobial resistance, AMR, MDR, poultry meat, shawarma, MALDI-TOF.

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Kirish

Antibiotiklarga chidamlilik (AMR – Antimicrobial Resistance) bugungi kunda inson va hayvonlar salomatligi, veterinariya amaliyoti hamda oziq-ovqat xavfsizligiga jiddiy ta’sir ko‘rsatayotgan global muammolardan biri hisoblanadi. Antibakterial preparatlardan keng va ayrim hollarda nazoratsiz foydalanish natijasida mikroorganizmlarda turli antibiotiklarga nisbatan chidamlilik mexanizmlari shakllanishi va rezistent shtammlarning atrof-muhitda keng tarqalishi kuzatilmoqda. Ayniqsa, oziq-ovqat mahsulotlari orqali antibiotiklarga chidamli mikroorganizmlarning inson organizmiga uzatilishi jamoat salomatligi nuqtai nazaridan alohida ahamiyat kasb etmoqda. Bunday holatlarda chorvachilik va parrandachilik sohalari antibiotiklarga chidamli bakteriyalarning shakllanishi va tarqalishida muhim tarmoqlaridan biri sifatida qaraladi. Parrandalarda bakterial kasalliklarni davolash, profilaktika qilish, shuningdek, ayrim sharoitlarda ishlab chiqarish samaradorligini oshirish maqsadida antibakterial preparatlardan foydalanish mikrob populyatsiyalarining ortishiga olib keladi. Antibiotiklarga sezgir bakteriyalar soni kamayib, rezistent xususiyatga ega mikroorganizmlar saqlanib qolishi va ko‘payishi kuzatiladi.

Tovuq go‘shti shaurma kabi tez tayyorlanadigan ko‘cha taomlarining asosiy xomashyolaridan biri sifatida keng qo‘llaniladi. Bunday mahsulotlarni tayyorlash jarayonida xom va pishirilgan mahsulotlarning o‘zaro kontakti, bir xil ishlov berish jihozlaridan foydalanish, yetarli bo‘lmagan termik ishlov, tayyor mahsulotni saqlash haroratiga rioya qilmaslik va xodimlarning shaxsiy gigienasi bilan bog‘liq omillar ikkilamchi mikrobiologik kontaminatsiyaga olib kelishi mumkin. Shu sababli xom tovuq go‘shti bilan bir qatorda undan tayyorlangan tez tayyor bo‘luvchi mahsulotlarda ham antibiotiklarga chidamli mikroorganizmlarni aniqlash muhim ilmiy va amaliy ahamiyatga ega.

Antibiotiklarga chidamli bakteriyalarning oziq-ovqat mahsulotlarida uchrashi faqat ularning patogenlik xususiyati bilan emas, balki antibiotiklarga chidamlilik determinantlarining boshqa mikroorganizmlarga gorizontal tarzda o‘tishi ehtimoli bilan ham ahamiyatlidir. Oziq-ovqat orqali inson organizmiga tushgan rezistent bakteriyalar ichak mikrobiotasi bilan o‘zaro ta’sirga kirishishi va chidamlilik genlarining tarqalishi uchun potensial rezervuar vazifasini bajarishi mumkin. Shu jihatdan ushbu muammo «Yagona salomatlik» (One Health) konsepsiyasi doirasida inson, hayvon, oziq-ovqat va atrof-muhit o‘rtasidagi o‘zaro bog‘liqlikni hisobga olgan holda baholanishi lozim.

Shu munosabat bilan mahalliy bozorlarda sotiladigan tovuq go‘shti hamda undan tayyorlangan shaurma mahsulotlarining mikrobiologik holatini o‘rganish, ulardan antibiotiklarga chidamli bakteriyalarni ajratib olish va antibiotiklarga sezgirlik xususiyatlarini baholash oziq-ovqat xavfsizligini ta’minlash nuqtai nazaridan dolzarb hisoblanadi.

Mazkur tadqiqotning **maqsadi** tovuq go‘shti va undan tayyorlangan shaurma namunalaridan ajratilgan bakteriyalarning ayrim antibiotiklarga nisbatan chidamlilik xususiyatlarini aniqlash hamda ularning potensial mikrobiologik xavfini baholashdan iborat**.**

Materiallar va metodlar

Tadqiqotlar O‘zR FA Mikrobiologiya institutining “Inson mikrobiomi” laboratoriyasida bajarildi. Namunalar sifatida mahalliy bozorlardagi tovuq go‘shtining son mushaklari, jigar, buyrak, yurak va boshqa to‘qimalari, shuningdek, tovuq go‘shtidan tayyorlangan shaurma olindi. Bakteriyalar go‘sht-pepton agar va antibiotik qo‘shilgan Myuller–Hinton agarda ajratildi. Izolyatlar morfologik va tinktorial (gramm musbat va gramm manfiy bo‘yalish) belgilari bo‘yicha baholandi. Antibiotiklarga sezgirlik 0,5 McFarland standartiga mos suspenziyada disk-diffuzion usul bilan aniqlandi; streptomitsin, sefotaksim, siprofloksatsin, tetrasiklin va ampitsillin qo‘llanildi. Ingibitsiya zonalari EUCAST mezonlari asosida S, I va R guruhlariga ajratildi. Rezistent izolyatlar MALDI-TOF mass-spektrometriyasida identifikatsiya qilindi.

Natijalar

Tovuq go‘shti mahsulotlaridan 34 ta, shaurmadan 14 ta bakteriya izolyati ajratildi. Yurak, jigar va buyrak namunalarida koloniyalar soni nisbatan ko‘proq qayd etildi. Antibiotiklarga

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sezgirlikda ingibitsiya zonalari 0–42 mm oralig‘ida bo‘ldi. Sefotaksim va siprofloksatsinga nisbatan 17–18 ta izolyat sezgir bo‘lib, 1–9 ta izolyatda rezistentlik qayd etildi. Ampitsillin va tetrasiklinga nisbatan esa 15–17 ta izolyatda yuqori rezistentlik kuzatildi. Ayrim izolyatlarda ingibitsiya zonasining mavjud emasligi to‘liq rezistentlikni ko‘rsatdi. MDR tahlilida 8 ta izolyatda bir nechta antibiotiklarga chidamlilik belgilari aniqlandi: 7, 12, 18 va 32-izolyatlar yuqori darajali, 14, 19, 24 va 34-izolyatlar o‘rtacha darajali MDR guruhiga kiritildi. MALDI-TOF tahlili rezistent izolyatlarning *Escherichia coli* turiga mansubligini tasdiqladi.

Olingan ma’lumotlar parranda mahsulotlarida antibiotiklarga chidamli *E. coli* izolyatlari uchrashini va ayniqsa ampitsillin hamda tetrasiklinga rezistentlik yuqori ekanligini ko‘rsatdi. Bu holat oziq-ovqat hayvonlarida antibiotiklardan foydalanishning AMR tarqalishiga ta’siri haqidagi xalqaro ma’lumotlarga mos keladi.

Xulosa

Tadqiqotda parranda go‘shti va shaurma namunalaridan antibiotiklarga turlicha sezgirlikka ega bakteriya izolyatlari ajratildi, 8 ta izolyatda MDR belgilari aniqlandi. Ampitsillin va tetrasiklinga nisbatan rezistentlik yuqori, sefotaksim va siprofloksatsinga sezgirlik esa nisbatan yuqoriroq bo‘ldi.

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ENDOGEN ANTIOKSIDANT HIMOYA TIZIMINI RAG‘BATLANTIRISH UCHUN ISTIQBOLLI PROBIOTIK SHTAMMLARNI TANLASH

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Annotatsiya: Tadqiqotda 18 ta sut kislotasi bakteriyasi shtammining DPPH, superoksid anioni va gidroksil radikallariga qarshi antioksidant faolligi baholandi. Yuqori faollik ko‘rsatgan *Lactiplantibacillus plantarum* TK1 va KA3 shtammlarining kultura suyuqligidagi erkin aminokislotalar tarkibi tahlil qilindi. Ushbu shtammlarda glutation biosintezi uchun zarur glutamat, sistein va glitsin miqdorining yuqoriligi aniqlandi. Natijalar TK1 va KA3 shtammlarining antioksidant va biotexnologik potensiali yuqori ekanligini ko‘rsatdi.

Kalit so‘zlar: glutation, antioksidant faollik, sut kislotasi bakteriyalari, *Lactiplantibacillus plantarum*, oksidlovchi stress.

Аннотация: В исследовании оценена антиоксидантная активность 18 штаммов молочнокислых бактерий в отношении DPPH, супероксид-аниона и гидроксильного радикала. Штаммы *Lactiplantibacillus plantarum* TK1 и KA3 проявили высокую антиоксидантную активность. В их культуральной жидкости выявлено повышенное содержание глутамата, цистеина и глицина, необходимых для биосинтеза глутатиона. Полученные результаты свидетельствуют о высоком антиоксидантном и биотехнологическом потенциале данных штаммов.

Ключевые слова: глутатион, антиоксидантная активность, молочнокислые бактерии, *Lactiplantibacillus plantarum*, окислительный стресс.

Abstract: The antioxidant activity of 18 lactic acid bacteria strains against DPPH, superoxide anion, and hydroxyl radicals was evaluated. *Lactiplantibacillus plantarum* TK1 and KA3 showed high antioxidant activity. Their culture supernatants contained increased levels of glutamate, cysteine, and glycine, which are required for glutathione biosynthesis. The results indicate the high antioxidant and biotechnological potential of these strains.

Keywords: glutathione, antioxidant activity, lactic acid bacteria, *Lactiplantibacillus plantarum*, oxidative stress.

Oksidlovchi stress — organizm va hujayralarda reaktiv kislorod turlari (RKT) hosil bo‘lishi hamda ularni neytrallovchi antioksidant himoya tizimlari o‘rtasidagi muvozanatning buzilishi natijasida yuzaga keladigan fiziologik va biokimyoviy holatdir. Reaktiv kislorod turlarining ortiqcha miqdorda to‘planishi hujayra membranalari lipidlarining peroksidlanishi, oqsillar strukturasi va funksiyasining buzilishi, nuklein kislotalarning shikastlanishi hamda metabolik jarayonlarning izdan chiqishiga olib kelishi mumkin. Shu sababli hujayralarning antioksidant himoya tizimi oksidlovchi stressning salbiy oqibatlarini kamaytirishda va hujayra gomeostazini saqlashda muhim ahamiyat kasb etadi [1].

Endogen antioksidant tizimning asosiy komponentlaridan biri glutation hisoblanadi. Glutation glutamat, sistein va glitsin aminokislotalaridan tashkil topgan tripeptid bo‘lib, hujayrada

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oksidlanish-qaytarilish muvozanatini saqlash, erkin radikallarni neytrallash, peroksid birikmalarini zararsizlantirish hamda turli oksidlovchi omillarga qarshi himoyani ta’minlashda faol ishtirok etadi. Bundan tashqari, glutation ko‘plab fermentativ reaksiyalarning kechishi, hujayra detoksikatsiyasi va antioksidant fermentlar faoliyatini qo‘llab-quvvatlashda ham muhim metabolik rol o‘ynaydi [2].

So‘nggi yillarda sut kislotasi bakteriyalarining nafaqat probiotik, balki antioksidant xususiyatlariga ham katta e’tibor qaratilmoqda. Sut kislotasi bakteriyalari ayrim erkin radikallarni bevosita neytrallash, antioksidant metabolitlar hosil qilish, hujayra redoks tizimlarini faollashtirish hamda oksidlovchi stress sharoitida yashovchanligini saqlash qobiliyati bilan tavsiflanadi. Ularning bunday xususiyatlari mikroorganizmlarning probiotik potensialini belgilovchi muhim mezonlardan biri hisoblanadi. Ayniqsa, glutation biosintezi bilan bog‘liq glutamat, sistein va glitsin kabi aminokislotalarni hosil qilish qobiliyatiga ega shtammlarni aniqlash funksional xususiyatlarga ega yangi probiotik mikroorganizmlarni tanlash nuqtai nazaridan istiqbolli yo‘nalishdir [3].

Sut kislotasi bakteriyalarining antioksidant faolligi shtammga xos xususiyat bo‘lib, turli mikroorganizmlar erkin radikallarga nisbatan bir xil darajada ta’sir ko‘rsatmaydi. Shu sababli istiqbolli shtammlarni tanlashda faqat bitta antioksidant test natijalariga asoslanish yetarli bo‘lmay, bir nechta erkin radikallarga nisbatan ingibirlovchi faollikni kompleks baholash muhim hisoblanadi. DPPH radikali, superoksid anioni va gidroksil radikali kabi reaktiv birikmalarga qarshi faollikni aniqlash mikroorganizmlarning antioksidant potensialini qiyosiy baholash imkonini beradi. Shu bilan birga, yuqori antioksidant faollik namoyon etgan shtammlarda glutation biosintezi uchun zarur bo‘lgan metabolik prekursorlarning miqdorini aniqlash ularning funksional va biotexnologik imkoniyatlarini yanada chuqurroq tavsiflashga xizmat qiladi [4].

Mazkur tadqiqotning **maqsadi** yuqori antioksidant faollik namoyon etuvchi, DPPH, superoksid anioni va gidroksil radikallarini samarali ingibirlash qobiliyatiga ega hamda glutation biosintezi uchun zarur glutamat, sistein va glitsin aminokislotalarini faol hosil qiluvchi istiqbolli sut kislotasi bakteriyalari shtammlarini aniqlashdan iborat.

Materiallar va usullar

Tadqiqot obyekti sifatida turli manbalardan, jumladan dorivor o‘simliklardan hamda fermentlangan oziq-ovqat mahsulotlaridan ajratilgan 18 ta sut kislotasi bakteriya shtammi tanlandi. Barcha izolyatlar “Inson mikrobiomi” laboratoriyasi kolleksiyasida 20% glitserinli eritmada −80 °C haroratda saqlangan.

Antioksidant faollik DPPH, superoksid anioni va gidroksil radikallarini ingibirlash asosida baholandi. DPPH spektrofotometrik usulda amalga oshirildi. Har bir tajriba uch marta takrorlandi. Yuqori antioksidant faollikka ega shtammlarning kultura suyuqligidagi erkin aminokislotalar tarkibi yuqori samarali suyuqlik xromatografiyasi (YuSSX) yordamida aniqlandi. Glutation biosintezi potensialini baholashda glutamat, sistein va glitsin miqdorlariga alohida e’tibor berildi.

Natijalar

Solishtirma musbat nazorat sifatida ishlatilgan vitamin C DPPH, superoksid anioni va gidroksil radikallarini mos ravishda 99%, 91,37% va 88,21% ingibirladi. 18 ta shtamm orasida *L. plantarum* TK1 va KA3 uchala radikal bo‘yicha nisbatan yuqori va barqaror faollik ko‘rsatdi. TK1 supernatanti DPPH ni 77%, superoksid anionini 80,5% va gidroksil radikalini 76,8% ingibirladi. KA3 supernatantida ushbu ko‘rsatkichlar mos ravishda 62%, 82,4% va 77,7% bo‘ldi. Butun hujayra fraksiyalarida TK1 uchun 85%, 77,6% va 70%, KA3 uchun 87%, 76,4% va 72% natijalar qayd etildi.

Erkin aminokislotalar tahlili TK1 va KA3 shtammlarida glutation biosintezi uchun muhim bo‘lgan komponentlarning yuqori miqdorini ko‘rsatdi. Nazorat sifatida shtammlarni faollantirish uchun foydalanilgan ozuqa muhit CDM (to‘liq tarkibli to‘yintirilgan ozuqa muhit) dan foydalanildi. Glutamat miqdori nazoratdagi 1,530 µg/µl ga nisbatan TK1 da 12,970 µg/µl va KA3 da 13,536 µg/µl bo‘ldi. Glitsin nazoratda va shtammlarda mos ravishda 1.636, 7,466 va 4,872 µg/µl, sistein esa nazoratda 1.443 µg/µl ga teng, shtammlarda 3,206 va 3,626 µg/µl ni tashkil etdi. Ushbu uchta

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aminokislotaning birgalikda yuqori miqdorda aniqlanishi TK1 va KA3 ning glutation biosintezi uchun zarur prekursorlarni hosil qilish potensialini ko‘rsatadi.

Olingan natijalarga ko‘ra, *L. plantarum* TK1 va KA3 shtammlari yuqori antioksidant faollik va glutation biosintezini qo‘llab-quvvatlovchi metabolik xususiyatlari sababli funksional oziq-ovqat va probiotik mahsulotlar uchun istiqbolli mikroorganizmlar sifatida tanlandi.

Xulosa

Tadqiqot natijalari 18 ta SKB shtammi orasida *L. plantarum* TK1 va KA3 ning yuqori kompleks antioksidant faollikka ega ekanligini ko‘rsatdi. Ushbu shtammlarda glutamat, sistein va glitsin miqdorining yuqoriligi ularning glutation biosintezi uchun zarur metabolik prekursorlarni hosil qilish potensialini tasdiqlaydi. TK1 va KA3 shtammlari funksional oziq-ovqat va probiotik mahsulotlar yaratish uchun istiqbolli nomzodlar sifatida keyingi tadqiqotlarga tavsiya etiladi.

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MAHALLIY SUT KISLOTALI BAKTERIYA SHTAMMLARIDAGI GABA BIOSINTEZIDA ISHTIROK ETADIGAN gadB VA gadC GENLARINI PZR USULI BILAN SEKVENIRLASH

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Kirish

Gamma-aminomoy kislotasi (GABA, GAMK) glyutamatdekarboksilaza tizimi orqali bir qator sut kislotasi bakteriyalari tomonidan sintez qilinadigan muhim neyroaktiv metabolit hisoblanadi. gadB geni glyutamatning GABAga aylanishini katalizlovchi glyutamatdekarboksilaza fermentini kodlaydi, gadC genlari esa glyutamat va GABAning hujayra membranasi orqali tashilishiga (transportiga) bog‘liq. Ushbu yo‘lning genetik determinantlarini o‘rganish GABA ishlab chiqaruvchi istiqbolli shtammlarni tanlab olishda katta ahamiyatga ega.

Tadqiqot maqsadi

polimeraza zanjir reaksiyasi (PZR) usuli yordamida sut kislotasi bakteriyalari shtammlarida gadB, gadC1 va gadC2 genlarini aniqlash.

Material va usullar

Beshta taksonomik guruhga mansub 22 ta sut kislotasi bakteriyalari shtammlari tadqiq qilindi. gadB, gadC1 va gadC2 genlarining mavjudligi o‘ziga xos (spetsifik) praymerlardan foydalangan holda PZR usuli bilan aniqlandi. Natijalar kutilgan o‘lchamdagi amplifikatsiya mahsulotlarining mavjudligiga qarab baholandi. Salbiy nazorat sifatida *Staphylococcus aureus* ATCC shtammidan foydalanildi.

Natijalar va ularning muhokamasi

PZR-skrining natijasida gadB geni tekshirilgan 22 ta shtammdan 7 tasida (31,8%) aniqlandi, jumladan, *Lactiplantibacillus plantarum* A4, K2, TM5, EB-2.2 va AA-2, *Limosilactobacillus reuteri* 1 hamda *Lactococcus lactis* R2 shtammlarida qayd etildi. Shu bilan birga, tekshirilgan shtammlarning birortasida ham gadC1 va gadC2 genlariga mos keladigan amplifikatsiya mahsulotlari topilmadi. gadB bo‘yicha pozitiv bo‘lgan shtammlarda amplikon o‘lchamlari kutilgan qiymatlarga mos keldi, salbiy nazoratda esa amplifikatsiya kuzatilmadi. Olingan natijalar o‘rganilgan kulturalarning bir qismida glyutamatdekarboksilaza yo‘lining genetik salohiyati mavjudligidan dalolat beradi. gadC1 va gadC2 amplifikatsiyasining yo‘qligi o‘rganilgan bakteriyalarda ushbu yo‘lning genetik tuzilishi o‘ziga xosligi, praymerlar bog‘lanish sohalaridagi ketma-ketliklar divergensiyasi (farqlanishi) yoki qo‘llanilgan metodikaning cheklovlari bilan bog‘liq bo‘lishi mumkin. Shu bilan birga, PZR mahsulotining yo‘qligi ushbu genlarning mutlaqo mavjud emasligini isbotlamaydi.

Xulosa

Tekshirilgan 22 ta sut kislotasi bakteriyalari shtammlaridan yettitasi gadB geni bo‘yicha ijobiy bo‘lib chiqdi, gadC1 va gadC2 genlari esa aniqlanmadi. Aniqlangan shtammlar ularning GABA ishlab chiqarish faolligini yanada chuqurroq o‘rganish uchun qiziqish uyg‘otadi. Ularning

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funksional salohiyatini tasdiqlash uchun GABA miqdorini aniqlash, glyutamatdekarboksilaza faolligini baholash va zarurat tug‘ilganda tegishli genetik sohalarni sekvenirlash talab etiladi.

Kalit so‘zlar: sut kislotasi bakteriyalari, GABA, gadB, gadC1, gadC2, PZR, glyutamatdekarboksilaza.

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ZIZIPHORA PEDICELLATA O‘SIMLIGIDAN ANTIBAKTERIAL FITOEKSTRAKTLAR AJRATIB OLISH TEXNOLOGIYASI

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Abstract: *Ziziphora pedicellata* is a valuable medicinal aromatic plant belonging to the Lamiaceae family, widely distributed in Central Asia. The species is rich in essential oils, flavonoids, phenolic compounds, and terpenoids, demonstrating significant antibacterial, antioxidant, and therapeutic properties. This study evaluates the technology of extraction of bioactive phytoextracts using various solvents and ultrasound-assisted extraction techniques, as well as their in vitro antibacterial efficacy against pathogenic bacteria including Staphylococcus aureus and Escherichia coli. Optimal extraction parameters were determined to achieve high yield and antimicrobial potency.

Keywords: *Ziziphora pedicellata*; Lamiaceae; phytoextract; antibacterial activity; ultrasound-assisted extraction; phenolic compounds; essential oil; pulegone; disc diffusion; minimum inhibitory concentration (MIC); pathogens; bioactive compounds.

Ziziphora pedicellata (Kiyiko‘t) – Lamiaceae (Yalpizdoshlar) oilasi, *Ziziphora* turkumiga mansub ko‘p yillik dorivor va efir moyli o‘simlik hisoblanadi. *Ziziphora* turkumining ilmiy tavsifi va taksonomiyasi o‘simliklar sistematikasida keng o‘rganilgan bo‘lib, u Markaziy Osiyo tog‘li va tog‘oldi hududlarida tabiiy holda keng tarqalgan. Ushbu turkum vakillarining kimyoviy tarkibi va biologik faolligini o‘rganishga ko‘plab mahalliy va xorijiy olimlar, jumladan, Sh.S. Sagdullaev, X.M. Komilov va boshqa tadqiqotchilar katta hissa qo‘shganlar.

Ziziphora pedicellata tarkibida yuqori miqdorda efir moylari (asosiy komponenti pulegon, menton va piperiton), flavonoidlar, oshlovchi moddalar, fenolkarbon kislotalari va triterpenoidlar mavjud. Bugungi kunda patogen mikroorganizmlarning sintetik antibiotiklarga nisbatan chidamliligi (rezistentligi) ortib borayotgani sababli tabiiy kelib chiqishiga ega bo‘lgan antibakterial va antiseptik vositalarni yaratish dolzarb masalalardan biridir. Tadqiqotlar *Z. pedicellata* ekstraktlarining gram-musbat va gram-manfiy bakteriyalarga nisbatan yuqori antimikrob faolligini ko‘rsatgan. Shu bois u farmatsevtika va oziq-ovqat sanoati uchun tabiiy antiseptik va nutrasevtik manba sifatida katta ahamiyatga ega.

Tarqalishi va ekologiyasi

Ziziphora pedicellata asosan dengiz sathidan 800–2500 metr balandlikdagi toshli-shag‘alli yonbag‘irlarda, tog‘ daralarida va quruq dasht mintaqalarida o‘sadi. U kserofit va geliofit o‘simlik bo‘lib, qurg‘oqchilikka va yuqori yorug‘lik intensivligiga moslashgan. O‘simlikning tarqalishi va biologik faol moddalar to‘planishida ekologik omillar — tuproq-iqlim sharoiti, quyosh insolatsiyasi hamda namlik darajasi muhim rol o‘ynaydi. Vegetatsiya davrining gullash pallasida o‘simlik xomashyosida efir moylari va fenol birikmalarining konsentratsiyasi maksimal darajaga yetadi.

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Morfologik va anatomik tuzilishi

Ziziphora pedicellata bo‘yi 10–40 sm ga yetadigan poyasining tubidan shoxlanuvchi yarimbutacha hisoblanadi. Poyasi to‘rt qirrali, ingichka, qisqa tuklar bilan qoplangan. Barglari qarama-qarshi joylashgan, shakli tuxumsimon yoki nashtarsimon, qisqa bandli, chetlari butun yoki biroz tishli, yuzasida efir moyi ajratuvchi bezchalar va tukchalar ravshan ko‘rinadi. Bu bezchalarda efir moylari va boshqa uchuvchan birikmalar to‘planadi. Gullari kichik, ikki jinsli, poya va shoxlarning uchida sharsimon yoki boshchasimon to‘pgullarni hosil qiladi. Gultojisi ikki labli, pushti-binafsha yoki binafsha rangda bo‘ladi. Mevasi — to‘rtta yong‘oqchadan iborat quruq meva. O‘simlik xomashyosining mikroskopik tahlilida barg epiderma hujayralarining tuzilishi hamda efir moyli bezchalarning joylashuvi muhim diagnostik taksonomik belgi hisoblanadi.

Ekstraksiya texnologiyasi va antibakterial faolligi

O‘simlik xomashyosidan biologik faol moddalarni maksimal darajada ajratib olish va ularning destruksiyasining oldini olish uchun zamonaviy ekstraksiya usullaridan foydalaniladi. Tajribalarda an’anaviy matseratsiya usuliga nisbatan ultratovush yordamida ekstraksiya qilish (UAE — Ultrasound-Assisted Extraction) usuli yuqori samaradorlik ko‘rsatdi. Erituvchi sifatida va vaqt parametrlari maqbul darajaga keltirilganda (70% li etanol erituvchisida, 35 kHz chastotada 30 daqiqa davomida) biologik faol moddalar va fenol birikmalarining ekstraksiyaga o‘tish unumi 1.8 baravarga ortgani kuzatildi. Olingan *Ziziphora pedicellata* fitoekstraktining antibakterial faolligi disk-diffuziya va ketma-ket suyultirish usullari yordamida *Staphylococcus aureus* (gram-musbat) hamda *Escherichia coli* (gram-manfiy) patogen bakteriya shtammlariga nisbatan o‘rganildi. Natijalarga ko‘ra: -*Staphylococcus aureus* ga nisbatan bakteriyalarning o‘sishini ingibitsiya qilish zonasi diametri **18.5 ± 0.4** mm ni tashkil etdi. -*Escherichia coli* ga nisbatan esa ingibitsiya zonasi **14.2 ± 0.3** mm ga teng bo‘ldi. Fitoekstraktning gram-musbat bakteriyalarga nisbatan yuqoriroq faollik ko‘rsatishi ularning hujayra devori tuzilishi (gram-manfiy bakteriyalardagi tashqi gidrofob lipopolisaxarid peptidoglikan qatlamining yo‘qligi) hamda ekstrakt tarkibidagi monoterpenoidlar va fenollarning hujayra membranasi o‘tkazuvchanligini buzishi va fermentativ tizimlarini ingibitsiya qilishi bilan izohlanadi. Xulosa qilib aytganda, *Ziziphora pedicellata* o‘simligidan ajratib olingan fitoekstraktlar yuqori antibakterial va biologik faollikka ega bo‘lib, farmatsevtika hamda tibbiyot amaliyotida tabiiy antimikrob va antiseptik preparatlar yaratishda istiqbolli manba hisoblanadi.

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ANTIBACTERIAL POTENTIAL OF THE ENDOPHYTIC FUNGAL ISOLATE S34 FROM *THERMOPSIS ALTERNIFLORA*

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Abstract: The ethyl acetate extract of the endophytic fungal isolate S34, obtained from *Thermopsis alterniflora* collected in Bostanliq District, Tashkent Region, was screened for antimicrobial activity by the agar disk-diffusion method. The extract inhibited *Bacillus subtilis* (12 ± 0.33 mm), *Pseudomonas aeruginosa* (9 ± 0.19 mm) and *Staphylococcus aureus* (7 ± 0.12 mm), whereas no activity was detected against *Escherichia coli* or *Candida albicans*.
Keywords: endophytic fungi, *Thermopsis alterniflora*, antimicrobial activity, disk diffusion, *Pseudomonas aeruginosa*.

Annotatsiya: Toshkent viloyati Bo‘stonliq tumanidan yig‘ilgan *Thermopsis alterniflora* o‘simligidan ajratilgan endofit zamburug‘ S34 izolyati etilatsetatli ekstraktining antimikrob faolligi agar-disk diffuziya usulida baholandi. Ekstrakt *Bacillus subtilis* (12 ± 0,33 mm), *Pseudomonas aeruginosa* (9 ± 0,19 mm) va *Staphylococcus aureus* (7 ± 0,12 mm) o‘sishini to‘xtatdi, *Escherichia coli* va *Candida albicans*ga nisbatan esa faollik kuzatilmadi.
Kalit so‘zlar: endofit zamburug‘lar, *Thermopsis alterniflora*, antimikrob faollik, disk-diffuziya, *Pseudomonas aeruginosa*.

Аннотация: Методом диффузии в агар (диско-диффузионный метод) оценена антимикробная активность этилацетатного экстракта эндофитного гриба S34, выделенного из растения *Thermopsis alterniflora*, собранного в Бостанлыкском районе Ташкентской области. Экстракт подавлял рост *Bacillus subtilis* (12 ± 0,33 мм), *Pseudomonas aeruginosa* (9 ± 0,19 мм) и *Staphylococcus aureus* (7 ± 0,12 мм), тогда как в отношении *Escherichia coli* и *Candida albicans* активность не выявлена.
Ключевые слова: эндофитные грибы, *Thermopsis alterniflora*, антимикробная активность, диско-диффузионный метод, *Pseudomonas aeruginosa*.

Introduction

Antimicrobial resistance has become one of the most serious threats to global health: in 2019 alone, an estimated 1.27 million deaths were directly attributable to resistant bacterial infections [1]. This situation creates an urgent need for new sources of antimicrobial compounds. Endophytic fungi, which colonize internal plant tissues without causing visible symptoms, are widely regarded as a prolific source of structurally diverse and biologically active secondary metabolites [2]. Plants of the genus *Thermopsis* (Fabaceae) are rich in quinolizidine alkaloids, and cytisine has been quantified in *T. alterniflora* [3]; however, the endophytic fungi inhabiting this plant have received little attention. The aim of this study was to evaluate the antimicrobial activity of the extract of the endophytic fungal isolate S34 obtained from *T. alterniflora*.

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Materials and methods

Plant material of *T. alterniflora* was collected in Bostanliq District, Tashkent Region, Uzbekistan, and isolate S34 was recovered from surface-sterilized plant tissues. The isolate was cultivated in potato dextrose broth for 21 days, after which the culture was extracted with ethyl acetate. The antimicrobial activity of the extract (20 mg/mL) was determined by the agar disk-diffusion method as described previously [4, 5] against Gram-positive (*Bacillus subtilis*, *Staphylococcus aureus*) and Gram-negative (*Escherichia coli*, *Pseudomonas aeruginosa*) bacteria and the yeast *Candida albicans*. Ampicillin/sulbactam, gentamicin and fluconazole served as positive controls for Gram-positive bacteria, Gram-negative bacteria and *C. albicans*, respectively. All assays were performed in triplicate, and the results are expressed as mean ± standard error (SE).

Results

The S34 extract was active against three of the five test organisms. The most sensitive strain was *B. subtilis*, with an inhibition zone of 12 ± 0.33 mm, which amounts to 40.0% of the zone produced by ampicillin/sulbactam (30 ± 0.21 mm). Against the Gram-negative *P. aeruginosa*, the extract formed a zone of 9 ± 0.19 mm, equal to 34.6% of the gentamicin effect (26 ± 0.41 mm). Only weak inhibition was observed for *S. aureus* (7 ± 0.12 mm; 26.9% of the ampicillin/sulbactam zone, 26 ± 0.28 mm), while *E. coli* and *C. albicans* were not susceptible to the extract.

Discussion

The activity of the extract against *P. aeruginosa* deserves particular attention, since this species is intrinsically resistant to many antibiotics owing to the low permeability of its outer membrane and its efficient efflux systems [6]. Anti-*Pseudomonas* activity has also been recorded for the ethyl acetate extract of *Alternaria alstroemeriae* S6, an endophyte of *Veronica acinifolia* previously studied by our group [4]. At the same time, the S34 extract did not affect the other Gram-negative species, *E. coli*, which may point to a species-selective mode of action of its active constituents; this assumption, however, requires further verification. Because the disk-diffusion assay is a qualitative screening method and the zone diameter also depends on how well compounds diffuse through agar [5], minimum inhibitory concentrations (MIC) must be determined for a quantitative assessment. In addition, the present data were obtained with a crude extract, and the metabolites responsible for the activity have not yet been identified.

Conclusion

The endophytic fungal isolate S34 from *T. alterniflora* produces metabolites that inhibit both Gram-positive and Gram-negative bacteria, including *P. aeruginosa*. Further work will include molecular identification of the isolate, determination of MIC values, and bioassay-guided fractionation of the extract followed by chemical characterization of the active compounds.

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MAHALLIY ASALARI (APIS MELLIFERA L.) PROPOLISINING STAPHYLOCOCCUS AUREUS VA ESCHERICHIA COLI SHTAMMLARIGA QARSHI ANTIBAKTERIAL FAOLLIGI

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Annotatsiya: Mahalliy Apis mellifera L. propolisining 70% li etanoldagi ekstrakti 25%, 50%, 75% va 100% konsentratsiyalarda Staphylococcus aureus ATCC 25923 hamda Escherichia coli ATCC 25922 ga qarshi disk-diffuziya usulida tekshirildi. Konsentratsiya oshishi bilan o‘sishni to‘xtatish zonasi kengaydi; 100% ekstraktda u mos ravishda 18,5 ± 0,4 va 12,2 ± 0,5 mm bo‘ldi. Natijalar propolisning tabiiy antibakterial vosita sifatidagi istiqbolini ko‘rsatadi.
Kalit so‘zlar: Apis mellifera L., propolis, antibakterial faollik, Staphylococcus aureus, Escherichia coli.

Аннотация: Изучена активность этанольного экстракта прополиса местных пчёл Apis mellifera L. в концентрациях 25–100% против Staphylococcus aureus ATCC 25923 и Escherichia coli ATCC 25922 методом диффузии в агар. При повышении концентрации зоны ингибирования увеличивались и при 100% составили 18,5 ± 0,4 и 12,2 ± 0,5 мм соответственно. Результаты показывают перспективность прополиса как природного антибактериального средства.
Ключевые слова: прополис, антибактериальная активность, Staphylococcus aureus, Escherichia coli.

Abstract: The antibacterial activity of local Apis mellifera L. propolis extract (25–100%) was tested against Staphylococcus aureus ATCC 25923 and Escherichia coli ATCC 25922 using disc diffusion. Inhibition zones increased with concentration, reaching 18.5 ± 0.4 mm and 12.2 ± 0.5 mm, respectively, at 100% extract. The findings support further study of propolis as a natural antibacterial agent.
Keywords: propolis, antibacterial activity, Staphylococcus aureus, Escherichia coli.

Kirish

Antibiotiklarga chidamli mikroorganizmlar ko‘payishi tabiiy antimikrob moddalarni o‘rganishni dolzarb qiladi. Propolis tarkibidagi flavonoidlar, fenol kislotalari va terpenoidlar biologik faollikka ega; shu sababli mahalliy propolisning teri va ichak infeksiyalari bilan bog‘liq Staphylococcus aureus hamda Escherichia coli ga ta’sirini qiyosiy baholash muhimdir [1].

Material va usullar

Mahalliy asalarichilik xo‘jaliklaridan olingan propolis 70% li etil spirti bilan xona haroratida, qorong‘i joyda 7 kun davomida ekstraksiya qilindi (vaqti-vaqti bilan aralashtirildi) va filtrlandi. Asosiy ekstraktdan 25%, 50%, 75% va 100% li ishchi konsentratsiyalar tayyorlandi.

Antibakterial faollik Myuller–Xinton agari (MHA)da disk-diffuziya usuli bilan aniqlandi. Test-shtammlar: S. aureus ATCC 25923 (gram-musbat) va E. coli ATCC 25922 (gram-manfiy). 0,5 Mak-Farland standartidagi suspenziyalar muhitga ekildi; 6 mm li steril disklarga ekstraktning har bir

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konsentratsiyasidan 10 mkl solindi. Nazorat sifatida 70% li etanol ishlatildi, inkubatsiya 37 °C da 24 soat davom etdi.

Har bir tajriba uch takrorlashda bajarildi (n = 3). O‘sishni to‘xtatish zonalari (mm) o‘lchanib, o‘rtacha qiymat va standart og‘ish (M ± SD) hisoblandi; guruhlar t-mezon va ANOVA yordamida solishtirildi, $p < 0,05$ statistik ahamiyatli deb olindi.

Natijalar va muhokama

Mahalliy propolis ekstraktining antibakterial faolligi konsentratsiyaga va bakteriya turiga bog‘liq bo‘ldi (1-jadval).

1-jadval. Propolis ekstrakti konsentratsiyasiga qarab bakteriya o‘sishini to‘xtatish zonalari (mm)

Propolis ekstrakti konsentratsiyasi	**Staphylococcus aureus ATCC 25923 Zona (mm)**	**Escherichia coli ATCC 25922 Zona (mm)**
25%	8,1 ± 0,3	Aniqlanmagan (0,0)*
50%	12,4 ± 0,4	7,5 ± 0,3
75%	15,6 ± 0,5	10,1 ± 0,4
100% (asosiy ekstrakt)	**18,5 ± 0,4**	**12,2 ± 0,5**
Nazorat (70% etanol)	Aniqlanmagan (0,0)	Aniqlanmagan (0,0)

**Izoh: qiymatlar M ± SD (n = 3). “Aniqlanmagan” — bakteriya o‘sishini to‘xtatish zonasi kuzatilmadi. Guruhlararo farqlar p < 0,05 darajasida statistik ahamiyatli.*

Konsentratsiya 25% dan 100% gacha oshganda har ikki shtammda zona kattalashdi. S. aureus eng sezgir bo‘lib, 100% ekstraktda 18,5 ± 0,4 mm zona hosil qildi; E. coli da ko‘rsatkich 12,2 ± 0,5 mm bo‘ldi ($p < 0,01$). E. coli ning nisbatan past sezgirligi gram-manfiy bakteriyalarning tashqi lipid membranasi faol moddalar kirishini cheklashi bilan izohlanishi mumkin [2, 3].

Xulosalar

Mahalliy A. mellifera L. propolisining etanolli ekstrakti S. aureus va E. coli ga qarshi konsentratsiyaga bog‘liq antibakterial faollik ko‘rsatdi. Ta’sir S. aureus ga nisbatan kuchliroq bo‘ldi (100% ekstraktda 18,5 ± 0,4 mm). Natijalar propolisni yangi tabiiy antibakterial preparatlar va dermatologik vositalar ishlab chiqishda istiqbolli xomashyo sifatida keyingi tadqiq etish zarurligini ko‘rsatadi.

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LIPASES FROM THERMOPHILIC BACTERIA: PROPERTIES AND PROSPECTS FOR FOOD AND INDUSTRIAL BIOTECHNOLOGY

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Abstract: Lipases from thermophilic bacteria combine catalytic versatility with high stability to temperature, alkaline pH and organic solvents. Based on an analysis of recent literature, this paper summarizes their sources, structural and biochemical features and the main areas of application, with emphasis on the food industry. Thermophilic bacterial lipases from the genera *Geobacillus*, *Anoxybacillus* and *Aeribacillus* are active at 50–75 °C and pH 8–11, tolerate organic solvents and detergents, and can be further stabilized by protein engineering. Their use is promising in dairy flavour development, fat processing, detergents and biodiesel production.

Keywords: thermophilic bacteria, lipase, *Geobacillus*, *Anoxybacillus*, *Aeribacillus*, thermostability, food biotechnology.

Annotatsiya: Zamonaviy adabiyotlar tahlili asosida termofil bakteriyalar lipazalarining manbalari, tuzilishi, biokimyoviy xususiyatlari va qo‘llanilish sohalari umumlashtirilgan. *Geobacillus*, *Anoxybacillus* va *Aeribacillus* turkumlari lipazalari 50–75 °C va pH 8–11 da faol, organik erituvchilar va detergentlarga chidamli bo‘lib, sut sanoati, yog‘larni qayta ishlash, yuvish vositalari va biodizel ishlab chiqarishda istiqbolli hisoblanadi.

Kalit so‘zlar: termofil bakteriyalar, lipaza, *Geobacillus*, *Anoxybacillus*, *Aeribacillus*, termobarqarorlik.

Аннотация: На основе анализа современной литературы обобщены источники, структурно-биохимические свойства и области применения липаз термофильных бактерий. Липазы бактерий родов *Geobacillus*, *Anoxybacillus* и *Aeribacillus* активны при 50–75 °C и pH 8–11, устойчивы к органическим растворителям и детергентам и перспективны для молочной промышленности, переработки жиров, производства моющих средств и биодизеля.

Ключевые слова: термофильные бактерии, липаза, *Geobacillus*, *Anoxybacillus*, *Aeribacillus*, термостабильность.

Introduction

Lipases (triacylglycerol hydrolases, EC 3.1.1.3) catalyse the hydrolysis of long-chain triacylglycerols at the oil–water interface and, under low-water conditions, the reverse reactions of esterification and transesterification. Most of them possess a mobile lid domain over the active site, whose opening at the interface is responsible for interfacial activation [1, 4]. Microbial lipases dominate industrial use, and bacterial enzymes are especially valued for their activity at neutral and alkaline pH [1]. Many technological processes, however, run at elevated temperatures, which inactivate mesophilic enzymes. Thermophilic microorganisms are therefore regarded as a key source of robust biocatalysts for industry [2]. The aim of this work was to systematize current data on lipases from thermophilic bacteria and to assess their application potential, especially in the food industry.

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Methods

The study is based on an analysis of recent (2023–2026) peer-reviewed publications on the production, characterization, engineering and application of microbial and thermophilic bacterial lipases. Data on enzyme sources, temperature and pH optima, stability and application areas were compared and generalized.

Results

Among the reported thermophilic producers of lipases are *Geobacillus*, *Bacillus*, *Anoxybacillus*, *Aeribacillus* and *Thermus* species, and thermophilic enzymes generally work best in the range of 50–80 °C [2]. Subfamily I.5, represented mainly by *Geobacillus* lipases, has been studied most thoroughly. Its members are proteins of roughly 43–45 kDa that bind calcium and zinc ions, a feature linked to their heat tolerance, and they retain their structure in the presence of organic solvents [3]. For example, the recombinant lipase Lip7 from the Antarctic thermophile *Geobacillus* sp. ID17 showed maximum activity at 50 °C and pH 11.0, and its activity increased up to 250% in 50% (v/v) ethanol [3]. The lipase of *G. zalihae* T1 has an optimum of 70 °C and pH 9; a single substitution (F180C) raised its optimum to 75 °C and its melting temperature from 73.5 to 78.2 °C, while also improving its stability in organic solvents [4]. Representatives of the less studied genera show similar properties. A lipase of about 73 kDa purified from *Anoxybacillus gonensis* UF7 was most active and stable at pH 8.0 and 60 °C, kept its activity when methanol, ethanol or non-ionic and anionic surfactants were added, and converted waste frying oil into biodiesel with a yield of 87.7% [6]. A lipase of about 34 kDa from *Aeribacillus pallidus* IO3, isolated from a geothermal spring in Erzurum (Türkiye), had its optimum at pH 8.0 and 50 °C, retained 45–69% of its activity after 2 h at 70–80 °C, preferred the long-chain substrate p-nitrophenyl palmitate and was activated by chloroform and surfactants [5]. In addition, a *Bacillus* sp. lipase with a pH optimum of 9.5 and a temperature optimum of 60 °C hydrolyses natural fats and oils, which is relevant for food processing [2].

Discussion

The combination of thermostability, alkaline tolerance and solvent resistance determines the practical value of these enzymes. In the food industry, microbial lipases are used for the controlled hydrolysis of milk fat to develop cheese flavour [1]. Thermostable variants are also of interest for the modification of fats and oils, where higher process temperatures keep substrates liquid, lower viscosity and reduce the risk of microbial contamination. Outside the food sector, these enzymes are used in laundry and cleaning formulations and for the enzymatic conversion of oils, including waste frying oil, into biodiesel [1, 5, 6]. Remaining challenges include relatively low yields in native strains, the cost of purification and immobilization, and the need to confirm the safety of producer strains for food use. Recombinant expression and rational protein engineering, as shown for *G. zalihae* T1, offer effective ways to overcome these limitations [3, 4].

Conclusion

Lipases from thermophilic bacteria of the genera *Geobacillus*, *Anoxybacillus* and *Aeribacillus* are promising biocatalysts for processes requiring high temperature, alkaline pH or organic solvents. Screening of thermophiles from local extreme habitats, such as the hot springs of Central Asia and the Caucasus, combined with protein engineering, may provide new enzymes for food, chemical and environmental biotechnology.

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БИОТЕХНОЛОГИЧЕСКАЯ ДЕТОКСИКАЦИЯ АФЛАТОКСИНА B_1 В СУХОФРУКТАХ

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Аннотация: В работе рассмотрены теоретические и научно-методические аспекты биологической детоксикации афлатоксина B_1 (AFB_1) в сухофруктах с использованием микроорганизмов и их ферментативных комплексов. Обоснованы механизмы адсорбции токсина клеточными структурами и его ферментативной биотрансформации, а также обозначена необходимость оценки токсикологической безопасности образующихся продуктов деградации.
Ключевые слова: сухофрукты, афлатоксин B_1, микотоксины, биотехнология, биодетоксикация, биотрансформация, микроорганизмы, ферменты, пищевая безопасность, микробная деградация.

Annotatsiya: Ushbu ishda quruq mevalarda uchraydigan aflatoksin B_1 (AFB_1) ni mikroorganizmlar va ularning fermentativ komplekslari vositasida biologik zararsizlantirishning nazariy hamda ilmiy-uslubiy asoslari tahlil qilingan. Toksinning hujayra tuzilmalari tomonidan adsorbsiyasi va fermentativ biotransformatsiyasi mexanizmlari asoslanib, hosil bo‘ladigan mahsulotlarning toksikologik xavfsizligini baholash zaruriyati yoritilgan.
Kalit so‘zlar: quruq mevalar, aflatoksin B_1, mikotoksinlar, biotexnologiya, biozararsizlantirish, biotransformatsiya, mikroorganizmlar, fermentlar, oziq-ovqat xavfsizligi, mikrob degradatsiyasi.

Abstract: This paper examines the theoretical and methodological aspects of biological detoxification of aflatoxin B_1 (AFB_1) in dried fruits using microorganisms and their enzymatic systems. The mechanisms of toxin adsorption by cell structures and enzymatic biotransformation are substantiated, emphasizing the need to assess the toxicological safety of degradation products.
Keywords: dried fruits, aflatoxin B_1, mycotoxins, biotechnology, biodetoxification, biotransformation, microorganisms, enzymes, food safety, microbial degradation.

Сухофрукты являются ценным пищевым продуктом с длительным сроком хранения, однако на этапах выращивания, сбора, сушки и хранения они могут подвергаться контаминации токсигенными микроскопическими грибами и микотоксинами. Среди наиболее значимых микотоксинов, выявляемых в сухофруктах, особое место занимают афлатоксины и охратоксин А [1]. Афлатоксин B_1 (AFB_1), преимущественно продуцируемый токсигенными штаммами Aspergillus flavus и Aspergillus parasiticus, представляет особую опасность вследствие высокой токсичности и канцерогенных свойств [1]. Разработка эффективных и безопасных методов снижения содержания AFB_1 в пищевых продуктах является актуальной задачей современной пищевой биотехнологии. Традиционные физические и химические способы детоксикации могут сопровождаться изменением пищевых и органолептических характеристик продукта, поэтому всё больше внимания уделяется биологическим методам, основанным на использовании микроорганизмов и их ферментативных систем [2]. Биологическая детоксикация может осуществляться посредством адсорбции AFB_1

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клеточными структурами микроорганизмов либо посредством ферментативной биотрансформации молекулы токсина [2, 3].

Особый интерес представляют молочнокислые бактерии, представители рода Bacillus и другие непатогенные микроорганизмы, способные связывать или трансформировать афлатоксин B_1 [2, 3]. Микробная деградация AFB_1 может быть связана с действием различных ферментативных систем, включая окислительно-восстановительные ферменты [2, 3]. При этом снижение концентрации исходного токсина не всегда означает его полную детоксикацию, поскольку необходимо учитывать химическую природу и токсикологические свойства образующихся продуктов биотрансформации [3].

Современные исследования подтверждают перспективность поиска микроорганизмов, способных осуществлять биотрансформацию AFB_1. В частности, для штамма Brevundimonas sp. LF-1 была установлена способность к биотрансформации афлатоксина B_1 и выявлены потенциально участвующие в данном процессе ферментативные системы [4]. Эти результаты демонстрируют возможность использования микроорганизмов как основы для разработки биотехнологических способов детоксикации микотоксинов.

Использование микробных и ферментативных систем является перспективным направлением снижения загрязнения сухофруктов афлатоксином B_1. Для практического применения данного подхода необходимо исследовать эффективность биологической обработки непосредственно в пищевой матрице, оптимизировать параметры процесса и подтвердить безопасность образующихся продуктов биотрансформации.

В качестве заключения можно изложить: представленный подход может способствовать разработке экологически ориентированной технологии повышения микробиологической и токсикологической безопасности сухофруктов без снижения их качественных характеристик.

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DON VA DON MAHSULOTLARINING MIKROBIOLOGIK XAVFSIZLIGI: PATOGEN MIKROORGANIZMLAR VA MIKOTOKSINLAR XAVFI

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Annotatsiya: Ushbu tezisda don va don mahsulotlarining mikrobiologik ifloslanishi, unda uchraydigan asosiy patogen hamda mikotoksin ishlab chiqaruvchi zamburug‘lar va bakteriyalarning turlari, ularning rivojlanish sharoitlari va inson salomatligiga ko‘rsatadigan zararlari ilmiy jihatdan tahlil qilingan. Shuningdek, don yetishtirish, saqlash va qayta ishlash bosqichlarida mikrobiologik xavfsizlikni ta’minlash, GOST va xalqaro standartlar asosida sifat nazoratini yo‘lga qo‘yish hamda aholi salomatligini muhofaza qilishning dolzarb masalalari yoritilgan.

Kalit so‘zlar: Don mahsulotlari, patogen mikroorganizmlar, mikotoksinlar, Aspergillus, Fusarium, Bacillus cereus, oziq-ovqat xavfsizligi, mikrobiologik nazorat.

Kirish

Qishloq xo‘jaligi va oziq-ovqat sanoatida don mahsulotlari aholining birinchi darajali oziq-ovqat zaxirasini tashkil etadi. Biroq donni yetishtirish, o‘rib-yig‘ib olish, tashish va omborxonalarda saqlash jarayonida texnologik va sanitariya-gigiyena talablarining buzilishi turli patogen mikroorganizmlarning rivojlanishiga olib keladi. Don va un mahsulotlarining mikrobiologik ifloslanishi nafaqat mahsulotning ozuqaviylik va texnologik sifatini pasaytiradi, balki insonlar orasida og‘ir intoksikatsiya va oziq-ovqatdan zaharlanish holatlarini keltirib chiqaradi. Dunyo miqyosida donning sifatini saqlash va toksikogen omillarning oldini olish global oziq-ovqat xavfsizligining eng ustuvor yo‘nalishlaridan biri bo‘lib qolmoqda.

Don va don mahsulotlarida uchraydigan asosiy patogenlar va ularning zararlari

Don mahsulotlarida fitopatogen va mikotoksikogen zamburug‘lar hamda bir qator sporali va sporasiz bakteriyalar keng tarqalgan. Ularning asosiy vakillari va zararlari quyidagilardan iborat:

1. Mikotoksikogen va fitopatogen zamburug‘lar

Fusarium avlodi zamburug‘lari (F. graminearum, F. oxysporum, F. sporotrichioides): Zarari: Dalada donning donadorlik davrida fuzarioz kasalligini keltirib chiqaradi. Zamburug‘lar hayot faoliyati davomida trixotetsenlar (T-2 toksin, HT-2 toksin), deoksinivalenol (DON/vomitoksin) va zearalenon kabi xavfli mikotoksinlarni ajratadi. Ushbu toksinlar don qayta ishlanganda ham (termik ishlov berilganda) parchalanmaydi. Inson va hayvonlar organizmida alimentar-toksik aleukiya, jig‘ildon va oshqozon-ichak trakti zararlanishi, qon yaratish tizimi funksiyasining buzilishi va gormonal disbalansni keltirib chiqaradi.

Aspergillus avlodi zamburug‘lari (A. flavus, A. parasiticus, A. niger): Zarari: Omborxona sharoitida, nisbiy namlik yuqori bo‘lganda faol rivojlanadi. A. flavus va A. parasiticus dunyodagi eng kuchli tabiiy kanserogenlardan biri bo‘lmish aflatoksinlarni (B1, B2, G1, G2) sintez qiladi. Aflatoksinlar jigar to‘qimalarini nekrozga uchratadi, jigar karsinomasini keltirib chiqaradi va mutagen ta’sirga ega. A. niger esa oxratoksin A ishlab chiqarib, buyrak faoliyatini og‘ir darajada zararlaydi.

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Penicillium avlodi zamburug‘lari (P. verrucosum, P. expansum): Zarari: Salqin va nam omborxonalarda don haroratining ko‘tarilishi (o‘z-o‘zidan qizish) va mog‘orlashiga sabab bo‘ladi. Ular sintez qiladigan citrinin va patulin toksinlari nefrotoksik xususiyatga ega bo‘lib, buyrak va hazm qilish organlarining surunkali kasalliklariga olib keladi.

2. Patogen va shartli patogen bakteriyalar. Bacillus cereus: Zarari: Sporali, gram-musbat tayoqcha. Sporalari pishirish va termik ishlov berish jarayonlariga juda chidamli. Un va dondan tayyorlangan mahsulotlar (non, bo‘tqalar, xamir ovqatlar) xona haroratida saqlanganda sporalar vegetativ shaklga o‘tib, emetik (qusish keltirib chiqaruvchi) va diarrheyik enterotoksinlar ajratadi. Bu tez rivojlanuvchi oziq-ovqat intoksikatsiyasiga sabab bo‘ladi.

Clostridium botulinum: Zarari: Anaerob sporali bakteriya. Don tuproq bilan kontaktda bo‘lganda sporalar bilan ifloslanadi. Anaerob sharoitda (zichlangan mahsulotlar, germetik idishlar) botulinotoksin sintez qiladi. Neyrotoksin markaziy nerv tizimini falajlaydi va o‘lim holatiga olib kelishi mumkin.

Enterobacteriaceae oilasi vakillari (Salmonella spp., Escherichia coli): Zarari: Don omborlarida kemiruvchilar, qushlar yoki nosog‘lom suv bilan kontakt oqibatida tushadi. Salmonella va patogen E. coli shtammlari alimentar gastrointestinal kasalliklar, ichburug‘, isitma va og‘ir suvsizlanishga sabab bo‘ladi.

Xulosa va amaliy takliflar

Don va don mahsulotlarining mikrobiologik xavfsizligini ta’minlash uchun mahsulotni yig‘ib olishdan to iste’molchiga yetkazgunga qadar bo‘lgan zanjirda kompleks nazorat choralarini amalga oshirish zarur: Dalada fuzarioz va boshqa fungal kasalliklarga qarshi agrotexnik hamda biologik himoya vositalarini o‘z vaqtida qo‘llash;

– Omborxonalarda don namligini kritik darajadan (13-14% dan) past ushlab turish va harorat-namlik rejimini qat’iy nazorat qilish;

– Mikrobiologik tahlillarni xalqaro va davlat standartlari (GOST) talablariga muvofiq, ekspress-metodlar va xromatografik usullar (XEX/GX) yordamida muntazam o‘tkazib borish.

Don mahsulotlarining mikrobiologik sofligini ta’minlash oziq-ovqat sanoatida sifat ko‘rsatkichlarini oshirish va aholi salomatligini muhofaza qilishning asosiy kafolatidir.

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PISHLOQ VA TVOROG ZARDOBINING KIMYOVIY TARKIBI HAMDA UNING *LACTOBACILLUS CASEI* UCHUN OZUQA MUHITI SIFATIDA YAROQLILIGI

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Annotatsiya: Maqolada pishloq (shirin) va tvorog (nordon) ishlab chiqarishda hosil bo‘ladigan sut zardoblarining kimyoviy tarkibi tahlil qilingan va ularning *Lactobacillus casei* probiyotik bakteriyasi uchun ozuqa muhiti sifatida yaroqliligi o‘rganilgan. Aniqlanishicha, shirin zardob tarkibida laktoza (4,6–4,9%) va oqsillar yuqori, pH ko‘rsatkichi esa *L. casei* o‘sishi uchun optimal hisoblanadi. Nordon zardobda laktoza miqdori kamroq (3,8–4,3%) bo‘lib, yuqori kislotalilik sababli neytrallashni talab etadi.

Kalit so‘zlar: shirin zardob, nordon zardob, laktoza, oqsil, mineral tarkib, *Lactobacillus casei*, ozuqa muhiti.

Аннотация: В статье проанализирован химический состав подсырной (сладкой) и творожной (кислой) сывороток и изучена их пригодность в качестве питательной среды для пробиотической бактерии *Lactobacillus casei*. Установлено, что сладкая сыворотка содержит больше лактозы (4,6–4,9%) и белков, а её уровень pH оптимален для роста *L. casei*. Кислая сыворотка содержит меньше лактозы (3,8–4,3%) и из-за высокой кислотности требует нейтрализации.

Ключевые слова: сладкая сыворотка, кислая сыворотка, лактоза, белок, минеральный состав, *Lactobacillus casei*, питательная среда.

Abstract: The article analyzes the chemical composition of cheese (sweet) and cottage cheese (acid) wheys and evaluates their suitability as a nutrient medium for the probiotic bacterium *Lactobacillus casei*. It was found that sweet whey has higher lactose (4.6–4.9%) and protein content, and its pH is optimal for *L. casei* growth. Acid whey contains less lactose (3.8–4.3%) and requires neutralization due to its high acidity.

Keywords: sweet whey, acid whey, lactose, protein, mineral composition, *Lactobacillus casei*, nutrient medium.

Kirish

Sut zardobi pishloq va tvorog ishlab chiqarish sanoatining asosiy qo‘shimcha mahsuloti bo‘lib, tarkibida qimmatli biologik komponentlarni saqlaydi. Biotexnologiyada zardobdan probiyotik madaniyatlar, xususan, *Lactobacillus casei* yetishtirishda arzon va samarali ozuqa muhiti sifatida foydalanish dolzarb yo‘nalish hisoblanadi. Zardob turi va uning kimyoviy tarkibi mikroorganizmlarning biomassa to‘plashi va metabolik faolligiga to‘g‘ridan-to‘g‘ri ta’sir ko‘rsatadi. Tadqiqotning maqsadi pishloq va tvorog zardoblarining kimyoviy ko‘rsatkichlarini solishtirish hamda ularning *L. casei* uchun ozuqa muhiti sifatida yaroqliligini baholashdan iborat.

Materiallar va metodlar

Tadqiqotda mahalliy sut korxonalaridan olingan pishloq (shirin) va tvorog (nordon) zardoblaridan foydalanildi. Zardoblarning pH ko‘rsatkichi pH-metr yordamida, quruq modda miqdori

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refraktometrik usulda aniqlandi. Laktoza miqdori atsidometrik, umumiy oqsil esa Kyeldal usuli bo‘yicha tahlil qilindi. Mineral tarkibi (Ca, P, K) atom-absorbsion spektrometriya yordamida o‘rganildi. Sinov obyekti sifatida *L. casei* shtammi olingan bo‘lib, u zardob muhitlarida 37 °C haroratda 24 soat davomida kultivatsiya qilindi. Bakteriyalar o‘sishi optik zichlik (OD600) va koloniya hosil qiluvchi birliklar (KHO‘B/ml) soni orqali baholandi.

Natijalar

Olingan natijalar pishloq va tvorog zardoblarining kimyoviy tarkibida sezilarli farqlar borligini ko‘rsatdi. Shirin (pishloq) zardobning pH ko‘rsatkichi 6,1–6,5 ni tashkil etib, tarkibidagi laktoza miqdori 4,8% ni, oqsillar esa 0,8% ni tashkil etdi. Nordon (tvorog) zardobda esa kislotali muhit (pH 4,4–4,6) kuzatildi, laktoza miqdori 4,1% gacha kamaygan, ammo unda erigan kalsiy (Ca) va fosfor (P) miqdori shirin zardobga nisbatan 1,5 barobar yuqori bo‘ldi. *L. casei* kultivatsiya qilinganda, shirin zardob muhitida qo‘shimcha neytrallashsiz ham yuqori biomassa ($8{,}9\times10^8$ KHO‘B/ml) olindi. Nordon zardobda esa bakteriyalar o‘sishi boshlang‘ich bosqichda sekin kechdi va faqat muhit pH ko‘rsatkichi 6,2 gacha korreksiya qilingandan so‘ng samarali ko‘payish ($7{,}4\times10^8$ KHO‘B/ml) kuzatildi.

Muhokama

Shirin zardob tarkibidagi uglevodlar (laktoza) va oqsillarning yuqori konsentratsiyasi sut kislotasi bakteriyalari uchun tayyor energiya va azot manbai bo‘lib xizmat qiladi. Nordon zardob tarkibidagi mineral tuzlarning (ayniqsa, kalsiy fosfat) ko‘pligi mikrob hujayralari osmoregulyatsiyasi uchun foydali bo‘lsa-da, uning past pH ko‘rsatkichi *L. casei* shtammlarining fermentatsiya jarayonini tormozlashi mumkin. Shu sababli, tvorog zardobidan ozuqa muhiti sifatida foydalanishda muhitni oldindan ishqoriy agentlar (NaOH yoki $CaCO_3$) bilan neytrallash hamda fermentativ gidrolizlash talab etiladi.

Xulosa

Tadqiqotlar shuni ko‘rsatdiki, pishloq (shirin) zardobi o‘zining tabiiy pH ko‘rsatkichi va yuqori laktoza miqdori tufayli *Lactobacillus casei*ni kultivatsiya qilish uchun eng qulay va iqtisodiy jihatdan yaroqli substrat hisoblanadi. Tvorog zardobi ham ozuqa muhiti sifatida ishlatilishi mumkin, biroq u dastlabki texnologik korreksiyani (pH ko‘rsatkichini optimallashtirishni) taqozo etadi.

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ANOR PO‘STLOG‘IDAN AJRATILGAN ELLAGITANINLARNING MIKROORGANIZMLARDA LAKTAZA FERMENTI FAOLLIGIGA TA’SIRI

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Annotatsiya: Mazkur tezisda anor po‘stlog‘i tarkibidan ajratib olinadigan ellagitaninlarning mikroorganizmlarda laktaza fermenti faolligiga ta’sirini o‘rganishning nazariy va amaliy jihatlari yoritilgan. Anor po‘stlog‘i polifenolik birikmalar, jumladan, gidrolizlanuvchi taninlar va ellagitaninlarga boy tabiiy xomashyo hisoblanadi. Ellagitaninlarning mikroorganizmlar (*Lactobacillus plantarum*) da laktaza ferment faolligiga ta’siri tavsiflandi.
Kalit so‘zlar: anor po‘stlog‘i, laktaza, ellagitaninlar, *Lactobacillus plantarum*.

Аннотация: В данной диссертации рассматриваются теоретические и практические аспекты изучения влияния эллагитаннинов, выделенных из кожуры граната, на активность фермента лактазы в микроорганизмах. Кожура граната — это природное сырье, богатое полифенольными соединениями, включая гидролизуемые дубильные вещества и эллагитаннины. Описано влияние эллагитаннинов на микроорганизмы (*Lactobacillus plantarum*) и активность фермента лактазы.
Ключевые слова: кожура граната, лактаза, эллагитаннины, *Lactobacillus plantarum*.

Abstract: This thesis explores the theoretical and practical aspects of the effect of ellagitannins-extracted from pomegranate peel-on the activity of the enzyme lactase in microorganisms. Pomegranate peel is a natural raw material rich in polyphenolic compounds, including hydrolyzable tannins and ellagitannins. The influence of ellagitannins on microorganisms *(Lactobacillus plantarum*) and the activity of the enzyme lactase is described.
Keywords: pomegranate peel, lactase, ellagitannins, *Lactobacillus plantarum.*

Kirish

Oziq-ovqat biotexnologiyasida o‘simlik ikkilamchi xomashyolaridan biologik faol moddalarni ajratib olish va amaliyotga tatbiq etish dolzarb masalalardan biridir. Anor (Punica granatum L.) po‘stlog‘i gidrolizlanuvchi taninlar, xususan ellagitaninlar va ellag kislotasiga boy xomashyo hisoblanadi. Laktaza fermenti sut mahsulotlarini biotexnologik qayta ishlash va laktoza miqdori kamaytirilgan mahsulotlar ishlab chiqarishda muhim o‘rin tutadi. Ushbu tadqiqotning maqsadi anor po‘stlog‘idan ajratilgan ellagitaninlarning *Lactobacillus plantarum* mikroorganizmidagi laktaza fermenti faolligiga va o‘sish kinetikasiga ta’sirini aniqlashdan iborat.

Materiallar va Metodlar

Anor po‘stlog‘i 40–45°C haroratda quritilib, maydalandi va suv-spirtli erituvchi yordamida ekstraksiya qilindi. Ekstrakt tarkibidagi umumiy fenollar spektrofotometrik, individual komponentlar esa HPLC yordamida tahlil qilindi. Model mikroorganizm sifatida *Lactobacillus plantarum* shtammidan foydalanildi. Bakteriyalar o‘sishi optik zichlik (OD_{600}) orqali, laktaza faolligi esa sintetik substrat - *o*-nitrofenil-β-D-galaktopiranozid (ONPG) gidrolizlanishi natijasida hosil bo‘lgan *o*-nitrofenol (ONP) miqdorini 420 nm to‘lqin uzunligida o‘lchash orqali baholandi [1].

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Natijalar

Mikroorganizm o‘sishi: Ellagitanin ekstraktining past konsentratsiyalarida (0.1–0.25 mg/mL) *Lactobacillus plantarum* biomassasi to‘planishida nazoratga nisbatan sezilarli o‘zgarish kuzatilmadi [2]. Konsentratsiya 1.0 mg/mL va undan yuqoriga oshirilganda, bakteriyalar o‘sishi 10–30% ga sekinlashdi [3].

Laktaza faolligi. Ekstraktning 0.1–0.25 mg/mL konsentratsiyasida ferment faolligi nazoratga nisbatan 102–105% atrofida saqlanib qoldi [4]. Yuqori konsentratsiyalarda (1.0–2.5 mg/mL) esa laktaza katalitik faolligining 20–40% gacha pasayishi (qisman ingibirlanishi) qayd etildi [5].

Muhokama

Laktaza faolligining yuqori konsentratsiyalarda pasayishi ellagitaninlar tarkibidagi gidroksil (–OH) guruhlarining ferment oqsili bilan vodorod va gidrofob bog‘lar hosil qilishi, bu esa konformatsion o‘zgarishlarga olib kelishi bilan izohlanadi [6,7]. Past konsentratsiyalardagi barqarorlik esa bakteriyalarning adaptiv javob reaksiyasi va ferment oqsillarining stabilizatsiyasi bilan bog‘liq [8]. Shuningdek, *Lactobacillus plantarum* shtammlarining ellagitaninlarga bo‘lgan sezgirligi ularning tanaza/ellagitanin-gidrolaza fermentativ faolligiga qarab farqlandi [9].

Xulosa

1. Anor po‘stlog‘idan ajratilgan ellagitaninlar *Lactobacillus plantarum* o‘sishi va laktaza faolligiga konsentratsiyaga bog‘liq ravishda ta’sir ko‘rsatadi.
2. Ekstraktning 0.1–0.25 mg/mL konsentratsiyasi laktaza faolligiga va bakteriya o‘sishiga salbiy ta’sir ko‘rsatmaydi.
3. Yuqori konsentratsiyalar (>1.0 mg/mL) fermentativ jarayonlarni qisman ingibirlaydi, bu esa probiotik va sut biotexnologiyalarida ellagitaninlar dozasini to‘g‘ri maqbullashtirish zarurligini ko‘rsatadi.

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OZUQA MUHITI VA *PEDIOCOCCUS ACIDILACTICI* K1–UzRSMMT-396 SHTAMMI TOMONIDAN BIOSURFAKTANT BIOSINTEZI SHAROITLARINI TANLASH

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Annotatsiya: Tadqiqotda *Pediococcus acidilactici* K1 shtammi tomonidan biosurfaktant biosinteziga ozuqa muhiti tarkibi va kultivatsiya sharoitlarining ta’siri bir omilli optimallashtirish (OFAT) usuli asosida baholandi. Sut zardobi, glyukoza va pepton konsentratsiyalari, shuningdek, muhitning boshlang‘ich pH qiymati, kultivatsiya harorati va davomiyligi bo‘yicha maqbul parametrlar tanlandi. Tajribalarda biosurfaktant miqdori 2,684–2,714 g/L, emulsifikatsiya indeksi (E24) 72,8–74,2% va sirt tarangligi 41,0–42,4 mN/m oralig‘ida qayd etildi. Olingan natijalar laboratoriya sharoitida biosurfaktant biosintezi uchun maqbul parametrlarni aniqlash imkonini berdi hamda jarayonni yanada optimallashtirish uchun ilmiy asos bo‘lib xizmat qiladi.
Kalit so‘zlar: *Pediococcus acidilactici*, biosurfaktant, sut zardobi, ozuqa muhiti, biosintez, emulsifikatsiya faolligi, optimallashtirish.

Аннотация: В исследовании оценено влияние состава питательной среды и условий культивирования на биосинтез биосурфактанта штаммом *Pediococcus acidilactici* K1 с применением метода однофакторной оптимизации (One-Factor-at-a-Time, OFAT). Выбраны наиболее благоприятные параметры концентрации молочной сыворотки, глюкозы и пептона, а также начального значения pH среды, температуры и продолжительности культивирования. В ходе экспериментов выход биосурфактанта составил 2,684–2,714 г/л, индекс эмульгирования (E24) — 72,8–74,2%, а поверхностное натяжение — 41,0–42,4 мН/м. Полученные результаты позволили определить благоприятные параметры биосинтеза биосурфактанта в лабораторных условиях и служат научной основой для дальнейшей оптимизации процесса.
Ключевые слова: *Pediococcus acidilactici*, биосурфактант, молочная сыворотка, питательная среда, биосинтез, эмульгирующая активность, оптимизация.

Abstract: This study evaluated the effects of culture medium composition and cultivation conditions on biosurfactant biosynthesis by *Pediococcus acidilactici* K1 using the One-Factor-at-a-Time (OFAT) optimization approach. Favorable parameters were selected for whey, glucose, and peptone concentrations, as well as initial medium pH, cultivation temperature, and duration. Across the experiments, biosurfactant yield ranged from 2.684 to 2.714 g/L, the emulsification index (E24) from 72.8 to 74.2%, and surface tension from 41.0 to 42.4 mN/m. The results enabled the identification of favorable parameters for biosurfactant biosynthesis under laboratory conditions and provide a scientific basis for further process optimization.
Keywords: *Pediococcus acidilactici*, biosurfactant, whey, culture medium, biosynthesis, emulsifying activity, optimization.

So‘nggi yillarda ekologik xavfsizligi, biologik parchalanish xususiyati va yuqori sirt-faolligi bilan tavsiflanadigan mikrob biosurfaktantlariga ilmiy va amaliy qiziqish ortib bormoqda. Biosurfaktantlar mikroorganizmlar tomonidan sintezlanadigan amfifil tabiatli birikmalar bo‘lib, sirt

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va fazalararo taranglikni kamaytirish, emulsiyalarni hosil qilish hamda barqarorlashtirish xususiyatlariga ega. Bundan tashqari, ayrim biosurfaktantlar antimikrob, antiadgeziv va antibiofilm faollikni ham namoyon etishi mumkin [1, 2]. Hozirgi vaqtda ko‘plab sanoat tarmoqlarida sintetik surfaktantlardan keng foydalanilmoqda. Biroq ayrim sintetik surfaktantlarning ekologik ta’siri va biologik parchalanish xususiyatlari bilan bog‘liq muammolar ularning muqobillarini izlashga turtki bermoqda. Shu munosabat bilan biologik kelib chiqishga ega sirt-faol birikmalarni ishlab chiqarish va amaliyotga joriy etish imkoniyatlarini kengaytirishga qaratilgan tadqiqotlar dolzarb hisoblanadi [2]. Shu bilan birga, biosurfaktantlarning sanoat miqyosida ishlab chiqarilishi yuqori mahsuldor produtsent shtammlarni tanlash, ozuqa muhiti tannarxini kamaytirish, biosintez samaradorligini oshirish hamda mahsulotni ajratib olish va tozalash jarayonlarini takomillashtirish bilan bog‘liq qator muammolar bilan cheklanmoqda [2]. Ushbu muammolarni hal etishda statistik tajriba dizayni va matematik modellashtirish usullaridan foydalanish alohida ahamiyatga ega. Xususan, javob sirtlari metodologiyasi (Response Surface Methodology — RSM) ozuqa muhiti komponentlari va kultivatsiya parametrlarining biosurfaktant sinteziga ta’sirini baholash, omillar o‘rtasidagi o‘zaro ta’sirlarni aniqlash hamda tajribalarni oqilona rejalashtirish imkonini beradi. Mazkur yondashuv tajribalar sonini maqbullashtirish va biosurfaktant ishlab chiqarish jarayonining samaradorligini oshirishda istiqbolli usul hisoblanadi [3].

Tadqiqot **maqsadi** — *Pediococcus acidilactici K1* shtammi tomonidan biosurfaktant ishlab chiqarish miqdorini oshirishda ozuqa muhiti tarkibi va kultivatsiya sharoitlarini optimallashtirish.

Materiallar va usullar

Biosurfaktant biosintezini oshirish va miqdoriy oshirish uchun ozuqa muhiti tarkibi hamda kultivatsiya sharoitlarini optimallashtirish bo‘yicha tajribalar olib borildi. Ozuqa muhiti tarkibini optimallashtirish jarayonida uglerod va azot manbalarining turi hamda konsentratsiyasi, shuningdek, sut zardobining biosurfaktant hosil bo‘lishiga ta’siri baholandi. Kultivatsiya sharoitlarini optimallashtirishda muhitning boshlang‘ich pH ko‘rsatkichi, inkubatsiya harorati va davomiyligi asosiy omillar sifatida o‘rganildi. Biosurfaktant hosil bo‘lish samaradorligi emulsifikatsiya indeksi (E24), kultural suyuqlikning sirt tarangligi va ajratib olingan biosurfaktant miqdori asosida baholandi.

O‘tkazilgan tadqiqotlar natijasida *Pediococcus acidilactici* K1 shtammi tomonidan biosurfaktant biosinteziga ozuqa muhiti tarkibi va kultivatsiya sharoitlarining ta’siri bir omilli optimallashtirish (One-Factor-at-a-Time, OFAT) usuli asosida baholandi.

Natijalar

Har bir omilning ta’sirini alohida o‘rganish natijasida biosurfaktant sintezi uchun maqbul parametrlar sifatida sut zardobi konsentratsiyasi 30% (hajm/hajm), glyukoza va pepton miqdori har biri 10 g/L, muhitning boshlang‘ich pH qiymati 6,5, kultivatsiya harorati 37 °C hamda davomiyligi 36 soat tanlandi. Ushbu parametrlarni tanlash jarayonida emulsifikatsiya indeksi (E24) 72,8–74,2%, sirt tarangligi 41,0–42,4 mN/m va biosurfaktant miqdori 2,684–2,714 g/L oralig‘ida qayd etildi. Olingan natijalar *P. acidilactici* K1 shtammi asosida biosurfaktant ishlab chiqarish jarayonini takomillashtirish uchun istiqbolli sharoitlarni belgilash imkonini berdi.

Olingan natijalar laboratoriya sharoitida tasdiqlanishini asoslash uchun tajribalar qilinganda, matematik ishlanma va laboratoriya natijalari aniqlik darajasi 75% dan yuqori ekanligi tasdiqlandi. Mazkur sharoitda emulsifikatsiya indeksining 72,8–74,2% oralig‘ida qayd etilishi sintezlangan biosurfaktantning emulsiya hosil qilish va uni barqarorlashtirish salohiyatini ko‘rsatadi. Shuningdek, sirt tarangligining 41–42 mN/m atrofida bo‘lishi kultural suyuqlikda sirt faol birikmalar mavjudligini tasdiqlovchi muhim funksional ko‘rsatkichlardan biri hisoblanadi. Sut zardobidan ozuqa muhiti komponenti sifatida foydalanish biosurfaktant ishlab chiqarish texnologiyasining iqtisodiy samaradorligini oshirish nuqtayi nazaridan ham istiqbolli hisoblanadi. Chunki sut zardobi tarkibidagi uglevodlar, azotli birikmalar va mineral komponentlar mikroorganizmlarning o‘sishi hamda metabolik faoliyatini ta’minlashda ishtirok etishi mumkin.

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Xulosa

O‘tkazilgan tajribalar natijalariga ko‘ra, o‘rganilgan parametrlarning quyidagi qiymatlari tanlandi: sut zardobi — 30 % (hajm/hajm), glyukoza va pepton — har biri 10 g/l, boshlang‘ich pH — 6,5, harorat — 37 °C, o‘stirish davomiyligi — 36 soat. Olingan ma’lumotlar *P. acidilactici* K1-UzRSMMT-396 shtammi yordamida biosurfaktant olish jarayonini yanada ishlab chiqish uchun asos bo‘lib xizmat qiladi. Tanlangan parametrlarni birgalikda qo‘llash samaradorligini alohida tajribada tasdiqlash zarur.

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БИОЛОГИЧЕСКАЯ ДЕТОКСИКАЦИЯ МИКОТОКСИНОВ В КОРМАХ С ИСПОЛЬЗОВАНИЕМ МОЛОЧНОКИСЛЫХ БАКТЕРИЙ

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Аннотация: Исследована антифунгальная активность молочнокислых бактерий в отношении микотоксигенного гриба *Aspergillus flavus*, выделенного из местных кормов. Штаммы *Lactiplantibacillus plantarum*, *Pediococcus pentosaceus*, *Enterococcus faecium* и *Weissella cibaria* проявили выраженную активность, формируя зоны подавления роста 43–47 мм. При совместном культивировании в течение 30 суток жизнеспособные клетки гриба не обнаруживались. Результаты свидетельствуют о перспективности исследованных бактерий для разработки биологических методов защиты кормов от микотоксигенных микромицетов.

Ключевые слова: микотоксины, корма, биологическая детоксикация, молочнокислые бактерии, *Aspergillus flavus*, афлатоксин B1, антифунгальная активность.

Annotatsiya: Mahalliy yemlardan ajratib olingan mikotoksin hosil qiluvchi *Aspergillus flavus* zamburug‘iga nisbatan sut kislotasi bakteriyalarining antifungal faolligi o‘rganildi. *Lactiplantibacillus plantarum*, *Pediococcus pentosaceus*, *Enterococcus faecium* va *Weissella cibaria* shtammlari yuqori faollik ko‘rsatib, zamburug‘ o‘sishini 43–47 mm zonada bostirdi. Bakteriyalar bilan 30 kun davomida birgalikda kultivatsiya qilinganda zamburug‘ning yashovchan hujayralari aniqlanmadi. Natijalar o‘rganilgan bakteriyalardan yemlarni mikotoksin hosil qiluvchi mikromitsetlardan biologik himoya qilish usullarini ishlab chiqishda foydalanish istiqbollarini ko‘rsatadi.

Kalit so‘zlar: mikotoksinlar, yem, biologik detoksikatsiya, sut kislotasi bakteriyalari, *Aspergillus flavus*, aflatoksin B1, antifungal faollik.

Abstract: The antifungal activity of lactic acid bacteria against the mycotoxigenic fungus *Aspergillus flavus*, isolated from local feed samples, was investigated. The strains *Lactiplantibacillus plantarum*, *Pediococcus pentosaceus*, *Enterococcus faecium*, and *Weissella cibaria* demonstrated strong antifungal activity, producing growth inhibition zones of 43–47 mm. No viable fungal cells were detected after 30 days of co-cultivation. These findings indicate the potential of the investigated bacteria for developing biological approaches to protect feed against mycotoxigenic fungi.

Keywords: mycotoxins, feed, biological detoxification, lactic acid bacteria, *Aspergillus flavus*, aflatoxin B1, antifungal activity.

Введение

Загрязнение кормов и продовольствия микотоксинами, продуцируемыми микромицетами, представляет угрозу здоровью людей и животных [1, 2]. В связи с ограничениями физических и химических методов детоксикации перспективно применение молочнокислых бактерий, способных связывать микотоксины, трансформировать их и подавлять развитие токсигенных грибов [3, 4]. Цель работы — оценить потенциал молочнокислых бактерий в биодеструкции микотоксинов и подавлении роста Aspergillus flavus, выделенного из местных кормов.

ДЛЯ ЦИТИРОВАНИЯ
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Материалы и методы

Микромицеты выделяли из образцов местных кормов классическими микробиологическими методами; идентификацию проводили по морфологическим признакам и молекулярно-генетически (секвенирование региона ITS, анализ в NCBI BLASTn, филогенетическое дерево методом Neighbor-Joining в MEGA 11, бутстреп-анализ – 1000 повторов). Микотоксигенность подтверждена наличием генов биосинтеза афлатоксинов (aflO, aflP, aflD, aflQ), качественно – методом ИФА, а образование афлатоксина B1 – методом ВЭЖХ-МС/МС (Waters XEVO TQ-S). Антагонистическую активность штаммов Lactiplantibacillus plantarum M1, Pediococcus pentosaceus A1, Enterococcus faecium A2 и Weissella cibaria определяли методом агаровых штрихов. Способность к биодеструкции изучали при совместном культивировании бактерий (в том числе Bacillus megaterium и B. subtilis) с *A. flavus* в жидкой питательной среде в течение 30 суток с ежедневным определением числа КОЕ.

Результаты

Изолят с тёмно-зелёными колониями и шаровидными вздутиями конидиеносцев идентифицирован как Aspergillus flavus Uz-Z3 (GenBank PV528914). По данным ИФА, при 30 °C на 14-е сутки содержание афлатоксина B1 составляло 12,08 мкг/л, а охратоксина — около 370 мкг/л. При 35 °C концентрация афлатоксина B1 достигала 18,4 мкг/л на 14-е сутки и 17,9 мкг/л на 30-е сутки. Наличие афлатоксина B1 подтверждено методом ВЭЖХ-МС/МС. Все исследованные штаммы молочнокислых бактерий проявили антифунгальную активность. Зоны подавления роста A. flavus составляли 45–47 мм для Lactiplantibacillus plantarum, 47 мм для Pediococcus pentosaceus и 43 мм для Enterococcus faecium. Weissella cibaria также проявила ингибирующее действие. При совместном культивировании в течение 30 суток титр молочнокислых бактерий сохранялся на уровне 10^7–10^8 КОЕ/мл, а Bacillus megaterium и B. subtilis — 10^6 КОЕ/мл. Жизнеспособные клетки A. flavus во всех вариантах опыта не обнаруживались.

Обсуждение

Полученные результаты подтверждают микотоксигенный потенциал A. flavus Uz-Z3 и зависимость концентрации афлатоксина B1 от условий культивирования. Более высокая концентрация токсина при 35 °C по сравнению с 30 °C указывает на влияние температуры на его накопление. Выраженная антифунгальная активность молочнокислых бактерий, особенно L. plantarum и P. pentosaceus, свидетельствует об их потенциале для биологического контроля микотоксигенных грибов. Отсутствие жизнеспособных клеток A. flavus после совместного культивирования указывает на полное подавление его роста в исследованных условиях. Однако этот результат сам по себе не доказывает разрушение уже образовавшихся микотоксинов. Для подтверждения детоксикации необходимо определить остаточные концентрации афлатоксина B1 и охратоксина после обработки бактериями, а также оценить токсичность возможных продуктов трансформации.

Выводы

Штаммы *L. plantarum M1, P. pentosaceus A1, E. faecium A2 и W. cibaria* обладают выраженной антифунгальной активностью в отношении микотоксигенного A. flavus и полностью подавляют его развитие при совместном культивировании, вытесняя токсигенный микромицет в процессе ферментации. Это позволяет рассматривать их как безопасных кандидатов для биологической детоксикации кормов и продовольствия, загрязнённых микотоксинами.

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DORIVOR O‘SIMLIKLAR EKSTRAKTLARINING ANTIMIKROB FAOLLIGI VA ULARNING MIKROBIOLOGIYADAGI ISTIQBOLLARI

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Annotatsiya: Ushbu tezisda dorivor o‘simliklar tarkibidagi biologik faol birikmalarning mikroorganizmlarga qarshi ta’siri, ularning ehtimoliy ta’sir mexanizmlari hamda mikrobiologiyada qo‘llash istiqbollari yoritilgan. O‘simlik ekstraktlarining antibakterial xususiyatlarini o‘rganish antibiotiklarga chidamli mikroorganizmlarga qarshi yangi biologik faol moddalarni izlashda muhim ilmiy yo‘nalish hisoblanadi. Shuningdek, ekstraktlarning kimyoviy tarkibi, tayyorlash usuli va mikroorganizmlar turiga bog‘liq holda ularning faolligi o‘zgarishi muhokama qilinadi.
Kalit so‘zlar: dorivor o‘simliklar, mikroorganizmlar, antimikrob faollik, o‘simlik ekstrakti, flavonoidlar, fenolik birikmalar, antibiotiklarga chidamlilik.

Аннотация: В тезисе рассматриваются антимикробное действие биологически активных соединений, содержащихся в лекарственных растениях, возможные механизмы их воздействия, а также перспективы их применения в микробиологии. Изучение антибактериальных свойств растительных экстрактов является важным научным направлением в поиске новых биологически активных веществ, направленных против микроорганизмов, устойчивых к антибиотикам. Кроме того, рассматривается изменение антимикробной активности экстрактов в зависимости от их химического состава, способа приготовления и вида микроорганизмов.
Ключевые слова: лекарственные растения, микроорганизмы, антимикробная активность, растительный экстракт, флавоноиды, фенольные соединения, антибиотикорезистентность.

Abstract: This thesis examines the antimicrobial effects of biologically active compounds found in medicinal plants, their possible mechanisms of action, and their prospects for application in microbiology. The study of the antibacterial properties of plant extracts is an important research area in the search for new biologically active substances against antibiotic-resistant microorganisms. In addition, changes in the antimicrobial activity of extracts depending on their chemical composition, preparation methods, and the types of microorganisms are discussed.
Keywords: medicinal plants, microorganisms, antimicrobial activity, plant extract, flavonoids, phenolic compounds, antibiotic resistance.

Kirish

Hozirgi vaqtda mikroorganizmlarning antimikrob preparatlarga chidamliligining ortishi tibbiyot va mikrobiologiyaning dolzarb muammolaridan biri hisoblanadi. Jahon sog‘liqni saqlash tashkilotining ma’lumotlariga ko‘ra, antimikrob rezistentlik infeksion kasalliklarni davolash samaradorligini pasaytirib, ularning tarqalishi va asoratlar xavfini oshiradi [1]. Shu sababli yangi antimikrob moddalarni izlash, tabiiy manbalarning biologik xususiyatlarini o‘rganish va mavjud preparatlarga muqobil vositalarni ishlab chiqish muhim ahamiyatga ega.

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Dorivor o‘simliklar biologik faol moddalarning tabiiy manbai bo‘lib, ularning tarkibida flavonoidlar, fenolik kislotalar, taninlar, alkaloidlar va terpenoidlar uchraydi. Ushbu birikmalarning ayrimlari bakteriyalar va zamburug‘larning o‘sishi hamda rivojlanishiga ta’sir ko‘rsatishi mumkin [2, 3].

Ilmiy adabiyotlarda dorivor o‘simlik ekstraktlarining turli mikroorganizmlarga qarshi faolligi keng o‘rganilgan. Xususan, ayrim o‘simliklardan olingan ekstraktlar *Staphylococcus aureus*, *Escherichia coli* va *Pseudomonas aeruginosa* kabi bakteriyalarga nisbatan laboratoriya sharoitida ingibirlovchi ta’sir ko‘rsatishi qayd etilgan [2]. Biroq bunday ta’sir o‘simlik turi, ishlatilgan qismi, ekstraksiya erituvchisi, faol moddalar konsentratsiyasi va sinov metodikasiga bog‘liq.

O‘simliklarning antimikrob faolligi bir necha mexanizm bilan izohlanadi. Ayrim fenolik birikmalar va terpenoidlar mikroorganizmlarning hujayra membranasi yaxlitligiga ta’sir qilishi, membrana o‘tkazuvchanligini o‘zgartirishi hamda hujayra ichidagi muhim biokimyoviy jarayonlarni buzishi mumkin. Flavonoidlar va boshqa fitokimyoviy moddalar ham bakterial fermentlar faoliyati va metabolik jarayonlarga ta’sir ko‘rsatishi ehtimoli mavjud [3].

Mikrobiologik tadqiqotlarda o‘simlik ekstraktlarining faolligini baholash uchun agar muhitida diffuziya usuli, minimal ingibirlovchi konsentratsiyani (MIK) aniqlash va boshqa standartlashtirilgan laboratoriya metodlaridan foydalaniladi. MIK mikroorganizmning ko‘zga ko‘rinadigan o‘sishini to‘xtatuvchi moddaning eng kichik konsentratsiyasini ifodalaydi. Ushbu ko‘rsatkich turli ekstraktlarning faolligini miqdoriy taqqoslashda muhimdir.

Shu bilan birga, laboratoriyada aniqlangan antibakterial faollik o‘simlik ekstraktining klinik jihatdan samarali yoki xavfsiz ekanini o‘z-o‘zidan isbotlamaydi. Faol moddalarning tarkibi va miqdorini aniqlash, toksikligini baholash, standartlashtirilgan sinovlarni o‘tkazish hamda ta’sir mexanizmlarini chuqur o‘rganish talab etiladi [2, 3]. O‘simlik ekstraktlarini antibiotiklar bilan birgalikda qo‘llash imkoniyatlarini o‘rganish ham istiqbolli yo‘nalishlardan biridir, biroq bunday kombinatsiyalarning samaradorligi tajribalar orqali alohida tasdiqlanishi lozim.

Material va metodlar

Mazkur mavzuni o‘rganishda ilmiy adabiyotlarni tahlil qilish, dorivor o‘simliklar tarkibidagi biologik faol birikmalarning xususiyatlarini umumlashtirish hamda ularning antimikrob faolligini baholashda qo‘llaniladigan mikrobiologik usullarni taqqoslash asosiy metodik yondashuv sifatida belgilanadi. Tahlilda o‘simlik ekstraktlarining kimyoviy tarkibi, mikroorganizmlar guruhlariga ta’siri va laboratoriya sharoitida faollikni aniqlash mezonlariga e’tibor qaratiladi.

Dorivor o‘simliklarning antimikrob xususiyatlarini eksperimental baholashda, avvalo, o‘simlik turini aniq identifikatsiya qilish, foydalaniladigan qismini belgilash va xomashyo sifatini nazorat qilish muhim hisoblanadi. Ekstrakt tarkibi o‘simlikning vegetatsiya davri, yig‘ib olish sharoiti, quritish usuli va ekstraksiya uchun tanlangan erituvchiga qarab farqlanishi mumkin. Shu sababli tadqiqot natijalarining ishonchliligi uchun xomashyo va ekstrakt tayyorlash sharoitlarini standartlashtirish talab etiladi.

Antimikrob faollikni baholashda agar-diffuziya usuli dastlabki skrining uchun qo‘llanilishi mumkin. Ushbu usulda mikroorganizm o‘sishining cheklanishi natijasida hosil bo‘lgan ingibitsiya zonasi o‘lchanadi. Biroq zona diametri faqat biologik faollikka emas, balki ekstrakt tarkibidagi birikmalarning agar muhitida tarqalish xususiyatiga ham bog‘liq. Shu bois mazkur usul natijalarini ekstraktning haqiqiy antimikrob kuchini belgilovchi yagona mezon sifatida qabul qilish to‘g‘ri emas [4, 5].

Ekstraktlarning faolligini miqdoriy baholashda suyuq muhitdagi mikrosuyultirish usuli muhim o‘rin tutadi. Ushbu usul yordamida mikroorganizmning ko‘zga ko‘rinadigan o‘sishini to‘xtatuvchi eng kichik konsentratsiya — minimal ingibirlovchi konsentratsiya (MIK) aniqlanadi. Zarur hollarda minimal bakteritsid konsentratsiyasi (MBK) ham baholanib, mikroorganizmlarning o‘sishi to‘xtashi bilan ularning nobud bo‘lishi o‘rtasidagi farq o‘rganiladi. Bunda nazorat

namunalari, erituvchining ta’siri va standart antimikrob preparat bilan taqqoslash natijalarning ishonchliligini oshiradi [4, 5].

Tadqiqotda *Staphylococcus aureus*, *Escherichia coli* va *Pseudomonas aeruginosa* kabi bakteriyalar model mikroorganizmlar sifatida ko‘rib chiqilishi mumkin. Ushbu turlar Gram-musbat va Gram-manfiy bakteriyalar vakillarini qamrab olgani sababli ekstraktlarning turli hujayra tuzilishiga ega mikroorganizmlarga ta’sirini taqqoslash imkonini beradi. Bunday tajribalar tegishli biosafety talablariga rioya qilinadigan laboratoriyada, standartlashtirilgan metodika asosida bajarilishi lozim.

Shuni ta’kidlash kerakki, mazkur tezis adabiyotlar tahliliga asoslangan. Unda mustaqil laboratoriya tajribasi o‘tkazilgani yoki muayyan ekstrakt uchun MIK va MBK qiymatlari aniqlangani da’vo qilinmaydi. Yuqorida keltirilgan laboratoriya usullari kelgusidagi eksperimental tadqiqotlar uchun metodik yondashuv sifatida tavsiya etiladi.

Natijalar va muhokama

Ilmiy adabiyotlar tahlili dorivor o‘simliklarning antimikrob xususiyatlari ularning kimyoviy tarkibi va ekstraksiya sharoitlariga chambarchas bog‘liqligini ko‘rsatadi. O‘simliklarning ikkilamchi metabolitlari hisoblangan fenolik birikmalar, flavonoidlar, taninlar va terpenoidlar mikroorganizmlarning hujayra membranasi, ferment tizimlari va boshqa muhim hujayraviy jarayonlariga ta’sir ko‘rsatishi mumkin [2, 3]. Biroq bir xil o‘simlikning turli erituvchilar yordamida olingan ekstraktlari ham tarkibi va biologik faolligi bo‘yicha farqlanishi mumkin.

Muhim jihatlardan biri — Gram-musbat va Gram-manfiy bakteriyalarning hujayra qobig‘i tuzilishidagi farqlardir. Gram-manfiy bakteriyalarda mavjud tashqi membrana ayrim kimyoviy birikmalarning hujayra ichiga kirishini cheklashi mumkin. Shu sababli o‘simlik ekstraktining turli bakteriyalarga ta’siri bir xil bo‘lmasligi ehtimoli mavjud. Biroq bu holatni barcha o‘simlik ekstraktlariga birdek tatbiq etib bo‘lmaydi, chunki antimikrob ta’sir faol birikmalarning tabiati va mikroorganizmning o‘ziga xos xususiyatlariga ham bog‘liq [3, 5].

Natijalarni baholashda metod tanlovi alohida ahamiyatga ega. Agar-diffuziya usulida ingibitsiya zonasining kichik bo‘lishi ekstraktning biologik faolligi pastligini har doim ham anglatmaydi. Ayrim gidrofob birikmalar agar muhitida sust tarqalishi sababli o‘z faolligini yetarlicha namoyon qilmasligi mumkin. Aksincha, suyuq muhitdagi mikrosuyultirish usuli ekstraktning o‘sishni cheklovchi konsentratsiyasini aniqlashga imkon beradi, ammo rangli yoki loyqa ekstraktlar o‘lchash natijalariga xalaqit berishi mumkin. Shuning uchun metodni tanlashda ekstraktning fizik-kimyoviy xususiyatlarini hisobga olish zarur [4, 5].

Dorivor o‘simliklarning antimikrob xususiyatlarini o‘rganish antibiotiklarga chidamlilik muammosiga qarshi yangi biologik faol birikmalarni izlash uchun istiqbolli yo‘nalishdir. Jahon sog‘liqni saqlash tashkilotining 2025-yilgi global hisobotida antimikrob rezistentlikni kuzatish va unga qarshi kurashish bo‘yicha standartlashtirilgan ma’lumotlarning ahamiyati ta’kidlangan [1]. Shu nuqtayi nazardan, tabiiy birikmalarni izlash, ularning ta’sir mexanizmlarini o‘rganish va laboratoriya natijalarini takrorlanuvchan usullar bilan tasdiqlash dolzarb ilmiy vazifa hisoblanadi.

Shu bilan birga, o‘simlik ekstraktining laboratoriya sharoitida antibakterial faollik ko‘rsatishi uning inson organizmida xavfsiz va samarali dori vositasi bo‘lishini anglatmaydi. Faol moddaning toksikligi, organizmda so‘rilishi, barqarorligi, dozasi va boshqa preparatlar bilan o‘zaro ta’siri alohida tekshirilishi kerak. Demak, dorivor o‘simliklarni mikrobiologiyada qo‘llash imkoniyatlarini baholashda an’anaviy bilimlar bilan zamonaviy fitokimyoviy va mikrobiologik usullarni uyg‘unlashtirish maqsadga muvofiq.

Umuman olganda, adabiyotlar tahlili dorivor o‘simliklar antimikrob faollikka ega birikmalarning istiqbolli manbai ekanini ko‘rsatadi. Kelgusida mahalliy dorivor o‘simliklar, jumladan, O‘zbekiston florasi vakillarining kimyoviy tarkibi va mikroorganizmlarga qarshi xususiyatlarini tizimli o‘rganish yangi ilmiy ma’lumotlar olishga xizmat qilishi mumkin.

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Xulosa

Dorivor o‘simliklar tarkibidagi biologik faol birikmalar yangi antimikrob moddalarni izlash uchun istiqbolli tabiiy manba hisoblanadi. Ularning ayrimlari laboratoriya sharoitida bakteriyalar va boshqa mikroorganizmlarning o‘sishini cheklashi mumkin. Kelgusidagi tadqiqotlarda mahalliy dorivor o‘simliklarning kimyoviy tarkibini aniqlash, antimikrob faolligini standart usullar yordamida baholash va faol birikmalarning ta’sir mexanizmlarini o‘rganishga e’tibor qaratish maqsadga muvofiq. Bunday yondashuv mikrobiologiya va farmakologiya sohalarida yangi ilmiy ma’lumotlar olishga xizmat qilishi mumkin.

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ASPERGILLUS TUBINGENSIS S23 AS A PROMISING SOURCE OF PHARMACEUTICALLY IMPORTANT SECONDARY METABOLITES

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Abstract: The biosynthetic potential of *Aspergillus tubingensis* S23, an endophytic fungus isolated from the medicinal plant *Eremostachys isochila*, was evaluated through whole-genome sequencing and comparative genome mining. Molecular phylogeny and phylogenomics supported its identification as *A. tubingensis*. antiSMASH predicted 95 biosynthetic gene cluster (BGC) regions, including regions similar to characterized clusters associated with kojic acid, yanuthone D, clavaric acid, TAN-1612, nidulanin A, and burnettiene A. These results indicate substantial potential for genome-guided natural-product discovery, although the production and biological activities of the predicted compounds require experimental verification.

Keywords: *Aspergillus tubingensis*; endophytic fungi; secondary metabolites; biosynthetic gene clusters; kojic acid; natural-product discovery.

Introduction

Endophytic fungi represent a promising source of structurally diverse secondary metabolites with potential applications in pharmaceutical biotechnology and drug discovery. These microorganisms inhabit internal plant tissues without causing apparent disease symptoms and possess complex biosynthetic pathways responsible for producing numerous biologically active compounds. Among endophytic fungi, species belonging to the genus *Aspergillus* are particularly attractive because of their ability to synthesize polyketides, nonribosomal peptides, terpenoids, and other specialized metabolites exhibiting a wide range of biological activities. However, the pharmaceutical potential of many fungal isolates remains insufficiently explored, particularly at the genomic and biosynthetic levels. The integration of whole-genome sequencing, biosynthetic gene cluster (BGC) mining, and metabolite characterization offers a powerful approach for identifying promising microbial producers of pharmaceutically relevant natural products. The present study investigates the biosynthetic potential of *Aspergillus tubingensis* S23, an endophytic fungus isolated from the medicinal plant *Eremostachys isochila*, with particular emphasis on its capacity to produce secondary metabolites of potential pharmaceutical importance.

Materials and Methods

The fungal strain S23 was isolated from healthy, asymptomatic tissues of *Eremostachys isochila* (Lamiaceae), a medicinal plant collected in Uzbekistan. Taxonomic identification was performed using internal transcribed spacer (ITS) sequencing, multilocus phylogenetic analysis of three protein-coding genes (*benA*, *CaM*, and *RPB2*), and genome-scale phylogenomic analysis. Whole-genome sequencing was conducted using the MGI DNBSEQ-T7 platform with 150 bp paired-end reads. Sequencing data were quality-filtered using fastp, and genome assembly was performed

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using SPAdes v3.15.5. The biosynthetic potential of the strain was evaluated using antiSMASH v8.0.4, while predicted gene clusters were compared with experimentally characterized biosynthetic pathways available in the MIBiG database.

Results and Discussion

Molecular identification and phylogenomic analyses confirmed that strain S23 belongs to *Aspergillus tubingensis*, a member of the section *Nigri*. Genome mining revealed substantial biosynthetic diversity, with 95 predicted biosynthetic gene cluster regions, including clusters associated with polyketide synthases, nonribosomal peptide synthetases, terpene biosynthesis, and other specialized metabolic pathways. This extensive biosynthetic repertoire indicates the potential of *A. tubingensis* S23 to produce chemically diverse secondary metabolites, including compounds of pharmaceutical interest.

Comparative analysis of the predicted BGCs revealed several pathways associated with known bioactive fungal metabolites, including yanuthone D, burnettiene A, nidulanin A, TAN-1612, and kojic acid. Notably, the yanuthone D-associated BGC was found to be complete in strain S23, whereas corresponding genomic regions were disrupted in its closest relatives (Table 1).

This observation suggests distinctive biosynthetic capabilities that may differentiate S23 from other closely related strains. The burnettiene A-associated cluster exhibited a distribution consistent with vertical inheritance and differential gene loss (Figure 1), while clusters related to nidulanin A and TAN-1612 were broadly conserved across the examined fungal lineages. In contrast, the kojic acid biosynthetic pathway showed lineage-specific patterns of gene retention, relocation, and loss, highlighting the evolutionary plasticity of fungal secondary metabolism.

Table 1. Biosynthetic gene clusters in strain S23 with similarity to characterized compounds of reported pharmaceutical, cosmetic, or antimicrobial potential

Compound	MIBiG similarity	Chemical class	Documented/reported bioactivity
Kojic acid	66%	Pyranone	Cosmetic potential, Antioxidant, Antimicrobial
Yanuthone D	90%	Meroterpenoid	Antifungal activity
Clavaric acid	100%	Triterpenoid	Anticancer activity
TAN-1612	100%	Anthraquinone-type polyketide	Broadly reported for antimicrobial and anticancer bioactivity
Nidulanin A	75%	Polyketide–nonribosomal peptide hybrid	Secondary metabolite of Aspergillus nidulans, bioactivity potential is uncharacterized.
Burnettiene A	100%	Polyketide	Bioactive potential has not yet been reported.

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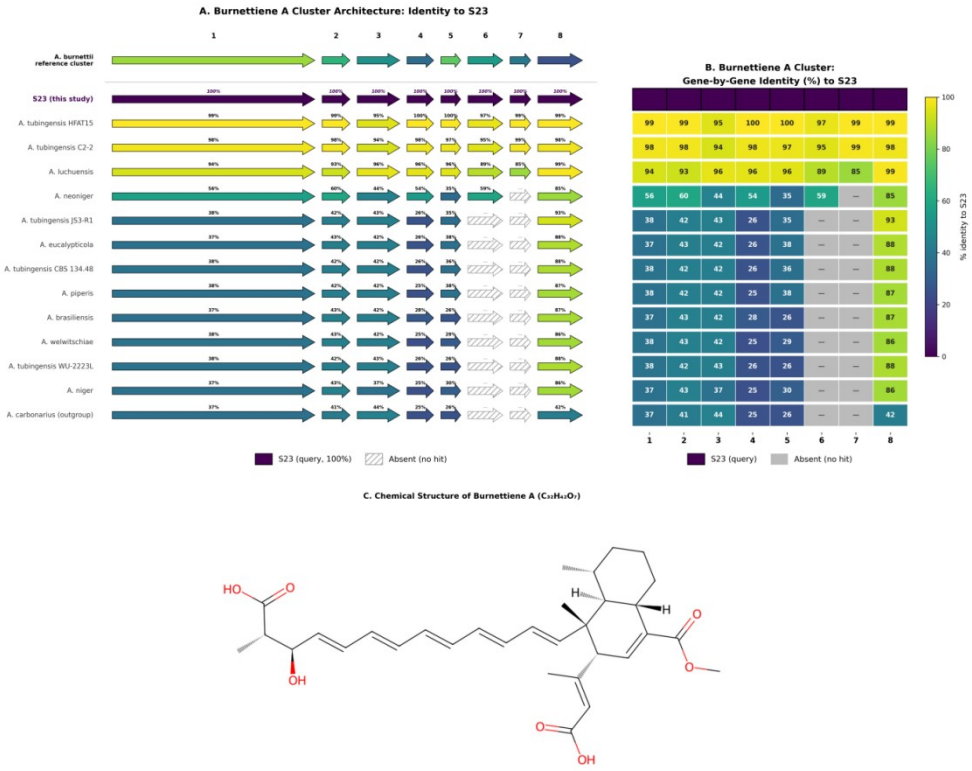


Figure 1. Burnettiene A biosynthetic gene cluster comparative and evolutionary analysis. (A) Gene architecture across all 14 genomes compared to the *A. burnettii* reference cluster (BGC0002139)

The findings demonstrate that *Aspergillus tubingensis* S23 possesses considerable potential as a microbial source of pharmaceutically relevant secondary metabolites. The identification of 95 predicted biosynthetic gene clusters, including pathways associated with kojic acid, yanuthone D, burnettiene A, nidulanin A, and TAN-1612, highlights the strain's extensive biosynthetic capacity. These results establish *A. tubingensis* S23 as a promising candidate for genome-guided natural-product discovery and provide a foundation for future metabolomic investigations, isolation of novel bioactive compounds, and development of potential pharmaceutical applications.

Discussion

The diverse predicted BGC repertoire suggests that S23 may synthesize multiple classes of specialized metabolites. The conservation and divergence of individual clusters across related genomes highlight the evolutionary complexity of fungal secondary metabolism. However, sequence similarity to characterized BGCs does not establish the production, chemical identity, yield, or pharmacological activity of the corresponding metabolites in S23. Metabolomic profiling, compound isolation, and targeted bioactivity assays are required to validate these predictions.

Conclusion

Aspergillus tubingensis S23 harbors 95 predicted BGC regions and several candidate pathways related to compounds of pharmaceutical or biotechnological interest. The findings support its selection for further genome-guided metabolite discovery and experimental characterization.

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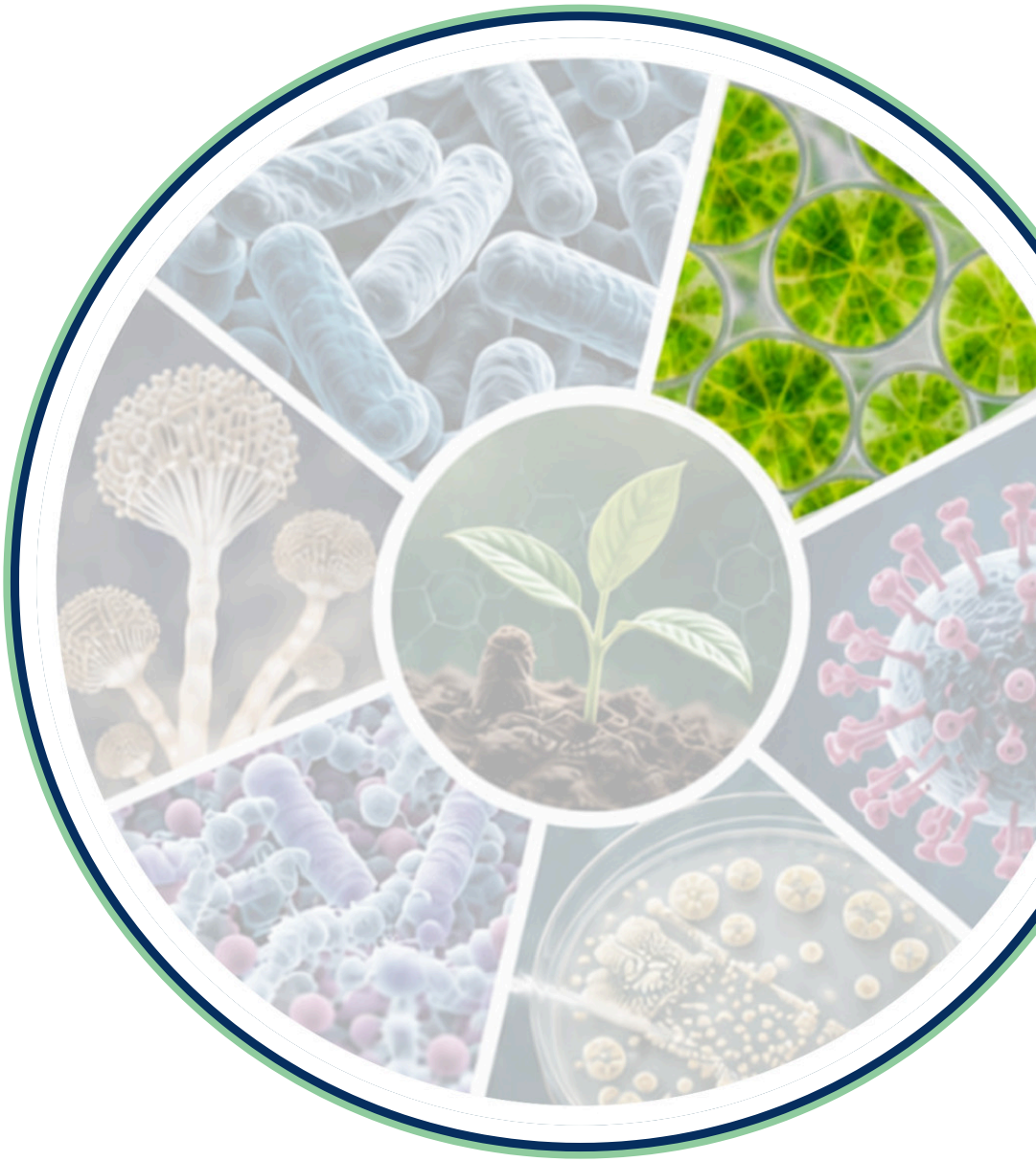
IV

BO‘LIM · SECTION · СЕКЦИЯ

TUPROQ, SUV, EKOLOGIYA VA SANITARIYA MIKROBIOLOGIYASI

Soil, Water, Ecological and Sanitary Microbiology

Почвенная, водная, экологическая и санитарная микробиология



33
ta maqola va tezis

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OLMA MEVASIDA PESTITSID QOLDIQLARINING MAVSUMIY VA HUDUDIY O‘ZGARISH XUSUSIYATLARI

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Annotatsiya: Mazkur maqolada olma mevasida pestitsid qoldiqlarining shakllanishi va miqdoriy o‘zgarishiga ta’sir etuvchi mavsumiy, hududiy hamda agrotexnik omillar ilmiy adabiyotlar asosida tahlil qilinadi. Pestitsidlarning qo‘llash muddati, mevaning yetilish bosqichi, iqlim sharoiti va faol moddalarning fizik-kimyoviy xususiyatlarining qoldiq miqdoriga ta’siri yoritiladi. Shuningdek, olma tarkibidagi pestitsid qoldiqlarini aniqlash va iste’mol bilan bog‘liq salomatlik xavfini baholashning ilmiy-amaliy ahamiyati ko‘rib chiqiladi.
Kalit so‘zlar: olma, pestitsid qoldiqlari, mavsumiy o‘zgarish, hududiy farqlar, agrotexnik omillar, pestitsid monitoringi, oziq-ovqat xavfsizligi, salomatlik xavfi.

Аннотация: В данной статье на основе анализа научной литературы рассматриваются сезонные, территориальные и агротехнические факторы, влияющие на формирование и количественные изменения остатков пестицидов в плодах яблони. Освещается влияние сроков применения пестицидов, стадии созревания плодов, климатических условий и физико-химических свойств действующих веществ на содержание их остатков. Также рассматривается научная и практическая значимость определения остатков пестицидов в яблоках и оценки потенциального риска для здоровья человека, связанного с их употреблением.
Ключевые слова: яблоко, остатки пестицидов, сезонные изменения, территориальные различия, агротехнические факторы, мониторинг пестицидов, безопасность пищевых продуктов, риск для здоровья.

Abstract: This article analyzes seasonal, regional, and agrotechnical factors affecting the formation and quantitative variation of pesticide residues in apples based on a review of scientific literature. It examines the influence of pesticide application timing, fruit ripening stage, climatic conditions, and the physicochemical properties of active substances on residue levels. The article also discusses the scientific and practical significance of determining pesticide residues in apples and assessing potential health risks associated with their consumption.
Keywords: apple, pesticide residues, seasonal variation, regional differences, agrotechnical factors, pesticide monitoring, food safety, health risk.

Kirish

Olma (*Malus domestica* Borkh.) inson oziqlanishida muhim o‘rin tutadigan mevalardan biri bo‘lib, uni yetishtirish jarayonida turli kasalliklar va zararkunandalarga qarshi pestitsidlardan keng foydalaniladi. Biroq o‘simliklarni himoya qilish vositalarining qo‘llanilishi meva tarkibida pestitsid qoldiqlarining saqlanib qolishiga olib kelishi mumkin. Vacková va hammualliflar (2025) tomonidan Chexiya bozorida sotilgan, turli geografik hududlarda yetishtirilgan 265 ta olma namunasi tahlil qilingan tadqiqotda namunalarning 98,1 foizida pestitsid qoldiqlari aniqlangan va jami 74 xil pestitsid

IQTIBOS UCHUN
Ismoilova O.L. Olma mevasida pestitsid qoldiqlarining mavsumiy va hududiy o‘zgarish xususiyatlari // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 290–293.
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qoldig‘i qayd etilgan. Mualliflar, shuningdek, olmalardagi pestitsid qoldiqlari tarkibi yetishtirilgan mamlakatga qarab farqlanishini ko‘rsatgan. Ushbu natijalar olma tarkibidagi pestitsid qoldiqlarini hududiy kesimda o‘rganish va ularning miqdoriga ta’sir etuvchi omillarni baholash muhimligini ko‘rsatadi (Vackova va boshqalar, 2025).

Olma mevasidagi pestitsid qoldiqlarini baholashda ularning miqdorini aniqlash bilan bir qatorda, saqlanish muddati davomida qoldiq miqdorining o‘zgarishini va iste’mol orqali inson salomatligiga yuzaga kelishi mumkin bo‘lgan xavfni o‘rganish ham muhimdir. Banshtu va hammualliflar (2025) tomonidan olib borilgan tadqiqotda hosil yig‘imidan keyin fludioxonil fungitsidi bilan ishlov berilgan olma mevalari va ulardan olingan sharbatdagi qoldiqlar o‘rganilgan. Tadqiqotda namunalar QuEChERS usuli asosida tayyorlanib, LC-MS/MS yordamida tahlil qilingan hamda pestitsid qoldiqlarining vaqt davomida saqlanishi va iste’mol bilan bog‘liq xavf baholangan. Ushbu tadqiqot olma tarkibidagi pestitsid qoldiqlarini zamonaviy instrumental usullar yordamida aniqlash va ularning inson salomatligi uchun ehtimoliy xavfini baholash zarurligini ko‘rsatadi. Shu asosda, mazkur maqolaning maqsadi olma mevasidagi pestitsid qoldiqlarining hududiy va vaqtga bog‘liq o‘zgarishlari hamda ularni aniqlash va xavfini baholash usullariga oid ilmiy adabiyotlarni tahlil qilishdan iborat.

Metodlar

Tadqiqotda olma mevalaridagi pestitsid qoldiqlarining mavsumiy va hududiy o‘zgarishlarini o‘rganishga oid ilmiy adabiyotlarni tahlil qilish, taqqoslash va umumlashtirish usullaridan foydalaniladi. Ilmiy ma’lumotlarni izlashda Scopus, Web of Science, ScienceDirect va Google Scholar bazalaridan foydalanish ko‘zda tutiladi. Manbalarni tanlashda pestitsid qoldiqlarining miqdori, namuna olingan hudud, mavsumiy farqlar va ularni aniqlash usullariga e’tibor qaratiladi. Olingan ma’lumotlar qiyosiy tahlil qilinib, olma mevalaridagi pestitsid qoldiqlarining o‘zgarish xususiyatlari umumlashtiriladi.

Natijalar

Tahlil qilingan ilmiy tadqiqotlarda olma mevalaridagi pestitsid qoldiqlari miqdori vaqt davomida o‘zgarishi aniqlandi. Xususan, 2024-yilda *Science of the Total Environment* jurnalida chop etilgan tadqiqotda xlorpirifos konsentratsiyasi 0,16 mg/kg dan 0,019 mg/kg gacha, karbendazim miqdori esa 2,16 mg/kg dan 0,35 mg/kg gacha kamaygan. Imidakloprid, asetamiprid va proxloraz qoldiqlari hosil yig‘imida aniqlash chegarasidan past bo‘lgan. Ushbu natijalar pestitsidlarning olma mevasidagi qoldiq miqdori vaqt o‘tishi bilan turlicha o‘zgarishini ko‘rsatadi. Biroq, mazkur tadqiqot natijalari mavsumlar va hududlar o‘rtasidagi farqlarni bevosita baholash uchun yetarli emas (Vang va boshqalar, 2024).

Olma mevalaridagi pestitsid qoldiqlarini aniqlashda zamonaviy spektroskopik usullardan foydalanish ham muhim ilmiy yo‘nalish hisoblanadi. Shi, Pan va Lu (2024) tadqiqotida olma tarkibidagi pimetrozin va karbendazim qoldiqlarini bir vaqtning o‘zida aniqlash uchun sirtni kuchaytiruvchi Raman sochilishi (SERS) usuli ko‘p o‘zgaruvchili tahlil bilan birlashtirilgan. Tadqiqotchilar spektral ma’lumotlarni qayta ishlash va bashorat modellarini yaratish orqali ikkala pestitsid miqdorini aniqlash imkoniyatini baholaganlar. Olma namunalarini tayyorlashda modifikatsiyalangan QuEChERS usulidan foydalanilgan, natijalar esa LC-MS/MS tahlili bilan taqqoslangan. Mazkur tadqiqot SERS va ko‘p o‘zgaruvchili tahlil kombinatsiyasi olma tarkibidagi bir nechta pestitsid qoldiqlarini tezkor aniqlash uchun istiqbolli yondashuv ekanini ko‘rsatadi. Bunday usullar pestitsid qoldiqlarini monitoring qilish jarayonini takomillashtirishga yordam berishi mumkin.

Olma mevalaridagi pestitsid qoldiqlarining tarqalishi turli hududlarda qo‘llaniladigan agrotexnik tadbirlar va pestitsidlardan foydalanish amaliyotiga ham bog‘liq. Polshada to‘qqiz yil davomida 696 ta olma namunasi 182 ta pestitsid bo‘yicha tekshirilgan tadqiqotda 34 xil pestitsid aniqlangan va namunalarning 3 foizida qoldiq miqdori maksimal ruxsat etilgan chegaradan (MRL) yuqori bo‘lgan (Łozowicka va boshq., 2015). Ushbu ma’lumotlar olma mevalaridagi pestitsid

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qoldiqlarini muntazam monitoring qilish hamda ularning miqdorini belgilangan me’yorlar bilan taqqoslash muhimligini ko‘rsatadi.

Shuningdek, Marokashda olma tarkibidagi pestitsid qoldiqlari va mikotoksinlarning tarqalishini baholashga qaratilgan meta-tahlilda 55 ta ilmiy tadqiqot natijalari umumlashtirilgan. Tadqiqotda olma namunalarining 70 foizida pestitsid qoldiqlari, 60 foizida esa mikotoksinlar aniqlangani qayd etilgan. Mualliflar tadqiqotlar o‘rtasidagi sezilarli farqlarni hududiy qishloq xo‘jaligi amaliyotlari va hosildan keyingi saqlash sharoitlari bilan bog‘liq holda muhokama qilganlar. Ushbu natijalar olma mevalaridagi ifloslantiruvchi moddalarni baholashda hududiy sharoitlar va tadqiqot metodlarini hisobga olish muhimligini ko‘rsatadi (Amar va boshq., 2026).

Nepalda olib borilgan tadqiqotda olma va banan mevalaridagi pestitsid qoldiqlari turli hududlar, fermer xo‘jaliklari va savdo nuqtalaridan olingan namunalar asosida o‘rganilgan. Bhandari va boshq. (2024) 51 turdagi pestitsid qoldig‘ini tahlil qilib, olma namunalarida tebuconazole, difenoconazole, propargite va imidacloprid kabi moddalar ko‘p uchraganini aniqlagan. Propargit olma namunalarida eng yuqori konsentratsiyani ko‘rsatgan va namunalarning 24 foizida uning miqdori maksimal qoldiq chegarasidan (MRL) oshgan. Tadqiqotda ayrim olma namunalarida yettitagacha turli pestitsid qoldig‘i aniqlangan. Mualliflar, shuningdek, propargit qoldiqlari mavjud olmani iste’mol qilish bolalar uchun ehtimoliy sog‘liq xavfini yuzaga keltirishi mumkinligini qayd etgan. Ushbu natijalar olma mevalaridagi pestitsid qoldiqlarini baholashda hududiy namuna olish, bir nechta pestitsidning birgalikda uchrashini aniqlash va iste’molchilar salomatligi uchun xavfni hisobga olish zarurligini ko‘rsatadi.

Import qilingan olmalardagi pestitsid qoldiqlarining hududiy farqlarini o‘rgangan Malhat va hammualliflar (2025) Misr bozorlarida Livan, Polsha, Italiya, Gretsiya va Suriyadan keltirilgan 10 176 ta olma namunasini tahlil qilgan. Tadqiqotda 430 turdagi pestitsid qoldig‘i gaz xromatografiyasi–tandem mass-spektrometriyasi (GC-MS/MS) va suyuqlik xromatografiyasi–tandem mass-spektrometriyasi (LC-MS/MS) usullari yordamida tekshirilgan. Natijalar pestitsid qoldiqlarining tarqalishi va maksimal qoldiq miqdoridan (MRL) oshish holatlari kelib chiqish mamlakatiga qarab farqlanishini ko‘rsatgan. Italiya olmalari nisbatan kam ifloslangan namunalar ulushi bilan ajralib turgan bo‘lsa, Suriya va Livan olmalari orasida MRL me’yoridan oshish holatlari ko‘proq kuzatilgan. Mualliflar barcha tekshirilgan namunalarda pestitsid qoldiqlari miqdori bir xil emasligini va ayrim namunalarda bir nechta pestitsid birgalikda uchrashini aniqlagan. Ushbu natijalar olma mevalaridagi pestitsid qoldiqlarini baholashda ularning kelib chiqish hududi, yetishtirish amaliyoti va me’yoriy talablarga muvofiqligini hisobga olish muhimligini ko‘rsatadi.

Muhokamalar

Tahlil qilingan ilmiy manbalar olma mevalaridagi pestitsid qoldiqlari miqdori qo‘llanilgan preparat turi, yetishtirish sharoiti, hududiy agrotexnik amaliyotlar va hosildan keyingi ishlov berish jarayonlariga qarab farqlanishi mumkinligini ko‘rsatadi. Xususan, import qilingan olmalarda pestitsid qoldiqlarining tarqalishi va maksimal qoldiq miqdoridan oshish holatlari kelib chiqish mamlakatiga qarab farqlangan (Malhat va boshq., 2025).

Olma mevalarida pestitsid qoldiqlarining vaqt davomida kamayishi ham muhim omil hisoblanadi. Ayrim tadqiqotlarda xlorpirifos va karbendazim qoldiqlari hosil yig‘imigacha kamaygani, boshqa tekshirilgan pestitsidlar esa aniqlash chegarasidan past darajaga tushgani qayd etilgan. Bu holat pestitsidlarning saqlanib qolish xususiyatlari bir xil emasligini ko‘rsatadi.

Biroq mavjud natijalarni taqqoslashda tadqiqotlar o‘rtasidagi farqlarni hisobga olish zarur. Namuna olingan hudud, olma navi, pestitsidlarni aniqlash usuli va me’yoriy chegaralarning turlicha bo‘lishi natijalarga ta’sir qilishi mumkin. Shu sababli pestitsid qoldiqlarining hududiy va mavsumiy o‘zgarishlarini ishonchli baholash uchun bir xil tahlil usullaridan foydalanilgan, turli davrlar va hududlarni qamrab olgan monitoring tadqiqotlari muhim ahamiyatga ega.

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Xulosa

Tahlil qilingan ilmiy adabiyotlar olma mevalaridagi pestitsid qoldiqlarining miqdori va tarqalishi pestitsid turi, yetishtirish sharoiti, kelib chiqish hududi hamda hosilni yig‘ib olishgacha bo‘lgan vaqtga qarab farqlanishini ko‘rsatdi. Ayrim tadqiqotlarda pestitsid qoldiqlarining vaqt o‘tishi bilan kamayishi kuzatilgan bo‘lsa, boshqa tadqiqotlarda turli mamlakatlardan keltirilgan olmalarda maksimal qoldiq miqdori me’yoridan oshish holatlari aniqlangan. Bu holatlar olma mahsulotlarining xavfsizligini ta’minlashda pestitsid qoldiqlarini muntazam monitoring qilish va ularni belgilangan me’yorlar bilan taqqoslash zarurligini ko‘rsatadi. Shuningdek, pestitsidlarning mavsumiy va hududiy o‘zgarishlarini aniq baholash uchun turli hududlarda va hosil yetishtirishning turli davrlarida olingan namunalarni bir xil analitik usullar yordamida tekshirish muhimdir. Kelgusida O‘zbekistonning turli hududlarida yetishtirilgan olma namunalarini o‘rganish pestitsid qoldiqlari tarqalishini baholash va iste’molchilar salomatligini muhofaza qilishga qaratilgan ilmiy asoslangan tavsiyalar ishlab chiqishga yordam beradi.

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ВЫДЕЛЕНИЕ И СКРИНИНГ МИКРООРГАНИЗМОВ, УСТОЙЧИВЫХ К ПЕСТИЦИДАМ

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Аннотация: В работе представлены результаты выделения и характеристики микроорганизмов, устойчивых к пестицидам, из загрязнённых почв Джизакской области. Методом накопительных культур на минеральной среде с γ-гексахлорциклогексаном (линданом) выделено более 90 бактериальных изолятов. Скрининг показал способность ряда изолятов к росту при концентрации пестицида 1,5%. Изучены их морфолого-культуральные и физиолого-биохимические свойства. Установлено, что устойчивые изоляты преимущественно относятся к родам *Bacillus* и *Pseudomonas*.

Ключевые слова: пестициды, γ-гексахлорциклогексан, устойчивые микроорганизмы, изоляты, *Bacillus*, *Pseudomonas*, скрининг, биодеградация.

Annotatsiya: Ushbu maqolada Jizzax viloyatidagi ifloslangan tuproqlardan pestitsidlarga chidamli mikroorganizmlarni ajratish va tavsiflash natijalari keltirilgan. γ-geksaxlorsiklogeksan (lindan) o‘z ichiga olgan mineral muhitda boyitish kulturalari yordamida 90 dan ortiq bakterial izolatlar ajratildi. Skrining ba’zi izolatlarning 1,5% pestitsid konsentratsiyasida o‘sish qobiliyatini ko‘rsatdi. Ularning morfologik, kultural, fiziologik va biokimyoviy xususiyatlari o‘rganildi. Chidamli izolatlar asosan *Bacillus* va *Pseudomonas* turkumlariga tegishli ekanligi aniqlandi.

Kalit so‘zlar: pestitsidlar, γ-geksaxlorsiklogeksan, chidamli mikroorganizmlar, izolatlar, *Bacillus*, *Pseudomonas*, skrining, bioparchalanish.

Abstract: This paper presents the results of the isolation and characterization of pesticide-resistant microorganisms from contaminated soils in the Jizzakh region. More than 90 bacterial isolates were isolated using enrichment cultures on a mineral medium containing γ-hexachlorocyclohexane (lindane). Screening demonstrated the ability of some isolates to grow at a pesticide concentration of 1.5%. Their morphological, cultural, physiological, and biochemical properties were studied. It was established that the resistant isolates primarily belong to the genera Bacillus and Pseudomonas.

Keywords: pesticides, γ-hexachlorocyclohexane, resistant microorganisms, isolates, *Bacillus*, *Pseudomonas*, screening, biodegradation.

Введение

Пестициды широко применяются в сельском хозяйстве для защиты растений, однако их остатки могут накапливаться в почве и воде и оказывать неблагоприятное воздействие на нецелевые организмы и экосистемы. Глобальное изменение климата (повышение температуры, изменение влажности, экстремальные погодные явления) может значительно влиять на эффективность биоремедиации. Оно меняет условия среды (температура, влажность, pH, состав микроорганизмов и др.), что может либо усиливать, либо ослаблять деградацию [1-3]. Во всем мире пестициды используются в объеме более 5,6 миллиарда фунтов в год [4]. Микроорганизмы обладают разнообразными метаболическими

ДЛЯ ЦИТИРОВАНИЯ
Кадырова Г.Х., Шонахунов Т.Э., Хусанов Т.С., Ибрагимов А.А. и др. Выделение и скрининг микроорганизмов, устойчивых к пестицидам // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 294–297.
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механизмами, позволяющими адаптироваться к присутствию ксенобиотиков и трансформировать или разлагать различные классы пестицидов. Поэтому выделение и скрининг устойчивых к пестицидам микроорганизмов представляет интерес для разработки биологических методов детоксикации загрязнённых объектов [1–3].

Цель исследования – выделить из образцов почвы микроорганизмы, устойчивые к воздействию пестицидов, и провести их первичный скрининг для выявления штаммов с потенциальной способностью к деградации пестицидов.

Методы

Образцы почвы отбирали с участков, подвергающихся воздействию пестицидов. Выделение устойчивых микроорганизмов проводили методом обогащения на питательной среде с добавлением исследуемого пестицида. После инкубации осуществляли последовательные пересевы и выделяли чистые культуры. Таксономический статус изолятов определяли на основании их морфолого-культуральных и физиолого-биохимических характеристик [5,6]. Первичный скрининг проводили по способности микроорганизмов расти в присутствии различных концентраций пестицида.

Все эксперименты проводили в трёхкратной повторности. Результаты представлены в виде средних значений (M) ± стандартное отклонение (SD). Для обработки данных применяли методы описательной статистики с использованием стандартных программных пакетов.

Результаты и обсуждение

Из загрязнённых пестицидами почв Джизакской области (посёлок Эгизбулак) было выделено более 90 бактериальных изолятов в чистой культуре. Полученные изоляты были протестированы на способность к росту и выживаемость в присутствии органохлорсодержащего пестицида γ-гексахлорциклогексана (γ-ГХЦГ, линдан) при концентрациях 0,75% и 1,5%.

Проведённый скрининг показал, что изоляты № 5e, 2e, 21e, 7e, 4e, 1e, 6e, 28e, 20e, 22e и 16e проявили устойчивость к высокой концентрации γ-ГХЦГ (1,5%) (рис. 1). Отобранные штаммы не только сохраняли жизнеспособность, но и продолжали активный рост в условиях, токсичных для большинства других культур. Наличие подобных устойчивых микроорганизмов свидетельствует об их возможной роли в процессах биодеградации пестицидов и указывает на перспективность их использования в технологиях биоремедиации.

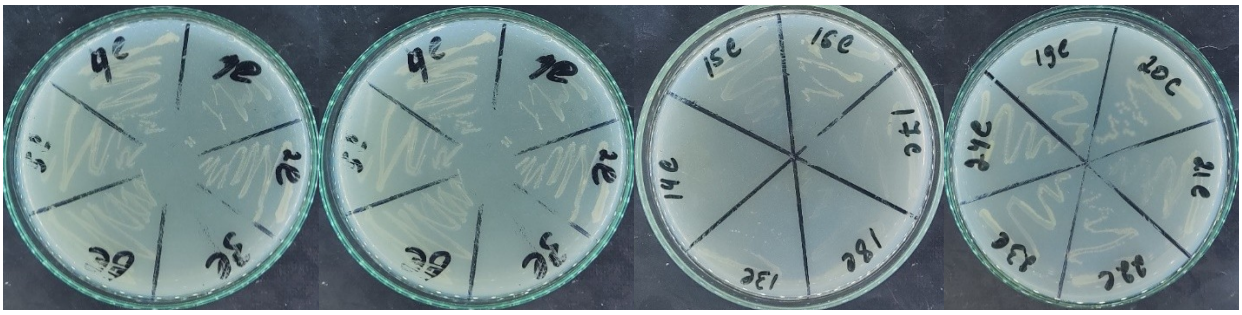


Рисунок 1. Рост и развитие изолированных культур при 1,5% концентрации пестицида (γ-ГХЦГ)

Для оценки биотехнологического потенциала устойчивых штаммов были изучены их морфолого-культуральные и физиолого-биохимические свойства.

Установлено, что изоляты 5e, 2e, 16e и 21e представлены грамположительными спорообразующими палочками, характерными для рода *Bacillus*. Они способны расти на стандартных питательных средах (например, Nutrient Agar) при оптимальной температуре около 30 °C. Данные штаммы проявляют устойчивость к стрессовым факторам, включая повышенную концентрацию NaCl (до 7,5%), широкий диапазон pH (5–9), а также температуры

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от 5 до 60 °C. Для них характерны положительные реакции на каталазу и утилизацию цитрата, при отрицательных результатах тестов на индол и метиловый красный.

Изоляты 7е и 4е также представлены грамположительными палочковидными бактериями. Изолят 7е проявляет положительные реакции на каталазу и оксидазу, тогда как у изолята 4е каталазная активность выражена слабо. Оба штамма способны ферментировать углеводы (глюкоза, арабиноза, ксилоза, маннитол, сахароза), а также гидролизовать амилозу, казеин и желатин. Выявлена выраженная липазная и протеолитическая активность. Изоляты 1е, 6е, 20е и 28е относятся к грамотрицательным, подвижным палочковидным бактериям, предположительно принадлежащим к роду *Pseudomonas* (рис.2). Они характеризуются оксидазоположительной реакцией и способностью к гидролизу желатина.

Изолят 22е представлен грамотрицательной подвижной палочкой, не образующей спор (рис.4). Колонии развиваются умеренно быстро, имеют жёлтую окраску, блестящую поверхность и куполообразную форму. Данный штамм продуцирует аммиак и липазы, а также способен расти при пониженных температурах (до 4 °C) (рис.3).

Rodríguez-Orozco et al. (2025) подчёркивают, что именно локальные штаммы лучше адаптированы к загрязнённой среде и демонстрируют повышенную эффективность в разрушении пестицидов [7]. Многочисленные работы показывают, что представители родов *Pseudomonas* и *Bacillus* являются ключевыми агентами биоремедиации. Они способны разлагать широкий спектр пестицидов благодаря разнообразию метаболических путей и ферментов [8].

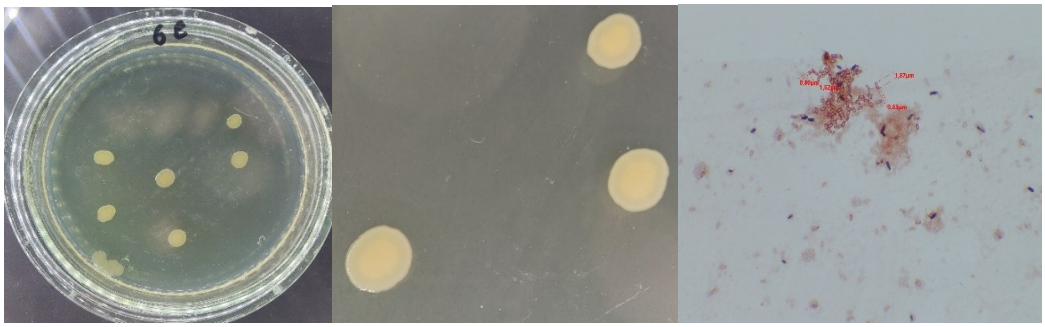


Рисунок 2. Морфолого-культуральные свойства изолята 1е: 1 – общий вид колоний, 2 – рост и развитие колоний, 3 – микрофотографии клеток (Увеличение 10х100)

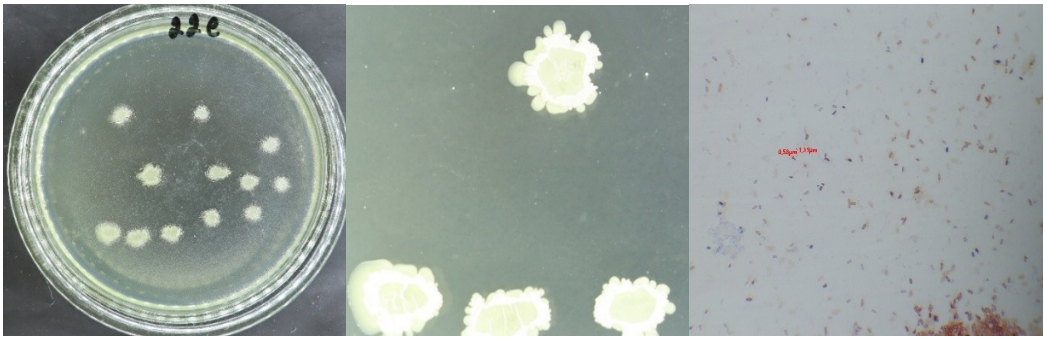


Рисунок 4. Морфолого-культуральные свойства изолята № 22е: 1 – общий вид колоний, 2 – рост и развитие колоний, 3 – микрофотографии клеток (Увеличение 10х100)

Заключение

Полученные в работе результаты согласуются с современными представлениями о том, что аборигенные микроорганизмы загрязнённых почв обладают повышенной устойчивостью к пестицидам и являются перспективными агентами биоремедиации. Подобно ранее описанным штаммам родов *Pseudomonas* и *Bacillus*, выделенные нами культуры демонстрируют способность к росту в присутствии высоких концентраций токсикантов, что указывает на их потенциальную роль в процессах биодеградации органохлоридных соединений. Таким

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образом, исследованные изоляты могут рассматриваться как перспективные кандидаты для разработки биотехнологических методов очистки загрязнённых экосистем.

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ALYUMINIY OKSIDLI KERAMIK QOPLAMALARNING *ESCHERICHIA COLI* BAKTERIYALARINI SORBSIYALASH XUSUSIYATINI TADQIQ ETISH

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Annotatsiya: Ushbu maqolada alyuminiy oksidli keramik qoplamalarning *Escherichia coli* bakteriyalarini sorbsiyalash samaradorligi tahlil qilindi. Tadqiqotda AMg6 va D16 alyuminiy qotishmalari hamda Zn–Al asosidagi kompozitsion qoplamalar mikroorganizmlar uchun qattiq tashuvchi sifatida o‘rganildi. Bakterial suspenziya tayyorlanib, qoplama namunalari bilan belgilangan sharoitda kontaktda saqlandi; sorbsiya samaradorligi kontaktdan oldin va keyin suspenziyada qolgan hujayralar sonining farqi bo‘yicha hisoblandi, sorbent yuzasiga birikkan hujayralarning holati esa elektron mikroskopiya yordamida baholandi. Tajriba natijalariga ko‘ra, sorbsiya samaradorligi AMg6 qoplamasida 51,0%, D16 qoplamasida 52,2% va Zn–Al qoplamasida 62,15% ni tashkil etdi. Eng yuqori ko‘rsatkich Zn–Al asosidagi qoplamada qayd etildi. Natijalar qoplama tarkibi va sirt xususiyatlari mikroorganizmlarning qattiq tashuvchiga birikishiga ta’sir ko‘rsatishini ko‘rsatadi.

Kalit so‘zlar: alyuminiy oksidi, keramik qoplama, sorbsiya, Escherichia coli, immobilizatsiya, qattiq tashuvchi, elektron mikroskopiya.

Аннотация: В данной статье проанализирована эффективность сорбции бактерий *Escherichia coli* керамическими покрытиями на основе оксида алюминия. В качестве твёрдых носителей для микроорганизмов изучались алюминиевые сплавы АМг6 и Д16, а также композиционные покрытия на основе Zn–Al. Была приготовлена бактериальная суспензия, которую контактировали с образцами покрытий в заданных условиях; эффективность сорбции рассчитывали по разности числа клеток до и после контакта, а состояние прикрепившихся клеток оценивали с помощью электронной микроскопии. Согласно полученным результатам, эффективность сорбции составила 51,0% для покрытия АМг6, 52,2% для покрытия Д16 и 62,15% для покрытия Zn–Al. Наибольшая эффективность отмечена у покрытия на основе Zn–Al. Результаты свидетельствуют о влиянии состава покрытия и свойств его поверхности на прикрепление микроорганизмов к твёрдым носителям.

Ключевые слова: оксид алюминия, керамическое покрытие, сорбция, Escherichia coli, иммобилизация, твёрдый носитель, электронная микроскопия.

Abstract: This article analyzes the sorption efficiency of aluminium oxide ceramic coatings for *Escherichia coli* bacteria. AMg6 and D16 aluminium alloys, as well as Zn–Al-based composite coatings, were investigated as solid carriers for microorganisms. A bacterial suspension was prepared and brought into contact with the coating samples under specified conditions; sorption efficiency was calculated from the difference in cell numbers before and after contact, and the

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Mamarayimova M.A., Axmedova Z.R., Abdullayeva Y.A. Alyuminiy oksidli keramik qoplamalarning Escherichia coli bakteriyalarini sorbsiyalash xususiyatini tadqiq etish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 298–301.
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condition of the attached cells was evaluated by electron microscopy. The sorption efficiency was 51.0% for the AMg6 coating, 52.2% for the D16 coating and 62.15% for the Zn–Al coating. The highest efficiency was observed for the Zn–Al-based coating. The results indicate that coating composition and surface properties influence the attachment of microorganisms to solid carriers.

Keywords: aluminium oxide, ceramic coating, sorption, Escherichia coli, immobilization, solid carrier, electron microscopy.

Kirish

Mikroorganizmlarni qattiq tashuvchilar yuzasiga biriktirish mikrobiologiya, biotexnologiya, ekologiya va sanoat mikrobiologiyasining muhim yo‘nalishlaridan biridir. Immobilizatsiya jarayoni mikroorganizmlarni ma’lum bir tashuvchi yuzasida ushlab turish orqali ularning texnologik jarayonlarda qo‘llanilish imkoniyatlarini kengaytiradi. Bunda tashuvchining kimyoviy tarkibi, sirt morfologiyasi, g‘ovakligi va fizik-kimyoviy xususiyatlari muhim ahamiyatga ega [2, 3].

Alyuminiy oksidi (Al_2O_3) asosidagi materiallar mexanik mustahkamligi, kimyoviy barqarorligi va sirt xususiyatlarini boshqarish imkoniyati tufayli istiqbolli qattiq tashuvchilar hisoblanadi. Bunday materiallarning mikroorganizmlar bilan o‘zaro ta’siri ularning sirt zaryadi, bakteriya hujayrasi qobig‘ining xususiyatlari va muhit sharoitlariga bog‘liq bo‘lishi mumkin [1, 5]. Shu bilan birga, alyuminiy oksidi yuzasining nanoo‘lchamli strukturasi ayrim bakteriyalarning adgeziyasini kamaytirishi ham qayd etilgan [1, 7], bu esa har bir qoplama turini mikroorganizmlar bilan o‘zaro ta’sirda alohida sinashni taqozo etadi.

Escherichia coli gram-manfiy bakteriya bo‘lib, mikrobiologik tadqiqotlarda model mikroorganizm sifatida keng qo‘llaniladi. Uning turli qattiq yuzalarga birikishini o‘rganish sorbentlarning mikroorganizmlarni ushlab qolish qobiliyatini baholash imkonini beradi; bakterial adgeziyaning hujayra darajasidagi mexanizmlari so‘nggi yillarda batafsil tavsiflangan [6].

Tadqiqotning maqsadi alyuminiy asosidagi turli kompozitsion keramik qoplamalarning *E. coli* hujayralarini sorbsiyalash samaradorligini taqqoslash va qoplama tarkibining ushbu jarayonga ta’sirini baholashdan iborat.

Materiallar va tadqiqot usullari

Tadqiqot obyekti sifatida *Escherichia coli* ATCC 25922 bakteriya shtammi hamda alyuminiy qotishmalari asosida tayyorlangan kompozitsion keramik qoplama namunalari olindi. Tadqiqotda uchta namuna taqqoslandi: AMg6 qotishmasi asosidagi qoplama, D16 qotishmasi asosidagi qoplama va Zn–Al asosidagi kompozitsion qoplama. Qoplamalarning tarkibi va sirt morfologiyasi bakteriya hujayralarining birikishiga ta’sir etuvchi asosiy omillar sifatida ko‘rib chiqildi. Namunalar tajribadan oldin avtoklavda 121 °C haroratda, 1 atm bosimda 20 daqiqa davomida sterilizatsiya qilindi.

Bakterial suspenziyani tayyorlash. Bakteriyalar go‘sht-peptonli bulonda 37 °C haroratda, 160 ayl/daq tezlikda 24 soat davomida o‘stirildi. O‘stirishdan so‘ng bakterial suspenziya ajratilib, hujayralar fiziologik eritma bilan oziqa muhiti qoldiqlari ketguncha yuvildi va fiziologik eritmada qayta suspenziyalandi. Suspenziyadagi hujayralar soni Goryaev kamerasi yordamida aniqlandi: ishchi suspenziyaning hajmi 50 ml ni, undagi hujayralarning umumiy soni esa 70 312 500 tani ($1{,}41\times10^6$ hujayra/ml) tashkil etdi.

Bakteriyalarning sorbent yuzasiga birikishini o‘rganish. Kompozitsion qoplama namunalari bakterial suspenziyaga joylashtirildi va 60 ayl/daq tezlikda 30 daqiqa davomida chayqatildi. Kontaktdan keyin namunalar fiziologik eritma bilan bir necha marta yuvildi; ushbu bosqichning maqsadi yuzaga birikmagan yoki zaif birikkan bakteriya hujayralarini ajratishdan iborat bo‘ldi. Namunalar keyingi tahlil uchun tayyorlanib, ularning sirtida qolgan bakteriya hujayralari elektron mikroskopiya yordamida o‘rganildi.

Sorbsiya samaradorligini hisoblash. Sorbsiya samaradorligi boshlang‘ich suspenziyadagi va sorbent bilan kontaktdan keyin suspenziyada qolgan hujayralar sonining farqi bo‘yicha quyidagi formula asosida hisoblandi:

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$$E = (N_0 - N_1) / N_0 \times 100\%$$

bu yerda E — sorbsiya samaradorligi, %; N_0 — boshlang‘ich suspenziyadagi bakteriyalar soni; N_1 — sorbent bilan kontaktdan keyin suspenziyada qolgan bakteriyalar soni.

Natijalar

O‘rganilgan uchala qoplama ham *E. coli* ATCC 25922 hujayralarini o‘z yuzasida ushlab qolish qobiliyatini namoyon qildi, biroq ularning samaradorligi bir xil bo‘lmadi. Eng past ko‘rsatkich AMg6 qoplamasida (51,0%), eng yuqorisi esa Zn–Al asosidagi kompozitsion qoplamada (62,15%) qayd etildi; D16 qoplamasi oraliq qiymatni (52,2%) namoyon etdi. Zn–Al qoplamasining ko‘rsatkichi AMg6 namunasiga nisbatan 11,15 foiz punktga, D16 namunasiga nisbatan esa 9,95 foiz punktga yuqori bo‘ldi. Shu bilan birga, AMg6 va D16 qoplamalari orasidagi farq atigi 1,2 foiz punktni tashkil etdi, ya’ni ikkala alyuminiy qotishmasi asosidagi qoplama bir-biriga yaqin natija berdi.

Elektron mikroskopiya natijalari. Elektron mikroskopiya yuvish bosqichidan so‘ng ham bakteriya hujayralarining qoplama yuzasida saqlanib qolishini tasdiqladi. Hujayralar sirt bo‘yicha notekis taqsimlangan bo‘lib, ayrim hududlarda guruh-guruh to‘planish kuzatildi.

Xulosa

1. *Escherichia coli* ATCC 25922 bakteriya hujayralarining AMg6, D16 alyuminiy qotishmalari hamda Zn–Al asosidagi kompozitsion qoplama yuzasida sorbsiyalanish xususiyatlari taqqoslandi; sorbsiya samaradorligi o‘rganilgan namunalarda 51,0–62,15% oralig‘ida bo‘ldi.

2. Eng yuqori sorbsiya samaradorligi Zn–Al asosidagi kompozitsion qoplamada — 62,15% ni tashkil etdi; bu ko‘rsatkich AMg6 namunasiga (51,0%) nisbatan 11,15 foiz punktga, D16 namunasiga (52,2%) nisbatan esa 9,95 foiz punktga yuqoridir.

3. Elektron mikroskopiya tasvirlari bakteriya hujayralarining qoplama yuzasida joylashishi va birikish holatlarini morfologik jihatdan baholash imkonini berdi; olingan natijalar qoplamaning tarkibi va sirt xususiyatlari hujayralarning qattiq yuzaga birikishiga ta’sir ko‘rsatishini anglatadi.

4. Zn–Al asosidagi kompozitsion qoplama mazkur tajriba sharoitida *E. coli* ATCC 25922 bakteriyalarini sorbsiyalash bo‘yicha eng yuqori ko‘rsatkichni namoyon etdi. Ushbu natijalar alyuminiy asosidagi qattiq tashuvchilarning mikroorganizmlarni immobilizatsiya qilish jarayonidagi imkoniyatlarini keyingi tadqiqotlarda o‘rganish uchun asos bo‘lib xizmat qiladi; bakteriyalarning hayotchanligi va tashuvchi yuzasida uzoq muddat saqlanishini baholash uchun alohida mikrobiologik sinovlar talab etiladi.

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BACILLUS MEGATERIUM BAKTERIYA SHTAMMINING BUG‘DOY O‘SIMLIGI FOTOSINTETIK PIGMENTLARI MIQDORIGA TA’SIRI

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Annotatsiya: Maqolada fotosintetik pigmentlar miqdoriga *Bacillus megaterium* bakteriyasi eritmalarining nisbatlari (1:1, 1:3, 1:5, 1:7 va 1:9) ta’sirini o‘rganish bo‘yicha ma’lumotlar o‘rin olgan. Tadqiqot obyekti sifatida kuzgi yumshoq (Triticum aestivum L) turiga mansub “Asr” navi olingan. Tadqiqot natijalari fotosintetik pigmentlar miqdori tuplanish, naychalash fazasiga nisbatan boshoqlash fazasida faollashganligi aniqlangan. Mazkur fazada 1:7 nisbatda Chl “a” 2,08, Chl “b” 1,53, va Car 0,53 mg/g teng ekanligi aniqlangan. *B. megaterium* bakteriyaning 1:7 nisbatli eritmasidan kuzgi bug‘doyning boshoqlash fazasida foydalanilganida Chl «a» miqdorini nazoratga nisbatan 24.0%ga, Chl «b»-11.8% ga va Car 74.1% oshganligi aniqlangan. Sug‘oriladigan tuproq iqlim sharoitida bug‘doy yetishtirishda B. megaterium bakteriyasining 1:7 nisbatli eritmasidan foydalanish tavsiya etilgan.

Kalit so‘zlar: kuzgi yumshoq bug‘doy, "Asr" navi, *Bacillus megaterium*, fotosintetik pigmentlar, xlorofil a, xlorofil b, karotinoidlar, tuplanish, naychalash, boshoqlash.

Аннотация: В статье представлены результаты исследования влияния различных соотношений растворов бактерии *Bacillus megaterium* (1:1, 1:3, 1:5, 1:7 и 1:9) на содержание фотосинтетических пигментов. Объектом исследования являлась озимая мягкая пшеница (Triticum aestivum L.) сорта «*Acp*». По результатам исследования установлено, что содержание фотосинтетических пигментов в фазе колошения повышалось по сравнению с фазами кущения и выхода в трубку. В фазе колошения при соотношении 1:7 содержание хлорофилла a (Chl a) составило 2,08 мг/г, хлорофилла b (Chl b) — 1,53 мг/г, а каротиноидов (Car) — 0,53 мг/г. Установлено, что применение раствора бактерии *B. megaterium* в соотношении 1:7 в фазе колошения озимой пшеницы способствовало увеличению содержания хлорофилла a на 24,0 %, хлорофилла b — на 11,8 %, а каротиноидов — на 74,1 % по сравнению с контрольным вариантом. Для выращивания озимой пшеницы в условиях орошаемого земледелия рекомендуется использовать раствор бактерии *B. megaterium* в соотношении 1:7

Ключевые слова: озимая мягкая пшеница, сорт «Acp», *Bacillus megaterium*, фотосинтетические пигменты, хлорофилл a, хлорофилл b, каротиноиды, кущение, выход в трубку, колошение.

Abstract: The effect of *Bacillus megaterium* solutions (1:1, 1:3, 1:5, 1:7 and 1:9 ratios) on the content of photosynthetic pigments (chlorophyll a, chlorophyll b, total chlorophyll and carotenoids) and on the Chl a/Chl b and ΣChl/Car ratios was studied in the winter bread wheat cultivar "*Asr*" at the tillering (22.11.2025), stem elongation (07.03.2026) and heading (09.04.2026) stages in the Boyavut area. The response depended on the growth stage and on the solution ratio. At tillering, the 1:3 ratio increased Chl a to 1.50 mg/g versus 1.27 mg/g in the control (about 18%), exceeding the mean±error range (1.24–1.34 mg/g); Chl b (0.72 mg/g) and carotenoids (0.45 mg/g) showed the same trend. At stem elongation, no positive effect on chlorophylls was observed; only the 1:9 ratio kept Chl a at the control level (1.46 mg/g) and raised carotenoids to 0.48 mg/g (control: 0.34 mg/g). The strongest effect occurred at heading: at 1:7, Chl a, Chl b, ΣChl and Car reached 2.08, 1.53, 3.61 and 0.53 mg/g,

IQTIBOS UCHUN
Mehmonova N.A., Ergasheva F.Sh. Bacillus megaterium bakteriya shtammining bug‘doy o‘simligi fotosintetik pigmentlari miqdoriga ta’siri // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 302–306.
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i.e. about 34%, 39% and 36% higher chlorophylls and nearly twofold higher carotenoids than the control. Thus, the effect of *B. megaterium* on pigment content is stage-specific: 1:3 was effective at tillering, 1:7 at heading, and no benefit was found at stem elongation.

Keywords: winter bread wheat, '*Asr*' cultivar, *Bacillus megaterium*, photosynthetic pigments, chlorophyll a, chlorophyll b, carotenoids, tillering, stem elongation, heading.

Kirish

Bug'doy O'zbekistonda oziq-ovqat xavfsizligini ta'minlovchi asosiy ekinlardan biridir. Uning hosildorligi va don sifati ko'p jihatdan o'simlikning fotosintetik faolligiga bog'liq. Fotosintetik apparatning holati xlorofil a, xlorofil b va karotinoidlar miqdori hamda ularning o'zaro nisbati orqali baholanadi.

Adabiyotlar tahlili

Bacillus megaterium* tuproq va rizosferada keng tarqalgan bakteriya. Uning fosfatlarni eritish va siderofor hosil qilish qobiliyati tasvirlangan. Siderofor sintezi eksponensial o'sish fazasida, sporulyatsiyadan oldin boshlanishi va uglerod manbaiga bog'liq ekani ko'rsatilgan [1]. Temir xlorofil biosintezi uchun zarur, shuning uchun bu xususiyat pigment tarkibiga bilvosita ta'sir qilishi mumkin [2]. Bug'doyda bu bakteriya asosan hosil elementlari va fosfor bilan ta'minlanish nuqtai nazaridan o'rganilgan. Misrda Beni Suef 5 navida *B. megaterium* bilan inokulyatsiya don hosili, o'simlik bo'yi, boshoqchalar va donlar sonini oshirgan, o'simlikdagi fosfor miqdori ham ortgan, ammo azot foizi sezilarli o'zgarmagan [3]. Boshqa tadqiqotda qurg'oqchilikka chidamli *B. megaterium* izolyati bilan ishlangan bug'doyda xlorofil va karotinoid miqdori hamda antioksidant fermentlar faolligi yaxshilangan (PMC9945272). Nikel stressida esa *B. megaterium* AFI1 shtammi xlorofil a, b va karotinoidlar miqdorini oshirgan, antioksidant himoyani faollashtirgan va o'simlikka nikel o'tishini kamaytirgan [4]. Umumiy xulosa shuki, bakteriya pigmentlarni asosan stressdan himoya qilish orqali saqlaydi, stressiz sharoitda esa ta'sir kuchsizroq va o'zgaruvchan bo'lishi mumkin [5].

Tadqiqot obyekti va usullari

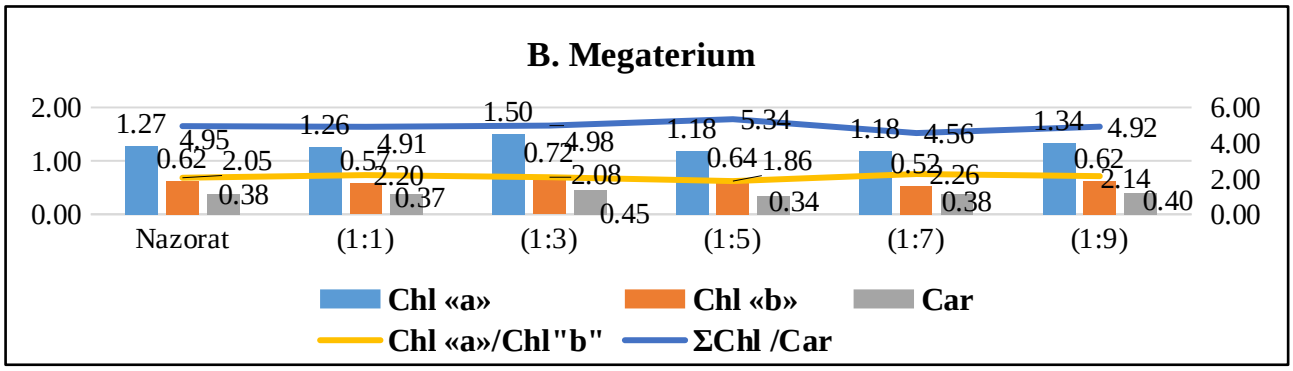
Tadqiqot obyekti sifatida (Triticum aestivum L) "Asr" navi olindi. Tadqiqot Guliston davlat universiteti qoshidagi Agrobiotexnologiya va biokimyo ilmiy tadqiqot ilmiy tadqiqot instituti va Don va dukkakli ekinlar ilmiy tadqiqot instituti Sirdaryo tajriba stansiyasi dala maydonida olib borildi. Pigmentlar miqdori spektrofotometrning (SF-2000) 470, 649 va 664 nm to'lqin uzunligida aniqlandi. Eritmani taqqoslash uchun 96.0% etil spirtidan foydalanildi [6].

Birlamchi ma'lumotlarni statistik tahlil qilishda SPSS-17 dasturidan foydalanildi [7,8].

Olingan natijalar

Tuplanish fazasi kuzgi bug'doyning muhim fazalaridan bo'lib unda morfologik va fiziologik o'zgarishlar sodir bo'ladi. Bunda o'simliklar tinim davriga kirishdan oldin oziqa moddalarni to'playdi va morfologik o'zgarish, qo'shimcha barglar hosil bo'ladi, barg yuza sathi ortadi. Mazkur fazada fotosintetik pigmentlar miqdoriga bakteriyalarning ta'sirini o'rganish bo'yicha olingan ma'lumotlarda (1-rasm) "Asr" navida nazoratda Chl «a» miqdori 1.27 mg/g teng bo'lgan bo'lsa bakteriyasining 1:1 nisbatli eritmasida 1.26; 1:3 nisbatda- 1.50; 1:5 nisbatda 1.18 1:7 nisbatda 1.18 va 1:9 nisbatda 1.34 mg/g teng bo'ldi.

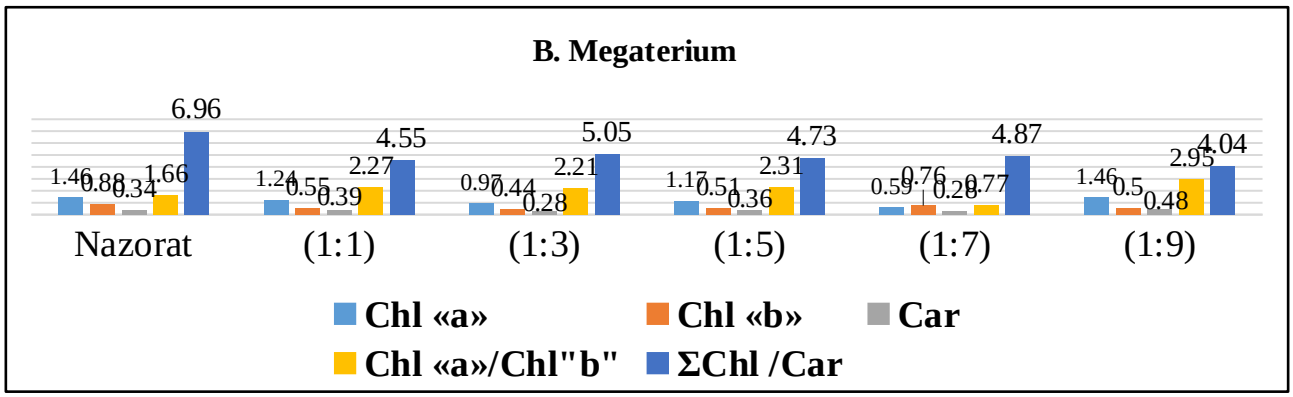
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1-rasm. Kuzgi bug‘doyning “Asr” navining tuplanishi fazasida fotosintetik pigmentlar miqdoriga

Ushbu ma’lumotlardan Chl «a»- miqdoriga eritma nisbatlari ta’sir etganligini ko‘rish mumkin. Ayniqsa, 1:3 nisbatli eritmada Chl «a» miqdori yuqori bo‘lib 1.50 mg/g teng bo‘ldi. Aynan shunday natija Chl «b» (0,72) Car(0.45) bo‘yicha ham qayd etildi. Xlorofillar (Chl «a»/Chl"b) va (ΣChl /Car) nisbatlari fotosintetik pigmentlarning sifatini baholaydi. Ilmiy manbalarda Chl «a»/"b nisbati 2.5 dan 3.5, ΣChl /Car 3:1 dan 5:1 gacha bo‘lishi e’tirof etilgan. Olingan natijalarda Chl «a»/"b" nisbati 1.86 dan 2.26 teng bo‘lgan bo‘lsa ΣChl /Car nisbati 4.56-5.34 teng bo‘ldi. Mazkur bakteriyaning 1:7 nisbatli eritmasida Chl «a»/"b" nisbati 2.26 teng ekanligi aniqlandi.

Naychalash fazasida bakteriya shtammlaridan tayyorlangan eritmalar ta’sirida Chl «a» miqdori o‘rtacha 1.15 mg/g teng bo‘lganligi aniqlandi. Eritma nisbati 1:1 bo‘lganida Chl «a» 1.24 mg/g; 1:3-0.97; 1:5-1.17; 1:7-0.59 va 1:9-1.46 mg/g ni tashkil etdi. Ushbu ma’lumotlardan, faqat 1:9 nisbatda xlorofill ”a” miqdori nazoratga teng bo‘lgan bo‘lsa qolgan variantlardan nazoratdan farq kuzatilmadi. Chl «b» miqdori nazoratda 0.88 mg/g teng bo‘lib o‘rtacha ko‘rsatkich 0.60mg/g teng bo‘ldi. Ushbu ma’lumotlardan naychalash fazasida Chl «b» miqdoriga bakteriya shtammlarining ta’sirida nazoratdan farq kuzatilmadi. Karotinoidlar miqdori o‘rtacha 0.35 mg/g teng bo‘lib nazoratda 0.34 mg/g ni tashkil etdi. Nisbatan yuqori ko‘rsatkich 1:9 nisbatli eritmada qayd etilib 0.48 mg/g teng bo‘ldi. Ushbu ma’lumotlardan mazkur bakteriyaning 1:9 nisbatli eritmasi fotosintetik pigmentlar faolligini oshirdi. Bunda karotinoidlar miqdori ortgan bo‘lsa Chl «a»/Chl"b" hamda ΣChl /Car nisbatlari 2.95 va 4.04 ni tashkil etdi.

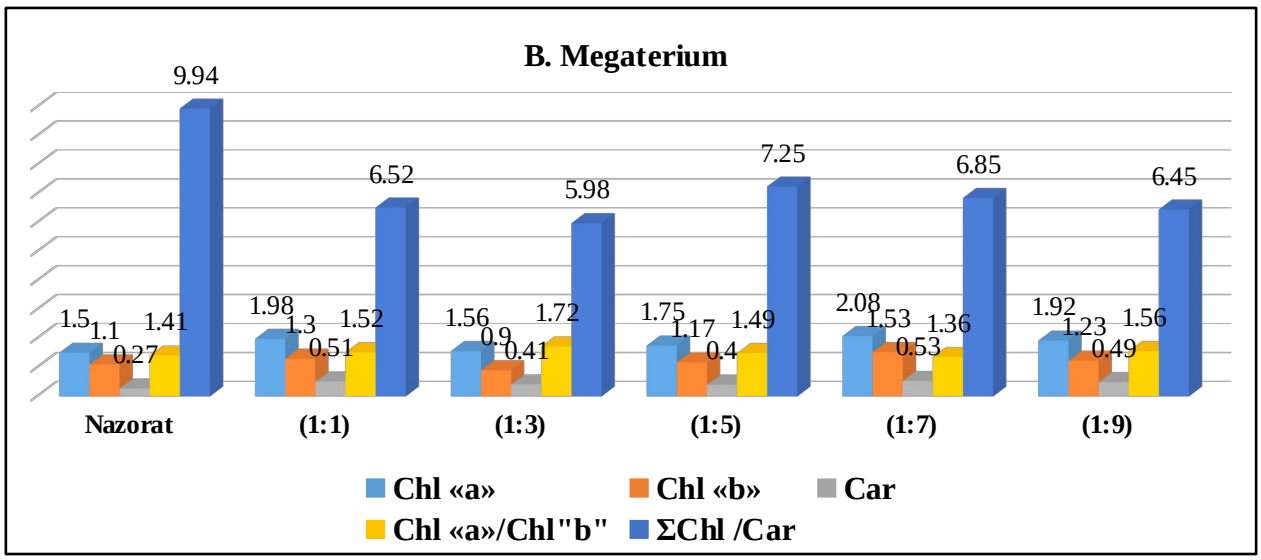


2-rasm. Kuzgi bug‘doyning “Asr” navining naychalash fazasida fotosintetik pigmentlar miqdori

Boshoqlash fazasi bug‘doyning o‘sish va rivojlanishning muhim fazalaridan hisoblanadi. Ushbu fazada bug‘doy boshog‘i hosil elementlari (boshoqdagi don soni, boshoqchalar soni, don soni) ham shakllanadi. Bu o‘simliklarning mineral moddalarga bo‘lgan talabini ortishiga olib kelib fotosintez jarayonini jadallashtirdi. Mazkur fazada B. megaterium bakteriya ta’sirida Chl «a» miqdori nazoratda 1.55 mng/g teng bo‘ldi. Eritma nisbati 1:1 teng bo‘lganida Chl «a»1.5, 1:3-1.56; 1:5-1.75; 1:7-2.08 va 1:9-1.91 mg/gni tashkil etdi. Ushbu ma’lumotlardan barcha eritma nisbatlarda Chl «a» miqdori ortganligi, ayniqsa 1:7 nisbatda eng yuqori bo‘lganligi aniqlandi. Chl «b» bo‘yicha ham shunday natija qayd etilib nazoratga nisbatan Chl «b» miqdori ortdi va nisbatan yuqori ko‘rsatkich 1:7 nisbatli eritmada qayd etilib 1.53 mg/g teng bo‘ldi. Karotinoidlar miqdori 0.27-0.53 mg teng bo‘lib

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1:7 nisbatda nisbatan yuqori ko‘rsatkich (0.53 mg/g) qayd etildi. Xlorofillar nisbati (Chl «a»/Chl"b") 1.36 dan 1.72 teng bo‘lgan bo‘lsa umumiy xlorofillarning karotinoidlarga nisbati (ΣChl /Car) 5.98-9.94 teng bo‘ldi**.**



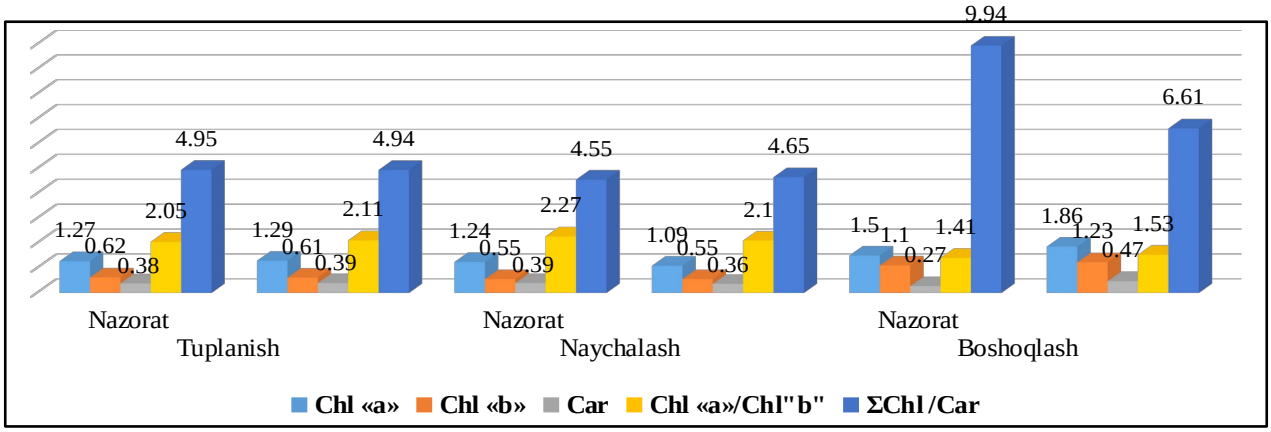
3-rasm. Kuzgi bug‘doyning “Asr” navining boshoqlash fazasida fotosintetik pigmentlar miqdori

Olingan natijalar muhokamasi

Olingan natijalar shuni ko‘rsatdiki, tuplanish fazasida Chl «a» nazoratda 1.27 teng bo‘lgan bo‘lsa B. megaterium bakteriyaning ta’sirida 1.29 teng bo‘ldi. Nazoratga nisbatan uning miqdori 0.2 qiymatga (yoki 1.57 %) ortganligi aniqlandi. Chl «b» miqdori tegishli ravishda 0.62 va 0.61 teng bo‘lib farq -0.01 yoki -1.61 % ni tashkil etdi (4-rasm). Car miqdori 0.38 dan 0.39 o‘zgarib farq 2.63 % ga ortganligi qayd etildi. Chl «a»/Chl"b" nisbati 2.05 dan 2.11 ortib farq 2.93% ni va ΣChl /Car nisbati 4.95 dan 4.94 kamayganligi aniqlandi. Ushbu ma’lumotlardan tuplanish fazasida mazkur bakteriyaning pigmentlar miqdoriga ta’siri kuzatilmadi. Nazoratga nisbatan farq statistik xatolik chegarasida qayd etildi.

Naychalash fazasida Chl «a» nazoratda 1.24 teng bo‘lgan bo‘lsa bakteriya ta’sirida 1.09 ni tashkil etdi. Bu xlorofill Chl «a» miqdori 12.1 % kamayganligini ko‘rsatdi. Chl «b» miqdori bo‘yicha farq kuzatilmadi. Car miqdori 0.39 dan 0.36, Chl «a»/Chl"b 2.27 dan 2.1 kamayganligi aniqlandi. ΣChl /Car nisbati 4.55 dan 4.65 ga ort**di.**

Boshoqlash fazasida Chl «a» miqdori nazoratda 1.50 teng bo‘lgan bo‘lsa bakteriya ta’sirida 1.86 teng bo‘lib Chl «b» miqdori tegishli ravishda 1.1 dan 1.23, Car 0.27 dan 0.47 ga Chl «a»/Chl"b" 1.41 dan 1.53 ortgan bo‘lsa ΣChl /Car nisbati 9.94 dan 6.61 ga kamaydi.



4-rasm. Kuzgi bug‘doyning “Asr” navida fotosintetik pigmentlar miqdorining fazalar kesimida o‘zgarishi (o‘rtacha ko‘rsatkichlar bo‘yicha)

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Yuqoridagi ma’lumotlardan, boshoqlash fazasida fotosintetik pigmentlar miqdoriga bakteriyaning ta’siri boshqa fazalarga nisbatan ortdi. Buni statistik tahlil natijalari ham isbotladi. Mazkur fazada quyidagi pigmentlarning birinchi faktor bo‘yicha yuklamalari ortdi, jumladan, Chl «a» (0.7539), Car (0.8252), Chl «a»/Chl"b" nisbati (0.9230) teng bo‘ldi. Bu mazkur ko‘rsatkichlar o‘rtasida kuchli korrelyasion bog‘lanish borligi hamda ular o‘xshash ekanligini ko‘rsatdi. Bu Chl «a» miqdorining ortishi Car miqdorini ham ortishiga olib keldi. Shu bilan birga mazkur faktorda Chl «b» (- 0.6230 va ΣChl /Car (-0.7024) yuklamalari minus bo‘ldi. Bu Chl «a» va Car miqdori ortganida Chl «b» - kamayganligidan dalolat berdi.

Xulosa

1. Fotosintetik pigmentlar miqdoriga B. megaterium bakteriyaning ta’siri fazalar kesimida o‘zgardi. Tuplanish fazasida nazoratda Chl «a» 1.27 teng bo‘lgan bo‘lsa Chl «b» 0.62, Car 0.39 teng bo‘ldi. Naychalash fazasida tegishli ravishda: 1.15; 0.6 va 0.35: boshoqlashda: 1.81; 1.20 va 0.43 teng bo‘lib mazkur fazada fotosintetik pigmentlar miqdori ortganligi kuzatildi.
2. Fotosintetik pigmentlar miqdori B. megaterium bakteriya shtammidan tayyorlangan eritma ta’siri etdi. Eritma konsentrasiyasi 1:1 teng bo‘lganida Chl «a» - 1.49; Chl «b»-0.80, Car -0.42, 1:3 da tegishli ravishda :1.34; 0.68 va 0.38; 1:5 –1.36; 0.77 va 0.39; 1:7 da 1.28; 0.77 va 0.36 va 1:9 da 1.57;0.78 va 0.37 teng bo‘lgan.
3. Boshoqlash fazasida B. megaterium bakteriyaning 1:7 nisbatli eritmasidan foydalanish fotosintetik pigmentlar miqdorini nazoratga nisbatan Chl «a» miqdorini 24.0%ga, Chl «b»-11.8% ga Car miqdorini 74.1% ga oshganligi aniqlandi

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ISSIQ BULOQ VA PAXTA RIZOSFERASIDAN AJRATILGAN BAKTERIYALARNING BIOKIMYOVIY XUSUSIYATLARI VA FERMENTATIV FAOLLIGINI BAHOLASH

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Annotatsiya: Ushbu tadqiqotda Qashqadaryo viloyati Koson tumanidagi Rayim So‘fi issiq bulog‘idan ajratilgan *Geobacillus sp. B1* hamda paxta rizosferasidan olingan Bacillus sp. M11, izolyatlarining morfologik, fiziologik va biokimyoviy xususiyatlari o‘rganildi. Izolyatlarning Gram bo‘yicha bo‘yalishi, katalaza faolligi, kazein, kraxmal va lipid gidrolizi baholandi. Geobacillus sp. B1 50 va 60 °C, *Bacillus* sp. izolyati esa 40, 45 va 55 °C haroratlarda tekshirildi. Natijalarga ko‘ra, *Geobacillus sp. B1*, izolyatlarida kazein hamda kraxmal gidrolizi kuzatildi, lipid gidrolizi esa izolyatlarda salbiy natija berdi. Katalaza sinovida *Geobacillus sp. B1* kuchli ijobiy, ijobiy, *Bacillus sp. M11* esa salbiy reaksiya ko‘rsatdi. Olingan natijalar izolyatlarning fermentativ xususiyatlari turlicha ekanligini ko‘rsatib, ularni keyingi biotexnologik tadqiqotlarda o‘rganish uchun asos yaratadi.

Kalit so‘zlar: termofil bakteriyalar, *Geobacillus*, *Bacillus*, issiq buloq, paxta rizosferasi, katalaza, kazein gidrolizi, kraxmal gidrolizi, lipaza.

Аннотация: В данном исследовании изучены морфологические, физиологические и биохимические свойства бактериального изолята *Geobacillus sp. B1*, выделенного из горячего источника Райим Суфи, расположенного в Касанском районе Кашкадарьинской области Узбекистана, а также трёх изолятов *Bacillus sp. M11*, *Bacillus* sp. B и *Bacillus* sp. C, полученных из ризосферы хлопчатника. Проведена оценка окрашивания изолятов по Граму, каталазной активности и способности к гидролизу казеина, крахмала и липидов. Изолят Geobacillus sp. B1 исследовали при температурах 50 и 60 °C, а изоляты *Bacillus* sp. — при 40, 45 и 55 °C. Установлено, что изоляты Geobacillus sp. B1, *Bacillus* sp. B и Bacillus sp. C проявляли положительные реакции гидролиза казеина и крахмала, тогда как гидролиз липидов не был выявлен ни у одного из четырёх изолятов. В тесте на каталазную активность изолят *Geobacillus sp. B1* продемонстрировал выраженную положительную реакцию, изоляты *Bacillus* sp. B и *Bacillus* sp. C — положительную, а *Bacillus sp. M11* — отрицательную реакцию. Полученные результаты свидетельствуют о различиях в ферментативных свойствах исследованных бактериальных изолятов и служат основой для дальнейшего изучения их биотехнологического потенциала.

Ключевые слова: термофильные бактерии, *Geobacillus*, *Bacillus*, горячий источник, ризосфера хлопчатника, каталаза, гидролиз казеина, гидролиз крахмала, липаза.

Abstract: This study investigated the morphological, physiological, and biochemical characteristics of Geobacillus sp. B1 isolated from the Rayim So‘fi hot spring in Koson District, Kashkadarya Region, Uzbekistan, and three bacterial isolates, *Bacillus sp. M11*, *Bacillus* sp. B, and *Bacillus* sp. C, obtained from the cotton rhizosphere. The isolates were evaluated for their Gram-staining characteristics, catalase activity, and ability to hydrolyze casein, starch, and lipids. *Geobacillus sp. B1* was examined at 50 and 60 °C, whereas the *Bacillus* sp. isolates were tested at

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40, 45, and 55 °C. The results showed that *Geobacillus sp. B1*, *Bacillus* sp. B, and *Bacillus* sp. C exhibited positive reactions for casein and starch hydrolysis, while lipid hydrolysis was not detected in any of the four isolates. In the catalase test, *Geobacillus sp. B1* showed a strongly positive reaction, *Bacillus* sp. B and *Bacillus* sp. C exhibited positive reactions, and *Bacillus sp. M11* showed a negative reaction. These findings demonstrate differences in the enzymatic properties of the bacterial isolates and provide a basis for further investigations into their biotechnological potential.

Keywords: thermophilic bacteria, *Geobacillus*, *Bacillus*, hot spring, cotton rhizosphere, catalase, casein hydrolysis, starch hydrolysis, lipase.

Kirish

Termofil mikroorganizmlar yuqori harorat sharoitida o‘sishga moslashgan bo‘lib, tabiiy issiq buloqlar va geotermal muhitlarda keng uchraydi. Ularning termostabil fermentlar ishlab chiqarish xususiyati sanoat biotexnologiyasi va ekologik jarayonlar uchun muhim ahamiyatga ega. Koreya Respublikasidagi beshta issiq buloqdan ajratilgan 29 ta termofil bakterial izolyatning 22 tasida kamida bitta gidrolitik ferment faolligi aniqlangan. Ushbu izolyatlarning 16S rRNK geni asosida identifikatsiyasi hamda amilaza, proteaza va lipaza faolligi o‘rganilgan [1]. *Geobacillus* turkumiga mansub bakteriyalar yuqori haroratli muhitlarga moslashganligi, ayrim shtammlarining termostabil fermentlar ishlab chiqarishi va organik substratlarni parchalash xususiyatlari bilan ajralib turadi. Biroq ularning fermentativ faolligi shtammga qarab farqlanadi [2]. Paxta rizosferasi ham foydali mikroorganizmlarning muhim tabiiy manbalaridan biridir. O‘zbekistonning yarim qurg‘oqchil hududlarida olib borilgan tadqiqotlarda rizosfera bakteriyalarining fermentativ faolligi, haroratga chidamliligi va ayrim fitopatogen zamburug‘larga qarshi antagonistik xususiyatlari o‘rganilgan [3]. Bakteriyalarning biokimyoviy xususiyatlarini baholashda kazein, kraxmal va lipid gidrolizi hamda katalaza sinovi keng qo‘llaniladi. Ushbu tahlillar mos ravishda proteolitik, amilolitik, lipolitik faollik va vodorod peroksidni parchalash qobiliyatini aniqlash imkonini beradi [4, 5].

Tadqiqotning maqsadi — issiq buloq va paxta rizosferasidan ajratilgan bakterial izolyatlarning morfologik, fiziologik hamda biokimyoviy xususiyatlarini baholash va ularning keyingi biotexnologik tadqiqotlar uchun istiqbolli belgilarini aniqlashdan iborat.

Tadqiqot usullari

Tadqiqotda ikki xil tabiiy ekologik manbadan ajratilgan to‘rtta bakterial izolyatdan foydalanildi. Birinchi manba Qashqadaryo viloyati Koson tumanidagi Rayim So‘fi issiq bulog‘idan namuna olingan vaqtda suv harorati 65 °C ni tashkil etdi. Ushbu manbadan ajratilgan bakterial izolyat *Geobacillus sp. B1* sifatida belgilandi. Ikkinchi manba paxta rizosferasi tuprog‘i bo‘lib, undan ajratilgan uchta izolyat *Bacillus sp. M11*, deb belgilandi.

Izolyatlarning haroratga bog‘liq o‘sish xususiyatlarini baholash maqsadida Geobacillus sp. B1 50 va 60 °C haroratlarda, paxta rizosferasidan ajratilgan *Bacillus* sp. izolyatlari esa 40, 45 va 55 °C haroratlarda inkubatsiya qilindi. Inkubatsiya davomiyligi mos ravishda yetti va uch kunni tashkil etdi.

Bakterial kulturalarning koloniya morfologiyasi, mikroskopik tuzilishi va Gram bo‘yicha bo‘yalish xususiyatlari tekshirildi. Biokimyoviy faollik kazein, kraxmal va lipid gidrolizi hamda katalaza sinovi orqali baholandi. Kazein gidrolizi oqsilli substratning parchalanishi, kraxmal gidrolizi esa yod eritmasi yordamida gidroliz zonasining aniqlanishiga asoslandi [4]. Lipolitik faollik lipidli substratning parchalanishi, katalaza faolligi esa vodorod peroksid ta’sirida gaz pufakchalari hosil bo‘lishi orqali qayd etildi [5].

Tadqiqot natijalari va muhokamasi

Kazein gidrolizi sinovida *Geobacillus sp. B1*, izolyatlari ijobiy natija ko‘rsatdi. *Bacillus sp. M11* izolyatida esa ushbu reaksiya aniqlanmadi. Kraxmal gidrolizi bo‘yicha ham xuddi shu uchta izolyatda ijobiy natija qayd etildi. Lipid gidrolizi barcha to‘rtta izolyatda salbiy bo‘ldi. Katalaza

sinovida *Geobacillus sp. B1* izolyatida kuchli ijobiy reaksiya (+++), izolyatlarida ijobiy reaksiya (+), *Bacillus sp. M11* izolyatida esa salbiy reaksiya kuzatildi.

1-jadval. Tanlangan bakterial izolyatlarning biokimyoviy xususiyatlari

Biokimyoviy ko‘rsatkich	Geobacillus sp. B1	Bacillus sp. M11
Kazein gidrolizi (proteolitik faollik)	+	+
Kraxmal gidrolizi (amilolitik faollik)	+	+
Tween 60 gidrolizi (lipolitik faollik)	–	–
Katalaza faolligi	+++	+

Izoh: (+) — musbat reaksiya; (−) — manfiy reaksiya; (+++) — kuchli musbat reaksiya sifatida qayd etilgan.

Issiq buloqdan ajratilgan *Geobacillus sp. B1* izolyati 50 va 60 °C haroratlarda besh kun davomida o‘stirildi. Paxta rizosferasidan ajratilgan uchta *Bacillus* sp. izolyatining o‘sishi 40, 45 va 55 °C haroratlarda uch kun davomida kuzatildi. Paxta rizosferasi izolyatlarining o‘sish darajasi harorat va izolyatga qarab farqlanishi qayd etildi. Ushbu natijalar izolyatlarning harorat sharoitlariga javobi bir xil emasligini ko‘rsatadi. Biroq o‘sishning miqdoriy ko‘rsatkichlari va optimal harorat qiymatlari keltirilmagani sababli, har bir izolyatning optimal o‘sish haroratini ushbu ma’lumotlarning o‘zi asosida belgilab bo‘lmaydi. Paxta rizosferasidan ajratilgan izolyatlarining ijobiy fermentativ faolligi ularni keyingi tadqiqotlarda o‘rganish uchun asos bo‘la oladi. Avvalgi tadqiqotlarda O‘zbekistonning yarim qurg‘oqchil hududlaridagi rizosfera bakteriyalari orasida ferment ishlab chiqaruvchi, haroratga chidamli va ayrim fitopatogenlarga qarshi antagonistik xususiyatga ega shtammlar aniqlangan [3]. Biroq mazkur tadqiqot izolyatlarining antagonistik faolligi tekshirilmaganligi sababli ularni biologik nazorat agentlari sifatida baholash hozircha mumkin emas.

Barcha izolyatlarda lipid gidrolizining salbiy natija berishi qo‘llanilgan tajriba sharoitida lipolitik faollik aniqlanmaganligini bildiradi. Bu bakteriyalarda lipaza fermenti mutlaqo mavjud emasligini anglatmaydi, chunki natijaga substrat turi, oziqa muhiti, inkubatsiya sharoiti va tahlil sezgirligi ta’sir ko‘rsatishi mumkin. Shu bois lipaza faolligini muqobil substratlar va tegishli nazoratlar yordamida qayta tekshirish maqsadga muvofiq.

Katalaza sinovida *Geobacillus sp. B1* izolyatining kuchli ijobiy reaksiya ko‘rsatishi, izolyatlarida esa oddiy ijobiy reaksiya kuzatilishi ularning vodorod peroksidni parchalash xususiyatlari turlicha ekanligini ko‘rsatadi. Shunga qaramay, «+++» belgisi standartlashtirilgan miqdoriy tahlil bilan tasdiqlanmaguncha ferment faolligining aniq ustunligi sifatida talqin qilinmasligi lozim.

Xulosa

Rayim So‘fi issiq bulog‘i va paxta rizosferasidan ajratilgan bakterial izolyatlarning morfologik, fiziologik va biokimyoviy xususiyatlari o‘rganildi. *Geobacillus sp. B1*, izolyatlarida kazein hamda kraxmal gidrolizi ijoeobacillus sp. izolyatida kuchli ijobiy, izolyatlarida ijobiy, *Bacillus sp. M11* izolyatida esa salbiy bo‘ldi.

Olingan bo‘lib, proteolitik va amilolitik faollik mavjudligiga mos kelishi aniqlandi. Barcha izolyatlarda lipid gidrolizi salbiy natija berdi. Katalaza faolligi G natijalar izolyatlarning fermentativ va fiziologik xususiyatlari turlicha ekanligini ko‘rsatdi. Kazein va kraxmalni gidrolizlagan izolyatlar keyingi miqdoriy fermentativ tadqiqotlar uchun istiqbolli hisoblanadi. Ularning optimal o‘sish harorati, fermentativ faolligi, taksonomik mansubligi va fitopatogenlarga qarshi antagonistik xususiyatlarini aniqlash uchun qo‘shimcha tadqiqotlar talab etiladi.

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MAHALLIY GLAUKONIT MINERALINING ASPERGILLUS NIGER ISHTIROKIDAGI BIOTEXNOLOGIK O‘ZGARISHLARINI DASTLABKI O‘RGANISH

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Annotatsiya: Ushbu tadqiqotda mahalliy glaukonit mineralining *Aspergillus niger* mikroskopik zamburug‘i ishtirokidagi dastlabki biotexnologik o‘zgarishlari o‘rganildi. Tajribada glaukonit suslali suyuq ozuqa muhitiga kiritilib, 11 kun davomida kuzatildi. Kuzatishlar davomida suyuqlik yuzasida zamburug‘simon tuzilmalar, mineral zarrachalari atrofida qatlamlar hamda yashil yoki to‘q yashil rangli cho‘kmalar qayd etildi. Ushbu o‘zgarishlar glaukonit va biologik tizim o‘rtasidagi ehtimoliy o‘zaro ta’sirni chuqurroq o‘rganish zarurligini ko‘rsatadi. Biroq mineral komponentlarining eruvchanligi va kimyoviy tarkibidagi o‘zgarishlarni tasdiqlash uchun qo‘shimcha laboratoriya tahlillari talab etiladi. Tadqiqot mahalliy mineral xomashyoni biotexnologik usullar yordamida o‘rganish va kelgusida mineral asosidagi o‘g‘itlar ishlab chiqish imkoniyatlarini baholashga qaratilgan.

Kalit so‘zlar: glaukonit, *Aspergillus niger*, biotexnologiya, mineral xomashyo, kaliy, organik kislotalar, biotexnologik faollashtirish.

Аннотация: В статье рассматриваются возможности биотехнологической активации местного глауконитового минерала Узбекистана с использованием микроскопического гриба *Aspergillus niger* и его применения при разработке фосфорсодержащих удобрений. Цель исследования заключается в изучении поведения глауконита в питательной среде и оценке потенциальных возможностей повышения подвижности минеральных компонентов при участии микроорганизмов. В предварительном эксперименте глауконит был внесён в жидкую питательную среду на основе сусла, после чего наблюдение проводилось в течение 11 суток. Органические кислоты, образуемые *Aspergillus niger*, потенциально способны влиять на растворимость отдельных минеральных компонентов. Для подтверждения эффективности процесса необходимы лабораторные определения pH среды, содержания водорастворимых форм фосфора и калия, а также изменений минерального состава. Работа направлена на создание научной основы для разработки удобрений с использованием местного минерального сырья и биотехнологических методов.

Ключевые слова: глауконит, *Aspergillus niger*, биотехнологическая активация, фосфорные удобрения, органические кислоты, минеральное сырьё, биоудобрение.

Abstract: This article examines the potential for biotechnological activation of a local Uzbek glauconite mineral using the filamentous fungus *Aspergillus niger* and its possible application in the development of phosphorus-containing fertilizers. The study aims to investigate glauconite in a nutrient medium and assess the potential for increasing the mobility of mineral components through microbial activity. In a preliminary experiment, glauconite was introduced into

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Oripova Z.M., Axmedova Z.R. Mahalliy glaukonit mineralining Aspergillus niger ishtirokidagi biotexnologik o‘zgarishlarini dastlabki o‘rganish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 311–314.
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a liquid wort-based medium and observed for 11 days. Organic acids produced by *Aspergillus niger* may influence the solubility of certain mineral components. However, the effectiveness of this process must be confirmed by laboratory measurements of medium pH, water-soluble phosphorus and potassium, and changes in mineral composition. The research is intended to establish a scientific basis for developing fertilizers from local mineral resources using biotechnological approaches.

Keywords: glauconite, *Aspergillus niger*, biotechnological activation, phosphorus fertilizers, organic acids, mineral resources, biofertilizer.

Kirish

Hozirgi vaqtda qishloq xo‘jaligida tuproq unumdorligini saqlash, o‘simliklarning mineral oziqlanishini yaxshilash va mahalliy mineral xomashyo resurslaridan samarali foydalanish muhim ilmiy-amaliy vazifalardan hisoblanadi. Mineral o‘g‘itlar ishlab chiqarishda tabiiy minerallardan foydalanish, ularning tarkibidagi oziq elementlarining o‘simliklar uchun o‘zlashtiriladigan shakllarini ko‘paytirish hamda resurs tejamkor texnologiyalarni ishlab chiqish dolzarb ahamiyatga ega. Shu nuqtayi nazardan, mineral xomashyoni mikroorganizmlar yordamida qayta ishlashga asoslangan biotexnologik usullar alohida ilmiy qiziqish uyg‘otadi. Glaukonit temir va kaliy saqlovchi qatlamli silikat minerali bo‘lib, yashil rangli tabiiy mineral xomashyo sifatida tavsiflanadi. Uning tarkibida kaliy, temir va boshqa elementlar mavjud bo‘lsa-da, ularning umumiy miqdori o‘simliklar tomonidan o‘zlashtirilish darajasini to‘liq ifodalamaydi. Glaukonit tarkibidagi ayrim elementlar mineral kristall panjarasi bilan bog‘langanligi sababli ularning ajralishi va eruvchan shakllarga o‘tishi mineralning kimyoviy tarkibi, zarracha o‘lchami hamda tashqi muhit sharoitlariga bog‘liq. Shu sababli glaukonitni qayta ishlashning fizik, kimyoviy va biologik usullarini o‘rganish uning qishloq xo‘jaligida qo‘llanish imkoniyatlarini kengaytirishga xizmat qilishi mumkin.

Mazkur tadqiqotda mahalliy glaukonit mineralining A. niger ishtirokidagi dastlabki o‘zgarishlarini o‘rganishga e’tibor qaratildi. Glaukonit suslali suyuq ozuqa muhitiga kiritilib, 11 kun davomida kuzatildi. Kuzatishlar davomida suyuqlik yuzasida zamburug‘simon tuzilmalar, mineral zarrachalari atrofida qatlamlar hamda yashil yoki to‘q yashil rangli cho‘kmalar qayd etildi.

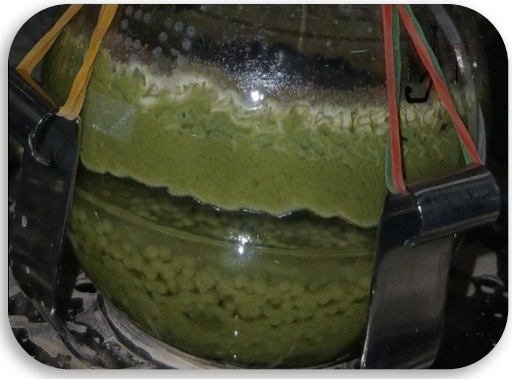
Materiallar va metodlar

Tadqiqot obyekti sifatida mahalliy glaukonit minerali va Aspergillus niger mikroskopik zamburug‘i tanlandi. Tajriba uchun glaukonit suslali suyuq ozuqa muhitiga kiritildi (1-rasm). Ozuqa muhiti mikroorganizmning rivojlanishini kuzatish va mineral bilan ehtimoliy o‘zaro ta’sirini o‘rganish uchun foydalanildi. Tajriba davomida glaukonit va A. niger ishtirokidagi tizim 11 kun davomida kuzatildi. Kuzatuvlarda zamburug‘simon tuzilmalarning paydo bo‘lishi va joylashuvi, suyuq muhit hamda mineral rangining o‘zgarishi, shuningdek, glaukonit zarrachalari atrofida qatlam va cho‘kmalarning hosil bo‘lishi qayd etildi (2-rasm). Kuzatuvlar tashqi morfologik belgilarni tavsiflashga qaratildi. Shu sababli tadqiqotning ushbu bosqichi glaukonit va mikroorganizm ishtirokidagi tizimning dastlabki kuzatuvi sifatida baholandi.

Jarayonning biotexnologik samaradorligini miqdoriy aniqlash uchun keyingi bosqichda ozuqa muhitining boshlang‘ich va yakuniy pH qiymatini o‘lchash, suyuq fazadagi kaliy miqdorini aniqlash hamda mineralning dastlabki va tajribadan keyingi tarkibini taqqoslash rejalashtiriladi. Shuningdek, mikroorganizm qo‘shilmagan glaukonitli nazorat namunasi bilan taqqoslash kuzatilgan o‘zgarishlarning biologik jarayon bilan bog‘liqligini baholash imkonini beradi.

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1-rasm. Glaukonit suslali suyuq ozuqa muhiti; 2-rasm. Mineral atrofidagi hosilalar

Natijalar va muhokama

Tajriba davomida mahalliy glaukonit minerali suslali suyuq ozuqa muhitida Aspergillus niger ishtirokida 11 kun davomida kuzatildi. Kuzatuvlar natijasida ozuqa muhiti va mineral namunasida ayrim tashqi morfologik o‘zgarishlar qayd etildi. Xususan, suyuqlik yuzasida va mineral zarrachalari atrofida zamburug‘simon tuzilmalar, shuningdek, yashil rangli qatlam va cho‘kma ko‘rinishidagi hosilalar kuzatildi (3-rasm). Muhit hamda mineral rangidagi o‘zgarishlar ham qayd etildi.

Kuzatilgan belgilar mikroorganizm va mineral ishtirokidagi tizimda muayyan o‘zgarishlar sodir bo‘lgan bo‘lishi mumkinligini ko‘rsatadi. Adabiyotlarda Aspergillus niger ning ayrim mineral xomashyolar, jumladan, fosfatli jinslardan fosforni eritmaga o‘tkazish jarayonidagi imkoniyatlari o‘rganilgan. Bunda mikroorganizm faoliyati davomida hosil bo‘ladigan organik kislotalar mineral komponentlarining eruvchanligiga ta’sir ko‘rsatishi mumkin.

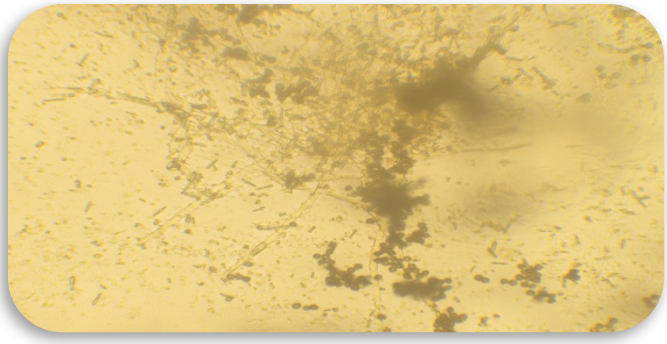
Ushbu tajribaning muhim jihati — mahalliy glaukonit mineralining zamburug‘ ishtirokidagi suyuq ozuqa muhitida dastlabki kuzatuvidir. Shuningdek, glaukonitdan kaliy ajralishi miqdoriy jihatdan aniqlanmagan. Ushbu tahlillar mahalliy glaukonitni biotexnologik usulda qayta ishlash imkoniyatlarini ilmiy asosda baholash uchun zarur.



3-rasm. Glaukonitning yashil rangli qatlami va cho‘kma ko‘rinishidagi hosilalari

Kuzatilgan belgilar tajriba tizimida fizik va biologik o‘zgarishlar yuz berganini ko‘rsatadi. Biroq yashil rangning paydo bo‘lishi mineral zarrachalarining tarqalishi, glaukonitning tabiiy rangi yoki boshqa jarayonlar bilan bog‘liq bo‘lishi mumkin. Zamburug‘simon tuzilmalarning aynan *A. niger* ga tegishliligi va mineral yuzasida biologik qatlam hosil bo‘lganligi mikroskopik tekshiruv orqali kuzatildi (4-rasm).

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4-rasm. Mineral yuzasida biologik qatlam hosil bo‘lganligining mikroskopik tekshiruvi

Ilmiy adabiyotlarda *A. niger* ning ayrim fosfatli minerallardan fosforni mobilizatsiya qilish imkoniyatlari ko‘rsatilgan. Ushbu ma’lumotlar mikroorganizmlar yordamida mineral xomashyoni qayta ishlashni o‘rganish uchun ilmiy asos bo‘lib xizmat qiladi.

Xulosa

O‘tkazilgan dastlabki tadqiqot davomida mahalliy glaukonit minerali suslali suyuq ozuqa muhitida Aspergillus niger ishtirokida 11 kun davomida kuzatildi. Tajriba natijasida ozuqa muhiti va mineral namunasida rang o‘zgarishlari, zamburug‘simon tuzilmalar hamda qatlam va cho‘kma ko‘rinishidagi hosilalar qayd etildi. Kuzatilgan o‘zgarishlar glaukonit va mikroorganizm ishtirokidagi tizimni yanada chuqurroq o‘rganish zarurligini ko‘rsatadi. Biroq glaukonit tarkibidagi kaliy ajralishi, mineralning biotexnologik faollashuvi yoki o‘g‘itbop xususiyatlarining yaxshilanishi uchun tajribalar davom etmoqda.

Foydalanilgan adabiyotlar

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OROL DENGIZI QURIGAN TUBI TUPROQLARIDA TARQALGAN AYRIM MIKROORGANIZMLARNING BIOLOGIK XILMA-XILLIGI

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O‘zbekiston Milliy universitetining Jizzax filiali

Annotatsiya: Mazkur tadqiqotda Orol dengizining qurigan tubi tuproqlarida tarqalgan ayrim mikroorganizmlarning biologik xilma-xilligi hamda kultural-morfologik xususiyatlari o‘rganildi. Mikroorganizmlarni ajratib olishda ketma-ket suyultirish va turli ozuqa muhitlariga ekish usullaridan foydalanildi. Kuzatuvlar davomida sariq, yashil va qaymoqsimon rangli koloniyalar aniqlandi. Koloniyalarning rang va tashqi ko‘rinishidagi farqlar o‘rganilgan namunalarda kultural xilma-xillik mavjudligini ko‘rsatdi. Olingan natijalar Orol dengizining qurigan tubi tuproqlaridagi mikroorganizmlarni tavsiflash hamda ularning ekstremal ekologik sharoitlarga moslanish xususiyatlarini keyingi tadqiqotlarda baholash uchun asos bo‘lib xizmat qiladi.

Kalit so‘zlar: Orol dengizi, mikroorganizm, tuproq mikrobiotasi, Kox usuli, bakterial izolyatlar, ekologik moslanish.

Аннотация: В данной работе изучены биологическое разнообразие и культурально-морфологические особенности некоторых микроорганизмов, распространённых в почвах высохшего дна Аральского моря. Для выделения микроорганизмов использовали метод последовательных разведений и посев на различные питательные среды. В ходе наблюдений были обнаружены колонии жёлтого, зелёного и кремового цветов. Различия в окраске и внешнем виде колоний свидетельствуют о наличии культурального разнообразия в исследованных образцах. Полученные результаты могут служить основой для дальнейшего изучения микроорганизмов почв высохшего дна Аральского моря и оценки их адаптации к экстремальным экологическим условиям.

Ключевые слова: Аральское море, микроорганизмы, почвенная микробиота, метод Коха, бактериальные изоляты, экологическая адаптация.

Abstract: This study investigated the biological diversity and cultural and morphological characteristics of selected microorganisms occurring in soils of the dried bed of the Aral Sea. Serial dilution and cultivation on different nutrient media were used to isolate the microorganisms. Yellow, green, and cream-colored colonies were observed during the study. Differences in colony pigmentation and appearance indicated cultural diversity among the microorganisms recovered from the investigated samples. The findings provide a basis for further characterization of microorganisms inhabiting the soils of the dried Aral Sea bed and for investigating their adaptation to extreme environmental conditions.

Keywords: Aral Sea, microorganisms, soil microbiota, Koch’s method, bacterial isolates, environmental adaptation.

Kirish

Orol dengizining qurigan tubida yuzaga kelgan ekstremal ekologik sharoitlar, xususan, tuproq sho‘rlanishi va namlik tanqisligi ushbu hududda tarqalgan mikroorganizmlarning biologik xilma-xilligi hamda ekologik moslanish xususiyatlarini o‘rganishni dolzarb ilmiy masalaga aylantirmoqda. Matzhanova va hammualliflarining (2021) tadqiqotlariga ko‘ra, 1973-2020-yillar davomida Orol

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Murodova S.S., Ortiqboyeva O.Q. Orol dengizi qurigan tubi tuproqlarida tarqalgan ayrim mikroorganizmlarning biologik xilma-xilligi // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 315–318.
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dengizining umumiy maydoni keskin qisqarib, qurigan dengiz tubi maydoni kengaygan. Suv tanqisligining kuchayishi Amudaryo deltasidagi tabiiy ko‘llarning suv bilan ta’minlanishiga ham salbiy ta’sir ko‘rsatgan [1].

Šimonovičová va hammualliflarining 2024-yildagi tadqiqotida Orol dengizi qurigan tubining turli qismlaridan olingan tuproq namunalarining kimyoviy va mikrobiologik xususiyatlari kompleks o‘rganilgan. Tadqiqotchilar tuproq muhitining ishqoriyligini va organik moddaning ayrim namunalarda juda past ekanligini qayd etgan. Jumladan, tadqiq qilingan namunalar pH qiymati taxminan 8,1-8,6 oralig‘ida bo‘lgan. Ayrim namunalarda gumus miqdori 0,17-1,03 % oralig‘ida farqlangan. Shuningdek, Na^+, Ca^{2+} va Mg^{2+} kabi ionlarning miqdori hudud va tuproq qatlamiga qarab sezilarli darajada o‘zgarishi aniqlangan [5].

Orol dengizi qurigan tubi tuproqlarining mikrobiologik tarkibini o‘rganish bo‘yicha zamonaviy tadqiqotlarda klassik kultivatsiya usullaridan tashqari molekulyar-genetik yondashuvlardan ham foydalanilmoqda. Šimonovičová va hammualliflari qurigan dengiz tubi tuproqlaridan 15 avlodga mansub 31 tur mikroskopik ipsimon zamburug‘ni aniqlagan. Bakteriyalar orasida esa *Arthrobacter, Bacillus, Massilia, Rhodococcus* va *Nocardiopsis* avlodlari vakillari aniqlangan. Tadqiqotchilar kultivatsion va yuqori o‘tkazuvchanlikka ega sekvenslash usullarining birgalikda qo‘llanilishi Orolqum mikrobiotasini to‘liqroq tavsiflash imkonini berishini ta’kidlagan [4].

Galofit o‘simliklar bilan bog‘liq mikroorganizmlarning yana bir muhim xususiyati — ularning yuqori sho‘rlanishga moslashganligi. Etesami va Beattie galofitlar rizosferasini sho‘r sharoitga chidamli o‘simliklarni qo‘llab-quvvatlovchi bakteriyalar uchun muhim tabiiy manba sifatida baholagan. Bunday bakteriyalar orasida *Halomonas, Bacillus, Streptomyces, Oceanobacillus* va *Pseudomonas* avlodlari ko‘p uchrashi qayd etilgan [8]. Ilangumaran va Smith PGPR yordamida sho‘rlanish stressini kamaytirish mexanizmlarini tizimli ravishda tahlil qilib, foydali bakteriyalar o‘simliklarda suv va oziqa moddalarining o‘zlashtirilishi, fotosintez, gormonal boshqaruv, ion gomeostazi va antioksidant himoya jarayonlariga ta’sir ko‘rsatishini qayd etgan. Mualliflar ekstremal muhitlardan, jumladan cho‘l va sho‘r suvli hududlardan ajratilgan mikroorganizmlar o‘simliklarning sho‘rlanishga chidamliligini oshirishda alohida istiqbolga ega ekanligini ko‘rsatadi [9].

Mishra va hammualliflarining sharhiga ko‘ra, tuzga chidamli PGP bakteriyalar o‘simliklarda osmotik moslashuv, ionlar muvozanatini saqlash, osmolitlar to‘planishi, oksidlovchi stressni kamaytirish va fitogormonlar sintezi orqali stressga chidamlilikni kuchaytiradi. Shu sababli ular sho‘rlangan tuproqlarning biologik unumdorligini tiklash va o‘simliklarning yashovchanligini oshirish uchun ekologik xavfsiz vosita sifatida qaralmoqda [10].

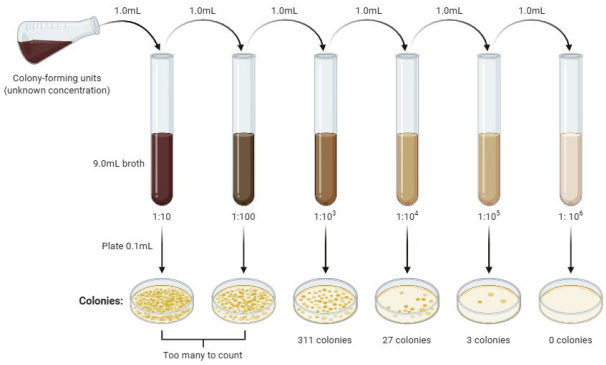
O‘simlik va mikroorganizmlar o‘rtasidagi munosabatlar rizosfera bilan cheklanmay, o‘simlikning ichki to‘qimalarida yashovchi endofit bakteriyalarni ham qamrab oladi. G‘arbiy Orolbo‘yi galofitlarini o‘rganish natijasida 9 ta o‘simlik namunasidan 289 ta bakterial izolyat ajratilgan bo‘lib, ular Firmicutes, Actinobacteria va Proteobacteria tiplariga mansub bo‘lgan. Izolyatlar orasida Bacillus (38,5 %), Staphylococcus (24,7 %) va Streptomyces (12,5 %) avlodlari ustunlik qilgan. Ayrim endofit bakteriyalarning fitopatogen zamburug‘larga qarshi antagonistlik xususiyati ularning o‘simliklarni biologik himoya qilishdagi potensial ahamiyatini ko‘rsatadi. Shu bois, Orolbo‘yi galofitlari bilan bog‘liq endofit mikroorganizmlar biologik preparatlar va biokontrol vositalarini yaratish uchun istiqbolli manba hisoblanadi [3].

Tadqiqot materiallari va usullari

Tadqiqot obyekti sifatida Orol dengizining qurigan tubi hududidan olingan tuproq namunalari tanlab olindi. Tadqiqot davomida tuproq namunalarini yig‘ish, laboratoriyaga yetkazish va tahlilga tayyorlash, mikroorganizmlarni ozuqa muhitlariga ekish, sof kulturalarni ajratib olish hamda ularning asosiy biologik xususiyatlarini o‘rganish usullaridan foydalanildi.

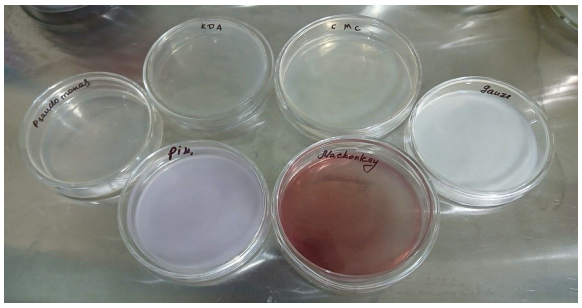
Tuproq namunalaridagi mikroorganizmlarni aniqlash uchun Kox usulida ketma-ket suyultirish amalga oshirildi. Bunda 1 g tuproq namunasi 9 ml steril eritmaga solinib, suspenziya ketma-ket suyultirildi.

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1-rasm. Kox usulida suyultirish

Tuproq namunalarida mavjud bo‘lgan mikroorganizmlarni ajratib olish va ularning kultural xususiyatlarini o‘rganish maqsadida go‘sht-pepton agar (GPA), nutrient agar (NA), kartoshka dekstrozali agar hamda tadqiqot maqsadiga muvofiq maxsus selektiv oziqa muhitlaridan MacConkey agar, Gauze, Pikovskiylardan foydalanildi. Tayyorlangan suyultirmalardan 0,1 ml dan olinib, steril sharoitda Petri idishlaridagi tegishli qattiq ozuqa muhitlari yuzasiga bir tekis taqsimlandi. Ekilgan namunalar qo‘llanilgan ozuqa muhiti va aniqlanishi mo‘ljallangan mikroorganizmlar guruhiga mos sharoitlarda inkubatsiya qilindi.



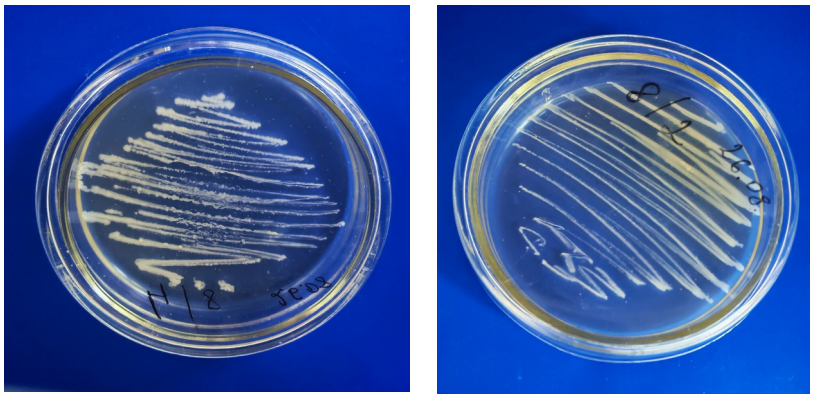
2-rasm. Mikroorganizmlarni ajratib olish uchun tayyorlangan ozuqa muhitlari

Bakterial izolyatlarning morfologik xususiyatlarini o‘rganish maqsadida preparatlar Gram usulida bo‘yaldi. Bunda bakterial surtma tayyorlanib, quritildi va fiksatsiya qilindi. Preparat ketma-ket kristall binafsha bo‘yoq, yod eritmasi, rangsizlantiruvchi eritma hamda safranin bilan ishlov berildi. So‘ng preparatlar mikroskop ostida kuzatildi.

Natijalar va ularning muhokamasi

Tadqiqot davomida Orol dengizining qurigan tubi tuproqlaridan ajratib olingan mikroorganizmlarning o‘sish xususiyatlari, koloniyalarining tashqi ko‘rinishi va morfologik belgilari o‘rganildi. Selektiv muhitlar bo‘yicha tahlil natijalari bakterial va zamburug‘li mikrobiotsenozning funksional xilma-xilligini ko‘rsatdi. Nutrient agar va umumiy muhitlarda bakterial o‘sishning yuqoriligi tuproqning umumiy mikrobiologik yuklamasi yuqori ekanligini tasdiqlaydi. MacConkey agarida gram-manfiy enterobakteriyalarning aniqlanishi esa tuproq tizimida fakultativ patogen yoki indikator guruhlarning mavjudligini ko‘rsatadi. Pikovskiy muhitida fosfat erituvchi va oligotrof mikroorganizmlarning aniqlanishi tuproqning oziqa elementlari cheklangan sharoitga qaramasdan mikroorganizmlar tomonidan samarali o‘zlashtirilayotganini bildiradi. Shuningdek, ayrim namunalar yuzasida pigment hosil qiluvchi koloniyalar (sariq, yashil va qaymoqsimon rangli koloniyalar) kuzatildi. Bu holat Orol hududiga xos ekstremal sharoitlarda (yuqori sho‘rlanish, qurg‘oqchilik va UV stress) rivojlangan galotolerant va stressga chidamli mikroorganizmlar mavjudligini ko‘rsatadi. Olingan natijalar Orol dengizi qurigan tubi ekotizimida mikrobiologik hayot to‘liq yo‘qolmaganligini, aksincha, u ekstremal sharoitlarga moslashgan maxsus mikrobiota shaklida saqlanib qolganligini ko‘rsatadi. Eng faol mikrobiologik zonalar o‘simlik ildiz tizimi atrofida aniqlanib, bu hududlar ekologik tiklanish jarayonlarida muhim rol o‘ynashi mumkin.

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3-rasm. Selektiv muhitda o‘sgan mikroorganizm namunalari

Tadqiqot davomida Orol dengizining qurigan tubi tuproqlaridan ajratib olingan mikroorganizmlarning kultural-morfologik xususiyatlari o‘rganildi. Sariq, yashil va qaymoqsimon rangli koloniyalarning aniqlanishi namunalarda kultural xilma-xillik mavjudligini ko‘rsatdi. Olingan natijalar mikroorganizmlarning ekstremal ekologik sharoitlarga moslanish xususiyatlarini chuqurroq o‘rganish hamda kelajakda Orolbo‘yi hududlarini ekologik tiklashda istiqbolli izolyatlardan foydalanish uchun asos bo‘lib xizmat qiladi.

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IDENTIFICATION OF MICROORGANISMS FOUND IN THE ROOTS OF PLANTS AND IN THE RHIZOSPHERIC SOIL OF THE DRIED BED OF THE ARAL SEA

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Abstract: In the context of global climate change and increasing environmental degradation, extreme ecosystems such as the dried bottom of the Aral Sea have become important natural laboratories for studying plant–microbe interactions under severe abiotic stress conditions. These environments, characterized by high salinity, aridity, and complex geochemical factors, significantly influence the structure and function of rhizosphere microbial communities. However, the diversity and ecological role of cultivable microorganisms associated with halophytic plants in such environments remain insufficiently explored.

The **aim** of the study was to identify cultivable microorganisms associated with the roots and rhizosphere of halophytic plants, particularly Salsola richteri, growing in the Aralkum region, and to evaluate their ecological and biotechnological potential.

Methods. The study employed classical microbiological and analytical approaches, including soil and root sampling from the Aral Sea dried seabed, serial dilution and streak plate techniques for isolation of pure bacterial cultures, and morphological, physiological, and Gram staining analyses. Precise taxonomic identification of isolates was carried out using MALDI-TOF mass spectrometry. Additionally, salt tolerance assays were performed to assess the adaptive capacity of isolates under hypersaline conditions.

Results. A total of 13 bacterial isolates were obtained, including 40% Gram-positive and 60% Gram-negative bacteria, predominantly rod-shaped forms. Taxonomic analysis revealed that the isolates mainly belonged to the genera Bacillus, Enterobacter, Providencia, Pseudomonas, and Rhodococcus. Among them, Rhodococcus ruber and Enterobacter cancerogenus were the most frequently detected species. Several isolates demonstrated high salinity tolerance, with the ability to grow at NaCl concentrations up to 12–14%, indicating strong physiological adaptation to extreme environmental conditions.

The predominance of halotolerant and stress-adapted microorganisms in the rhizosphere suggests their active involvement in plant survival under harsh conditions. These microorganisms likely contribute to plant adaptation through mechanisms such as osmotic regulation, nutrient mobilization, and stimulation of plant growth.

Conclusion. The obtained results highlight the ecological significance of rhizosphere microbiota in the Aral Sea region and demonstrate their potential application in phytomelioration, soil restoration, and the development of biofertilizers. The identified strains represent promising candidates for future biotechnological applications aimed at improving plant resilience in saline and arid environments.

Keywords: Aral Sea, *Salsola richteri*, rhizosphere microorganisms, saline soil, extreme environment, MALDI-TOF MS, *Bacillus*, *Enterobacter*, *Rhodococcus*, phytomelioration.

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Hyper-extreme ecosystems, such as salt lakes and the areas formed as a result of their desiccation, are distributed worldwide; however, they differ in salinity levels and chemical composition, which are largely determined by local geological characteristics (de la Haba et al., 2011). In addition to their hypersaline nature, these ecosystems are often characterized by other environmental extremes, including high alkalinity, low oxygen availability, and intense ultraviolet (UV) radiation (Edwardson & Hollibaugh, 2018).

A prominent example of such environments is the Aral Sea and its desiccated seabed. The Aral Sea is an endorheic saline lake located between Kazakhstan in the north and Uzbekistan in the south. It began to shrink in the 1960s and had largely transformed into a desert by the 2010s (Wikipedia contributors, n.d.).

As a consequence of the Aral Sea's desiccation, sandy landscapes have formed within its former basin (Song et al., 2024), initiating processes of soil formation (Jabbarov et al., 2024). Currently, these newly formed areas cover approximately 5.2 million hectares, of which 3.2 million hectares are located within the territory of Uzbekistan.

The distribution of vegetation across the dried seabed of the Aral Sea varies by region—southern, eastern, western, northern, and central zones. In the southern region alone, 216 plant species have been identified (UzDaily, 2024), whereas in the western region, 27 plant species belonging to four genera have been recorded (Shomurodov et al., 2021).

Over the years, changes in the composition of vegetation in the dried bed of the Aral Sea have been observed. In particular, a significant transformation has occurred in mesophytic plant communities as a result of the decline in groundwater levels. In addition, the movement and redistribution of salts have led to the emergence of new plant species, while others have disappeared (Adilov et al., 2021). The primary factor influencing the gradual transformation of vegetation is soil salinization (Duan et al., 2024). Furthermore, as a result of desertification processes, approximately 68% of the dried Aral Sea bed has undergone degradation (Song et al., 2021).

In the northern part of the dried Aral Sea basin, the main processes of soil degradation include anthropogenic salinization, wind erosion, and soil alkalization (Issanova et al., 2022). Initially, the water of the Aral Sea was not highly saline; however, over time, it became increasingly saline, which contributed to severe soil salinization and the formation of solonchaks (Panin et al., 2024). At present, the dried bed of the Aral Sea is predominantly covered by halophytic and psammophytic plant species, whose projective cover changes over time (Issanova et al., 2023). Periodic climatic changes further influence the distribution patterns of vegetation (He et al., 2022). The intensification of soil salinity has a negative impact on plant growth and development (Micklin et al., 2020).

Among the plants tolerant to salinity and drought in the Aral Sea region, *Glycyrrhiza glabra* (licorice) is recognized as a species highly resistant to various ecological stresses (Jabborova et al., 2023). Another stress-tolerant plant found in different parts of the dried Aral Sea basin is *Chenopodium quinoa* (Reimov & Fayzieva, 2014).

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Figure 1. The plant *Salsola richteri*, which occurs on the dried bottom of the Aral Sea

The study of *Salicornia* L., which is widely distributed throughout the Aral Sea surroundings, and the isolation of bacteria from its rhizosphere for application to plants in other regions have demonstrated positive results under stress conditions (Zhang et al., 2019).

In addition, *Salsola richteri* (Fig. 1), *Haloxylon aphyllum*, species belonging to the genus *Calligonum*, and other plants are present in this region as dominant species characterized by high biomass production.

The analysis of the above-mentioned literature indicates that studying the plants distributed on the dried bottom of the Aral Sea, particularly *Salsola richteri*, as well as the microorganisms inhabiting its rhizosphere zone, is of significant scientific relevance. In particular, the composition of these microorganisms and their precise identification have not been sufficiently elucidated, making research in this area highly important from both ecological and biotechnological perspectives.

Materials and Methods

Soil and root samples were collected from the rhizosphere zone (at a depth of 25–30 cm) of selected plant species growing on the dried bottom of the Aral Sea. The sampling was conducted in November 2025. The map of the Aral Sea and the geographical location of the sampling sites are presented in Figure 2.

During the study period, meteorological and weather conditions remained stable. Throughout the observation period, sunny weather prevailed, with an average daytime air temperature of approximately 22 °C (Figure 2).

Soil and root samples were collected under aseptic conditions, placed into sterile plastic containers, and transported to the laboratory within 1–2 days.

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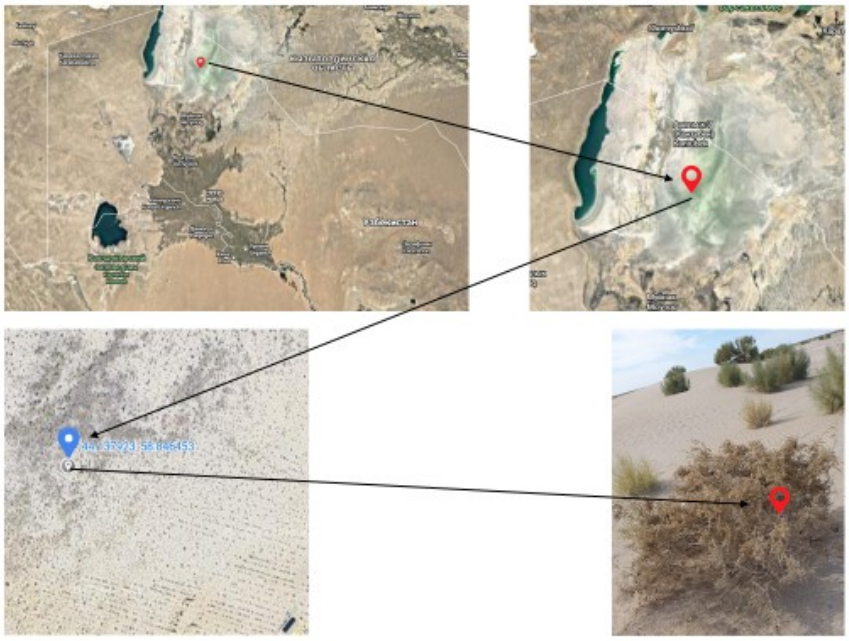


Figure 2. Sampling site of soil samples

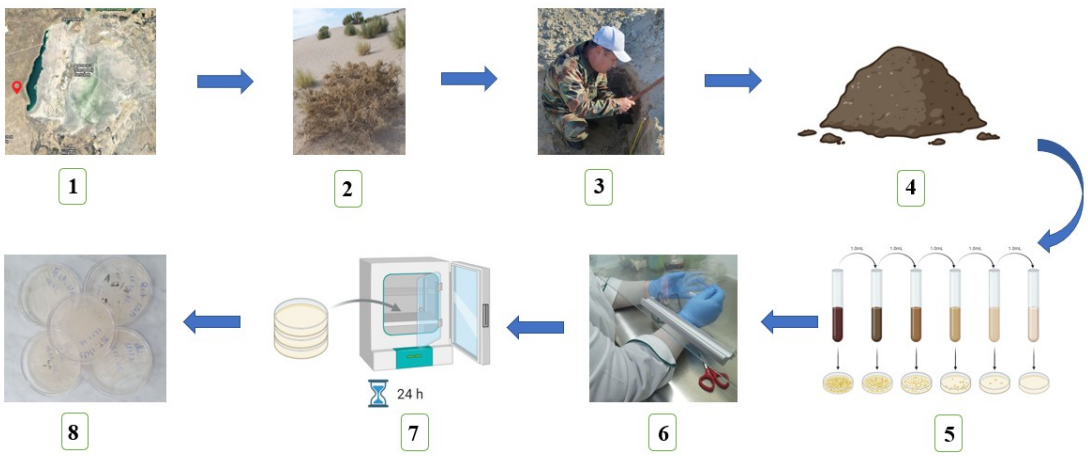
The map was created using Google Maps (https://www.google.com/maps)

A nutrient agar medium was selected for the isolation of bacteria. In this study, bacteria were isolated from soil samples using serial dilution and the streak plate method.

Nutrient agar is a general-purpose culture medium designed for the cultivation of microorganisms. It supports the growth of a wide range of non-fastidious organisms, including various bacteria and fungi. Due to its rich composition, nutrient agar provides essential nutrients required for microbial growth and is widely used in microbiological studies.

Serial dilution is a stepwise dilution technique used to reduce the concentration of a substance in a solution. To perform serial dilution, a small volume of a well-mixed sample is transferred into a new container, and an appropriate amount of diluent (such as sterile water or buffer solution) is added to achieve dilution. The resulting diluted sample serves as the basis for subsequent dilutions. When this process is repeated multiple times, a series of solutions with progressively decreasing concentrations is obtained.

The number of dilution steps and the dilution factor depend on the initial concentration and the desired range for analysis. Serial dilutions are commonly performed in tenfold (1:10) or hundredfold (1:100) increments. For example, a 1:10 dilution is prepared by mixing one part of the sample with nine parts of the diluent, whereas a 1:100 dilution involves mixing one part of the sample with ninety-nine parts of the diluent.



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Figure 3. Pure Culture Isolation Process: 1. Selection of the sampling site 2. *Salsola richteri* plant 3. Collection of soil samples 4. Transportation of soil samples to the laboratory 5. Serial dilution method 6. Inoculation (culturing) of microorganisms 7. 24-hour incubation 8. Obtaining a pure culture

The figures were created using BioRender (https://www.biorender.dev/).

For instance, mixing 100 µL of the original sample with 900 µL of water results in a 1:10 dilution. The final volume becomes 1000 µL (1 mL), and the concentration is reduced to one-tenth of the original sample. This is commonly referred to as a tenfold (10×) dilution.

The streak plate method is a widely used technique for isolating pure bacterial colonies from mixed cultures. In this study, a small amount of soil suspension was aseptically collected using a sterile inoculating loop. The inoculum was then streaked across the surface of a pre-prepared nutrient agar plate in a series of successive streaks, enabling gradual dilution of the sample.

The inoculating loop was sterilized between each streak to prevent contamination and ensure effective isolation. The plates were incubated at 37°C for 24–48 hours. Following incubation, well-isolated colonies were selected for subsequent morphological and biochemical analyses.

This method ensures the separation of individual bacterial cells and facilitates the growth of pure colonies suitable for further identification (Figure 3).

The cultivated bacteria were initially differentiated into Gram-positive and Gram-negative groups, and their cellular morphology and arrangement were examined using the Gram staining method developed by HC (1884). A bacterial smear was prepared on a clean glass slide and then gently heat-fixed using a spirit lamp. Subsequently, 2–3 drops of crystal violet were applied to the smear and allowed to stand for one minute. The excess stain was carefully rinsed off with tap water, and the slide was gently dried using absorbent paper.

Thereafter, Gram's iodine was applied for one minute, followed by brief washing. Decolorization was carried out using 96% ethanol for approximately 10 seconds. Next, several drops of safranin were added and left for one minute. The slide was then rinsed again with water to stop the decolorization process and allowed to air dry. Finally, the stained smear was observed and analyzed under a microscope.

The isolated microbial strains were identified using a MALDI-TOF Mass Spectrometry EXS 2600 (Zybio) system. During the analysis, a centrifuge, vortex mixer, pipettes, and a reagent kit (Matrix solution, Microorganism lysate I, and Microorganism lysate II) were utilized, along with distilled water and 96% ethanol.

For the identification procedure, pure and well-isolated colonies grown on nutrient media were selected. A volume of 300 µL of ultrapure water was added to 1.5 mL microcentrifuge tubes, followed by the addition of 1–5 mg of an individual colony. The resulting suspension was thoroughly homogenized using a vortex mixer until a uniform consistency was achieved. Subsequently, 900 µL of absolute ethanol was added to each tube, mixed again, and centrifuged at 12,000 rpm for 2–3 minutes.

After centrifugation, the supernatant was carefully discarded, and 20 µL of Microorganism lysate I reagent was added to the remaining pellet and mixed thoroughly. Then, 20 µL of Microorganism lysate II reagent was added, and the mixture was homogenized using a pipette. The obtained mixture was centrifuged again for 2 minutes.

The MALDI-TOF target plate was disinfected with 96% ethanol prior to sample application. For each sample, 1 µL of the supernatant was spotted onto the designated wells of the plate and allowed to air-dry at room temperature. After complete drying, 1 µL of Matrix solution was added on top of each spot and again allowed to dry.

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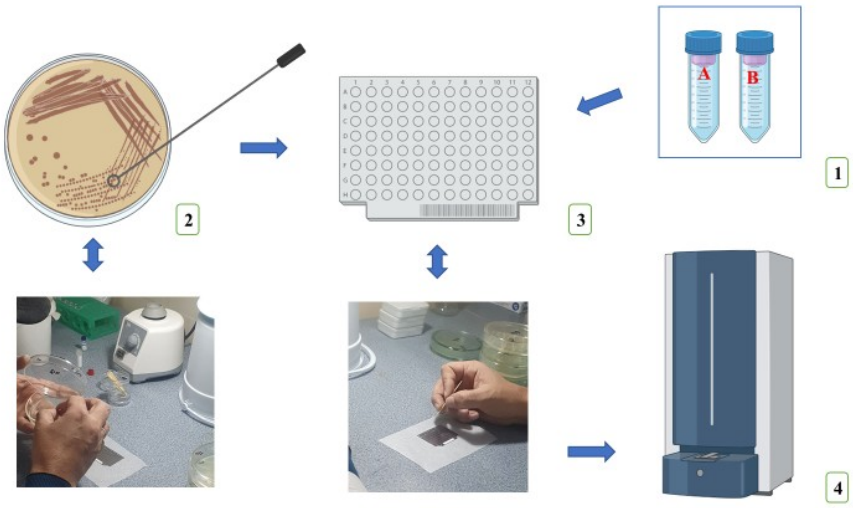


Figure 4. Identification process using a MALDI-TOF instrument: 1 – Treatment with reagents, 2 – Processing of samples obtained from pure cultures, 3 – Drying of the target plate, 4 – Placement into the MALDI-TOF device followed by microbial identification
The figures were created using BioRender (https://www.biorender.dev/).

Finally, the prepared target plate was inserted into the MALDI-TOF instrument, and microbial identification was performed (Figure 4).

Results

During the course of the study, a total of 13 bacterial isolates were obtained from soil samples collected from the rhizosphere of selected plants growing on the dried bottom of the Aral Sea (Figure 6).

The isolated colonies exhibited significant morphological diversity in terms of colony color, shape, size, texture, and growth characteristics under saline conditions. Such morphological variability among the isolates indicates a diverse microbial community adapted to the extreme environmental conditions of the dried Aral Sea region, particularly high salinity and low moisture content. The observed differences in salt tolerance among the isolates further suggest that these microorganisms possess different physiological adaptation mechanisms to saline environments.

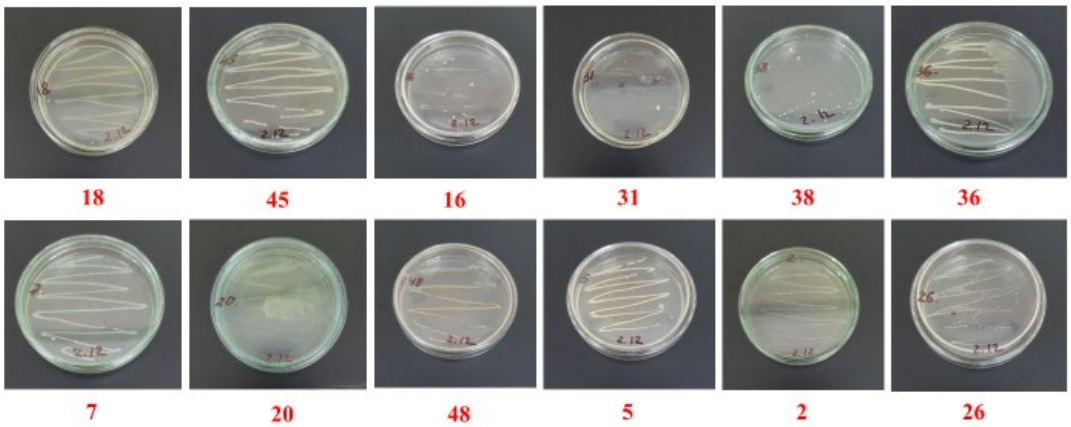


Figure 5. Isolates obtained from the roots of certain plants and the surrounding rhizosphere soil collected from the dried bottom of the Aral Sea

According to the Gram staining results, 6 (60.0%) of the isolated strains were identified as Gram-negative bacteria, while 7 (40.0%) were identified as Gram-positive bacteria. Microscopic examination revealed that the isolates were predominantly rod-shaped and partially coccoid in morphology (Table 1).

Table 1. Gram staining results of the isolates

Isolates obtained from the roots of selected plants and the surrounding rhizosphere soil from the dried bottom of the Aral Sea	2	Gram-negative
	5	Gram-positive
	7	Gram-negative
	26	Gram-negative
	45	Gram-positive
	7	Gram-negative
	16	Gram-positive
	18	Gram-negative
	20	Gram-positive
	31	Gram-positive
	36	Gram-positive
	38	Gram-positive
	48	Gram-negative

The identification of the bacterial isolates was performed using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS). This method allows rapid and reliable identification of microorganisms based on protein spectral profiles. According to the obtained mass spectra and database matching results, the isolated microorganisms were assigned to the genera *Bacillus*, *Providencia*, *Pseudomonas*, *Rhodococcus*, and *Enterobacter*.

Among the identified bacteria, the most frequently detected species were *Rhodococcus ruber* and *Enterobacter cancerogenus*, indicating that these species are widely distributed in the rhizosphere and root-associated soil of plants growing in the dried Aral Sea region. The presence of representatives of the genera *Bacillus* and *Pseudomonas* is particularly important, as these microorganisms are known for their plant growth-promoting properties, stress tolerance, and ability to survive under saline and arid environmental conditions.

The identification results suggest that the microbial community associated with the roots of desert plants consists of ecologically adapted and physiologically active bacteria, which may play an important role in plant adaptation to extreme environmental conditions such as high salinity, drought, and nutrient deficiency (Table 2).

Table 2. Identification of the isolates by MALDI-TOF MS

2	Rhizosphere soil of *Salsola richteri*	***Providencia rettgeri***	Bacteria	2.42
5	Shuvoq tuproq	***Rhodococcus ruber***	Actinomycetes	2.12
7	Root of *Salsola richteri*	***Enterobacter cloacae***	Bacteria	2.25
26	Root of *Salsola richteri*	***Enterobacter cancerogenus***	Bacteria	2.40
45	Rhizosphere soil of *Salsola richteri*	***Bacillus cereus***	Bacteria	2.34
7	Root of *Salsola richteri*	***Enterobacter cloacae***	Bacteria	2.25
16	Rhizosphere soil of *Aristida pennata*	***Bacillus infantis***	Bacteria	2.38
18	Stem of *Lugaion aphyllum*	***Pseudomonas azotoformans***	Bacteria	2.12
20	Stem of *Lugaion aphyllum*	***Bacillus subtilis***	Bacteria	2.25
31	Rhizosphere soil of *Aristida pennata*	***Bacillus simplex***	Bacteria	2.13
36	Rhizosphere soil of *Aristida pennata*	***Bacillus atrophaeus***	Bacteria	2.17
38	Rhizosphere soil of *Aristida pennata*	***Bacillus firmus***	Bacteria	2.06
48	Rhizosphere soil of *Haloxylon aphyllum*	***Pseudomonas koreensis***	Bacteria	2.16

The salt tolerance of the isolated microorganisms was evaluated by culturing the strains on nutrient media supplemented with different NaCl concentrations (7%, 10%, 12%, and 14%). The results showed that the salt tolerance of the isolates varied significantly depending on the genus and species of microorganisms.

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Most of the isolates demonstrated growth at 7% NaCl, indicating their ability to tolerate moderately saline conditions. Among the tested strains, *Rhodococcus ruber* showed the highest salt tolerance, as it was able to grow at all tested NaCl concentrations (7–14%), indicating its high adaptability to saline environments. Similarly, *Providencia rettgeri* and *Enterobacter cloacae* showed growth up to 12% NaCl, but no growth was observed at 14% NaCl, suggesting that these strains belong to the group of moderate halophilic or halotolerant microorganisms.

Species of the genus *Bacillus* showed different levels of salt tolerance. In particular, *Bacillus subtilis*, *Bacillus firmus*, and *Bacillus cereus* were able to grow at 7–10% NaCl, while growth inhibition was observed at higher salt concentrations (12–14% NaCl). *Bacillus infantis* demonstrated limited salt tolerance and grew mainly at 7% NaCl, with weak or no growth at higher salt concentrations.

In contrast, isolates belonging to the genus *Pseudomonas*, particularly *Pseudomonas azotoformans* and *Pseudomonas koreensis*, showed low salt tolerance and did not grow at high NaCl concentrations, indicating that these bacteria are likely non-halophilic or weakly halotolerant microorganisms.

Based on the obtained results and according to the Kushner classification, most of the isolated strains can be classified as moderate halophiles or halotolerant microorganisms, as they were able to grow at NaCl concentrations between 7% and 10%, and some strains up to 12–14% NaCl. These results indicate that microorganisms isolated from the rhizosphere of plants growing in the dried Aral Sea region possess significant adaptive potential to saline soil conditions and may be promising for use in agricultural biotechnology under saline environments (Table 3).

Table 3. Salt tolerance of the isolates at different NaCl concentrations

T/r	Microorganisms	7%	10%	12%	14%
2	***Providencia rettgeri***	+	+	+	-
5	***Rhodococcus ruber***	+	+	+	+
7	***Enterobacter cloacae***	+	+	+	-
16	***Bacillus infantis***	+	+	-	-
18	***Pseudomonas azotoformans***	-	-	-	-
20	***Bacillus subtilis***	-	-	-	-
26	***Bacillus infantis***	+	-	-	-
31	***Pseudomonas azotoformans***	+	-	-	-
36	***Bacillus subtilis***	+	+	+	-
38	***Bacillus firmus***	+	+	-	-
45	***Bacillus cereus***	+	-	-	-
48	***Pseudomonas koreensis***	-	-	-	-

Discussion

The dried bottom of the Aral Sea (Aralkum), characterized by hypersaline and anthropogenically disturbed soils, represents an extreme ecological filter for microbial communities. In our study, the predominance of isolates belonging to the genera *Bacillus*, *Enterobacter*, and *Rhodococcus*, obtained from the rhizosphere of *Salsola richteri*, is directly associated with the unique geochemical and mineralogical properties of this environment.

As reported by Jiang et al. (2021), the concentration of total soluble salts (TSS) in soils increases with distance from the Aral Sea shoreline, resulting in a significant reduction in microbial diversity. The occurrence of the bacterial isolates identified in our study in association with evaporite minerals such as gypsum and calcite indicates that these microorganisms are adapted not only to high salinity but also to the mineralogical composition of the soil. In particular, the presence of representatives of the genus *Bacillus* in all samples confirms their ability to survive under adverse environmental conditions due to their endospore-forming capability, which allows long-term persistence in extreme habitats.

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The isolated strains, particularly *Rhodococcus ruber* and *Enterobacter cloacae*, demonstrated the ability to grow under high NaCl concentrations (12–14%). As explained by Kumawat (2022), such bacteria employ a “compatible solute” strategy, synthesizing organic osmolytes such as betaine, ectoine, or trehalose within the cell. This mechanism helps balance the osmotic pressure between the intracellular environment and the external medium, thereby preventing cellular dehydration and maintaining metabolic activity under saline stress conditions.

Halophytic plants such as *Salsola richteri* form specialized microbiomes in the rhizosphere that enable them to survive in highly saline soils. The bacteria identified in our study are capable of producing the enzyme ACC deaminase, which reduces stress-induced ethylene levels in plants and promotes root system development under saline conditions. Furthermore, the ability of *Enterobacter* and *Bacillus* species to solubilize phosphate and produce siderophores provides a scientific basis for their application in phytomelioration programs in nutrient-poor environments such as the Aral Sea region.

Although MALDI-TOF MS used in this study enabled rapid identification of culturable microorganisms, multi-omics approaches such as metagenomics and transcriptomics are required to fully elucidate the ecological roles of unculturable microorganisms in the Aralkum ecosystem. The integration of these advanced molecular approaches will significantly enhance the potential for biotechnological utilization of biological resources from the dried Aral Sea region in the future.

Conclusions

This study was devoted to investigating the composition of microorganisms inhabiting the root and rhizosphere zones of *Salsola richteri*, a halophytic plant growing under the extremely saline and arid conditions of the dried bottom of the Aral Sea, and to their precise identification using MALDI-TOF mass spectrometry. During the study, a total of five pure bacterial isolates were obtained using classical microbiological methods, and their morphological characteristics, Gram staining properties, and modern mass spectrometric analyses were carried out.

The results obtained demonstrated that the rhizosphere and root zone of *Salsola richteri* harbor a diverse community of microorganisms, among which bacteria belonging to the genera *Bacillus*, *Enterobacter*, and *Providencia*, as well as actinomycetes belonging to the genus *Rhodococcus*, were predominant. In particular, the high occurrence frequency of *Rhodococcus ruber* and *Enterobacter cancerogenus* indicates that these microorganisms are well adapted to saline and arid environmental conditions.

The identified microorganisms may play an important ecological role in increasing plant tolerance to extreme environmental conditions, maintaining rhizosphere stability, and reducing soil degradation processes. Furthermore, these isolates can be considered as promising biological resources for future applications in phytomelioration, development of microbial biopreparations, restoration of saline soils, and other biotechnological applications.

The results of this study provide an important scientific basis for the investigation of microbial resources in the Aral Sea region, identification of microorganisms associated with the rhizosphere of halophytic plants, and the development of sustainable ecological technologies based on these microorganisms.

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Conflict of Interest

The authors declare no conflict of interest.

Information

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СКРИНИНГ И ОЦЕНКА УСТОЙЧИВОСТИ МИКРООРГАНИЗМОВ К РАЗЛИЧНЫМ КОНЦЕНТРАЦИЯМ ИОНОВ СВИНЦА (Pb^{2+})

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Аннотация: Изучена устойчивость изолированных штаммов из загрязненных тяжелыми металлами почв и коллекционных штаммов микроорганизмов к воздействию ионов Pb^{2+} в концентрациях 48,0; 95,9 и 287,7 мг/л. Проведён скрининг, оценена оптическая плотность культур при 600 нм и исследованы морфологические изменения клеток. Установлено, что *Rhodococcus ruber* 318, *Bacillus cereus* 138, *Bacillus paralicheniformis, Bacillus subtilis, Bacillus atrophaeus* сохраняли рост при высоких концентрациях Pb^{2+}. При 287,7 мг/л Pb^{2+} значения $ОП_{600}$ *B. cereus* 138 и *B. paralicheniformis* превышали контрольные показатели. Выявленные устойчивые штаммы перспективны для дальнейшего изучения механизмов устойчивости к свинцу и оценки их потенциала в биоремедиации загрязнённых сред.

Ключевые слова: тяжёлые металлы, свинец, Pb^{2+}, устойчивость микроорганизмов, *Bacillus*, *Rhodococcus*, биоремедиация.

Annotatsiya: Og‘ir metallar bilan ifloslangan tuproqlardan ajratib olingan shtammlar hamda mikroorganizmlarning kolleksiya shtammlarining 48,0; 95,9 va 287,7 mg/l konsentratsiyadagi Pb^{2+} ionlariga chidamliligi o‘rganildi. Skrining olib borildi, 600 nm to‘lqin uzunligida kulturaning optik zichligi baholandi va hujayralardagi morfologik o‘zgarishlar tekshirildi. Aniqlanishicha, *Rhodococcus ruber* 318, *Bacillus cereus* 138, *Bacillus paralicheniformis, Bacillus subtilis, Bacillus atrophaeus* shtammlari Pb^{2+} ning yuqori konsentratsiyalarida ham o‘sishni davom ettirgan. Pb^{2+} konsentratsiyasi 287,7 mg/l bo‘lgan sharoitda *B. cereus* 138 va *B. paralicheniformis* shtammlarining OD_{600} ko‘rsatkichlari nazorat darajasidan yuqori bo‘lgan. Aniqlangan chidamli shtammlar qo‘rg‘oshin ta’siriga chidamlilik mexanizmlarini chuqurroq o‘rganish hamda ifloslangan muhitni bioremediatsiya qilishdagi salohiyatini baholash uchun istiqbolli nomzodlar hisoblanadi.

Kalit so‘zlar: og‘ir metallar, qo‘rg‘oshin, Pb^{2+}, mikrobial chidamlilik, *Bacillus*, *Rhodococcus*, bioremediatsiya.

Abstract: The resistance of strains isolated from heavy-metal-contaminated soils and collection strains of microorganisms to Pb^{2+} ions at concentrations of 48.0, 95.9, and 287.7 mg/L was investigated. Screening was conducted, culture optical density at 600 nm was evaluated, and morphological changes in cells were examined. It was found that *Rhodococcus ruber* 318, *Bacillus cereus* 138, *Bacillus paralicheniformis, Bacillus subtilis, Bacillus atrophaeus* maintained growth at high Pb^{2+} concentrations. At a Pb^{2+} concentration of 287.7 mg/L, the OD_{600} values for *B. cereus* 138 and *B. paralicheniformis* exceeded control levels. The identified resistant strains are promising candidates for further study of lead resistance mechanisms and for the assessment of their potential in the bioremediation of contaminated environments.

Keywords: heavy metals, lead, Pb^{2+}, microbial resistance, *Bacillus*, *Rhodococcus*, bioremediation.

ДЛЯ ЦИТИРОВАНИЯ
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Введение

Загрязнение почв тяжёлыми металлами является одной из актуальных экологических проблем, поскольку такие элементы, как свинец (Pb), отличаются высокой токсичностью, устойчивостью и способностью длительно сохраняться в окружающей среде. В отличие от органических загрязнителей, тяжёлые металлы не подвергаются биологическому разложению, что способствует их накоплению в почве и поступлению в трофические цепи. Свинец оказывает неблагоприятное воздействие на живые организмы, поэтому поиск эффективных и экологически безопасных методов снижения его подвижности и биодоступности имеет важное значение [1,2].

Микроорганизмы, обитающие в загрязнённых почвах, способны адаптироваться к повышенным концентрациям тяжёлых металлов и формировать различные механизмы устойчивости к Pb^{2+}, включая биосорбцию, внеклеточную секвестрацию, связывание металла клеточными компонентами, активный вынос и биоминерализацию [3,4]. Выделение устойчивых местных микроорганизмов непосредственно из загрязнённых почв представляет особый интерес, поскольку такие штаммы уже адаптированы к условиям техногенной нагрузки и могут рассматриваться как перспективные объекты для биоремедиационных исследований. Показано, что устойчивые к свинцу бактерии способны участвовать в иммобилизации и удалении Pb^{2+} из загрязнённых сред, что определяет перспективность их дальнейшего практического применения [3,4].

Цель исследования – провести сравнительную оценку устойчивости штаммов микроорганизмов, изолированных из загрязненных тяжелыми металлами почв, и коллекционных штаммов микроорганизмов к различным концентрациям ионов Pb^{2+} с использованием чашечного метода и количественной оценки образования биомассы по показателям $ОП_{600}$.

Методы

В качестве объектов исследования использовали местные штаммы микроорганизмов, выделенные из почв, загрязнённых тяжёлыми металлами, Кашкадарьинской и Самаркандской областей: *Bacillus paralicheniformis, Bacillus subtilis, Bacillus atrophaeus*, *Enterobacter cloacae* и штаммы, которые хранятся в Коллекции промышленно важных культур Института микробиологии: *Pseudomonas putida 133, Bacillus cereus 138, Pseudomonas fluorescens 206* и *Rhodococcus ruber 318.*

Первичный скрининг устойчивости штаммов к ионам Pb^{2+} проводили чашечным методом на питательной среде с добавлением свинца в концентрациях 48,0; 95,9 и 287,7 мг/л. Устойчивость оценивали по способности микроорганизмов сохранять рост в присутствии исследуемых концентраций Pb^{2+}.

Для количественной оценки влияния свинца на рост микроорганизмов определяли образование биомассы по оптической плотности культуры при 600 нм ($ОП_{600}$). Значения $ОП_{600}$ исследуемых культур при различных концентрациях Pb^{2+} сравнивали с контролем без добавления свинца. По полученным значениям оценивали степень ингибирования роста и относительную устойчивость исследуемых штаммов к воздействию ионов свинца [5].

Результаты и обсуждение

Для оценки устойчивости исследуемых микроорганизмов к воздействию ионов тяжёлых металлов культуры выращивали в присутствии Pb^{2+} в концентрациях 48,0; 95,9 и 287,7 мг/л. Первичный скрининг проводили чашечным методом, после чего влияние Pb^{2+} на рост микроорганизмов оценивали по оптической плотности культуры при 600 нм ($ОП_{600}$). Согласно полученным результатам, среди исследованных коллекционных культур *Rhodococcus ruber* 318 и *Bacillus cereus* 138, а также среди изолированных резистентных культур *Bacillus paralicheniformis* и *Bacillus atrophaeus* сохраняли способность к росту при всех исследованных концентрациях Pb^{2+}, включая 287,7 мг/л, что позволяет рассматривать

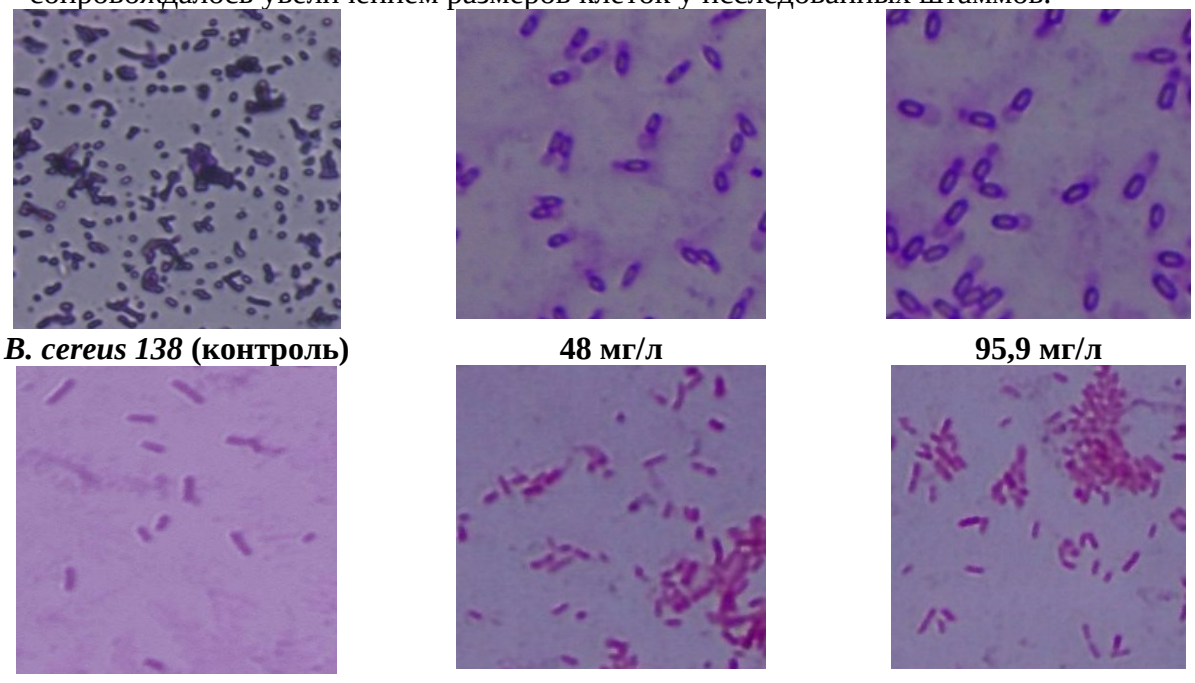
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данные штаммы как перспективные объекты для дальнейшего изучения механизмов устойчивости к свинцу (табл. 1).

Таблица 1. Титр клеток микроорганизмов при различных концентрациях ионов Pb^{2+}

№	Культуры	Контроль	Концентрации ионов Pb^{2+}, мг/л		
			48,0	95,9	287,7
1	*Rhodococcus ruber 318*	$4,9 \times 10^8$	$3,4 \times 10^7$	$2,1 \times 10^6$	$1,0 \times 10^5$
2	*Pseudomonas putida 133*	$5,4 \times 10^7$	$3,2 \times 10^6$	$1,3 \times 10^5$	0
3	*Pseudomonas fluorescens 206*	$2,2 \times 10^7$	$1,8 \times 10^6$	$3,1 \times 10^5$	0
4	*Bacillus cereus 138*	$4,7 \times 10^8$	$2,1 \times 10^7$	$1,6 \times 10^7$	$1,3 \times 10^6$
5	*Bacillus paralicheniformis*	$5,4 \times 10^8$	$6,5 \times 10^7$	$5,4 \times 10^7$	$4,3 \times 10^7$
6	*Bacillus subtilis*	$5,2 \times 10^8$	$4,1 \times 10^7$	$3,4 \times 10^7$	$2,8 \times 10^7$
7	*Bacillus atrophaeus*	$5,1 \times 10^8$	$4,6 \times 10^7$	$3,8 \times 10^7$	$2,4 \times 10^7$
8	*Enterobacter cloacae*	$4,6 \times 10^7$	$4,2 \times 10^6$	$2,1 \times 10^6$	$1,8 \times 10^6$

Микроскопическое исследование показало, что воздействие Pb^{2+} сопровождалось изменениями морфометрических характеристик отдельных штаммов. Известно, что содержание в среде ионов тяжелых металлов даже в низких концентрациях негативно влияет на жизнедеятельность организмов [6]. При концентрации Pb^{2+} 48,0 мг/л выраженных изменений морфологии клеток по сравнению с контролем не наблюдалось. При увеличении концентрации свинца до 95,9 мг/л у *Pseudomonas putida* 133 отмечалось изменение формы клеток, выражавшееся в их укорочении и увеличении ширины. Данные изменения могут отражать морфологическую адаптацию клеток к воздействию повышенной концентрации тяжёлого металла, однако для установления конкретного механизма необходимы дополнительные исследования. При высокой концентрации Pb^{2+} (287,7 мг/л) более выраженные морфометрические изменения наблюдались у *Rhodococcus ruber* 318 и *Bacillus paralicheniformis* (рис. 1). У *R. ruber* 318 отмечалось увеличение размеров клеток приблизительно в 1,5 раза по сравнению с контролем. Размеры клеток в контрольном варианте составляли около 1,5–2,0 мкм в длину и 0,6–0,9 мкм в ширину. Для *B. paralicheniformis* в контрольном варианте размеры клеток составляли 2,5–3,2 мкм в длину и 0,4–0,6 мкм в ширину, тогда как при концентрации Pb^{2+} 287,7 мг/л длина клеток увеличивалась до 3,8–4,5 мкм, а ширина – до 0,8–1,0 мкм (рис. 1). Таким образом, воздействие высокой концентрации Pb^{2+} сопровождалось увеличением размеров клеток у исследованных штаммов.



***B. cereus 138* (контроль)** **48 мг/л** **95,9 мг/л**

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***B. paralicheniformis* (контроль)**	**48 мг/л**	**95,9 мг/л**

Рисунок 1. Микрофотографии микроорганизмов в присутствии различных концентраций ионов Pb^{2+} (Увеличение:

Количественная оценка роста по показателю $ОП_{600}$ также продемонстрировала отсутствие выраженного подавления роста отдельных устойчивых штаммов при высокой концентрации свинца. На 7-е сутки культивирования $ОП_{600}$ *B. cereus* 138 в контрольном варианте составляла 0,724, тогда как в присутствии 287,7 мг/л Pb^{2+} достигала 0,896. Для *B. paralicheniformis* соответствующие значения составляли 0,886 и 1,174. Таким образом, при исследованной концентрации Pb^{2+} значения $ОП_{600}$ у обоих штаммов были выше, чем в контроле.

Заключение

Проведён скрининг устойчивости местных штаммов микроорганизмов, выделенных из почв, загрязнённых тяжёлыми металлами, и коллекционных штаммов микроорганизмов к воздействию ионов Pb^{2+} в концентрациях 48,0; 95,9 и 287,7 мг/л. Установлено, что исследуемые микроорганизмы характеризовались различной степенью устойчивости к свинцу. Коллекционные штаммы *Rhodococcus ruber* 318 и *Bacillus cereus* 138 сохраняли рост при всех исследованных концентрациях Pb^{2+}. У ряда штаммов воздействие высокой концентрации свинца сопровождалось изменением морфометрических характеристик клеток. Значения $ОП_{600}$ *B. cereus* 138 и *B. paralicheniformis* при концентрации Pb^{2+} 287,7 мг/л превышали контрольные показатели, что свидетельствует о сохранении способности данных культур к образованию биомассы в присутствии высокой концентрации свинца. Полученные штаммы представляют интерес для дальнейшего изучения механизмов устойчивости к тяжёлым металлам и оценки их потенциального применения в биоремедиационных технологиях.

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SPORA HOSIL QILUVCHI BAKTERIYALARNI ALYUMINIY OKSIDLI YANGI AVLOD SORBENTLARIGA IMMOBILLASH ORQALI ULARNING YASHOVCHANLIK KO‘RSATKICHLARINI BAHOLASH

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Annotatsiya: Ushbu tadqiqotda mikroyoyli oksidlanish (MYO) usuli bilan olingan, g‘ovakligi va kimyoviy tarkibi turlicha bo‘lgan alyuminiy oksidli yangi avlod sorbentlarining (AlMg6, D16 va ZnAl(O,Si)) mikroorganizmlarni biriktirish (immobillash) va ularning yashovchanligini saqlash samaradorligi o‘rganildi. Modelli mikroorganizm sifatida spora hosil qiluvchi *Bacillus subtilis* bakteriyalari tanlandi. Sorbsion sig‘im kontaktdan keyin erkin qolgan hujayralarni sanash, desorbsiyadan keyingi yashovchanlik esa go‘sht-peptonli agarda koloniya hosil qiluvchi birliklarni (KHB) aniqlash orqali baholandi. Natijalar alyuminiy oksidli sorbentlar yuqori sorbsion sig‘imga ega bo‘lishini (AlMg6 namunasida 75%) va desorbsiyadan so‘ng bakteriyalarning yashovchanligi 88–93% darajasida saqlanishini ko‘rsatdi; nazorat namunasida bu ko‘rsatkich 82% ni tashkil etdi.

Kalit so‘zlar: Bacillus subtilis, alyuminiy oksidi, mikroyoyli oksidlanish (MYO), sorbsiya, immobillash, desorbsiya, yashovchanlik.

Аннотация: В данном исследовании изучена эффективность сорбентов нового поколения на основе оксида алюминия (AlMg6, D16 и ZnAl(O,Si)) с различной пористостью и химическим составом, полученных методом микродугового оксидирования (МДО), в отношении связывания (иммобилизации) микроорганизмов и сохранения их жизнеспособности. В качестве модельного микроорганизма выбраны спорообразующие бактерии *Bacillus subtilis*. Сорбционную ёмкость оценивали по числу свободных клеток после контакта, жизнеспособность после десорбции — по числу колониеобразующих единиц (КОЕ) на мясо-пептонном агаре. Результаты показали, что сорбенты обладают высокой сорбционной ёмкостью (75% для AlMg6) и сохраняют жизнеспособность бактерий на уровне 88–93% после десорбции против 82% в контроле.

Ключевые слова: Bacillus subtilis, оксид алюминия, микродуговое оксидирование (МДО), сорбция, иммобилизация, десорбция, жизнеспособность.

Abstract: This study investigated the efficiency of new-generation aluminium oxide sorbents (AlMg6, D16 and ZnAl(O,Si)) of different porosity and chemical composition, obtained by micro-arc oxidation (MAO), in binding (immobilizing) microorganisms and maintaining their viability. Spore-forming *Bacillus subtilis* bacteria were selected as the model microorganism. Sorption capacity was assessed by counting the cells remaining free after contact, and post-desorption viability by colony-forming unit (CFU) counts on nutrient agar. The results showed that aluminium oxide sorbents have a high sorption capacity (75% for AlMg6) and retain bacterial viability at 88–93% after desorption, compared with 82% in the control.

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Turdibekova O.J., Axmedova Z.R., Abdullayeva Y.A. Spora hosil qiluvchi bakteriyalarni alyuminiy oksidli yangi avlod sorbentlariga immobillash orqali ularning yashovchanlik ko‘rsatkichlarini baholash // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 334–337.
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Keywords: Bacillus subtilis, aluminium oxide, micro-arc oxidation (MAO), sorption, immobilization, desorption, viability.

Kirish

Oqova suvlarni va atrof-muhitni sanoat chiqindilari, og‘ir metallar hamda patogen mikroorganizmlardan tozalash zamonaviy ekologik biotexnologiyaning eng dolzarb muammolaridan biridir. Suvlarni tezkor va samarali tozalashda turli fizik-kimyoviy usullar orasida sorbsiya usuli yuqori samaradorligi, arzonligi va ekologik xavfsizligi bilan ajralib turadi. So‘nggi yillarda nafaqat kimyoviy birikmalarni, balki tirik mikrob hujayralarini ham biriktira oladigan (immobillaydigan) universal sorbentlarni yaratishga bo‘lgan talab ortib bormoqda.

Mikroorganizmlarning mineral zarrachalar va sorbent yuzasiga birikishi (adgeziya) murakkab biofizik jarayon bo‘lib, u hujayra devori zaryadiga hamda sorbent yuzasining funksional guruhlariga bog‘liq [2, 3]. Gram-musbat bakteriyalar, xususan *Bacillus subtilis*, yuzasida manfiy zaryadga ega. Bu zaryad peptidoglikan (PG) makropolimeridagi karboksil guruhlari, teyxoy kislotalari (TK) va lipoteyxoy kislotalari (LTK) hamda anionli polimerlar mavjudligi bilan izohlanadi [4].

Kremniy va alyuminiy tutgan oksidli materiallar, xususan alyuminiy oksidi, g‘ovakli strukturasi va tarkibini sintez bosqichida boshqarish imkoniyati yuqori bo‘lgani uchun istiqbolli sorbentlar hisoblanadi [1, 5]. Belarus Milliy fanlar akademiyasining Birlashgan mashinasozlik institutida mikroyoyli oksidlanish (MYO) usuli bilan olingan alyuminiy qoplamalari qalinligi 300 mikrongacha va undan ortiq yuqori g‘ovakli struktura hosil qilish imkonini beradi [6, 7]. Shu bilan birga, qoplama yuzasining rel’efi va faza tarkibi bakteriyalar adgeziyasiga turlicha ta’sir ko‘rsatishi mumkinligi qayd etilgan [1, 5], shuning uchun har bir yangi qoplama turini mikroorganizmlar bilan o‘zaro ta’sirda alohida sinash talab etiladi.

Tadqiqotning maqsadi spora hosil qiluvchi *Bacillus subtilis* bakteriyalarini alyuminiy oksidli yangi avlod sorbentlariga immobillash, sorbsiya samaradorligini hamda desorbsiyadan so‘ng ularning yashovchanligini baholashdan iborat.

Materiallar va tadqiqot usullari

Tadqiqot obyekti sifatida O‘zR FA Mikrobiologiya instituti kolleksiyasidan olingan *Bacillus subtilis* shtammi hamda alyuminiy qotishmalari asosida MYO usuli bilan tayyorlangan kompozitsion keramik qoplama namunalari olindi.

Sorbent tashuvchilari. Tadqiqotda uch xil sorbent tashuvchisi (nositel) taqqoslandi:

1. AlMg6 — AlMg6 qotishmasi yuzasida shakllantirilgan keramik qoplama. Tarkibi α-Al_2O_3 va γ-Al_2O_3 fazalaridan (70:30 nisbatda) iborat. Qoplama qalinligi 60–70 mkm, sirt g‘ovakligi 40–50%, g‘ovaklar o‘lchami 0,5 dan 5 mkm gacha.

2. D16 — D16 qotishmasida shakllantirilgan qoplama. Asosan γ-Al_2O_3 modifikatsiyasidan tashkil topgan. G‘ovak o‘lchamlari 0,5–5 mkm (ba’zilari 20 mkm gacha), g‘ovaklik darajasi 40–50%.

3. ZnAl(O,Si) — ZnAl qotishmasida olingan kompozit qoplama. Tarkibi alyuminiy oksidi (α-Al_2O_3), rux alyuminati va mullit aralashmasidan iborat. Yirik g‘ovaklar o‘lchami 10–30 mkm, shuningdek, 1–3 mkm li lokal maydonlar mavjud.

Barcha namunalar tajribadan oldin avtoklavda 121 ^{0}C haroratda, 1 atm bosimda 20 daqiqa davomida sterilizatsiya qilindi va steril sharoitda sovitildi.

Bakterial suspenziyani tayyorlash. Bakteriyalar go‘sht-peptonli bulonda 37 ^{0}C haroratda, 160 ayl/daq tezlikda 24 soat davomida o‘stirildi. O‘stirishdan so‘ng bakterial suspenziya sentrifugalash yo‘li bilan ajratildi, hujayralar fiziologik eritma bilan oziqa muhiti qoldiqlari ketguncha yuvildi va fiziologik eritmada qayta suspenziyalandi. Ishchi suspenziyadagi hujayralar soni go‘sht-peptonli agarda ketma-ket o‘nlik suyultirish va KHB ni sanash usuli bilan aniqlandi.

Bakteriyalarning sorbent yuzasiga birikishini o‘rganish. Kompozitsion qoplama namunalari bakterial suspenziyaga joylashtirildi va 60 ayl/daq tezlikda 30 daqiqa chayqatildi.

Kontaktdan keyin namunalar yuzaga birikmagan yoki zaif birikkan hujayralarni ajratish maqsadida fiziologik eritma bilan bir necha marta yuvildi. Sorbsiyalangan hujayralar soni boshlang‘ich suspenziyadagi va kontaktdan keyin erkin qolgan hujayralar sonining ayirmasi bo‘yicha hisoblandi, sorbsiya samaradorligi esa boshlang‘ich hujayralar soniga nisbatan foizda ifodalandi. Namunalar yuzasida qolgan bakteriya hujayralari elektron mikroskopiya yordamida o‘rganildi.

Desorbsiya va yashovchanlikni aniqlash. Hujayralar sorbent yuzasidan desorbsiya qilindi. Desorbatdagi tirik hujayralar soni go‘sht-peptonli agarda KHB ni sanash orqali aniqlandi va sorbsiyalangan hujayralar soniga nisbatan foizda ifodalandi. Nazorat sifatida sorbentsiz, xuddi shu sharoitda va shu muddat davomida ushlab turilgan bakterial suspenziya ishlatildi.

Natijalar

Sorbsion sig‘im. Uchala qoplama ham *Bacillus subtilis* hujayralarini o‘z yuzasida ushlab qolish qobiliyatini namoyon qildi. AlMg6 namunasida boshlang‘ich 300 mln hujayradan 225 mln tasi sorbsiyalandi, bu 75% ni tashkil etadi. ZnAl(O,Si) sorbentida sorbsiyalangan hujayralarning umumiy soni 186,66 mln dan oshdi.

Yashovchanlik ko‘rsatkichlari. Sorbent yuzasidan desorbsiya qilingan *Bacillus subtilis* hujayralarining yashovchanligi ZnAl(O,Si) sorbentida 93% ni, AlMg6 da 90% ni, D16 da 88% ni tashkil etdi; nazorat namunasida bu ko‘rsatkich 82% ga teng bo‘ldi. Shunday qilib, uchala sorbent ham nazoratga nisbatan hujayralar yashovchanligini 6–11% ga yuqoriroq darajada saqladi.

Xulosa

1. Mikroyoyli oksidlanish usuli bilan olingan alyuminiy oksidli sorbentlar (AlMg6, D16, ZnAl(O,Si)) spora hosil qiluvchi *Bacillus subtilis* bakteriyalarini immobillash uchun mos g‘ovakli strukturaga ega; AlMg6 namunasida sorbsiya samaradorligi 75% ni tashkil etdi.

2. Sorbent yuzasidan desorbsiya qilingan hujayralarning yashovchanligi yuqori darajada saqlanadi: ZnAl(O,Si) sorbentida 93%, AlMg6 da 90%, D16 da 88%, nazoratda esa 82%.

3. Sorbsion sig‘im va yashovchanlik ko‘rsatkichlari qoplamaning g‘ovaklik strukturasi va faza tarkibiga bog‘liq holda o‘zgaradi: mayda g‘ovakli AlMg6 ko‘proq hujayra biriktirsa, yirik g‘ovakli ZnAl(O,Si) hujayralar yashovchanligini yaxshiroq saqlaydi.

4. Ushbu yangi avlod sorbentlari biotexnologik jarayonlarda hamda bakterial preparatlarni matritsalarda saqlashda qo‘llanilishi istiqbolli hisoblanadi; saqlash muddatining yashovchanlikka ta’siri keyingi tadqiqotlarda baholanishi lozim.

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SHO‘RLANGAN TUPROQLARDA SILIKAT BAKTERIYALARDAN FOYDALANISHNING ISTIQBOLLARI

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Annotatsiya: Sho‘rlanish qishloq xo‘jaligi ekinlarining o‘sishi, rivojlanishi va hosildorligini cheklovchi asosiy abiotik stress omillaridan biridir. Tuproqda eruvchan tuzlarning, ayniqsa Na^+ va Cl^- ionlarining ortiqcha to‘planishi o‘simliklarda osmotik stress, ionlar muvozanatining buzilishi, oksidlovchi stress va oziqa elementlarining o‘zlashtirilishining pasayishiga olib keladi. Bunday sharoitda biologik usullardan foydalanish, jumladan, o‘simliklarning rizosferasida faoliyat yurituvchi foydali mikroorganizmlardan foydalanish sho‘rlanish oqibatlarini kamaytirishning istiqbolli yo‘nalishlaridan hisoblanadi. Silikatlarni erituvchi bakteriyalar mineral silikatlarning biologik erishini tezlashtirib, tuproqda kremniyning o‘simliklar uchun mavjud shakllarini ko‘paytirishi mumkin. Ushbu mikroorganizmlar organik kislotalar, ligandlar, ekzopolisaxaridlar va boshqa metabolitlar ishlab chiqarish orqali silikat minerallarining parchalanishiga ta’sir ko‘rsatadi. Kremniyning o‘simliklarda ion muvozanatini saqlash, suv almashinuvini tartibga solish, antioksidant tizimni faollashtirish va tuz stressiga chidamlilikni oshirishdagi roli ko‘plab tadqiqotlarda ko‘rsatilgan.

Kalit so‘zlar: silikat bakteriyalar, sho‘rlangan tuproq, silikatlarni eritish, kremniy, NaCl, rizosfera, *Bacillus*, o‘simliklarning tuz stressiga chidamliligi, bioo‘g‘it.

Аннотация: Засоление почв является одним из основных абиотических стрессовых факторов, ограничивающих рост, развитие и продуктивность сельскохозяйственных культур. Избыточное накопление растворимых солей в почве, особенно ионов Na^+ и Cl^-, приводит к возникновению осмотического стресса у растений, нарушению ионного баланса, окислительному стрессу и снижению усвоения питательных элементов. В этих условиях применение биологических методов, в частности полезных микроорганизмов, обитающих в ризосфере растений, рассматривается как перспективное направление снижения негативных последствий засоления. Бактерии, растворяющие силикаты, могут ускорять биологическое выветривание силикатных минералов и повышать содержание доступных для растений форм кремния в почве. Данные микроорганизмы воздействуют на процессы разрушения силикатных минералов посредством продуцирования органических кислот, лигандов, экзополисахаридов и других метаболитов. Во многих исследованиях показана роль кремния в поддержании ионного баланса растений, регуляции водного обмена, активации антиоксидантной системы и повышении устойчивости к солевому стрессу.

Ключевые слова: силикатрастворяющие бактерии, засолённая почва, растворение силикатов, кремний, NaCl, ризосфера, *Bacillus*, устойчивость растений к солевому стрессу, биоудобрение.

Abstract: Soil salinity is one of the major abiotic stress factors limiting the growth, development, and productivity of agricultural crops. The excessive accumulation of soluble salts in

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soil, particularly Na^+ and Cl^- ions, induces osmotic stress, disrupts ionic homeostasis, causes oxidative stress, and reduces nutrient uptake in plants. Under these conditions, the application of biological approaches, particularly beneficial microorganisms inhabiting the plant rhizosphere, represents a promising strategy for mitigating the adverse effects of soil salinity. Silicate-solubilizing bacteria can accelerate the biological weathering of silicate minerals and potentially increase the availability of plant-accessible forms of silicon in soil. These microorganisms contribute to the dissolution of silicate minerals through the production of organic acids, ligands, exopolysaccharides, and other metabolites. Numerous studies have demonstrated the role of silicon in maintaining ionic homeostasis, regulating water relations, activating antioxidant defense systems, and enhancing plant tolerance to salt stress.

Keywords: silicate-solubilizing bacteria, saline soil, silicate dissolution, silicon, NaCl, rhizosphere, *Bacillus*, plant salt-stress tolerance, biofertilizer.

Bilamizki, tuproq sho‘rlanishi dunyo qishloq xo‘jaligida o‘simlik mahsuldorligini cheklovchi muhim ekologik muammolardan biridir. Sho‘rlanish natijasida tuproq eritmasining osmotik potensiali pasayadi, o‘simlik ildizlarining suvni o‘zlashtirishi qiyinlashadi va Na^+ hamda Cl^- kabi ionlarning o‘simlik to‘qimalarida ortiqcha to‘planishi yuzaga keladi [1,2]. Sho‘rlanishning o‘simlikka ta’siri odatda uchta asosiy mexanizm orqali namoyon bo‘ladi:

- Osmotik stress - suv o‘zlashtirilishining kamayishi;
- Ion stress - Na^+ va Cl^- toksikligi;
- Oksidlovchi stress - reaktiv kislorod shakllarining (ROS) ortiqcha hosil bo‘lishi. Kuchli sho‘rlanish sharoitida ushbu jarayonlar fotosintez, mineral oziqlanish, fermentativ faoliyat va hujayra metabolizmining buzilishiga olib kelishi mumkin [1,6]. Shu sababli sho‘rlangan tuproqlarda o‘simliklarning chidamliligini oshirish uchun mineral, kimyoviy va agrotexnik usullar bilan bir qatorda biologik va mikrobiologik yondashuvlar ham muhim ahamiyat kasb etmoqda [3]. Sho‘rlanishning o‘simliklar fiziologiyasiga ta’siri quyidagicha bo‘ladi: sho‘rlangan tuproqda NaCl konsentratsiyasining oshishi dastlab ildiz atrofidagi suv potensialining pasayishiga sabab bo‘ladi. Natijada o‘simlik ildizi tuproqdan suvni o‘zlashtirish uchun yuqori energiya sarflaydi. Uzoq davom etgan sho‘rlanish esa hujayralarda Na^+ va Cl^- ionlarining to‘planishiga olib kelib, metabolik jarayonlarni buzadi [1]. Na^+ ning ortiqcha to‘planishi K^+ bilan raqobatga kirishadi. Kaliy ko‘plab fermentlarning faolligi, stomalarning ishlashi va hujayra osmotik muvozanatini saqlash uchun zarur bo‘lganligi sababli Na^+/K^+ nisbatining buzilishi o‘simlikning normal fiziologik faoliyatiga salbiy ta’sir ko‘rsatadi [1,6]. Sho‘rlanish, shuningdek, ROS - superoksid anioni, vodorod peroksid va boshqa reaktiv kislorod shakllarining ko‘payishiga sabab bo‘lishi mumkin. Ular membrana lipidlari, oqsillar va nuklein kislotalarga zarar yetkazishi mumkin [6]. Shuning uchun sho‘rlangan tuproqlarda o‘simlikning:

- Na^+ ni cheklashi;
- K^+/Na^+ nisbatini saqlashi;
- suvni samarali o‘zlashtirishi;
- antioksidant himoyani kuchaytirishi;
- osmotik muvozanatni saqlashi tuz stressiga chidamlilikning muhim ko‘rsatkichlari hisoblanadi [1,6].

Kremniy (Si) ko‘plab o‘simliklarda klassik ma’noda majburiy oziqa elementi hisoblanmasada, stress sharoitlarida o‘simliklarning fiziologik holatini yaxshilovchi foydali element sifatida keng o‘rganilgan [6,7]. Kremniyning sho‘rlanishga chidamlilikdagi ta’siri bir nechta mexanizmlar bilan bog‘liq. Xususan, Si o‘simlikning Na^+ va Cl^- ionlarini ortiqcha o‘zlashtirishini cheklashi va K^+/Na^+ muvozanatini yaxshilashi mumkin [6]. Masalan, bodringda olib borilgan tajribada 75 mM NaCl stressi o‘simlik biomassasini sezilarli kamaytirgan, Si qo‘llanilishi esa ildiz va poya biomassasi, ildiz uzunligi, ildiz yuzasi va boshqa o‘sish ko‘rsatkichlarini yaxshilagan. Shu tadqiqotda Si qo‘llanilishi o‘simlik poyasidagi Cl^- miqdorining kamayishi bilan ham bog‘langan [8]. Bundan tashqari, sho‘rlanish vaqtida ROS hosil bo‘lishining kuchayishi oksidlovchi stressni yuzaga keltiradi. Si o‘simlikning antioksidant tizimini qo‘llab-quvvatlab, oksidlovchi zararni kamaytirishga yordam

berishi mumkin [6]. 2026-yilgi tadqiqotda *Bacillus* - Si kombinatsiyasi tuz-qurg‘oqchilik stressiga uchragan *Glycyrrhiza uralensis* o‘simliklarida antioksidant fermentlar va boshqa antioksidant metabolitlarning faoliyatini yaxshilagani ko‘rsatilgan [9,10]. Silikatlarni erituvchi bakteriyalar - qiyin eruvchan silikat minerallarining biologik erishini tezlashtirish qobiliyatiga ega mikroorganizmlar guruhidir. Ular orasida quyidagi bakterial guruhlar uchrashi mumkin: *Bacillus, Paenibacillus*, *Pseudomonas*, *Enterobacter*, *Aeromonas* va boshqa rizosfera bakteriyalari.

Ayrim izolyatlar silikatlarni eritishdan tashqari fosfataza va ACC-deaminaza kabi o‘simlik o‘sishini rag‘batlantiruvchi xususiyatlarga ham ega bo‘lgan [8]. Bu juda muhim jihat, chunki silikat bakteriyalar faqat Si mobilizatsiyasi bilan cheklanib qolmasdan, bir vaqtning o‘zida o‘simlik o‘sishini rag‘batlantiruvchi ko‘plab funksiyalarga ega bo‘lishi mumkin. Silikat bakteriyalarning asosiy biotexnologik xususiyati - qiyin eruvchan mineral shakllardagi Si va boshqa elementlarni harakatchan holatga o‘tkazishidir. Jarayonni quyidagicha ifodalash mumkin: silikat minerali - bakteriyaning mineral yuzasiga kolonizatsiyasi - organik kislotalar va boshqa metabolitlarning ajralishi - mineral kristall strukturasining yemirilishi - Si, K, Mg, Fe va boshqa elementlarning ajralishi – o‘simlik uchun mavjud elementlar - o‘simlikning oziqlanishi va stressga chidamliligining yaxshilanishi. Sho‘rlangan tuproqlarda silikat bakteriyalarning ahamiyatini ikki tomonlama ko‘rish mumkin:

Birinchi yo‘nalish - Si mobilizatsiyasi. Bakteriyalar qiyin eruvchan silikatlarni parchalab, kremniyning o‘simlik tomonidan o‘zlashtirilishi mumkin bo‘lgan shakllarini ko‘paytiradi [4,5].

Ikkinchi yo‘nalish - o‘simlikning tuz stressiga chidamliligini qo‘llab-quvvatlash. Bakterial Si mobilizatsiyasi natijasida o‘simlikning Si bilan ta’minlanishi yaxshilansa, Si o‘z navbatida ion muvozanati, antioksidant himoya va suv almashinuvini qo‘llab-quvvatlashi mumkin [6, 7]. Shu sababli: silikat bakteriya - Si mobilizatsiyasi - o‘simlikning Si bilan ta’minlanishi - Na^+/K^+ muvozanati - antioksidant himoya - sho‘rlanishga chidamlilik modelini taklif qilish mumkin. Mazkur yo‘nalish O‘zbekiston sharoitida alohida ilmiy-amaliy ahamiyatga ega. Qurg‘oqchil iqlim, sug‘oriladigan dehqonchilik va ayrim hududlarda tuproq sho‘rlanishi mikrobiologik biotexnologiyalarni qo‘llash uchun dolzarb sharoit yaratadi. O‘zbekiston va Markaziy Osiyo sharoitida sho‘r tuproqlardan ajratib olingan tuzga chidamli rizobakteriyalar o‘simliklarning sho‘rlanish sharoitidagi o‘sishini yaxshilashi mumkinligi bo‘yicha tadqiqotlar mavjud. Egamberdieva va hammualliflar sho‘r tuproqlardan ajratilgan tuzga chidamli PGPR bakteriyalarni sho‘rlangan agroekotizimlarni tiklashda qo‘llash istiqbollarini ko‘rsatgan [3].

Xulosa

Sho‘rlangan tuproqlarda silikat bakteriyalardan foydalanish tuproq mikrobiologiyasi, o‘simlik fiziologiyasi va biotexnologiyaning kesishgan istiqbolli yo‘nalishlaridan biridir. Silikat bakteriyalar qiyin eruvchan mineral shakllardan Si va boshqa elementlarning mobilizatsiyasini kuchaytirishi, o‘simliklarning mineral oziqlanishini yaxshilashi va Si orqali sho‘rlanish stressiga chidamlilikni bilvosita qo‘llab-quvvatlashi mumkin. Ayniqsa, *Bacillus* turkumiga mansub bakteriyalar noqulay sharoitlarda yashab qolish, rizosferani kolonizatsiya qilish va o‘simlik o‘sishini rag‘batlantirish xususiyatlari sababli amaliy jihatdan qiziq hisoblanadi. So‘nggi tadqiqotlar esa silikat erituvchi mikroorganizmlarni faqat Si mobilizatori sifatida emas, balki o‘simlik–mikrobiom–tuproq tizimining faol komponenti sifatida o‘rganish zarurligini ko‘rsatmoqda.

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SHARG‘UN KO‘MIR KONI CHIQINDISINI MAHALLIY *BACILLUS* SHTAMMLARI YORDAMIDA BIODEGRADATSIYA QILISH

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Annotatsiya: Ushbu maqolada Sharg‘un ko‘mir koni chiqindisidan ajratilgan *Bacillus cabrialesii SH16* va *Bacillus subtilis SH29* shtammlari ko‘mirning organik qismini qay darajada parchalay olishi gravimetrik, FTIR va UV–Vis usullari yordamida tekshirildi. Eng sezilarli natijaga *B. subtilis SH29* erishdi — sof massa yo‘qotishi 3,01% ni tashkil etdi, FTIR spektrida esa karbonil guruhlarining paydo bo‘lishi qayd etildi. Dala tajribasida konsorsium qo‘llanilgan tuproq namunasida ham o‘xshash spektral siljishlar kuzatildi. Bu ma’lumotlar mahalliy shtammlarning ko‘mir chiqindisini bioremediatsiya qilishda amaliy ahamiyatga ega bo‘lishini ko‘rsatadi.
Kalit so‘zlar: ko‘mir biodegradatsiyasi, *Bacillus cabrialesii*, *Bacillus subtilis*, FTIR spektroskopiyasi, UV–Vis, bioremediatsiya.

Аннотация: В настоящей работе изучена способность штаммов *Bacillus cabrialesii SH16* и *Bacillus subtilis SH29*, выделенных из отходов угольного разреза Шаргунь, разлагать органическую часть угля — с применением гравиметрического, ИК-Фурье (FTIR) и УФ-видимого (UV–Vis) анализа. Наиболее выраженный эффект показал штамм *B. subtilis SH29*: чистая потеря массы достигла 3,01%, а в его ИК-спектре появились полосы, характерные для карбонильных групп. Схожие спектральные изменения зафиксированы и в почве, обработанной консорциумом в полевых условиях. Полученные данные указывают на практическую пригодность местных штаммов для биоремедиации угольных отходов.
Ключевые слова: биодеградация угля, *Bacillus cabrialesii*, *Bacillus subtilis*, FTIR-спектроскопия, UV–Vis, биоремедиация.

Abstract: This paper examines the capacity of *Bacillus cabrialesii SH16* and *Bacillus subtilis SH29*, isolated from Shargun coal mine waste, to degrade the organic fraction of coal, assessed through gravimetric, FTIR, and UV–Vis analyses. The most pronounced effect was shown by *B. subtilis SH29*, with a net mass loss of 3.01%, while its FTIR spectrum revealed new bands attributable to carbonyl groups. Similar spectral shifts were detected in soil treated with the consortium under field conditions. These findings point to the practical relevance of local strains for coal-waste bioremediation.
Keywords: coal biodegradation, *Bacillus cabrialesii*, *Bacillus subtilis*, FTIR spectroscopy, UV–Vis, bioremediation.

Kirish

Ko‘mir koni chiqindilari hajmining yildan-yilga ortishi ularni arzon va ekologik xavfsiz yo‘l bilan qayta ishlash masalasini dolzarb qilmoqda. Chiqindining organik qismini mahalliy muhitdan ajratilgan shtammlar yordamida mikrobiologik parchalash istiqbolli yo‘nalishlardan biri hisoblanadi, zero *Bacillus* avlodiga mansub bakteriyalar ko‘mirdagi murakkab organik birikmalarni gumin kislotalariga qadar transformatsiya qilish xususiyatiga ega [1]. Shu bois ushbu ishning maqsadi — Sharg‘un koni chiqindisidan ajratilgan shtammlarni molekulyar aniqlash hamda

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ularning ko‘mirni parchalash faolligini gravimetrik, FTIR va UV–Vis usullari orqali baholashdan iborat.

Materiallar va metodlar

Ko‘mirli muhitda boshqalariga nisbatan faolroq o‘sgan ikkita izolyat — SH16 va SH29 — 16S rRNK genining ketma-ketligini aniqlash orqali identifikatsiya qilindi. So‘ngra har bir shtamm alohida, shuningdek ularning konsorsiumi steril mineral muhitda ko‘mir chiqindisi qatnashida inkubatsiya qilindi. Namunadagi massa o‘zgarishi gravimetrik yo‘l bilan o‘lchandi; qattiq fazadagi funksional guruhlar esa FTIR spektroskopiyasi orqali (400–4000 sm^{-1} oralig‘ida) baholandi, bunda mineral va organik komponentlarning polosalarini ajratishda ilgari qo‘llanilgan yondashuvlarga tayanildi [2]. Suyuq fazaga o‘tgan mahsulotlar UV–Vis spektrofotometriyasi yordamida, xususan E_4/E_6 nisbatini hisoblash orqali tahlil qilindi — bu ko‘rsatkich guminsimon moddalarning kondensatsiyalanganlik darajasini baholash uchun ancha avval taklif etilgan [3]. Bundan tashqari, SH16 va SH29 asosida tayyorlangan konsorsium Sharg‘un koni atrofidagi tuproqqa dala sharoitida qo‘llanildi va 3 oy o‘tgach olingan namunaning FTIR spektri dastlabki holat bilan solishtirildi.

Natijalar

Sekvenslash natijalari SH16 izolyatining *Bacillus cabrialesii, SH29* esa *Bacillus subtilis* turiga tegishli ekanini ko‘rsatdi (mos ravishda GenBank PZ299317.1 va PZ299319.1 raqamlari bilan ro‘yxatga olingan). Gravimetrik o‘lchovlarda eng yuqori ko‘rsatkich *B. subtilis* SH29 shtammida qayd etildi: abiotik nazoratga nisbatan sof massa kamayishi 3,01% ni tashkil qildi, SH16 da bu ko‘rsatkich 2,01%, konsorsiumda esa 1,34% bo‘ldi — ya’ni ikki shtammni birlashtirish kutilganidan farqli ravishda qo‘shimcha sinergik samara bermadi. FTIR spektrlarida e’tiborga molik jihat shundan iboratki, barcha uchta bakterial variantda 1700 sm^{-1} atrofida ilgari mavjud bo‘lmagan, karbonil guruhlarga xos yangi polosalar paydo bo‘ldi [4], bunda kvars va kaolinitga tegishli mineral polosalar deyarli o‘zgarmasdan qoldi [2]. Bu konsorsium namunasining spektri kimyoviy jihatdan, kutilganidan ko‘ra ko‘proq, SH29 namunasiga yaqin chiqqanini ham anglatadi. Kultura filtratlarining UV–Vis spektrlarida olingan E_4/E_6 qiymatlari guminsimon eruvchan birikmalarning hosil bo‘lganini tasdiqlaydi [3]. Shuni ham qayd etish kerakki, dala sharoitida konsorsium bilan ishlov berilgan tuproq namunasida, 3 oy o‘tgach, gidroksil va organik C–H guruhlariga tegishli sohalarda sezilarli spektral siljishlar kuzatildi — bu natija laboratoriya sharoitidagi kuzatuvlarni tasdiqlagandek ko‘rinadi.

Muhokama

Karbonil guruhlarining hosil bo‘lishi va kvars/kaolinit asosining barqarorligi ko‘mir yuzasida bakterial oksidlanish jarayonlari kechayotganini ko‘rsatuvchi belgilardan biri hisoblanadi, bu esa boshqa tadqiqotchilar tomonidan qayd etilgan natijalarga mos keladi [1, 4]. Shu bilan birga, SH16 va SH29 shtammlarini birga qo‘llash kutilgan sinergik samarani bermagani diqqatga sazovor — bunga o‘xshash holat, aslida, *Bacillus* avlodiga mansub turli shtammlarda organik substratlarni parchalashda hamkorlik emas, balki raqobat ustunlik qilishi mumkinligini ko‘rsatuvchi adabiyotlardagi ma’lumotlar bilan ham izohlanishi mumkin [5]. Konsorsiumning FTIR profili SH29 namunasiga yaqin chiqqani esa, ehtimol, aralashmada aynan shu shtamm faolroq bo‘lganidan dalolat beradi — bu masalani aniqlashtirish uchun shtammlar orasidagi o‘zaro ta’sir mexanizmini alohida o‘rganish talab etiladi. Dala tajribasidagi natijalar qiziqarli bo‘lsa-da, parallel ravishda ishlov berilmagan nazorat uchastkasi bo‘lmagani sababli ularni ehtiyot bilan, dastlabki kuzatuv sifatida qabul qilish ma’qul.

Xulosa

Olib borilgan tajribalar mahalliy *Bacillus* shtammlari — ayniqsa *B. subtilis* SH29 — Sharg‘un ko‘mir chiqindisining organik qismini ma’lum darajada biologik yo‘l bilan o‘zgartira olishini ko‘rsatdi. Bu natijalar yakuniy xulosa chiqarish uchun hali yetarli emas: takroriy o‘lchovlar, kattalashtirilgan namuna hajmi va dala sharoitida nazorat uchastkasining mavjudligi kelgusi

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tadqiqotlarda hisobga olinishi lozim bo‘lgan jihatlardir. Shunga qaramay, olingan dastlabki ma’lumotlar mahalliy shtammlarni ko‘mir chiqindilarini bioremediatsiya qilish yo‘nalishida yanada chuqur o‘rganishga arzigulik obyekt sifatida ko‘rsatadi.

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POLIETILEN PARCHALANISHINI TEZLASHTIRUVCHI BAKTERIAL SHTAMMLARNI *(PSEUDOMONAS SPP., BACILLUS SPP.)* MAHALLIY HUDUDLARDAN AJRATIB OLISH VA IDENTIFIKATSIYA QILISH

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Annotatsiya: Polietilen chiqindilarining atrof-muhitga salbiy ta’sirini kamaytirish maqsadida mahalliy chiqindi poligonlari tuproqlaridan polietilenni samarali parchalovchi *Pseudomonas spp.* va *Bacillus spp.* bakterial shtammlarini ajratib olish va identifikatsiya qilish masalalari o‘rganilgan. Seleksiya jarayonida uglerodning yagona manbasi sifatida polietilen plyonkalar qo‘llanilgan Mineral Salt Medium ozuqa muhitidan foydalanildi. 60 kunlik laboratoriya tajribalari davomida *Pseudomonas putida* va *Bacillus subtilis* shtammlari yuqori destruktiv faollik ko‘rsatib, polietilen plyonka o‘lchamini mos ravishda 16.4% va 14.8% ga kamaytirgani aniqlandi. FTIR-spektroskopiya va SEM (skanerlovchi elektron mikroskopiya) tahlillari orqali polimer sirtida oksidlanish va struktura yemirilishi sodir bo‘lgani ilmiy jihatdan tasdiqlandi.

Kalit so‘zlar: Polietilen, biodegradatsiya, *Pseudomonas*, *Bacillus*, Mineral Salt Medium, FTIR-spektroskopiya, SEM, bioremediatsiya.

Аннотация: Выделение и идентификация бактериальных штаммов *Pseudomonas spp*. и *Bacillus spp*., эффективно разлагающих полиэтилен, из почв местных полигонов отходов с целью снижения негативного воздействия пластиковых отходов на окружающую среду. В процессе селекции использовалась минеральная питательная среда (Mineral Salt Medium), где полиэтиленовые пленки служили единственным источником углерода. В ходе 60-дневных лабораторных экспериментов штаммы *Pseudomonas putida* и *Bacillus subtilis* показали высокую деструктивную активность, снизив массу полиэтиленовой пленки на 16.4% и 14.8% соответственно. Методы FTIR-спектроскопии и СЭМ (сканирующая электронная микроскопия) научно подтвердили процессы окисления и структурного разрушения на поверхности полимера.

Ключевые слова: Полиэтилен, биодеградация, *Pseudomonas*, *Bacillus*, минеральная среда, FTIR-спектроскопия, СЭМ, биоремедиация.

Abstract: The isolation and identification of *Pseudomonas spp*. and *Bacillus spp*. bacterial strains capable of efficiently degrading polyethylene from local waste landfill soils, aiming to mitigate the adverse environmental impact of plastic waste. Selection was carried out using a Mineral Salt Medium where polyethylene films served as the sole carbon source. During 60-day laboratory experiments, *Pseudomonas putida* and *Bacillus subtilis* strains demonstrated high destructive activity, reducing the weight of the polyethylene film by 16.4% and 14.8%, respectively. FTIR spectroscopy and SEM (Scanning Electron Microscopy) analyses scientifically confirmed oxidation and structural degradation processes on the polymer surface.

Keywords: Polyethylene, biodegradation, *Pseudomonas*, *Bacillus*, Mineral Salt Medium, FTIR spectroscopy, SEM, bioremediation.

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Kirish

Hozirgi vaqtda sintetik polimerlar, xususan, past va yuqori zichlikdagi polietilen mahsulotlarining haddan tashqari ko‘p ishlatilishi global ekologik inqiroz muammosini keltirib chiqarmoqda. Polietilenning kimyoviy jihatdan inertligi uning tabiatda yuzlab yillar davomida parchalanmasdan saqlanishiga olib keladi. An’anaviy utilizatsiya usullari (yoqish, ko‘mib tashlash) ikkilamchi ekologik xavflarni (toksik gazlar ajralishi) yuzaga keltiradi.[1] Shu sababli, tuproq va chiqindi poligonlaridan polietilenni samarali parchalovchi mikroorganizmlarni ajratib olish hamda ularning destruktiv holatini o‘rganish biotexnologiya va ekologiyaning eng ustuvor yo‘nalishlaridan biri hisoblanadi. Xususan, *Pseudomonas* va *Bacillus* turkumiga mansub bakteriyalar o‘zlarining yuqori fermentativ faolligi va ekologik moslashuvchanligi bilan ajralib turadi.

Materiallar va metodlar

Namuna olish va seleksiya**:** Tuproq namunalari Toshkent viloyati va boshqa hududlardagi maishiy chiqindi poligonlarining polietilen chiqindilari uzoq vaqt yig‘ilib qolgan qatlamlaridan olindi. Shtammlarni tanlab olish uchun uglerodning yagona manbai sifatida sterillangan polietilen plyonkalar kiritilgan *Mineral Salt Medium (MSM)* suyuq va qattiq ozuqa muhitidan foydalanildi. Destruksiya faoliyatini baholash: Polietilen plyonkalarning parchalanish jarayoni 30 va 60 kunlik inkubatsiya davrida vazn yo‘qotish foizi (**weight loss %**) orqali hisoblandi.[2] Spektroskopik va mikroskopik tahlil: Polietilen yuzasidagi strukturaviy o‘zgarishlar va funksional guruhlarning o‘zgarishi FTIR-spektroskopiyasi yordamida, sirt morfologiyasidagi yemirilishlar SEM qurilmasida tekshirildi. Molekulyar identifikatsiya**:** Bakterial DNK ajratib olinib, 16S rRNK geniga xos universal praymerlar yordamida PZR reaksiyasi bajarildi va sekvens qilindi.

Natijalar va muhokamalar

Seleksiya jarayonida polietilendan yagona uglerod manbai sifatida foydalana oladigan jami 18 ta faol bakterial izolyat olindi. Morfologik va biokimyoviy tahlillar ularning 10 tasi *Bacillus* turkumiga (*Bacillus subtilis*, *Bacillus cereus*, *Bacillus megaterium*) va 8 tasi *Pseudomonas* turkumiga (*Pseudomonas putida*, *Pseudomonas aeruginosa*) mansubligini ko‘rsatdi. Laboratoriya sharoitida o‘tkazilgan 60 kunlik tajribalarda *Pseudomonas putida* B-1 va *Bacillus subtilis* P-2 shtammlari yuqori destruktiv faollik ko‘rsatib, polietilen plyonka vaznini mos ravishda **16.4%** va **14.8%** ga kamaytirishga erishdi. Bu mikroorganizmlar ajratib chiqargan maxsus fermentlar (masalan, lakkaza, alkogoldegidrogenaza) ta’sirida polimer zanjirlarining oksidlanib parchalanganidan dalolat beradi. [3,4] SEM tahlillari bakteriyalar ta’sirida polietilen plyonka sirtida yoriqlar, g‘ovaklar va yemirilish hududlari hosil bo‘lganini aniq ko‘rsatdi.

Xulosa

Mahalliy hududlardan ajratib olingan *Pseudomonas putida* va *Bacillus subtilis* shtammlari polietilenni biologik parchalashda yuqori samaradorlikka ega ekanligi ilmiy jihatdan asoslandi. Mazkur shtammlar asosida polimer chiqindilarni utilizatsiya qiluvchi lokal biotexnologik qurilmalar va bioremediatsiya usullarini ishlab chiqish tavsiya etiladi.

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GALOFIT O‘SIMLIKLAR RIZOSFERASIDAN AJRATILGAN BAKTERIYA SHTAMMLARINING TURLI NaCl KONSENTRATSIYALARIDA O‘SISH FAOLLIGI

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Tuproqning sho‘rlanishi qishloq xo‘jaligi ishlab chiqarishi va ekologik xavfsizlikka tahdid soladigan keng tarqalgan to‘siqdir. Sho‘r tuproqlarda tuzning yuqori konsentratsiyasi asosan osmotik stress, ion toksikligi va oksidlovchi stress tufayli yuzaga keladi, bu esa o‘simliklarning o‘sishi va rivojlanishiga salbiy ta’sir ko‘rsatadi. Sho‘r tuproqda Na^+ va Cl^- ionlarining yuqori konsentratsiyasi o‘simliklarning suv va ozuqa moddalarini o‘zlashtirishiga to‘sqinlik qilishi mumkin. Yuqori tuz konsentratsiyasida (>200 mM NaCl) yashab qolish qobiliyatiga ega bo‘lgan, tuzga chidamli o‘simliklar galofitlar deb ataladi. Ushbu turlar o‘ziga xos tuzilmalarga, masalan, ortiqcha miqdordagi Na^+ ionlarini vakuolalarida to‘plovchi epidermal pufaksimon hujayralarga ega bo‘lib, bu ularga yuqori sho‘rlanish sharoitiga moslashish imkonini beradi.

Galotolerant bakteriyalar yuqori tuz konsentratsiyalariga ma’lum darajada bardosh bera olishi bilan ajralib turadi. Bunday mikroorganizmlarni aniqlash sho‘rlangan tuproqlarning mikrobiologik xususiyatlarini o‘rganish, biologik preparatlar yaratish va qishloq xo‘jaligida sho‘rlanish sharoitiga mos mikroorganizmlardan foydalanish uchun ilmiy ahamiyatga ega. Biroq bakteriyalarning tuzga chidamliligi tur va shtammga, o‘stirish muhitiga, inkubatsiya sharoitiga hamda tuz konsentratsiyasiga qarab farqlanadi.

Galofit o‘simliklar rizosferasidagi bakteriyalarni sho‘rlanishga chidamlilik xususiyatlari bo‘yicha o‘rganish ularning ekologik moslashganligini baholash imkonini beradi.

Tadqiqotning maqsadi galofit o‘simliklar rizosfera tuprog‘idan ajratilgan bakteriyalarning o‘sish faolligiga natriy xlorid tuzining turli xil konsentratsiyalarining ta‘sirini o‘rganishdan iborat.

Tadqiqot obyekti sifatida galofit o‘simliklar — *Atriplex undulata* (Moq.) D.Dietr., *Cynanchum acutum* L., *Tamarix* L. va *Capparis spinosa* L. rizosferasidan ajratilgan 10 ta bakteriya shtammi (*Bacillus simplex* AU1, *Bacillus licheniformis* AU2, AU4, CA1, *Bacillus firmus* AU3, *Bacillus* spp. CA4, T4, T5, CS1 va CS2) olindi. Bakteriya shtammlarining o‘sish faolligi NaCl tuzining 0, 5, 7, 10, 15, 20, 25 va 30% konsentratsiyalarini saqlovchi pepton-glyukozali suyuq ozuqa muhitida 1, 3 va 5 kun davomida o‘rganildi. Bakteriyalarning o‘sish faolligi spektrofotometr yordamida 600 nm to‘lqin uzunligida optik zichlik (OZ_{600}) ko‘rsatkichi bo‘yicha baholandi. Shu bilan birga, ozuqa muhitining kislotalilik-ishqoriylik holati pH-metr yordamida aniqlandi.

Galofit o‘simliklar rizosferasidan ajratilgan bakteriya shtammlarining NaCl tuzining turli konsentratsiyalariga chidamliligi 1, 3 va 5 kun davomida optik zichlik (OZ_{600}) ko‘rsatkichi asosida baholandi. Olingan natijalarda bakteriya shtammlarining o‘sish faolligida tuz konsentratsiyasiga va o‘stirish davomiyligiga qarab sezilarli farqlanish kuzatildi.

Tadqiqotning birinchi kunida nazorat variantida bakteriyalarning optik zichligi 0,024–0,300 oralig‘ida bo‘lib, eng yuqori ko‘rsatkich *Bacillus* sp. CS2 shtammida (0,300), *B. licheniformis* AU4 shtammida esa 0,274 ni tashkil etdi. NaCl konsentratsiyasining 5% gacha oshirilishi ko‘pchilik

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shtammlarning o‘sish faolligini keskin pasaytirdi. *B. simplex* AU1 shtammida OZ_{600} nazoratdagi 0,215 dan 0,020 gacha, *B. firmus* AU3 shtammida 0,245 dan 0,098 gacha pasaydi. NaCl konsentratsiyasining 10–30% gacha oshirilishi birinchi sutkada bakteriyalarning o‘sishini yanada chekladi. Biroq ayrim shtammlarda yuqori tuz konsentratsiyalarida ham optik zichlik qayd etildi. Xususan, *Bacillus* sp. CS2 shtammida 15, 20, 25 va 30% NaCl sharoitida OZ_{600} mos ravishda 0,031; 0,026; 0,022 va 0,012 ni tashkil etdi. Bu natijalar CS2 shtammining yuqori tuz konsentratsiyalarida ham o‘sish faolligini saqlab qolganini ko‘rsatdi.

Tadqiqotning uchinchi kunida nazorat variantlarida OZ_{600} ko‘rsatkichlari AU1, AU2, AU3 va AU4 shtammlarida mos ravishda 0,593; 0,424; 0,571 va 0,875 ni tashkil etdi. Bu ko‘rsatkichlar dastlabki sutkaga nisbatan o‘sish faolligining ortib borganligini ko‘rsatadi. 5% NaCl sharoitida AU1 va AU3 shtammlarining optik zichligi mos ravishda 0,646 va 0,586 ni tashkil etdi. AU1 shtammidagi ushbu ko‘rsatkich nazorat variantidan ham yuqori ekanligini ko‘rsatdi. 7% NaCl sharoitida AU3 shtammi 0,300, AU2 shtammi esa 0,159 optik zichlik ko‘rsatkichiga ega bo‘ldi. Biroq 10% va undan yuqori konsentratsiyalarda ko‘pchilik shtammlarda o‘sish faolligi keskin pasaydi. 15% NaCl da AU1 va AU3 shtammlarida OZ_{600} mos ravishda 0,026 va 0,019 bo‘lgan bo‘lsa, T4, CS1, CA4 va T5 shtammlarida esa 15–30% NaCl sharoitida juda past ko‘rsatkichlar yoki umuman o‘smaganligi qayd etildi. CS2 shtammi yuqori tuz konsentratsiyalarida ham boshqa shtammlarga nisbatan barqarorroq o‘sish faolligini ko‘rsatdi.

Tajribaning beshinchi kunida ayrim shtammlarning o‘sish faolligi sezilarli darajada oshganligi kuzatildi. AU3 shtammi 5 va 7% NaCl sharoitida mos ravishda 1,437 va 1,486 OZ_{600} ko‘rsatkichlariga erishdi. CA1 shtammida ham ushbu konsentratsiyalarda optik zichlik 1,120 va 1,240 ni tashkil etdi. AU2 shtammida 5% NaCl da 0,842, 7% NaCl da esa 0,685 ko‘rsatkich qayd etildi. AU3, CA1 va AU2 shtammlari past va o‘rtacha tuz konsentratsiyalarida o‘sish faolligini saqlash qobiliyatiga ega ekanligini ko‘rsatdi. AU4 shtammida 7% NaCl sharoitida OZ_{600} 1,005 gacha yetdi, 10% NaCl da esa 0,365 ni tashkil etdi. T4 va CS1 shtammlarida 10% NaCl da mos ravishda 0,551 va 0,594 ko‘rsatkichlar qayd etildi. Bu holat ayrim shtammlarda tuz ta’siriga javob sifatida o‘sish dinamikasi vaqt o‘tishi bilan o‘zgarishini ko‘rsatadi. Demak, tadqiqot natijalari rizobakteriya shtammlarining NaCl tuziga chidamliligi bir xil emasligini ko‘rsatdi va NaCl tuzining 5–7% konsentratsiyalarida AU3, AU2, AU4, CA1 shtammlari nisbatan yuqori faollikni namoyon etdi.

Bakteriya shtammlarining turli NaCl konsentratsiyalarida o‘sish faolligini baholash bilan bir qatorda, ozuqa muhitining pH ko‘rsatkichlari ham o‘rganildi. Tadqiqot davomida muhitning pH ko‘rsatkichlari asosan 3,2–5,9 oralig‘ida bo‘ldi.

Shunday qilib, tadqiqot natijalari galofit o‘simliklar rizosferasidan ajratilgan bakteriya shtammlarining NaCl ta’siriga chidamliligi shtammlarning o‘ziga xos xususiyatlari va o‘sish davomiyligiga bog‘liq ekanligini ko‘rsatdi. Ko‘pchilik shtammlarda NaCl konsentratsiyasining oshishi dastlabki o‘sish faolligining pasayishi bilan namoyon bo‘ldi. Biroq *Bacillus firmus* AU3, *Bacillus licheniformis* AU2 va AU4 hamda CA1 shtammlarida 5–7% NaCl sharoitida tadqiqotning beshinchi kuniga kelib nisbatan yuqori optik zichlik ko‘rsatkichlari qayd etildi. Bu natijalar mazkur shtammlarning past va o‘rtacha tuz konsentratsiyalarida o‘sish faolligini saqlash qobiliyatiga ega ekanligini ko‘rsatadi. *Bacillus* sp. CS2 shtammida esa 15–30% NaCl sharoitida ham nisbatan past bo‘lsa-da, o‘sish faolligini saqlab qolganligi kuzatildi. Ozuqa muhiti pH ko‘rsatkichlarining dinamikasi bakteriya shtammlari ta’sirida muhitning kislotalilik-ishqoriylik holati turlicha o‘zgarishini ko‘rsatdi. Ayrim variantlarda pH ko‘rsatkichlari nisbatan barqaror saqlangan bo‘lsa, boshqalarida sezilarli o‘zgarishlar kuzatildi. Bu holat bakteriya shtammlarining metabolik faolligi va ozuqa muhiti xususiyatlari o‘rtasidagi ehtimoliy bog‘liqlikni ko‘rsatadi.

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HYDROLYTIC ENZYME ACTIVITY AND SALT TOLERANCE OF *BACILLUS INAQUOSORUM* STRAIN J13 ISOLATED FROM OIL-CONTAMINATED SOIL

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Abstract: This study investigated the hydrolytic enzyme activity and salt tolerance of *Bacillus inaquosorum* strain J13 isolated from oil-contaminated soil in Surkhandarya Region, Uzbekistan. The taxonomic affiliation of the strain was assessed by BLAST comparison of its 16S rRNA gene sequence. Activities of protease (47 mm), lipase (42 mm), xylanase (37 mm), cellulase (34 mm), and amylase (30 mm) were detected, whereas pectinase activity was not observed. The strain was able to grow at NaCl and Na_2SO_4 concentrations of up to 2 M. These findings support further evaluation of strain J13 as a candidate for bioremediation research.

Keywords: Bacillus inaquosorum J13, oil-contaminated soil, bioremediation, hydrolytic enzymes, lipase, protease, salt tolerance, hydrocarbons.

Annotatsiya: Ushbu tadqiqotda Surxondaryo viloyatining neft bilan ifloslangan tuprog‘idan ajratilgan *Bacillus inaquosorum* J13 shtammining gidrolitik ferment faolligi va tuzga chidamliligi o‘rganildi. Shtammning taksonomik mansubligi 16S rRNK geni ketma-ketligini BLAST orqali taqqoslash asosida baholandi. Proteaza (47 mm), lipaza (42 mm), ksilanaza (37 mm), sellulaza (34 mm) va amilaza (30 mm) faolligi qayd etildi, pektinaza faolligi aniqlanmadi. Shtamm NaCl va Na_2SO_4 ning 2 M gacha konsentratsiyalarida o‘sish qobiliyatini saqladi. Natijalar J13 izolyatini bioremediatsiya uchun istiqbolli nomzod sifatida keyingi tadqiqotlarda baholash zarurligini ko‘rsatadi.

Kalit so‘zlar: Bacillus inaquosorum J13, neft bilan ifloslangan tuproq, bioremediatsiya, gidrolitik fermentlar, lipaza, proteaza, tuzga chidamlilik, uglevodorodlar.

Аннотация: В исследовании изучены гидролитическая ферментативная активность и устойчивость к солям штамма *Bacillus inaquosorum* J13, выделенного из загрязнённой нефтью почвы Сурхандарьинской области. Таксономическую принадлежность оценивали путём сравнения последовательности гена 16S рРНК с использованием BLAST. Обнаружена активность протеазы (47 мм), липазы (42 мм), ксиланазы (37 мм), целлюлазы (34 мм) и амилазы (30 мм); активность пектиназы не выявлена. Штамм сохранял способность к росту при концентрациях NaCl и Na_2SO_4 до 2 М. Полученные результаты позволяют рассматривать изолят J13 как перспективный объект для дальнейшего изучения его потенциала в биоремедиации.

Ключевые слова: Bacillus inaquosorum J13, загрязнённая нефтью почва, биоремедиация, гидролитические ферменты, липаза, протеаза, солеустойчивость, углеводороды.

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Introduction

Contamination of soil with petroleum hydrocarbons during oil extraction, transportation, and refining adversely affects its physicochemical properties, fertility, and microbiological balance. One of the most promising approaches to the remediation of contaminated soils is bioremediation, which relies on the biodegradation potential of microorganisms [1]. Bacteria of the genus *Bacillus* are distinguished by their ability to form spores, their tolerance to adverse conditions, and, in some strains, the ability to synthesize biosurfactants [2, 3].

Soil lipase activity is one of the indicators used to assess biological processes in oil-contaminated environments [4]; however, enzyme activity alone does not prove the direct degradation of petroleum hydrocarbons. *Bacillus inaquosorum* was originally described as a subspecies of *B. subtilis* and was later elevated to species rank [5, 6]. Surfactin and other lipopeptides have been identified in *B. inaquosorum* strain KR2-7 [7]. The aim of the present study was to evaluate the taxonomic affiliation, hydrolytic enzyme activity, and salt tolerance of isolate J13 obtained from oil-contaminated soil.

Materials and Methods

The object of the study was bacterial isolate J13, obtained from oil-contaminated soil in Surkhandarya Region. Colony morphology, cell shape, and Gram reaction were examined. Taxonomic affiliation was assessed by BLAST comparison of the 16S rRNA gene sequence (1,501 bp) with sequences in the NCBI database. Amylase, cellulase, xylanase, pectinase, protease, and lipase activities were tested by spot inoculation on solid media containing the corresponding substrates. The plates were incubated at 30 °C for 72 h. Amylase activity was detected with iodine solution, and cellulase, xylanase, and pectinase activities with 0.5% Congo red. Protease activity was assessed on skim milk medium, and lipase activity on medium containing Tween 80 or tributyrin. Activity was expressed as the diameter of the hydrolysis zone (mm); gelatinase activity was determined by liquefaction of gelatin medium. Salt tolerance was assessed by growth on nutrient media containing various concentrations of NaCl and Na_2SO_4. The highest concentration at which growth was observed was recorded as the salt tolerance of the strain under laboratory conditions.

Results and Discussion

On meat-peptone agar, isolate J13 exhibited colony characteristics typical of the genus *Bacillus*. The cells were rod-shaped, Gram-positive, and spore-forming. Based on BLAST comparison of the 16S rRNA gene sequence, the isolate was identified as *Bacillus inaquosorum* J13. Confirmation by additional phylogenetic analysis is advisable to reliably distinguish closely related species within the *B. subtilis* species complex.

In the enzymatic assays, the largest hydrolysis zones were recorded for protease (47 mm) and lipase (42 mm). Xylanase, cellulase, and amylase activities produced zones of 37, 34, and 30 mm, respectively. Gelatinase activity was positive, whereas pectinase activity was not detected. Protease and lipase activities indicate the potential of the strain to hydrolyze the corresponding organic substrates. Although lipase activity is a useful preliminary indicator in studies of oil-contaminated environments, the extent of oil degradation needs to be determined in a separate experiment [4].

The detection of biosurfactants in *B. inaquosorum* KR2-7 [7] provides a basis for testing whether isolate J13 also produces such compounds; however, this property was not directly measured in the present study. Isolate J13 retained the ability to grow at NaCl and Na_2SO_4 concentrations of up to 2 M. This result indicates potential tolerance to high salt concentrations, but bioremediation efficiency in naturally saline soils must be confirmed in separate trials.

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Conclusion

Isolate J13, obtained from oil-contaminated soil in Surkhandarya Region, was identified as *Bacillus inaquosorum*. The strain exhibited protease (47 mm), lipase (42 mm), xylanase (37 mm), cellulase (34 mm), and amylase (30 mm) activities, while pectinase activity was not detected. In addition, the isolate grew at NaCl and Na_2SO_4 concentrations of up to 2 M. These properties provide a basis for further evaluation of isolate J13 as a promising candidate for bioremediation. Future studies should directly determine the extent of petroleum hydrocarbon degradation, biosurfactant synthesis, and the stability of the strain under environmental conditions.

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TUPROQ BAKTERIYALARIDAN OLINGAN BIOFAOL METABOLITLARNING SITOTOKSIK XUSUSIYATLARI

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Annotatsiya: O‘zbekiston Respublikasi Qashqadaryo viloyati tuprog‘idan bakteriya izolyatlari ajratib olindi va 16S rRNK geni ketma-ketligi tahlili asosida identifikatsiya qilindi. Tadqiqotda 30 dan ortiq izolyat olindi; ulardan to‘rtta shtamm antimikroblik va yallig‘lanishga xos xususiyatlariga ko‘ra tanlab olindi va ular: *Bacillus atrophaeus* AD80, *Priestia endophytica* AD81, *Paenibacillus lautus* AD83 va *Peribacillus frigoritolerans* AD90 sifatida aniqlandi. Tanlangan shtammlarning xom ekstraktlari inson ko‘krak bezi adenokarsinomasi MCF-7 va bachadon bo‘yni saratoni HeLa hujayralariga nisbatan CCK-8 testi yordamida baholandi. *B. atrophaeus* AD80 ekstrakti eng yuqori sitotoksik faollikni ko‘rsatib, IC_{50} qiymatlari MCF-7 hujayralarida 174,4 µg/ml va HeLa hujayralarida 151,0 µg/ml ni tashkil etdi. P. endophytica AD81 ekstrakti MCF-7 hujayralariga nisbatan kuchsizroq faollik ko‘rsatdi (IC_{50} = 765,8 µg/ml). *P. lautus* AD83 va *P. frigoritolerans* AD90 ekstraktlari 1000 µg/ml gacha bo‘lgan konsentratsiyada hujayra hayotchanligini 50% ga kamaytirmadi. Natijalar *B. atrophaeus* AD80 shtammini keyingi tadqiqotlar uchun istiqbolli biofaol metabolitlar manbai sifatida ko‘rsatadi.

Kalit so‘zlar: tuproq bakteriyalari, ikkilamchi metabolitlar, sitotoksik faollik, IC_{50}, MCF-7, HeLa, 16S rRNK.

Аннотация: Из почвы Кашкадарьинской области Республики Узбекистан были выделены бактериальные изоляты и идентифицированы на основе анализа нуклеотидной последовательности гена 16S рРНК. В ходе исследования было получено более 30 изолятов. По результатам оценки антимикробных и противовоспалительных свойств были отобраны четыре штамма: *Bacillus atrophaeus* AD80, *Priestia endophytica* AD81, *Paenibacillus lautus* AD83 и *Peribacillus frigoritolerans* AD90. Цитотоксическую активность сырых экстрактов отобранных штаммов оценивали с помощью теста CCK-8 на клеточных линиях аденокарциномы молочной железы человека MCF-7 и рака шейки матки человека HeLa. Наибольшую цитотоксическую активность проявил экстракт *B. atrophaeus* AD80: значения IC_{50} составили 174,4 мкг/мл для клеток MCF-7 и 151,0 мкг/мл для клеток HeLa. Экстракт *P. endophytica* AD81 продемонстрировал более низкую активность в отношении клеток MCF-7 (IC_{50} = 765,8 мкг/мл). Экстракты *P. lautus* AD83 и *P. frigoritolerans* AD90 не снижали жизнеспособность клеток на 50% при концентрациях до 1000 мкг/мл. Полученные результаты указывают на перспективность штамма *B. atrophaeus* AD80 в качестве источника биоактивных вторичных метаболитов для дальнейших исследований.

Ключевые слова: почвенные бактерии, вторичные метаболиты, антимикробная активность, противовоспалительная активность, цитотоксическая активность, IC_{50}, MCF-7, HeLa, 16S рРНК.

Abstract: Bacterial isolates were obtained from soil in the Kashkadarya Region of the Republic of Uzbekistan and identified based on analysis of the 16S rRNA gene nucleotide sequences.

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Alimova D., Murodullayev D., Temirova M., Rayimberdiyeva S. va boshq. Tuproq bakteriyalaridan olingan biofaol metabolitlarning sitotoksik xususiyatlari // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 353–355.
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More than 30 isolates were recovered during the study. Four strains were selected based on their antimicrobial and anti-inflammatory properties: *Bacillus atrophaeus* AD80, *Priestia endophytica* AD81, *Paenibacillus lautus* AD83, and *Peribacillus frigoritolerans* AD90. The cytotoxic activity of crude extracts from the selected strains was evaluated against human breast adenocarcinoma MCF-7 cells and human cervical cancer HeLa cells using the CCK-8 assay. The *B. atrophaeus* AD80 extract exhibited the highest cytotoxic activity, with IC_{50} values of 174.4 µg/mL against MCF-7 cells and 151.0 µg/mL against HeLa cells. The *P. endophytica* AD81 extract showed weaker activity against MCF-7 cells, with an IC_{50} value of 765.8 µg/mL. The extracts of *P. lautus* AD83 and *P. frigoritolerans* AD90 did not reduce cell viability by 50% at concentrations of up to 1,000 µg/mL. These findings indicate that *B. atrophaeus* AD80 is a promising source of bioactive secondary metabolites for further investigation.

Keywords: soil bacteria, secondary metabolites, antimicrobial activity, anti-inflammatory activity, cytotoxic activity, IC_{50}, MCF-7, HeLa, 16S rRNA.

Materiallar va metodlar

Tadqiqot davomida O‘zbekistonning Qashqadaryo viloyati tuprog‘idan 30 dan ortiq bakterial izolyat ajratib olindi. 16S rRNK geni nukleotid ketma-ketligi tahlili asosida to‘rtta vakil shtamm antimikroblik va yallig‘lanishga xos xususiyatlariga ko‘ra tanlab olindi: *Bacillus atrophaeus* AD80, *Priestia endophytica* AD81, *Paenibacillus lautus* AD83 va *Peribacillus frigoritolerans* AD90 sifatida identifikatsiya qilindi. Tanlangan shtammlardan olingan xom ekstraktlarning sitotoksik faolligi inson ko‘krak bezi adenokarsinomasi MCF-7 va inson bachadon bo‘yni saratoni HeLa hujayralarida CCK-8 testi yordamida baholandi. Ekstraktlar 62,2-1000 µg/ml konsentratsiya oralig‘ida 24 soat davomida sinovdan o‘tkazildi.

Natija va muhokama

16S rRNK geni ketma-ketligi tahlili natijasida to‘rtta bakteriya shtammi identifikatsiya qilindi. Sitotoksiklik sinovida *B. atrophaeus* AD80 ekstrakti eng yuqori faollikni namoyon etdi: uning IC_{50} qiymati MCF-7 hujayralariga nisbatan 174,4 µg/ml, HeLa hujayralariga nisbatan 151,0 µg/ml bo‘ldi. *P. endophytica* AD81 ekstrakti MCF-7 hujayralariga nisbatan IC_{50} = 765,8 µg/ml qiymat bilan kuchsizroq ta’sir ko‘rsatdi. *P. lautus* AD83 va *P. frigoritolerans* AD90 ekstraktlari 1000 µg/ml gacha bo‘lgan konsentratsiyada hujayra hayotchanligini 50% ga kamaytirmadi. *P. endophytica* AD81 ekstraktining HeLa hujayralariga nisbatan IC_{50} qiymati ham tekshirilgan konsentratsiyalar oralig‘ida aniqlanmadi. Natijalar o‘rganilgan shtammlar xom ekstraktlarining sitotoksik faolligi bir xil emasligini ko‘rsatdi. *B. atrophaeus* AD80 ekstrakti ikkala hujayra liniyasida ham eng past IC_{50} qiymatlarini namoyon etgani sababli, ushbu shtamm keyingi izlanishlar uchun ustuvor nomzod sifatida qaralishi mumkin. Ammo bu natijalar ekstrakt tarkibidagi muayyan birikmaning saratonga qarshi ta’sirini yoki klinik samaradorlikni isbotlamaydi. Faollik xom ekstraktga tegishli bo‘lib, faol komponentlarni aniqlash uchun ularni ajratish, tozalash va kimyoviy tuzilishini o‘rganish zarur.

Xulosa

Qashqadaryo viloyati tuprog‘idan ajratilgan bakteriyalar orasidan to‘rtta shtamm 16S rRNK geni ketma-ketligi asosida identifikatsiya qilindi. Ularning xom ekstraktlari ichida *B. atrophaeus* AD80 MCF-7 va HeLa saraton hujayralariga nisbatan eng yuqori sitotoksik faollikni ko‘rsatdi. Ushbu shtamm biofaol ikkilamchi metabolitlarni keyingi bosqichda o‘rganish uchun istiqbolli manba hisoblanadi. Faol birikmalarni ajratish va tavsiflash hamda saraton bo‘lmagan hujayralardagi selektivligini tekshirish bo‘yicha qo‘shimcha tadqiqotlar talab etiladi.

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ALYUMINIY OKSIDLI KOMPOZIT KERAMIK QOPLAMALARNING MIKROORGANIZMLARNI IMMOBILIZATSIYALASH VA UZOQ MUDDATLI SAQLASHDAGI ISTIQBOLLARI

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Annotatsiya: Tezisda alyuminiy oksidli kompozit keramik qoplamalarning mikroorganizmlarni immobilizatsiyalash va kolleksion shtammlarni uzoq muddat saqlashdagi istiqbollari ilmiy adabiyotlar asosida tahlil qilindi. Mikroyoyli oksidlash usulida olingan qoplamalarning tuzilishi va adsorbsion xususiyatlariga oid ma’lumotlar umumlashtirildi. Ular istiqbolli tashuvchi material bo‘lsa-da, uzoq muddatli saqlashdagi samaradorligini aniqlash uchun maxsus tajribalar zarur.
Kalit so‘zlar: alyuminiy oksidi, kompozit keramik qoplama, mikroorganizmlar, kolleksion shtammlar, immobilizatsiya, adsorbsiya, yashovchanlik, uzoq muddatli saqlash.

Аннотация: В тезисе на основе научной литературы рассмотрены перспективы применения композиционных керамических покрытий на основе оксида алюминия для иммобилизации микроорганизмов и длительного хранения коллекционных штаммов. Обобщены данные о структуре покрытий и их сорбционных свойствах. Обоснована необходимость экспериментального изучения влияния условий хранения на жизнеспособность клеток.
Ключевые слова: оксид алюминия, композиционное керамическое покрытие, иммобилизация микроорганизмов, коллекционные штаммы, длительное хранение, жизнеспособность.

Abstract: Based on published literature, this thesis analyzes the prospects of aluminum oxide composite ceramic coatings for the immobilization of microorganisms and the long-term preservation of collection strains. Data on the structure and adsorption properties of micro-arc oxidation coatings are summarized. Their effectiveness for long-term preservation requires dedicated experimental studies.
Keywords: aluminum oxide, ceramic coating, microorganisms, collection strains, immobilization, adsorption, cell viability, long-term preservation.

Kirish

Mikroorganizmlarning kolleksion shtammlarini uzoq muddat saqlash mikrobiologiya va biotexnologiyaning muhim yo‘nalishlaridan biri bo‘lib, tadqiqotlarning takrorlanuvchanligi va biotexnologik jarayonlar barqarorligini ta’minlaydi [5]. Amaliyotda kriokonservatsiya (glitserin, dimetilsulfoksid kabi krioprotektorlar bilan) va quritish, jumladan, liofilizatsiya qo‘llanadi; ularning natijasi mikroorganizm turi, himoya moddalari va saqlash sharoitlariga bog‘liq bo‘lib, universal usul mavjud emas [3–5]. Shu sababli mikroorganizmlarni qattiq tashuvchilarga immobilizatsiyalash, xususan, alyuminiy qotishmalari yuzasida mikroyoyli oksidlash usulida

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olingan kompozit keramik qoplamalardan foydalanish dolzarb hisoblanadi [1, 2]. Biroq sirtga adsorbsiyalanish hujayralarning uzoq muddat yashovchanligini kafolatlamaydi [2, 4].

Tadqiqot usullari

Ilmiy adabiyotlarni tahlil qilish, taqqoslash va umumlashtirish usullari qo‘llanildi. Qoplamalarning tuzilishi va adsorbsion xususiyatlari monografiya va maqolalar [1, 2], an’anaviy saqlash usullari esa ilmiy sharhlar [3–5] asosida o‘rganildi. *Escherichia coli*, *Pseudomonas aeruginosa*, *Bacillus subtilis*, *Staphylococcus aureus*, *Candida albicans* va *Aspergillus niger* bo‘yicha e’lon qilingan natijalar ko‘rib chiqildi. Ish yangi laboratoriya tajribalariga emas, avval e’lon qilingan natijalar tahliliga asoslangan.

Natijalar va muhokama

Mikroyoyli oksidlash usulida hosil qilingan qoplamalarning sirt morfologiyasi va kimyoviy tarkibi ularning sorbsion xususiyatlarini belgilaydi [1, 2]. Akhmedova va boshq. (2026) ma’lumotiga ko‘ra, boshlang‘ich konsentratsiya 3×10^8 hujayra/ml bo‘lganda *E. coli* hujayralarining Zn–Al qoplamasiga adsorbsiyalanish zichligi $0{,}9 \times 10^6$ hujayra/mm² gacha yetgan va bu D16 qotishmasi asosidagi qoplamadan taxminan 30 % yuqori bo‘lgan [2]. *A. niger* sporalarining Al–Mg6 qoplamasiga adsorbsiyalanish darajasi 67,5 % ni tashkil etgan [1]. Biroq bu ko‘rsatkichlar saqlash davomida yashovchanlik va biologik xususiyatlar saqlanganini bevosita isbotlamaydi. Shu bois uzoq muddatli saqlash texnologiyasini ishlab chiqishda immobilizatsiyadan keyingi yashovchanlik, saqlash davomiyligi, harorat va namlik ham hisobga olinishi kerak [3–5]. Kelgusida immobilizatsiyalangan shtammlarning yashovchanligi va biologik xususiyatlarini belgilangan vaqt oralig‘ida an’anaviy usullar bilan taqqoslab baholash maqsadga muvofiq.

Xulosa

Mikroyoyli oksidlash usulida olingan alyuminiy oksidli kompozit keramik qoplamalar mikroorganizmlarni immobilizatsiyalash uchun istiqbolli tashuvchi hisoblanadi; ularning tarkibi va sirt morfologiyasi adsorbsiyaga ta’sir ko‘rsatadi [1, 2]. Ammo adsorbsiyalanish darajasini uzoq muddatli saqlash samaradorligi bilan tenglashtirib bo‘lmaydi: buni saqlash davomiyligi, harorat va namlikni hisobga olgan maxsus eksperimental tadqiqotlar orqali baholash zarur [3–5].

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SHO‘RLANGAN TUPROQDAN AJRATILGAN *BACILLUS* AVLODI VAKILLARINING NaCl STRESSIGA CHIDAMLILIGI

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Annotatsiya: Sho‘rlangan tuproqdan ajratilgan bakterial izolyatlarning taksonomik mansubligi, NaCl ga chidamliligi va fitogormonlar bilan bog‘liq funksional potensiali baholandi. MALDI-TOF MS tahlili izolyatlarning Bacillus halotolerans, B. rugosus, B. safensis va B. pumilus turlariga mansubligini ko‘rsatdi. NaCl konsentratsiyasi 5% dan 15% gacha oshirilganda o‘sishni saqlagan izolyatlar ulushi 84,6% dan 53,8% gacha kamaydi. Ayrim izolyatlar yuqori tuz stressi va fitogormonlar bilan bog‘liq kolorimetrik faollikni birgalikda namoyon etdi.

Kalit so‘zlar: sho‘rlangan tuproq, *Bacillus*, NaCl stressi, MALDI-TOF MS, IAA, gibberellin.

Аннотация: Проведена оценка таксономической принадлежности бактериальных изолятов, выделенных из засоленной почвы, их устойчивости к NaCl и функционального потенциала, связанного с фитогормонами. Анализ MALDI-TOF MS показал принадлежность изолятов к видам *Bacillus halotolerans, B. rugosus, B. safensis* и *B. pumilus*. При повышении концентрации NaCl с 5 до 15% доля изолятов, сохранивших способность к росту, снизилась с 84,6 до 53,8%. Некоторые изоляты одновременно проявляли устойчивость к высокому солевому стрессу и колориметрическую активность, связанную с фитогормонами.

Ключевые слова: засоленная почва, *Bacillus*, солевой стресс, NaCl, MALDI-TOF MS, ИУК, гиббереллин.

Abstract: The taxonomic affiliation, NaCl tolerance, and phytohormone-related functional potential of bacterial isolates recovered from saline soil were evaluated. MALDI-TOF MS analysis identified the isolates as *Bacillus halotolerans, B. rugosus, B. safensis,* and *B. pumilus*. As the NaCl concentration increased from 5% to 15%, the proportion of isolates retaining growth ability decreased from 84.6% to 53.8%. Some isolates simultaneously exhibited tolerance to high salt stress and phytohormone-related colorimetric activity.

Keywords: saline soil, *Bacillus*, NaCl stress, MALDI-TOF MS, IAA, gibberellin.

Kirish

Tuproq sho‘rlanishi o‘simliklarning o‘sishi, mineral oziqlanishi va hosildorligini cheklovchi muhim abiotik stress omillaridan biridir. Sho‘rlangan muhitda shakllangan galotolerant bakteriyalar yuqori osmotik bosim va ion konsentratsiyalariga moslashish qobiliyati bilan birga o‘simlik o‘sishini rag‘batlantiruvchi ayrim funksional xususiyatlarni ham namoyon qilishi mumkin. Shu sababli mahalliy sho‘rlangan tuproqlardan istiqbolli bakterial izolyatlarni ajratish va ularning tuzga chidamliligi hamda funksional potensialini baholash qishloq xo‘jaligi uchun biologik vositalar yaratishning muhim dastlabki bosqichidir [1, 2]. Tadqiqotning maqsadi Qashqadaryo viloyatining sho‘rlangan tuprog‘idan ajratilgan bakterial izolyatlarni identifikatsiya qilish, ularning NaCl ga chidamliligi va IAA hamda gibberellin bilan bog‘liq funksional potensialini qiyosiy baholashdan iborat.

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Materiallar va metodlar

Tuproq namunalari Qashqadaryo viloyati Qamashi tumanidagi sho‘rlangan hududdan (38.874484° N, 66.505119° E) 0–30 cm chuqurlikdan olindi. Kompozit namunaning pH qiymati 7,8, elektr o‘tkazuvchanligi esa 4–8 dS m^{-1} ni tashkil etdi. Bakteriyalar ketma-ket suyultirish usulida tuproqli agar va Nutrient Agar muhitlarida ajratildi. Izolyatlar morfo-kultural va mikroskopik belgilar bo‘yicha tavsiflandi hamda MALDI-TOF MS yordamida taksonomik identifikatsiya qilindi. Tuzga chidamlilik 5, 10 va 15% (w/v) NaCl saqlagan Nutrient Agar muhitida 30–32 °C da 48 soat davomida baholandi. O‘sish mavjudligi “+”, o‘sish kuzatilmasligi “–” sifatida qayd etildi. Tanlangan izolyatlarning IAA va gibberellinlar bilan bog‘liq funksional potensiali hujayrasiz kultura filtratlarida kolorimetrik usulda baholandi; absorbans mos ravishda 450 va 750 nm da o‘lchandi.

Natijalar va muhokama

MALDI-TOF MS tahliliga ko‘ra, tekshirilgan izolyatlar B. halotolerans, B. rugosus, B. safensis va B. pumilus turlariga mansub bo‘ldi. NaCl konsentratsiyasining oshishi bilan o‘sish qobiliyatini saqlagan izolyatlar ulushi izchil kamaydi: 5% NaCl da 13 izolyatdan 11 tasi (84,6%), 10% da 10 tasi (76,9%) va 15% da 7 tasi (53,8%) o‘sdi. Eng yuqori sinov konsentratsiyasida B. halotolerans 1, 4, 5, 7 va 12 hamda B. rugosus 6 va 9 izolyatlari o‘sish qobiliyatini saqladi. B. rugosus 2 va 3 izolyatlarida esa 5% NaCl sharoitida ham ko‘rinadigan o‘sish qayd etilmadi. Bu holat tuzga chidamlilik bir tur doirasida ham izolyat darajasida sezilarli farqlanishi mumkinligini ko‘rsatadi.

Fitogormonlar bilan bog‘liq kolorimetrik skriningda eng yuqori gibberellin bilan bog‘liq javob B. rugosus 13 izolyatida (OD_{750}=0,805), undan keyin B. halotolerans 7 (0,734) va B. safensis 8 (0,541) izolyatlarida qayd etildi. IAA bilan bog‘liq reaksiyada eng yuqori absorbans B. pumilus 10 (OD_{450}=0,776), B. safensis 8 (0,608) va B. rugosus 13 (0,525) izolyatlarida kuzatildi. Tuzga chidamlilik va funksional ko‘rsatkichlarni birgalikda baholashda B. halotolerans 7 alohida qiziqish uyg‘otdi: ushbu izolyat 15% NaCl da o‘sishni saqlashi bilan birga gibberellin bilan bog‘liq yuqori kolorimetrik javob namoyon etdi. Biroq kolorimetrik absorbans qiymatlari fitogormonlarning mutlaq konsentratsiyasini ifodalamaydi; shu sababli istiqbolli izolyatlarning PGP xususiyatlarini keyinchalik miqdoriy tahlillar va o‘simlik tajribalarida tasdiqlash zarur.

Xulosa

Sho‘rlangan tuproqdan ajratilgan Bacillus izolyatlari NaCl ga chidamlilik va fitogormonlar bilan bog‘liq kolorimetrik faollik bo‘yicha sezilarli farqlandi. Yetti izolyat 15% NaCl sharoitida o‘sishni saqladi. Ko‘p mezonli dastlabki saralash B. halotolerans 7 ni yuqori tuzga chidamlilik va gibberellin bilan bog‘liq funksional faollikni birlashtirgan istiqbolli izolyatlardan biri sifatida ko‘rsatdi. Olingan natijalar mahalliy Bacillus izolyatlarini sho‘rlangan agroekotizimlarda qo‘llash imkoniyatini keyingi vegetatsion va miqdoriy PGP tadqiqotlarida baholash uchun asos yaratadi.

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PHOSPHATE-SOLUBILIZING ACTIVITY OF BACTERIAL STRAINS IMMOBILIZED ON PHOSPHORITE FLOUR AFTER STORAGE

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Phosphate-solubilizing bacteria play an important role in transforming poorly soluble soil phosphorus compounds into forms available for plant uptake. The use of these microorganisms represents a promising approach to developing biological fertilizers that improve phosphorus nutrition in plants.

Immobilization of bacterial cells on mineral and organomineral carriers is a promising strategy for developing effective microbial preparations for agricultural applications. Suitable carriers provide a matrix for cell immobilization, may help maintain microbial viability and functional activity, and facilitate the production and application of biopreparations. Locally available mineral materials, particularly phosphorite flour, are of special interest because they can serve not only as carriers for bacterial cells but also as additional sources of phosphorus-containing compounds.

An important direction in improving microbial fertilizers is the development of dry formulations that are convenient to store, transport, and apply to soil. Immobilization on solid mineral carriers may contribute to maintaining microbial viability during storage and facilitate the release of bacterial cells after application to soil. However, the effectiveness of such preparations depends on the bacterial strain, carrier properties, formulation technology, and storage conditions. Therefore, investigating the phosphate-solubilizing activity of bacteria after storage is important for assessing the potential of phosphorite flour-based dry microbial preparations.

Accordingly, the aim of this study was to evaluate the phosphate-solubilizing activity of bacterial strains immobilized on phosphorite flour and ammonium sulfate-activated phosphorite flour after three months of storage, in order to assess their potential for developing dry microbial formulations.

The study investigated *Bacillus megaterium* strains 5F, 9T, and 22R, *Bacillus subtilis* strain 7R, and *Bacillus proteolyticus* strain 33S immobilized on phosphorite flour (FM) and activated phosphorite flour (FMA). The phosphate-solubilizing activity of *B. megaterium* strains 5F, 9T, and 22R and *B. subtilis* strain 7R was assessed in Pikovskaya medium, whereas that of *B. proteolyticus* strain 33S was evaluated in NBRIP medium. Tricalcium phosphate, $Ca_3(PO_4)_2$, was used as a poorly soluble mineral phosphorus source. Phosphorite flour (FM) and phosphorite flour pretreated with ammonium sulfate (FMA) were used as mineral carriers. The phosphate-solubilizing activity of the immobilized bacterial strains was evaluated by measuring the concentration of soluble phosphorus in the culture medium on days 3, 6, and 10 of cultivation following three months of storage. The results were expressed as mg P_2O_5 per 100 mL.

In Pikovskaya medium, the highest phosphate-solubilizing activity was observed for *B. subtilis* strain 7R immobilized on FM. The soluble phosphorus concentration increased from below

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the detection limit on day 3 to 2.65 mg P_2O_5/100 mL on day 6 and 40.85 mg P_2O_5/100 mL on day 10. When FMA was used as the carrier, the corresponding values were below the detection limit, 1.70, and 5.59 mg P_2O_5/100 mL. On day 10, the soluble phosphorus concentration in the FM treatment was approximately 7.3 times higher than that in the FMA treatment.

For *B. megaterium* strain 5F immobilized on FMA, the soluble phosphorus concentration was 1.06 mg P_2O_5/100 mL on day 3, increased to 1.24 mg P_2O_5/100 mL on day 6, and subsequently decreased to 0.86 mg P_2O_5/100 mL on day 10. In *B. megaterium* strain 9T, the concentration increased progressively from 0.72 to 0.78 and 1.28 mg P_2O_5/100 mL on days 3, 6, and 10, respectively. For *B. megaterium* strain 22R, the soluble phosphorus concentration was below the detection limit on day 3, reached 0.24 mg P_2O_5/100 mL on day 6, and increased to 0.61 mg P_2O_5/100 mL on day 10.

In NBRIP medium, *B. proteolyticus* strain 33S immobilized on FM showed soluble phosphorus concentrations below the detection limit on days 3 and 6, followed by an increase to 29.64 mg P_2O_5/100 mL on day 10. When FMA was used as the carrier, the concentrations were also below the detection limit on days 3 and 6, whereas the value on day 10 reached 1.86 mg P_2O_5/100 mL. Thus, the final soluble phosphorus concentration in the FM treatment was approximately 15.9 times higher than that in the FMA treatment.

Following three months of storage, the immobilized bacterial preparations retained the ability to promote the accumulation of soluble phosphorus during subsequent cultivation. The highest final values were recorded for *B. subtilis* strain 7R immobilized on phosphorite flour in Pikovskaya medium (40.85 mg P_2O_5/100 mL) and *B. proteolyticus* strain 33S immobilized on phosphorite flour in NBRIP medium (29.64 mg P_2O_5/100 mL). These findings indicate the potential of phosphorite flour as a mineral carrier for phosphate-solubilizing bacteria in the development of microbial fertilizers.

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GLIFOSAT GERBITSIDIGA CHIDAMLI *BACILLUS PUMILUS XGR7* SHTAMMINING AYRIM MORFOLOGIK, FIZIOLOGIK-BIOKIMYOVIY XUSUSIYATLARI

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Annotatsiya: Ushbu tezisda glifosat gerbitsidiga chidamli *Bacillus pumilus XGR7* shtammining ayrim morfologik va fiziologik-biokimyoviy xususiyatlari o‘rganilgan. Tadqiqot davomida bakteriya shtammining morfologik belgilari hamda amilaza, lipaza va sellulaza fermentlari faolligi baholangan. Olingan ma’lumotlar shtammning biologik xususiyatlarini tavsiflash va uning bioremediatsion imkoniyatlarini kelgusida o‘rganishda muhim ahamiyatga ega.
Kalit so‘zlar: *Bacillus pumilus*, glifosat, EPSPS, morfologik xususiyatlar.

Аннотация: В данном тезисе изучены некоторые морфологические и физиолого-биохимические свойства штамма *Bacillus pumilus XGR7*, устойчивого к гербициду глифосату. В ходе исследования оценены морфологические признаки бактериального штамма, а также активность ферментов амилазы, липазы и целлюлазы. Полученные данные имеют важное значение для характеристики биологических свойств штамма и дальнейшего изучения его биоремедиационного потенциала.
Ключевые слова: *Bacillus pumilus*, глифосат, EPSPS, морфологические свойства.

Abstract: This thesis examines certain morphological, physiological, and biochemical characteristics of a glyphosate-resistant *Bacillus pumilus XGR7* strain. The study evaluates the morphological features of the bacterial strain and the activities of amylase, lipase, and cellulase enzymes. The findings are important for characterizing the biological properties of the strain and provide a basis for further investigation of its bioremediation potential.
Keywords: *Bacillus pumilus*, glyphosate, EPSPS, morphological characteristics.

Kirish

Glifosat gerbitsidi — N-(fosfonometil)glitsin keng ta’sir doirasiga ega bo‘lgan biotsid bo‘lib, 1974-yilda qishloq xo‘jaligi ekin maydonlarida begona o‘tlarga qarshi kurashish maqsadida qo‘llanila boshlangan. Glifosat o‘simliklarning barglari orqali o‘zlashtiriladi va o‘simlikning barcha qismlariga tarqaladi, natijada bir necha kundan so‘ng o‘simlik nobud bo‘ladi.[1] 1974-yilda qo‘llanila boshlanganidan buyon glifosat pestitsidlar bozorida yetakchi o‘rinni egalladi. Glifosatning ta’sir mexanizmi, o‘simlik to‘qimalari bo‘ylab tez harakatlanishi (translokatsiyasi) hamda o‘simliklarning ushbu gerbitsidni detoksifikatsiya qilish qobiliyatining cheklanganligi uning yuqori samaradorligini ta’minladi va ko‘plab qishloq xo‘jaligi ishlab chiqaruvchilari uchun birinchi tanlovga aylanishiga sabab bo‘ldi. Glifosatning o‘simliklarga ta’sir qilish mexanizmi 5-enolpiruvilshikimat-3-fosfat sintaza (EPSPS) fermentini ingibitsiya qilish orqali shikimat metabolik yo‘lining buzilishiga asoslanadi. Bu jarayon hayotiy muhim aromatik aminokislotalar — fenilalanin, tirozin va triptofanning biosinteziga salbiy ta’sir ko‘rsatadi. Natijada oqsil sintezi va o‘simlikning o‘sish jarayonlari susayadi, bu esa oxir-oqibat hujayra faoliyatining izdan chiqishiga va hujayraning nobud bo‘lishiga olib keladi.[2] Glifosatdan intensiv foydalanish atrof-muhit va o‘simliklarda uning qoldiq

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miqdorining ortishiga olib kelgan. Glifosat molekulasi tarkibidagi barqaror uglerod–fosfor (C–P) bog‘i tufayli uning parchalanishi nisbatan qiyin kechadi. Shunga qaramay, glifosat nobud bo‘lgan o‘simlik qoldiqlari va tuproqda turli mikroorganizmlar tomonidan parchalanadi.[1] Glifosat tuproqda asosan zamburug‘lar va bakteriyalar tomonidan parchalanadi. Ushbu mikroorganizmlar glifosatdan fosfor manbai sifatida foydalanib glitsin yoki uglerod manbai sifatida foydalanib aminometilfosfon kislota (AMPA) hosil qiladi. Glifosat gerbitsidi bilan ifloslangan tuproqlarni bakteriyalar yordamida tozalash iqtisodiy jihatdan samarali va ekologik xavfsiz bioremediatsiya usuli hisoblanadi.[3] Bacillus avlodi bakteriyalari endospora hosil qilishi, turli ekologik sharoitlarda saqlanishi va ekstrasellyulyar fermentlar ishlab chiqarishi bilan ajralib turadi. Glifosatga chidamli shtammning morfologik va fermentativ faolligini o‘rganish keyingi bioremediatsion baholash uchun dastlabki bosqichdir.

Material va metodlar

Tadqiqot obyekti sifatida avvalgi tajribalarda glifosat mavjud muhitda o‘sish qobiliyatiga ko‘ra saralab olingan *Bacillus pumilus XGR7* bakterial shtammidan foydalaniladi. Bakterial shtammning ayrim morfologik, fiziologik-biokimyoviy xususiyatlarini o‘rganish uchun Egorov A.E. va Netrusov A.I. ning qo‘llanmalarida keltirib o‘tilgan ozuqa muhitlaridan foydalanildi.[4] Vegetativ hujayra Gram usulida bo‘yaldi va yorug‘lik mikroskopida kuzatildi. Ayrim gidrolitik fermentlar faolligini aniqlashda, amilaza faolligini aniqlash uchun kraxmaldan, lipaza faolligini aniqlash uchun zaytun yog‘idan va selluloza faolligini aniqlash uchun karboksimetilsellulozadan foydalanildi.

Tajriba

Ajratib olingan *Bacillus pumilus XGR7* shtammning ayrim morfologik xususiyatlarini o‘rganish uchun tayyor ozuqa muhiti **MPA** (Go‘sht pepton agar)da 30℃ 24-48 soat davomida o‘stirildi. Qattiq ozuqa muhitida koloniyaning rangi, shakli, cheti, yuzasi kuzatildi. Gram bo‘yash orqali hujayraning bo‘yalishi, shakli, gram-musbat yoki gram-manfiy ekanligi ko‘rildi. Fiziologik-biokimyoviy tekshiruvlar uchun ayrim gidrolitik fermentlar faolligi (selluloza, lipaza, amilaza) o‘rganildi. Bunda MSM muhitiga 1% tegishli tijorat substratlari va 2% agar qo‘shildi. Tayyorlangan muhit steril Petri kosachalariga quyildi va qotgandan so‘ng bakterial izolyatlar standart mikrobiologik usulda (nuqtaviy inokulyatsiya orqali) ekildi. Inokulyatsiya qilingan Petri kosachalari 30°C haroratda 24-120 soat davomida inkubatsiya qilindi va har 24 soatda o‘sish va zona hosil qilishi kuzatildi. Inkubatsiya yakunida fermentativ faollik substratlarning gidrolizi natijasida hosil bo‘lgan zonalar orqali aniqlashtirildi. Amilaza va lipaza faolligini aniqlash uchun Petri kosachalari Lugol eritmasi (yod eritmasi) bilan ishlov berildi. Agar kraxmal va zaytun yog‘i parchalansa shtamm atrofida rangsiz zonalar hosil bo‘ladi. Sellulyaza faolligini aniqlash uchun Petri kosachalari 0,5% kongo qizili eritmasi bilan bo‘yaldi. Kongo qizili sellyuloza bilan bog‘lanadi, ammo fermentativ parchalanish sodir bo‘lgan hududlarda ya’ni karboksimetilsellulyaza gidrolizlangan qismida rangsiz (shaffof) zonalar hosil bo‘ladi.

Natijalar va muhokama

MPA muhitida o‘stirilgan *Bacillus pumilus XGR7* shtammi oqish-kulrang yoki kremrang, asosan yumaloq koloniyalar hosil qildi. Koloniya chetlari tekis, ayrim hollarda to‘lqinsimon, yuzasi esa silliq yoki biroz notekis ko‘rinishda bo‘ldi. Kuchli pigmentatsiya kuzatilmadi. Gram usulida bo‘yalgan preparatlarda Gram-musbat, tayoqchasimon vegetativ hujayralar aniqlandi. Fermentativ faollikni aniqlash uchun o‘tkazilgan tajribada uchala substratli muhitda gidroliz zonalari qayd etildi. Amilolitik faollik uchun zona diametri 38 mm, lipolitik faollik uchun 42 mm, sellulolitik faollik uchun 25 mm bo‘ldi. Kuzatilgan zonalar shtammda tegishli substratlarni gidrolizlash bilan bog‘liq fermentativ faollik mavjudligini ko‘rsatdi. Adabiyotlarda shtammning o‘sishi uchun optimal harorat 30-37℃, ba’zi mezofil shtammlari 25-45℃, pH-6-9 neytral va biroz ishqoriy muhit, kislorodga talabi bo‘yicha aerob, o‘sish tezligi 24-48 soat ekanligini aniqladik.

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Xulosa

Tadqiqotda glifosat mavjud muhitda o‘sish qobiliyatiga ko‘ra ilgari saralangan *Bacillus pumilus XGR7* shtammining ayrim morfologik va fiziologik-biokimyoviy belgilari tavsiflandi. Shtammning oqish-kulrang yoki kremrang koloniyalar hosil qilishi, Gram-musbat tayoqchasimon hujayralarga ega ekanligi hamda kraxmal, zaytun yog‘i va KMS saqlovchi muhitlarda gidroliz zonalarini hosil qilishi aniqlandi. Amilaza, lipaza va sellulaza sinovlarida qayd etilgan zonalar mos ravishda 38, 42 va 25 mm bo‘ldi. Ushbu natijalar shtammning gidrolitik faolligini ko‘rsatadi va uning biologik xususiyatlarini chuqurroq tadqiq qilish uchun asos yaratadi.

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TIBBIYOT BUYUMLARI ISHLAB CHIQARUVCHI KORXONALARDA MIKROBIOLOGIK MONITORING TIZIMINI TAKOMILLASHTIRISH VA UNING SAMARADORLIGINI BAHOLASH

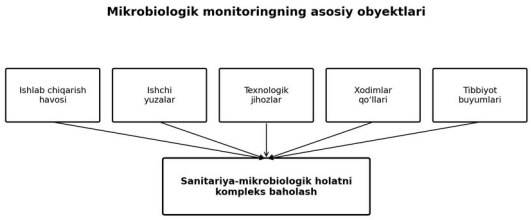
Nukus Med Tex korxonasi mikrobiologi
Jabborova Sabohat Jalil qizi

Annotatsiya: Tezisda tibbiyot buyumlari ishlab chiqaruvchi korxonalarda mikrobiologik monitoring tizimini tashkil etish, takomillashtirish va samaradorligini baholash masalalari yoritilgan. Ishlab chiqarish muhiti mikrobiologik holatini muntazam nazorat qilish mahsulot xavfsizligini ta’minlash va biologik xavflarning oldini olishga xizmat qiladi. Monitoringda ishlab chiqarish havosi, ishchi yuzalar, texnologik jihozlar, xodimlar qo‘llari va ishlab chiqarilayotgan buyumlar nazorat qilinadi. Natijalarni tizimli qayd etish va dinamik tahlil qilish profilaktik hamda tuzatuvchi choralarni o‘z vaqtida belgilash imkonini beradi.

Kalit so‘zlar: tibbiyot buyumlari, mikrobiologik monitoring, mikrobiologik nazorat, ishlab chiqarish muhiti, havo mikroflorasi, ishchi yuzalar, sanitariya-gigiyena, dezinfeksiya, mikrobiologik xavfsizlik.

Kirish

Ishlab chiqarish muhitidagi mikroorganizmlar mahsulotning mikrobiologik holatiga ta’sir ko‘rsatishi mumkin. Shu sababli ishlab chiqarish xonalari va texnologik jarayonlarning sanitariya-mikrobiologik holatini muntazam nazorat qilish zarur. Monitoring kontaminatsiya darajasini aniqlash, uning dinamikasini kuzatish va potensial xavf manbalarini o‘z vaqtida aniqlash imkonini beradi. Bunda mikroorganizmlar havodan, xodimlar faoliyatidan hamda ishchi yuzalar va jihozlardan mahsulotga o‘tishi mumkin. Shu sababli nazorat faqat tayyor buyumlar bilan cheklanmay, ishlab chiqarish muhitining mikrobiologik holatini ham qamrab olishi lozim. Nazorat natijalarini belgilangan mezonlar asosida baholash va muntazam qayd etish biokontaminatsiya manbalarini aniqlashga yordam beradi [2, 3].



1-rasm. Mikrobiologik monitoringning asosiy obyektlari

Tadqiqotning maqsadi

Mikrobiologik monitoring tizimini takomillashtirish, ishlab chiqarish muhitining mikrobiologik holatini kompleks baholash va mikrobiologik nazorat samaradorligini oshirishga qaratilgan amaliy yondashuvlarni ishlab chiqish.

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Materiallar va usullar

Ishlab chiqarish havosi, ishchi yuzalar, texnologik jihozlar va xodimlar qo‘llaridan namunalar olinadi. Havo holatini baholashda sedimentatsion usuldan foydalanish mumkin: oziqlantiruvchi muhitli Petri kosachalari belgilangan vaqt ochiq qoldirilib, inkubatsiyadan so‘ng koloniyalar hisoblanadi. Ishchi yuzalar va qo‘llardan steril tampon yordamida namuna olinib, oziqlantiruvchi muhitlarga ekiladi va inkubatsiyadan keyin o‘sish baholanadi.



2-rasm. Mikrobiologik monitoring jarayonining umumiy ketma-ketligi

Natijalar va muhokama

Kompleks monitoring ishlab chiqarish muhitidagi potensial mikrobiologik xavf manbalarini aniqlash imkonini beradi. Havo, ishchi yuzalar, xodimlar qo‘llari va buyumlarni birgalikda nazorat qilish sanitariya-mikrobiologik holat haqida tizimli ma’lumot beradi. Ko‘rsatkichlar oshganda tozalash va dezinfeksiya sifati, xodimlar gigiyenasi, texnologik jarayonlarga amal qilinishi va boshqa kontaminatsiya manbalari qayta baholanadi. Natijalarni jurnal yoki elektron bazada qayd etish va davriy tahlil qilish profilaktik hamda tuzatuvchi choralarni o‘z vaqtida ishlab chiqishga yordam beradi.

Xulosa

Mikrobiologik monitoringni tizimli va kompleks tashkil etish ishlab chiqarish muhitining sanitariya-mikrobiologik holatini nazorat qilishda muhim. Havo, ishchi yuzalar, jihozlar, xodimlar qo‘llari va ishlab chiqarilayotgan buyumlarni muntazam nazorat qilish potensial kontaminatsiya manbalarini aniqlash va oldini olish imkoniyatini oshiradi. Natijalarni tizimli qayd etish, dinamik tahlil qilish hamda profilaktik va tuzatuvchi choralarni o‘z vaqtida amalga oshirish mikrobiologik nazorat samaradorligi va mahsulot xavfsizligini oshiradi.

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JIZZAX VILOYATI QURG‘OQCHIL MAYDON TUPROQLARINING AYRIM FIZIK-KIMYOVIY XUSUSIYATLARI HAMDA MIKROBIOLOGIK HOLATINING QIYOSIY TAHLILI

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Annotatsiya: Mazkur tezisda Jizzax viloyatining qurg‘oqchil hududlarida tarqalgan tuproqlarning fizik-kimyoviy ko‘rsatkichlari va mikrobiologik holatini o‘zaro bog‘liqlikda o‘rganishning ilmiy-amaliy ahamiyati tahlil qilinadi. Tuproq namligi, mexanik tarkibi, gumus miqdori, pH va sho‘rlanish darajasi mikroorganizmlar soni hamda ekologik faoliyatiga ta’sir etuvchi muhim omillar sifatida ko‘rib chiqiladi. Ish adabiyotlar tahliliga asoslangan bo‘lib, aniq laboratoriya natijalari sifatida talqin qilinmasligi lozim.
Kalit so‘zlar: Jizzax viloyati, qurg‘oqchil tuproq, gumus, pH, sho‘rlanish, bakteriyalar, aktinomitsetlar, mikroskopik zamburug‘lar.

Аннотация: В тезисе рассматривается научно-практическое значение комплексного изучения физико-химических показателей и микробиологического состояния почв засушливых территорий Джизакской области. Влажность, механический состав, содержание гумуса, pH и засоление рассматриваются как факторы, влияющие на численность и активность почвенных микроорганизмов. Работа основана на анализе научной литературы и не представляет собственные лабораторные результаты.
Ключевые слова: Джизакская область, засушливые почвы, гумус, pH, засоление, бактерии, актиномицеты, микроскопические грибы.

Abstract: This thesis discusses the scientific and practical importance of studying the physicochemical properties and microbiological status of soils in arid areas of the Jizzakh region. Soil moisture, texture, humus content, pH and salinity are considered important factors affecting the abundance and activity of soil microorganisms. The work is based on a review of published literature and does not present original laboratory results.
Keywords: Jizzakh region, arid soil, humus, pH, salinity, bacteria, actinomycetes, microscopic fungi.

Kirish

Qurg‘oqchil hududlarda yog‘in miqdorining kamligi, bug‘lanishning yuqoriligi va sug‘orish suvidan foydalanish xususiyatlari tuproqning suv-tuz rejimiga sezilarli ta’sir ko‘rsatadi. Jizzax viloyati sug‘oriladigan yerlarida arid iqlim va sho‘rlanish xavfi tuproq unumdorligi hamda biologik jarayonlarni birgalikda baholashni talab etadi [1]. Tuproq mikroorganizmlari organik qoldiqlarning parchalanishi, uglerod va azot aylanishi, oziqa elementlarining o‘simliklar uchun o‘zlashtiriladigan shakllarga o‘tishida muhim rol o‘ynaydi. Sho‘rlanish esa osmotik bosim va ionlar ta’siri orqali mikrob jamoalarining tarkibi va funksional faolligini o‘zgartirishi mumkin [2, 3]. Shu sababli tuproqning fizik-kimyoviy xususiyatlarini mikrobiologik ko‘rsatkichlar bilan qiyosiy tahlil qilish dolzarbdir.

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Tadqiqotning maqsadi

Jizzax viloyatining qurg‘oqchil maydon tuproqlarida ayrim fizik-kimyoviy ko‘rsatkichlar va mikrobiologik holat o‘rtasidagi ehtimoliy bog‘liqliklarni ilmiy adabiyotlar asosida tahlil qilish hamda kelgusidagi dala-laboratoriya tadqiqotlari uchun taqqoslash mezonlarini belgilash.

Tadqiqot materiallari va usullari

Tezisni tayyorlashda ilmiy maqolalarni tahlil qilish, taqqoslash va umumlashtirish usullaridan foydalanildi. Kelgusidagi amaliy tadqiqotda Sharof Rashidov, Zafarobod va Arnasoy tumanlarining qurg‘oqchil maydonlaridan bir xil chuqurlikda tuproq namunalari olinib, mavsum va namuna olish sharoitlari qayd etilishi mumkin. Fizik-kimyoviy ko‘rsatkichlardan tuproq namligi, mexanik tarkib, pH, elektr o‘tkazuvchanlik yoki sho‘rlanish darajasi va gumus miqdorini aniqlash; mikrobiologik ko‘rsatkichlardan esa umumiy kultivatsiyalanadigan bakteriyalar, aktinomitsetlar va mikroskopik zamburug‘lar sonini standart ekish usullari bilan baholash taklif etiladi. Natijalarni hududlar va sho‘rlanish darajalari bo‘yicha solishtirish, o‘lchovlar takroriyligini ta’minlash zarur. Ushbu tezisda bunday laboratoriya o‘lchovlari bajarilgani yoki raqamli natijalar olingani da’vo qilinmaydi.

Natijalar va muhokama

Adabiyotlarda qurg‘oqchil va sho‘rlangan tuproqlarda mikroorganizmlarning tarqalishi tuproqning namligi, organik modda miqdori, tuzlar tarkibi va mavsumiy sharoitlarga bog‘liqligi qayd etiladi. Jizzax dashtining sug‘oriladigan sho‘rlangan tuproqlarini o‘rgangan Murodova va hammualliflar mikroorganizmlar rivojlanishi sho‘rlanish darajasi va mavsumga qarab farqlanishini, o‘rta va kuchli sho‘rlangan tuproqlarda nitrifikatsiyalovchi mikroorganizmlar miqdori past bo‘lishi mumkinligini ko‘rsatgan [2]. Bu ma’lumotlar viloyat tuproqlarini o‘rganishda faqat mikroorganizmlarning umumiy sonini emas, balki funksional guruhlar va mavsumiy o‘zgarishlarni ham hisobga olish zarurligini ko‘rsatadi.

Zamonaviy sharhlarda sho‘rlanish mikrob jamoalarining xilma-xilligi, fermentativ faolligi va uglerod-azot aylanishi bilan bog‘liq jarayonlarga ta’sir etishi ta’kidlangan [3, 4]. Biroq javob barcha tuproqlarda bir xil bo‘lmaydi: ayrim tuzga chidamli mikroorganizmlar saqlanib qolishi yoki muayyan sharoitlarda faollashishi mumkin. Gumus miqdori organik substrat zaxirasini tavsiflaydi, pH esa ko‘plab mikrob guruhlari uchun muhim ekologik omildir. Namlikning yetishmasligi mikroblarning metabolik faolligini cheklashi mumkin, lekin bu ta’sir tuproqning mexanik tarkibi va tuz miqdori bilan birgalikda namoyon bo‘ladi.

Shu nuqtayi nazardan, Sharof Rashidov, Zafarobod va Arnasoy tumanlaridan olingan namunalarni bir xil metodika asosida tekshirish hududlararo farqlarni aniqlashga yordam beradi. Fizik-kimyoviy ko‘rsatkichlar va mikrob guruhlari o‘rtasidagi korrelatsiyalar hisoblanishi mumkin, ammo korrelatsiya o‘z-o‘zidan sabab-oqibat munosabatini isbotlamaydi. Ishonchli xulosa chiqarish uchun yetarli namuna soni, takroriy tahlillar va mavsumiy monitoring talab etiladi.

Xulosa

Jizzax viloyatining qurg‘oqchil maydon tuproqlarini baholashda fizik-kimyoviy va mikrobiologik ko‘rsatkichlarni birgalikda o‘rganish muhimdir. Ilmiy adabiyotlar sho‘rlanish, namlik, pH va organik modda zaxirasi tuproq mikroorganizmlarining tarkibi hamda faoliyatiga ta’sir ko‘rsatishini tasdiqlaydi. Kelgusida Sharof Rashidov, Zafarobod va Arnasoy tumanlari tuproqlarida gumus, pH, sho‘rlanish, namlik hamda bakteriyalar, aktinomitsetlar va mikroskopik zamburug‘lar miqdorini yagona metodika bilan aniqlash, hududlar va mavsumlar kesimida taqqoslash tavsiya etiladi. Ushbu ish adabiyotlar tahlili bo‘lib, o‘z laboratoriya natijalari bilan to‘ldirilishi kerak.

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ПОЛУЧЕНИЕ И ИССЛЕДОВАНИЕ ВЫСОКОЭФФЕКТИВНЫХ ХИМИЧЕСКИ МОДИФИЦИРОВАННЫХ СОРБЕНТОВ

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Аннотация: Установлено, что химическая модификация базальтов является эффективным способом улучшения их сорбционных свойств и повышения адсорбционной способности по отношению к различным ионным формам загрязняющих веществ, включая ионы меди и фосфат-ионы. Показано, что изменение химического состава и структуры базальта посредством введения модифицирующих компонентов позволяет целенаправленно регулировать его физико-химические характеристики и расширять возможности практического применения в процессах очистки водных растворов. Особое внимание уделено использованию поликатионов в качестве пилларирующих агентов, обеспечивающих формирование более устойчивой межслоевой структуры глинистого минерала. Установлено, что введение ионов Cu^{2+} в состав пилларирующего катиона способствует повышению его устойчивости, что может положительно влиять на сохранение структурных и функциональных характеристик модифицированного сорбента. Полученные результаты свидетельствуют о перспективности химически модифицированных базальтов для разработки высокоэффективных сорбционных материалов, предназначенных для удаления ионов тяжёлых металлов и фосфатов из водных сред.
Ключевые слова: сорбент, базальт, модификация, очистка, адсорбция, устойчивость.

Annotatsiya: Bentonitlarning kimyoviy modifikatsiyasi ularning sorbsion xususiyatlarini yaxshilash va turli ifloslantiruvchi moddalarning ion shakllariga, jumladan, mis ionlari va fosfat-ionlarga nisbatan adsorbsion qobiliyatini oshirishning samarali usuli ekanligi aniqlandi. Bentonitning kimyoviy tarkibi va tuzilishini modifikatsiyalovchi komponentlarni kiritish orqali o‘zgartirish uning fizik-kimyoviy xususiyatlarini maqsadli ravishda boshqarish hamda suvli eritmalarni tozalash jarayonlarida amaliy qo‘llash imkoniyatlarini kengaytirishi ko‘rsatildi. Qatlamli gilli mineralning qatlamlararo tuzilmasini yanada barqaror shakllantirishni ta’minlaydigan pillarlovchi agentlar sifatida polikationlardan foydalanishga alohida e’tibor qaratildi. Pillarlovchi kation tarkibiga Cu^{2+} ionlarini kiritish uning barqarorligini oshirishga yordam berishi aniqlandi. Bu esa modifikatsiyalangan sorbentning strukturaviy va funksional xususiyatlarini saqlab qolishga ijobiy ta’sir ko‘rsatishi mumkin. Olingan natijalar kimyoviy modifikatsiyalangan bentonitlar suvli muhitlardan og‘ir metall ionlari va fosfatlarni ajratib olishga mo‘ljallangan yuqori samarali sorbsion materiallarni ishlab chiqishda istiqbolli ekanligini ko‘rsatadi.
Kalit so‘zlar: bazalt, kimyoviy modifikatsiya, sorbent, adsorbsion qobiliyat, pillarlash, mis ionlari, fosfat-ionlar, qatlamlararo tuzilma, suvni tozalash.

Abstract: Chemical modification of bentonites has been found to be an effective approach for improving their sorption properties and enhancing their adsorption capacity toward various ionic forms of pollutants, including copper ions and phosphate ions. It has been demonstrated that modifying the chemical composition and structure of bentonite through the incorporation of modifying agents enables the targeted regulation of its physicochemical properties and expands its

ДЛЯ ЦИТИРОВАНИЯ
Сагдиев Х.Т., Жумаева А.А. Получение и исследование высокоэффективных химически модифицированных сорбентов // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 370–373.
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potential applications in aqueous solution treatment processes. Particular attention has been paid to the use of polycations as pillaring agents, which promote the formation of a more stable interlayer structure in the clay mineral. The incorporation of Cu^{2+} ions into the composition of the pillaring cation has been found to contribute to increased stability, which may positively affect the preservation of the structural and functional characteristics of the modified sorbent. The results obtained indicate that chemically modified bentonites are promising materials for the development of high-performance sorbents designed to remove heavy metal ions and phosphates from aqueous media.

Keywords: sorbent, basalt, modification, purification, adsorption, stability.

Цель исследования

Загрязнение природной воды нефтью и нефтепродуктами имеет серьезные экологические последствия. Гидрофобная нефть, попавшая на поверхность водоемов, образует тонкую пленку, которая мешает нормальному газо- и теплообмену между атмосферой и гидросферой. Эти изменения могут вызвать изменение климата на планете. Нефть и нефтепродукты также могут негативно влиять на жизнедеятельность водных организмов.

Часто промышленные и бытовые стоки сбрасываются в водоемы без должной очистки от вредных примесей. Большое количество сточных вод, содержащих нефтепродукты, попадает в городскую канализацию. Нефтепродукты отрицательно влияют на работу биологических очистных сооружений. Опыт работы с такими станциями показывает, что периодические поступления значительных количеств нефтепродуктов и жиров создают трудности в их эксплуатации.

Существующие сорбенты, полученные на основе естественных или искусственных материалов, такие как активированный уголь и другие, действенны при очистке воды от нефтепродуктов и других органических веществ, но оказываются неэффективными при удалении тяжелых металлов. Поэтому разработка сорбента, способного эффективно удалять из воды как тяжелые металлы, так и органические загрязнители, является актуальной задачей.

Широко распространенными и экологически безопасными считаются адсорбенты на основе углерода, силикагеля, естественных и искусственных цеолитов, а также различных силикатов. Путем сочетания сорбционных свойств этих адсорбентов и различных методов их модификации можно достичь наилучшего удаления различных загрязнителей. Глины также обладают высокой сорбционной и ионообменной активностью, и именно на этих свойствах основана их способность удерживать тяжелые металлы, такие как цинк, кремний, свинец, никель, ртуть, кадмий и другие, в ионной форме [1-2].

Методы

Асмансайский базальт был исследован для создания интеркалированных систем. Оптимальные условия получения интеркалированных материалов на основе изучаемых базальтов и полиоксокатионов Fe были установлены: наиболее эффективным оказывается сухой метод с обработкой при температуре 50°C и соотношении Me^{n+}/глина, равным 10 ммоль/г. Исследования показали, что введение ионов Cu^{2+} в состав пилларирующего катиона способствует повышению его устойчивости. Анализ экспериментальных данных указывает на то, что синтез поликатионов следует проводить при значениях pH в диапазоне 2,0-2,2, а также с использованием гидролизующих агентов NaOH и NH_4OH.

Результаты и обсуждение

Модифицированный базальт МШБ имеет примерно в 3 раза большую сорбционную способность по ионам PO_4^{3-} в сравнении с исходными алюмосиликатами. Адсорбционная способность по фосфатам следует следующему порядку: МШЗБ > МШБ > ХМШЗБ > ХМШБ

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> ОШБ > ОШЗБ. Это соответствует изменению общей удельной поверхности и доступных микропор сорбентов.

Таким образом, модификация базальтов позволяет значительно увеличить их адсорбционную способность по различным ионам, включая ионы меди и фосфаты. Эти результаты могут быть полезны для разработки эффективных методов очистки воды от загрязняющих веществ.

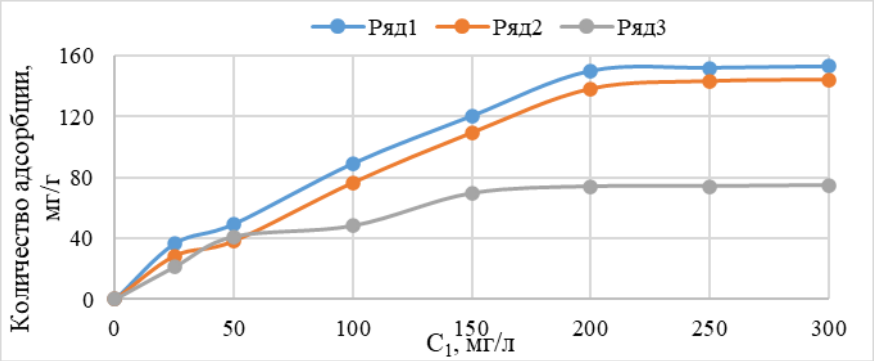


Рисунок 1. Изотермы адсорбции PO_4^{3+} на образцах: 1) МШБ; 2) МШЗБ; 3) ОШБ

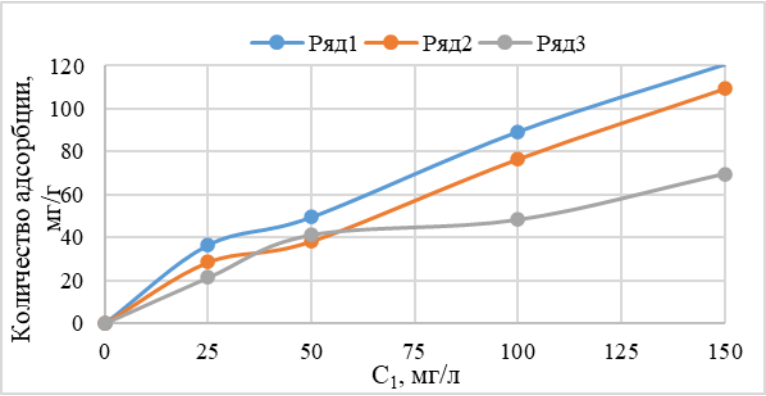


Рисунок 2. Изотермы адсорбции PO_4^{3-} на образцах: 1) МШБ; 2) МШЗБ; 3) ОШБ

Таблица 1. Значения количества адсорбции неорганических ионов на исследуемых материалах

Адсорбаты	ОШБ	ОШЗБ	МШБ	МШЗБ	ХМШБ	ХМШЗБ
Cu^{2+}	108,3	96,2	128,5	112,1	123,4	106,5
PO_4^{3-}	74,8	69,5	153,3	120,4	144,9	109,2

Заключение

Анализ данных из таблицы показывает, что модифицированные базальты МШБ, МШЗБ, ХМШБ и ХМШЗБ демонстрируют улучшенную адсорбционную активность по сравнению с исходными образцами ОШБ и ОШЗБ для обоих типов адсорбатов – Cu^{2+} и PO_4^{3-}. Среди всех исследуемых образцов МШБ обладает наивысшей адсорбционной активностью к Cu^{2+} и PO_4^{3-}. Эти результаты свидетельствуют о том, что процесс модификации базальта способствует повышению его адсорбционных свойств, особенно в отношении неорганических ионов.

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МЕТОДЫ КУЛЬТИВИРОВАНИЯ ЦИАНОБАКТЕРИЙ: НАУЧНЫЕ ОСНОВЫ И СОВРЕМЕННЫЕ ПОДХОДЫ

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Аннотация: Цианобактерии — фотосинтезирующие прокариоты, обладающие значительным экологическим и биотехнологическим потенциалом. Обобщены научные данные об их культивировании, включая выбор питательной среды, регулирование освещённости, температуры, pH, газообмена и минерального питания. Рассмотрены применение среды BG-11, особенности выращивания азотфиксирующих форм и оценка роста культур. Параметры культивирования влияют на накопление биомассы, содержание фотосинтетических пигментов и физиологическое состояние культуры. Для штаммов из аридных и засоленных регионов Узбекистана необходим индивидуальный подбор и стандартизация условий выращивания.

Ключевые слова: цианобактерии, культивирование, BG-11, питательная среда, биомасса, фотосинтез, азотфиксация, аридные территории.

Annotatsiya: Siyanobakteriyalar yuqori ekologik va biotexnologik salohiyatga ega fotosintetik prokariotik mikroorganizmlardir. Ozuqaviy muhitni tanlash va yoritish, harorat, pH, gaz almashinuvi va mineral oziqlanishni nazorat qilish yondashuvlari umumlashtirilgan. BG-11 muhitiga, azotni fiksatsiya qiluvchi siyanobakteriyalarni yetishtirishga va unumdorlikni baholashga alohida e’tibor qaratilgan. Ayniqsa, O‘zbekistonning qurg‘oqchil va sho‘r hududlaridan siyanobakteriyalar bilan ishlashda ma’lum bir shtammning xususiyatlarini hisobga olish zarurati ta’kidlangan.

Kalit so‘zlar: siyanobakteriyalar, yetishtirish, ozuqaviy muhit, biomassa, azot fiksatsiyasi, qurg‘oqchil hududlar.

Abstract: Cyanobacteria are photosynthetic prokaryotes with considerable ecological and biotechnological potential. This paper summarizes key approaches to their cultivation, including culture media, light, temperature, pH, gas exchange and mineral nutrition. Attention is given to BG-11 medium, nitrogen-fixing cyanobacteria and methods for assessing culture growth. Cultivation conditions affect biomass accumulation, photosynthetic pigments and physiological status. Strains from arid and saline regions of Uzbekistan require strain-specific optimization and standardized cultivation conditions.

Keywords: cyanobacteria, cultivation, BG-11, culture medium, biomass, photosynthesis, nitrogen fixation, arid regions.

Kirish

Цианобактерии осуществляют кислородный фотосинтез и встречаются в водоёмах, почвах, пустынях и засоленных местообитаниях. Они участвуют в круговороте углерода и азота, формировании микробных сообществ и изменении свойств субстрата; отдельные представители способны фиксировать атмосферный азот [1, 2]. Их биомасса и продукты метаболизма представляют интерес для экологических, сельскохозяйственных и

ДЛЯ ЦИТИРОВАНИЯ
Кахорова К.С. Методы культивирования цианобактерий: научные основы и современные подходы // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 374–376.
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биотехнологических исследований. Воспроизводимость результатов зависит от состава среды, освещённости, температуры, pH, газообмена и доступности минеральных элементов [4–6]. Цель работы — обобщить методы культивирования цианобактерий и определить факторы, значимые для разных физиологических групп, включая штаммы из аридных и засоленных территорий.

Materiallar va metodlar

Работа выполнена в формате обзорного научного тезиса на основе опубликованных исследований по выделению и поддержанию чистых культур, применению питательных сред, включая BG-11, влиянию освещения и температуры, регулированию pH и газообмена, выращиванию азотфиксирующих форм и оценке биомассы [1–6]. При анализе учитывалось, что оптимальные параметры зависят от штамма и условий опыта, поэтому результаты отдельных работ не рассматривались как универсальные нормативы.

Natijalar

BG-11 является распространённой минеральной средой для выращивания многих цианобактерий, однако потребности штаммов различаются [5, 6]. Для азотфиксирующих форм применяют среды с ограниченным содержанием связанного азота или без него, чтобы изучать использование атмосферного N_2 [1, 2, 6]. Недостаточное освещение ограничивает фотосинтез и накопление биомассы, тогда как чрезмерная интенсивность света может вызвать стресс. Температура и pH влияют на рост, ферментативную активность, доступность питательных веществ и метаболизм. Источником неорганического углерода служит воздух или дополнительно подаваемый CO_2; его эффект зависит от штамма и условий культивирования [5, 6]. Рост оценивают по оптической плотности, сухой массе, содержанию хлорофилла a и фикобилинов, скорости накопления биомассы, изменению pH и показателям азотного обмена.

Muhokama

Универсального протокола культивирования цианобактерий не существует [5–8]. BG-11 может служить исходной средой, но условия следует оптимизировать для конкретного штамма. Для организмов из экстремальных местообитаний важно оценивать устойчивость к температурным колебаниям, интенсивному свету, солёности и дефициту воды. Последовательное изменение отдельных факторов и экспериментальная оценка их сочетаний позволяют определить диапазон устойчивости местных штаммов. Для цианобактерий Узбекистана перспективно сочетать морфологическую и молекулярную идентификацию с контролируемым культивированием. Исследование чистых культур раскрывает свойства отдельного штамма, а изучение природных сообществ помогает оценить экологические связи [1, 4].

Xulosa

Эффективность культивирования определяется взаимодействием состава питательной среды, освещения, температуры, pH, газообмена и минерального питания. BG-11 подходит как базовая среда для многих цианобактерий, но требует корректировки с учётом физиологических особенностей штамма. Для азотфиксирующих форм важны условия проявления азотфиксации, а для организмов из аридных и засоленных местообитаний — устойчивость к солевому, температурному и водному стрессу. Для Узбекистана перспективны выделение и молекулярная идентификация местных штаммов и разработка стандартизированных условий их выращивания для дальнейшего изучения физиологических свойств и экологического потенциала.

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GLYCYRRHIZA GLABRA L. O‘SIMLIGINING ILDIZ TIZIMIDAN AJRATIB OLINGAN BAKTERIYA SHTAMMLARIDAN PREPARAT OLISH TEXNOLOGIYASI

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Annotatsiya: *Glycyrrhiza glabra* L. o‘simligi ildiz tizimidan ajratib olingan bakteriya shtammlarining mikrobiologik xususiyatlariga ko‘ra qishloq xo‘jaligida keng foydalanish imkoniyatlari ishlab chiqildi. Buning uchun ajratib olingan bakteriya shtammlaridan biotexnologik yondashuvlar asosida biopreparatlar yaratishga alohida e’tibor berildi.
Kalit so‘zlar: Glycyrrhiza glabra L., Rizosfera bakteriya, “Mikrobiovak”, omil, shtamm, preparat, bug‘doy, paxta.

Аннотация: Glycyrrhiza glabra L. благодаря микробиологическим свойствам штаммов бактерий, растение которых было выделено из корневой системы, было разработано для широкого использования в сельском хозяйстве. Для этого особое внимание было уделено созданию биопрепаратов на основе биотехнологических подходов из выделенных штаммов бактерий.
Ключевые слова: Glycyrrhiza glabra L., Ризосферные бактерии, "Микробиовак", фактор, штамм, препарат, пшеница, хлопок.

Abstract: Based on the microbiological properties of bacterial strains isolated from the root system of Glycyrrhiza glabra L., possibilities for their widespread use in agriculture have been developed. For this purpose, special attention was paid to the creation of biopreparations based on biotechnological approaches from the isolated bacterial strains.
Keywords: Glycyrrhiza glabra L., Rhizosphere bacteria, "Microbiovac", factor, strain, preparation, wheat, cotton.

Kirish

Bugungi kunda qishloq xo‘jaligida kam mablag‘ sarflab, kichik ekin maydonlarida hosildorlik va hosil sifatini oshirish hamda kimyoviy vositalar ishlatmagan holda ekologik xavfsiz mahsulotlar olishga alohida e’tibor berilmoqda. Shu bilan birga, qishloq xo‘jaligi o‘simliklarining sho‘rlanish va suvsizlikka chidamliligini oshirish ham dolzarb masalalardan biridir. Olib borilgan tadqiqot natijalariga ko‘ra bakteriyalarning o‘simlikning o‘sishi va rivojlanishiga nisbatan samaradorlik ko‘rsatkichlarining nisbatan yuqori bo‘lishi qayd etiladi, shuningdek, antagonistik xususiyatlariga ko‘ra ularning sinergetik effekti ham mavjudligi aniqlandi.

Materiallar va metodlar

Yuqoridagi tadqiqot natijalarida ko‘rsatilgani kabi shtammlarning biologik faol moddalarining birgalikdagi ta’siri natijasida, o‘simliklarning o‘sishi va rivojlanishini tezlashtirishi hamda tuproq unumdorligini oshirishi, stress omillarga chidamlilik berishi kabi polifunktsional xususiyatli ekologik toza mahsulot – biopreparat olish imkonini berishi mumkin, degan xulosaga kelindi. Bunday preparatni olish uchun maxsus texnologiyani ishlab chiqish zarur bo‘ladi. Shuning

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uchun ham ishlarimiz aynan ana shunday texnologiyani shakllantirishga qaratildi. Olib borilgan tadqiqotlar shuni ko‘rsatdiki, *Glycyrrhiza glabra* L. o‘simligi ildiz tizimidan ajratib olingan bakteriyalar xususiyatlariga ko‘ra yuqori biologik faollikka ega ekan.



1-rasm. Bakteriyalarning o‘zaro munosabat ko‘rsatkichlari

Natijalar

Bakteriyalarning o‘simliklarning o‘sishi va rivojlanishiga ta’sirini e’tiborga olgan holda mikrobiopreparat yaratish bo‘yicha xulosaga kelindi. Shunga ko‘ra *Glycyrrhiza glabra* L. o‘simligi ildiz tizimidan ajratib olingan bakteriya shtammlarining ozuqa muhitida o‘zaro munosabatini aniqladik (1-rasm).

Olingan ma’lumotlar va rasmdagi holatdan ko‘rinadiki, bakteriyalar izolyatlari orasida o‘zaro bir-biriga nisbatan antagonistik munosabat shakllanmagan. Izolyatlar o‘zaro bir-biriga zararsiz holda rivojlanish imkoniyatiga ega ekanligi kuzatildi.

Muhokama

Olingan natijalar asosida mahalliy shirinmiya *Glycyrrhiza glabra* L. o‘simligi ildiz tizimidan ajratib olingan rizosfera bakteriyalarning kompleks ta’sir etuvchi xususiyatlari asosida mikrobiologik ta’sir etuvchi majmua – biologik preparat olish imkoniyati paydo bo‘ldi. Ushbu preparatning nomini “Mikrobiovak” deb nomladik. Ushbu mikrobiologik preparat yordamida bug‘doy, paxta va shirinmiya o‘simliklariga ishlov berilganda o‘zining ijobiy natijasini ko‘rsatdi.

Xulosa

Tadqiqotimiz davomida *shirinmiya* o‘simligi ildizidan ajratib olingan bakteriya Olingan natijalar asosida mahalliy shirinmiya *Glycyrrhiza glabra* L. o‘simligi ildiz tizimidan ajratib olingan rizosfera bakteriyalarning kompleks ta’sir etuvchi xususiyatlari asosida mikrobiologik ta’sir etuvchi majmua – biologik preparat olish imkoniyati paydo bo‘ldi. Ushbu preparatning nomini “Mikrobiovak” deb nomladik. Ushbu mikrobiologik preparat yordamida bug‘doy, paxta va shirinmiya o‘simliklariga ishlov berilganda o‘zining ijobiy natijasini ko‘rsatdi.

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ВЫДЕЛЕНИЕ И ИДЕНТИФИКАЦИЯ БАКТЕРИЙ ГРУППЫ ESKAPE ИЗ ВОДНЫХ ОБЪЕКТОВ СЕЛЬСКОХОЗЯЙСТВЕННОГО НАЗНАЧЕНИЯ И ПЕРВИЧНЫЙ СКРИНИНГ ИХ РОСТА В ПРИСУТСТВИИ АНТИБИОТИКОВ

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Ключевые слова: ESKAPE, сельскохозяйственные водные объекты, антибиотики, фенотипический скрининг, MALDI-TOF MS.

Актуальность

Сельскохозяйственные водные объекты могут служить резервуарами бактерий и генетических детерминант антимикробной резистентности. Поступление животноводческих стоков и поверхностного стока с удобряемых навозом угодий создаёт потенциальные пути их распространения в окружающей среде [1, 2]. Особый интерес представляет выявление бактерий группы ESKAPE в воде, используемой для сельскохозяйственных нужд.

Цель исследования

Выделить и идентифицировать бактерии группы ESKAPE из водных объектов сельскохозяйственного назначения и провести первичный скрининг их способности к росту в присутствии антибактериальных препаратов.

Материалы и методы

Исследовали образцы воды из пяти источников, включавших тепличные системы водоснабжения и каналы. Проведено три последовательных этапа отбора с интервалом 30 дней. После поступления образцов определяли pH. Количество культивируемых микроорганизмов оценивали методом глубинного посева десятикратных разведений на Nutrient Agar с инкубацией при 37 °C и учётом колоний через 24, 48 и 72 ч; результаты выражали в КОЕ/мл.

Для повышения выявляемости бактерий 100 мл воды фильтровали через мембраны с размером пор 0,22 мкм. Мембраны переносили в Tryptic Soy Broth и Mossel Broth и инкубировали при 37 °C в течение 24–48 ч. Результаты после обогащения использовали только для качественного обнаружения бактерий, а не для расчёта их исходной концентрации. Чистые культуры получали последовательными пересевами; предварительную дифференциацию проводили на селективных и дифференциально-диагностических средах, идентификацию проводили методом MALDI-TOF MS.

Первичный скрининг проводили посевом 100 мкл накопительной культуры на Mueller–Hinton Agar с антибиотиками. Регистрировали видимый рост, рассчитывая долю положительных посевов для каждой комбинации препарата и концентрации. Данная схема не являлась стандартизованным определением антибиотикочувствительности; категории S, I и R не присваивали.

ДЛЯ ЦИТИРОВАНИЯ
Махсумханова М., Саидова И., Алимова Б.Х., Пулатова О.М. и др. Выделение и идентификация бактерий группы ESKAPE из водных объектов сельскохозяйственного назначения и первичный скрининг их роста в присутствии антибиотиков // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 380–381.
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Результаты и обсуждение

Культивируемые микроорганизмы обнаружены во всех исследованных образцах воды. Методом MALDI-TOF MS идентифицировано 148 изолятов. Среди них выявлены следующие представители классической группы ESKAPE: *Klebsiella pneumoniae* — 15 изолятов (10,1 %), *Enterococcus faecium* — 8 (5,4 %), *Pseudomonas aeruginosa* — 17 (11,5 %) и *Acinetobacter baumannii* — 4 (2,7 %). Суммарно указанные представители группы ESKAPE составили 44 изолята (29,7 % от общего числа идентифицированных изолятов). *Staphylococcus aureus* не выявлен. Кроме того, идентифицировано 42 изолята *Escherichia coli* (28,4 %) и 4 изолята *Enterococcus faecalis* (2,7 %). Выделенные *E. coli* и *E. faecalis* не относятся к классической группе ESKAPE, однако представляют интерес для исследования антимикробной резистентности. Остальные 58 изолятов (39,2 % от общего числа идентифицированных изолятов) были отнесены к другим бактериальным таксонам.

Выводы

В исследованных водных объектах сельскохозяйственного назначения выявлены представители классической группы ESKAPE — *K. pneumoniae*, *E. faecium*, *P. aeruginosa* и *A. baumannii*, суммарно составившие 29,7 % идентифицированных изолятов. Первичный скрининг показал сохранение бактериального роста в присутствии ряда антибактериальных препаратов при заданных экспериментальных концентрациях. Полученные результаты обосновывают дальнейшее стандартизованное определение антибиотикочувствительности выделенных чистых культур и исследование генетических детерминант устойчивости.

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OROL DENGIZINING QURIGAN TUBI TUPROQ-IQLIM SHAROITIDA O‘SIMLIKLARNI YETISHTIRISHDA FLOKULYANTLARGA IMMOBILLANGAN MIKROB PREPARATLARIDAN FOYDALANISH

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Orol dengizi qurigan tubida tuproq paydo bo‘lish jarayonlari dengiz suvlarining chekinishi, allyuvial va dengiz yotqiziqlarining tarkibi, relyef sharoiti, grunt suvlari sathi hamda cho‘l iqlimi ta’sirida shakllanmoqda. Tadqiqot hududida tuproq-gruntlar hali to‘liq shakllangan tuproqlar darajasiga yetmagan bo‘lib, ularda gidromorf sharoitdan yarim gidromorf va avtomorf sharoitga o‘tish, sho‘rxoklanish, taqirlanish va cho‘llanish jarayonlari bir vaqtning o‘zida kechayotganligi kuzatiladi.

Tadqiqot hududida cho‘l o‘simliklaridan saksovul, cherkez, baliqko‘z, olabuta kabilar ekildi. O‘simliklarga immobillangan biopreparatlarni qo‘llash uchun ekish oldidan vegetatsiya davrida 20 l dan bo‘lgan miqdorda Zamin-M va Rizo-to‘plam biopreparatlaridan $1*10^8$ KHB miqdorda foydalanildi. Immobillash uchun Zamin-M biopreparatining alginat Ca asosidagi gidrogelidan foydalanildi. Bakteriyalarning $1x10^8$ KHB miqdordagi suspenziyasi 3% li Na alginat eritmasi gel hosil qiluvchi alginat sifatida 12% li CaCl eritmasida granulalar shakliga keltirildi.

Mikroorganizmlar *Bacillus subtilis, Bacillus megaterium, Pseudomonas stutzeri* – 1:1:1 kompozitsiyasi (Zamin-M) va *Enterobacter cloacae, Paenibacillus polymyxa* – 1:1 aralashmasi (Rizo-to‘plam) sinergetik samaraga ega ekanligi isbotlandi.

Mazkur mikroorganizmlar asosida tayyorlangan immobillangan Zamin-M va Rizo-to‘plam biopreparatlari saksovul, teresken, cherkez, baliqko‘z, cho‘g‘on va olabuta kabi cho‘l o‘simliklarida stimulyator sifatida qo‘llanilganda saksovul o‘simligi unuvchanligi bo‘yicha immobillangan Zamin-M va Rizo-to‘plam variantlarida nazoratga nisbatan urug‘ unuvchanligiga ijobiy ta’sir ko‘rsatishi aniqlandi. Cherkez o‘simligining unuvchanligi immobillangan Zamin-M variantida nazoratga nisbatan 9,6%, Rizo-to‘plam variantida esa 6,4%, mos ravishda cho‘g‘on o‘simligida 10% va 4.8% ga, olabuta o‘simligida 3,6%, Rizo-to‘plam variantida esa 1,4% ortganligi aniqlanib, olingan natijalar cho‘llanishga qarshi kurashish hamda degradatsiyaga uchragan cho‘l o‘simlik qoplamini hosil qilishda immobillangan biopreparatlardan, xususan «Zamin-M»dan samarali stimulyator sifatida foydalanish samarali bo‘lishi mumkinligini isbotladi.

Stimulyator sifatida qo‘llanilgan immobillangan Zamin-M va Rizo-to‘plam biopreparatlari nazoratga nisbatan poya uzunligiga ijobiy ta’sir ko‘rsatishi aniqlandi. Jumladan, cherkez o‘simligining unuvchanligi immobillangan Zamin-M variantida nazoratga nisbatan 5,3 marta, Rizo-to‘plam variantida esa 3,9 baravar, mos ravishda cho‘g‘on o‘simligida 1,39 va 2,28, olabuta o‘simligida 1,88 va 1,6, teresken o‘simligida 6,1 va 4,2 marta yuqori bo‘lganligi qayd etildi.

Umuman olganda, tajriba natijalari asosida immobillangan Zamin-M va ayniqsa Rizo-to‘plam preparatlari o‘simlikning biometrik ko‘rsatkichlarining yaxshilanishiga samarali vosita ekanligi aniqlandi. Olingan natijalar ushbu preparatlarni kelgusida cho‘l va sho‘rlangan hududlarda o‘simliklarning yashovchanligini oshirish hamda urug‘ unuvchanligini yaxshilash maqsadida qo‘llash imkoniyatini ko‘rsatadi.

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TOSHKENT SHAHRI HAVOSIDAGI O‘SIMLIK GULCHANGLARINING AEROBIOLOGIK VA EKOLOGIK TAHLILI

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Annotatsiya: Ushbu tezisda Toshkent shahri atmosfera havosidagi o‘simlik gulchanglarining tarkibi, mavsumiy tarqalishi va ularga ta’sir etuvchi ekologik omillar tahlil qilindi. Aerobiologik monitoring Lanzoni VPPS-2010 volumetrik chang tutqichi yordamida amalga oshirildi. Kuzatuvlarda sarvdoshlar (*Cupressaceae*), chinor (*Platanus*) va qarag‘ay (*Pinus*) gulchanglariga alohida e’tibor qaratildi. Olingan natijalar o‘simliklarning gullash fenologiyasi, meteorologik sharoit va shahar ko‘kalamzorlashtirish tizimi atmosfera havosidagi gulchanglar miqdoriga bevosita ta’sir qilishini ko‘rsatdi.

Kalit so‘zlar: aerobiologiya, gulchang, atmosfera havosi, *Cupressaceae*, *Platanus*, *Pinus*, allergen, ekologik monitoring, Toshkent shahri.

Kirish

Atmosfera havosida tarqaladigan biologik zarrachalar, jumladan, o‘simlik gulchanglari shahar ekologik muhitining muhim tarkibiy qismi hisoblanadi. Ayrim o‘simliklarning gulchanglari allergenlik xususiyatiga ega bo‘lib, ular mavsumiy allergik rinit, rinokonyunktivit va bronxial astma belgilarining kuchayishiga sabab bo‘lishi mumkin [1,2]. Toshkent shahrida manzarali daraxt va butalarning ko‘p ekilishi, shuningdek, iqlim sharoitining o‘zgarishi gulchanglanish mavsumining davomiyligi va intensivligiga ta’sir ko‘rsatadi. Shu sababli havodagi gulchanglarni muntazam kuzatish muhim ilmiy-amaliy ahamiyatga ega [3].

Tadqiqot maqsadi

Toshkent shahri havosida uchraydigan asosiy o‘simlik gulchanglarini aniqlash, ularning mavsumiy o‘zgarishini baholash hamda tarqalishiga ta’sir etuvchi ekologik omillarni tahlil qilish.

Materiallar va usullar

Atmosfera havosidan namunalar Lanzoni VPPS-2010 rusumli Hirst tipidagi volumetrik chang tutqichi yordamida olindi. Uskunadagi yopishqoq lenta yetti kun davomida havodagi biologik zarrachalarni uzluksiz yig‘di. Olingan lentadan laboratoriya preparatlari tayyorlanib, yorug‘lik mikroskopida tekshirildi. Gulchanglar morfologik belgilariga ko‘ra taksonomik guruhlarga ajratildi va miqdoriy hisoblandi. Tahlilda, asosan, *Cupressaceae*, *Platanus* va *Pinus* gulchanglarining uchrash chastotasi hamda mavsumiy dinamikasi o‘rganildi.

Natijalar va muhokama

Monitoring natijalariga ko‘ra, Toshkent shahri havosidagi gulchanglar tarkibi mavsum davomida o‘zgarib turadi. Erta bahorda *Cupressaceae* oilasi vakillarining gulchanglari faol tarqaladi. Keyingi davrda chinor va qarag‘ay gulchanglarining havodagi ulushi ortadi. Gulchanglar miqdorining o‘zgarishi o‘simliklarning gullash muddati bilan bir qatorda, havo harorati, nisbiy namlik, yog‘ingarchilik va shamol tezligiga ham bog‘liq.

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Iliq va quruq ob-havo gulchanglarning havoga ajralishi hamda uzoq masofalarga tarqalishiga qulay sharoit yaratadi. Yog‘ingarchilik esa gulchanglarni atmosfera havosidan yuvib, ularning miqdorini vaqtincha kamaytiradi. Shahar hududida allergenligi yuqori o‘simliklarning keng ekilishi aerobiologik yuklamaning ortishiga olib kelishi mumkin. Shu jihatdan ko‘kalamzorlashtirishda o‘simliklarning nafaqat manzarali, balki allergenlik xususiyatlarini ham hisobga olish zarur.

Xulosa va tavsiyalar

Toshkent shahri atmosfera havosining gulchang tarkibi o‘simliklarning mavsumiy gullashi va meteorologik-ekologik omillar ta’sirida shakllanadi. *Cupressaceae*, *Platanus* va *Pinus* shaharning muhim aerobiologik komponentlari hisoblanadi. Uzluksiz monitoring gulchanglanish mavsumining boshlanishi, eng yuqori davri va yakunlanishini aniqlash imkonini beradi. Olingan ma’lumotlar asosida gulchanglanish kalendarini yaratish, aholiga allergenlik xavfi yuqori kunlar haqida tezkor axborot berish hamda shahar ko‘kalamzorlashtirish dasturlarida kam allergen o‘simliklardan foydalanish tavsiya etiladi.

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СРАВНИТЕЛЬНАЯ ОЦЕНКА ЭФФЕКТИВНОСТИ ПИТАТЕЛЬНЫХ СРЕД НА ОСНОВЕ МЕСТНОГО СЫРЬЯ ДЛЯ КУЛЬТИВИРОВАНИЯ БАКТЕРИЙ, УСТОЙЧИВЫХ К ТЯЖЕЛЫМ МЕТАЛЛАМ

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Аннотация: В работе проведена сравнительная оценка роста бактерий, устойчивых к тяжелым металлам Cd, Co, Cr и Cu, на жидких питательных средах на основе местного сырья. Установлено, что наиболее высокие показатели $ОП_{590}$ для большинства исследованных культур получены на мелассной среде, что характеризует ее как перспективную основу для получения бактериальной биомассы.
Ключевые слова: бактерии, тяжелые металлы, устойчивость, биомасса, меласса, местное сырье, питательные среды, культивирование

Annotatsiya: Ushbu tadqiqot mahalliy xomashyo asosidagi suyuq ozuqa muhitlarida og‘ir metallarga (Ni, Cd, Co, Cr va Cu) chidamli bakteriyalar o‘sishining qiyosiy bahosini taqdim etadi. Aniqlanishicha, o‘rganilgan bakteriya kulturalarining aksariyati uchun eng yuqori OD_{590} qiymatlari melassa asosidagi muhitda qayd etilgan bo‘lib, bu mazkur muhitni bakterial biomassa ishlab chiqarish uchun istiqbolli substrat sifatida belgilaydi.
Kalit so‘zlar: bakteriyalar, og‘ir metallar, chidamlilik, biomassa, melassa, mahalliy xomashyo, ozuqa muhitlari, kultivatsiyalash.

Abstract: This study presents a comparative assessment of the growth of bacteria resistant to heavy metals (Ni, Cd, Co, Cr, and Cu) in liquid nutrient media based on local raw materials. It was found that the highest OD_{590} values for the majority of the studied cultures were obtained using a molasses-based medium, identifying it as a promising substrate for bacterial biomass production.
Keywords: bacteria, heavy metals, resistance, biomass, molasses, local raw materials, nutrient media, cultivation.

Введение

Загрязнение окружающей среды тяжелыми металлами является одной из актуальных экологических проблем, поскольку такие элементы характеризуются высокой токсичностью, устойчивостью и способностью накапливаться в природных экосистемах. В отличие от органических загрязнителей, тяжелые металлы не подвергаются биологическому разложению, однако микроорганизмы способны связывать, аккумулировать и трансформировать их, что создает предпосылки для применения бактерий в биоремедиации загрязненных объектов [1,3]. Бактерии, устойчивые к тяжелым металлам, представляют особый интерес благодаря способности сохранять жизнеспособность и метаболическую активность в присутствии токсичных концентраций металлов. Механизмы устойчивости включают связывание металлов клеточной стенкой, внутриклеточное накопление, активный транспорт и трансформацию металлов в менее биодоступные формы [1,4]. Поэтому получение достаточного количества бактериальной биомассы является важным этапом при разработке биотехнологических подходов к очистке загрязненных сред.

ДЛЯ ЦИТИРОВАНИЯ
Туракулова Д.Э., Кадырова Г.Х. Сравнительная оценка эффективности питательных сред на основе местного сырья для культивирования бактерий, устойчивых к тяжелым металлам // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 386–388.
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Одновременно использование стандартных питательных сред может увеличивать стоимость культивирования микроорганизмов. Перспективным направлением является применение недорогого местного сырья и побочных продуктов сельскохозяйственного и пищевого производства в качестве компонентов питательных сред [2,5]. В частности, меласса и пшеничные отруби показали возможность использования в качестве источников питательных веществ для получения бактериальной биомассы. В связи с этим представляет интерес сравнительная оценка различных видов местного сырья для культивирования бактерий, устойчивых к тяжелым металлам.

Цель исследования — сравнительная оценка эффективности дешевых питательных сред на основе местного сырья для культивирования и получения биомассы бактерий, устойчивых к тяжелым металлам Ni, Cd, Co, Cr и Cu.

Методика исследования

Бактерии, устойчивые к тяжелым металлам Ni, Cd, Co, Cr и Cu, культивировали в жидких питательных средах на основе мясо-пептонной среды (МПБ), картофеля, мелассы, кукурузы и пшеничных отрубей. Культивирование проводили в течение 7 суток. После завершения культивирования определяли оптическую плотность (ОП) культуральной жидкости на спектрофотометре при длине волны 590 нм ($ОП_{590}$). Полученные значения использовали для сравнительной оценки интенсивности роста и накопления биомассы бактерий на различных питательных средах.

Результаты исследования

На 7-е сутки культивирования рост исследуемых микроорганизмов существенно различался в зависимости от состава питательной среды. Оценку накопления биомассы проводили по показателям оптической плотности культуральной жидкости при 590 нм ($ОП_{590}$). Наиболее выраженный рост большинства исследованных культур наблюдался на **мелассной среде**. Значения $ОП_{590}$ на данной среде варьировали от 0,828 до 2,467 (табл. 1). Максимальное значение отмечено у *Lactobacillus sakei* 28 — **2,467**, несколько ниже показатели были у *Acinetobacter lwoffii* 1 — **2,251** и *Pseudomonas aeruginosa* 18 — **2,235**. На МПБ наиболее высокие значения $ОП_{590}$ отмечены у *Bacillus licheniformis* 10K (**2,134**) и *Bacillus cereus* 17 (**2,029**). На картофельной среде значения $ОП_{590}$ в большинстве случаев были ниже, за исключением *Lactobacillus sakei* 28 (**1,000**). Среда на основе пшеничных отрубей обеспечивала более выраженный рост *L. sakei* 28 (**2,223**) и *A. lwoffii* 1 (**1,641**). На суспензии кукурузы максимальное значение $ОП_{590}$ отмечено у *B. licheniformis* 10K (**1,603**) и *Bacillus atrophaeus 17* (**1.681**) (табл. 1).

Таблица 1. Рост бактерий на различных питательных средах на 7-е сутки культивирования

№	Культура	Питательная среда				
		МПБ	Картофельный экстракт	Меласса	Пшеничные отруби	Суспензия кукурузы
1	*Bacillus licheniformis 10K*	**2.134**	0.487	**2.106**	0.446	**1.603**
2	*Bacillus atrophaeus 17*	1.701	0.289	1.908	0.373	**1.681**
3	*Bacillus cereus 17*	**2.029**	0.402	1.941	0.794	1.518
4	*Pseudomonas aeruginosa*	0.555	0.535	**2.235**	0.662	1.165
5	*Pseudomonas putida*	0.765	0.291	0.828	0.525	0.909
6	*Enterobacter ludwigii 11*	1.130	0.663	1.737	0.831	1.027

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7	*Enterobacter cloacae 5*	1.166	**0.712**	**2.111**	1.406	1.292
8	*Acinetobacter lwoffii*	0.381	0.356	**2.251**	**1.641**	1.533
9	*Lactobacillus sakei 28*	0.583	**1,000**	**2.467**	**2.223**	0.918
10	*Rhodococcus ruber*	0.923	0.580	1.212	0.699	1.392

Примечание: $ОП_{590}$ — оптическая плотность культуральной жидкости при длине волны 590 нм. Жирным шрифтом выделены максимальные значения для каждой культуры.

Заключение

Полученные результаты показали, что эффективность исследованных питательных сред существенно зависит от вида микроорганизма. Наиболее высокие значения $ОП_{590}$ для большинства исследованных культур получены на среде на основе мелассы, что свидетельствует о ее высокой эффективности для накопления биомассы бактерий. Среды на основе пшеничных отрубей и кукурузы также обеспечивали рост ряда культур и могут рассматриваться как перспективные субстраты на основе местного сырья. Полученные данные подтверждают возможность использования недорогих питательных сред на основе местного сырья для культивирования бактерий, устойчивых к тяжелым металлам.

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PROSPECTS FOR SUSTAINABLE SOIL CARBON STORAGE AND CLIMATE CHANGE MITIGATION USING BIOCHAR

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Abstract: Biochar plays an important role in climate change mitigation by promoting long-term soil carbon storage and potentially reducing greenhouse gas emissions. Its relatively stable carbon compounds contribute to increasing soil carbon stocks. In addition, biochar can improve soil water retention, nutrient availability, and biological activity. Its effectiveness depends on feedstock type, pyrolysis temperature, and soil characteristics. Therefore, biochar represents a promising approach to enhancing carbon sequestration, reducing soil degradation, and promoting sustainable agriculture.

Keywords: Biochar, soil carbon storage, carbon sequestration, climate change mitigation, pyrolysis, greenhouse gas emissions, soil fertility, sustainable agriculture.

Annotatsiya: Biochar tuproqda uglerodni uzoq muddat saqlash va iqlim o‘zgarishini yumshatishda muhim ahamiyatga ega bo‘lgan uglerodga boy material hisoblanadi. U organik biomassani kislorod cheklangan sharoitda piroliz qilish orqali olinadi. Biochar tarkibidagi nisbatan barqaror uglerod birikmalari tuproqdagi uglerod zaxiralarini oshirishga yordam beradi. Shuningdek, u tuproqning suvni ushlab turish qobiliyati, oziq moddalar mavjudligi va biologik faolligini yaxshilashi mumkin. Biocharning samaradorligi xomashyo turi, piroliz harorati hamda tuproq-iqlim sharoitlariga bog‘liq. Shu sababli biochar uglerod sekvestratsiyasini kuchaytirish, tuproq degradatsiyasini kamaytirish va barqaror qishloq xo‘jaligini rivojlantirishning istiqbolli vositasi hisoblanadi.

Kalit so‘zlar: biochar, tuproq uglerodi, uglerod sekvestratsiyasi, iqlim o‘zgarishini yumshatish, piroliz, issiqxona gazlari emissiyasi, tuproq unumdorligi, barqaror qishloq xo‘jaligi.

Аннотация: Биоуголь (biochar) представляет собой богатый углеродом материал, который играет важную роль в долгосрочном накоплении углерода в почве и смягчении последствий изменения климата. Он производится путём пиролиза органической биомассы в условиях ограниченного доступа кислорода. Относительно стабильные углеродные соединения биоугля способствуют увеличению запасов углерода в почве. Кроме того, его применение может улучшать водоудерживающую способность почвы, доступность питательных веществ и биологическую активность. Эффективность биоугля зависит от вида исходного сырья, температуры пиролиза и почвенно-климатических условий. Таким образом, биоуголь является перспективным средством повышения секвестрации углерода, снижения деградации почв и развития устойчивого сельского хозяйства.

Ключевые слова: биоуголь, почвенный углерод, секвестрация углерода, смягчение изменения климата, пиролиз, выбросы парниковых газов, плодородие почвы, устойчивое сельское хозяйство.

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Introduction

According to the latest Intergovernmental Panel on Climate Change (IPCC) assessment report, human activities have caused a considerable increase in greenhouse gases (GHG) emissions to the atmosphere with the carbon dioxide (CO_2) concentration reaching up to 422 ppm in 2024. It is predicted that the concentration of CO_2 in the atmosphere will reach to 600–700 ppm by the end of this century, if no concrete actions are taken to reduce their emissions at the global level [1]. Thus, in recent years, significant efforts have been made worldwide to develop novel strategies to reduce GHG emissions/carbon footprints to combat global warming, control climate change and protect the planet. In recent years, biomass-derived carbon materials (e.g., biochar) are receiving much attention as they can provide a nature-based green solution to enhance the carbon sequestration capacity of soil and thus the mitigation of climate change.

Materials and Methods

This study was based on a literature review of the role of biochar in soil carbon sequestration and climate change mitigation. Scientific publications addressing biochar production from plant biomass, carbon stability, soil organic carbon (SOC) interactions, and greenhouse gas emissions were analyzed. Particular attention was given to the effects of feedstock type, carbon-to-nitrogen (C/N) ratio, and pyrolysis conditions on biochar properties and its potential for long-term carbon storage. The selected studies were compared to identify the mechanisms through which biochar may influence soil carbon dynamics and CO_2 emissions. The analysis was based on previously published findings, and no new laboratory or field experiments were conducted [1,2].

Results

The literature analysis showed that biochar application can increase soil carbon sequestration by an average of 61% (95% confidence interval: 36–90%) [1]. Biochar can also improve soil porosity, water retention, and nutrient availability [3]. Its carbon stability depends on feedstock type, pyrolysis temperature, and soil conditions [4]. However, its effects on greenhouse gas emissions vary depending on environmental conditions. Overall, biochar is a promising approach to long-term soil carbon storage and sustainable agriculture.

Discussion

Biochar can enhance soil carbon sequestration by influencing microbial activity and nutrient cycling. It may promote beneficial bacteria such as *Bacillus* and *Pseudomonas*, which contribute to nutrient availability and organic matter transformation. Nitrogen-fixing bacteria, including *Rhizobium* and *Azotobacter*, may also respond positively to biochar application under suitable soil conditions. However, these effects depend on biochar properties, soil pH, moisture, and application rate. Therefore, biochar selection should consider both carbon stability and its effects on soil microbial communities to support sustainable agriculture and climate change mitigation.

Overall, the interplay between soil, climate and biochar characteristics drives its weathering and weathering dynamics. Soil pH, mineralogy, redox potential, microbial activity, and organic matter content collectively control biochar stability and functionality in soil systems which are in the meantime driven by climate conditions. As a result, a comprehensive understanding of these processes and their interaction would facilitate optimized biochar applications for sustainable soil management [4]. In addition to increasing the amount of organic carbon in the soil, BC amendments alter the soil's porosity, cation exchange capacity, and redox potential. On the contrary, research has demonstrated that the introduction of BC can enhance both soil biochemistry and plant physiology in the presence of abiotic stressors. The longevity of BC's effects on soil quality and its role in carbon sequestration also make it a strategic tool for environmental applications. It assists in creating a long-lasting positive impact on soil health and has the potential to store carbon for thousands of years, contributing to climate change mitigation efforts [5].

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NEFT QAZIB OLISH VA TASHISH TIZIMLARIDA MIKROBIOLOGIK KORROZIYANING TADQIQ ETILISHI VA ULARNI ANIQLASH USULLARI

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Annotatsiya: O‘zbekistonning Qashqadaryo va Buxoro viloyatlaridagi neft konlari hamda texnologik uskunalardan olingan namunalarda mikrobiologik korroziya bilan bog‘liq bakteriyalar o‘rganildi. 52 ta namunadan 70 dan ortiq mikroorganizm ajratildi; saralash natijasida 51 ta uglevodorod oksidlovchi va 5 ta sulfatni qaytaruvchi izolyat aniqlandi. Asosiy model shtammlar MALDI-TOF va 16S rRNK sekvenslash orqali *Serratia marcescens* va *Pseudomonas putida* sifatida identifikatsiya qilindi.

Kalit so‘zlar: mikrobiologik korroziya, neft quvurlari, sulfatni qaytaruvchi bakteriyalar, uglevodorod oksidlovchi bakteriyalar, *Serratia marcescens*, *Pseudomonas putida*, MALDI-TOF, 16S rRNK.

Аннотация: Изучены бактерии, связанные с микробиологической коррозией, в образцах с нефтяных месторождений и технологического оборудования Кашкадарьинской и Бухарской областей Узбекистана. Из 52 образцов выделено более 70 микроорганизмов; после скрининга выявлены 51 углеводородокисляющий и 5 сульфатредуцирующих изолятов. Основные модельные штаммы идентифицированы методом MALDI-TOF и секвенированием 16S рРНК как Serratia marcescens и Pseudomonas putida.

Ключевые слова: микробиологическая коррозия, нефтепроводы, сульфатредуцирующие бактерии, углеводородокисляющие бактерии, *Serratia marcescens*, *Pseudomonas putida*, MALDI-TOF, 16S рРНК.

Abstract: Bacteria associated with microbiologically influenced corrosion were studied in samples collected from oil fields and technological equipment in the Kashkadarya and Bukhara regions of Uzbekistan. More than 70 microorganisms were isolated from 52 samples; screening revealed 51 hydrocarbon-oxidizing and 5 sulfate-reducing isolates. The principal model strains were identified by MALDI-TOF and 16S rRNA sequencing as Serratia marcescens and Pseudomonas putida.

Keywords: microbiologically influenced corrosion, oil pipelines, sulfate-reducing bacteria, hydrocarbon-oxidizing bacteria, *Serratia marcescens*, *Pseudomonas putida*, MALDI-TOF, 16S rRNA.

Kirish

Mikrobiologik korroziya (MIC – microbiologically influenced corrosion) neft qazib olish, saqlash va tashish tizimlarida uchraydigan eng muhim texnologik muammolardan biri hisoblanadi. Ushbu jarayon metall konstruksiyalar, quvurlar, rezervuarlar va boshqa sanoat uskunalarining muddatidan oldin yemirilishiga, ularning mustahkamligi pasayishiga hamda avariya holatlarining yuzaga kelishiga sabab bo‘lishi mumkin. Ayniqsa, neft quvurlari va rezervuarlarining ichki yuzalarida namlik, uglevodorodlar, mineral tuzlar va turli mikroorganizmlarning mavjudligi mikrobiologik korroziya rivojlanishi uchun qulay sharoit yaratadi.

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Yodgorova F.Sh., Mavloniy M.E., Yodgorov I.Sh. Neft qazib olish va tashish tizimlarida mikrobiologik korroziyaning tadqiq etilishi va ularni aniqlash usullari // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 392–394.
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Mikrobiologik korroziya murakkab biokimyoviy va elektrokimyoviy jarayon bo‘lib, unda turli fiziologik guruhlarga mansub mikroorganizmlar ishtirok etadi. Anaerob sharoitda faoliyat yurituvchi sulfatni qaytaruvchi bakteriyalar (SQB) korroziya jarayonida alohida ahamiyatga ega. Ular sulfatlarni elektron akseptori sifatida o‘zlashtirib, metabolizm jarayonida vodorod sulfid (H_2S) hosil qiladi. Hosil bo‘lgan H_2S metall yuzasi bilan reaksiyaga kirishib, temir sulfidi birikmalarining shakllanishiga olib keladi va elektrokimyoviy korroziya jarayonlarini tezlashtiradi. Shu bilan birga, H_2Sning to‘planishi ishlab chiqarish tizimlarida toksik va korroziv muhitning yuzaga kelishiga sabab bo‘lishi mumkin.

Neft qazib olish va tashish tizimlarida mikrobiologik korroziyaning rivojlanish darajasi ko‘plab omillarga, jumladan harorat, muhit pH i, tuzlar miqdori, suvning mavjudligi, oksidlanish-qaytarilish potensiali va mikroorganizmlar tarkibiga bog‘liq. Shu sababli korroziya bilan bog‘liq mikroorganizmlarni ajratish, ularning fiziologik-biokimyoviy xususiyatlarini o‘rganish va tur darajasida aniq identifikatsiya qilish neft sanoati obyektlarida samarali profilaktik choralarni ishlab chiqishda muhim ahamiyat kasb etadi.

Tadqiqotning maqsadi mahalliy neft konlari va neftni tashish tizimlaridan korroziya jarayoni bilan bog‘liq mikroorganizmlarni ajratish, ularni saralash, morfologik, fiziologik va biokimyoviy xususiyatlarini baholash hamda zamonaviy usullar yordamida identifikatsiya qilishdan iborat bo‘ldi.

Natijalar va muhokama

Tadqiqot davomida namunalardan 61 dan ortiq mikroorganizm kulturasi ajratilib, selektiv saralash natijasida 51 ta uglevodorod oksidlovchi va 5 ta sulfatni qaytaruvchi, jami 56 ta mikrobiologik korroziya bilan potensial bog‘liq izolyat aniqlandi. Korroziya bilan bog‘liq izolyatlarning 91,1 % ini uglevodorod oksidlovchi, 8,9 % ini esa sulfatni qaytaruvchi bakteriyalar tashkil etdi. Keyingi saralashda 30 ta faol izolyat orasidan Ko‘kdumaloq-20, Ko‘kdumaloq-23, Ko‘kdumaloq-25 va Shimoliy O‘rtabuloq-5 yuqori o‘sish faolligi va barqaror yashovchanligi bilan ajralib turdi.

Model izolyatlarning fiziologik faolligini baholashda *Serratia marcescens* uchun Raymondo muhitida OD_{600} 0,62, go‘sht-peptonli muhitda 0,80; *Pseudomonas putida* uchun esa mos ravishda 0,57 va 0,75 ni tashkil etdi. *S. marcescens* kulturasida pH 7,0±0,2 dan 32 soat davomida 5,4 gacha pasaydi, bu uning metabolik faolligi natijasida kislotali mahsulotlar hosil bo‘lishi mumkinligini ko‘rsatadi. *P. putida* da esa pH 7,1–7,3 oralig‘ida nisbatan barqaror saqlandi. Mazkur farqlar shtammlarning uglevodorodli muhitdagi metabolik xususiyatlari turlicha ekanligini ko‘rsatdi.

MALDI-TOF tahlilida Ko‘kdumaloq-20, Ko‘kdumaloq-23 va Ko‘kdumaloq-25 izolyatlari *S. marcescens*, Shimoliy O‘rtabuloq-5 esa *P. putida* sifatida identifikatsiya qilindi. 16S rRNK sekvenslash natijasida *Serratia* spp. K25 izolyatining *S. marcescens* bilan 100 % o‘xshashligi (PX453256), *Pseudomonas* spp. 5 izolyatining esa *P. putida* bilan 99,93 % o‘xshashligi (PX453285) tasdiqlandi. MALDI-TOF va molekulyar-genetik tahlil natijalarining o‘zaro mosligi identifikatsiyaning ishonchliligini ko‘rsatdi.

Xulosa

Olingan natijalar neft konlari va neftni tashish tizimlarida uglevodorodlarni o‘zlashtirishga moslashgan hamda muhitning fizik-kimyoviy ko‘rsatkichlariga ta’sir ko‘rsata oladigan bakteriyalar mavjudligini ko‘rsatdi. *S. marcescens* va *P. putida* shtammlari mikrobiologik korroziya jarayonlarini keyingi bosqichlarda chuqur o‘rganish uchun istiqbolli model mikroorganizmlar sifatida tanlandi.

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EFFECT OF VARIOUS SODIUM CHLORIDE CONCENTRATIONS ON THE DYNAMICS OF indolyl-3-acetic ACID SYNTHESIS BY SALT-TOLERANT SOIL BACTERIA

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Soil salinity is a major factor limiting the growth and productivity of agricultural crops. Elevated salt concentrations in the soil solution disrupt plant water balance, reduce nutrient availability, and negatively affect the development of soil microorganisms. Under these conditions, salt-tolerant rhizobacteria – capable of maintaining physiological activity amidst high salinity and producing phytohormones that regulate plant growth – assume particular importance.

Indolyl-3-acetic acid (IAA) is a key growth-promoting compound synthesized by bacteria. It plays a role in regulating cell division and elongation, as well as root system formation and lateral root development. The ability of bacteria to synthesize IAA under saline conditions is of interest for the development of microbial preparations aimed at enhancing plant tolerance to salt stress.

The aim of this study was to investigate the effect of various sodium chloride concentrations on the synthesis of indolyl-3-acetic acid by salt-tolerant soil bacteria during the course of cultivation.

The study investigated 11 strains of soil bacteria: *Brevibacillus fluminis* 1A, *Bacillus subtilis* 7A, *B. rugosus* 8A, 9A, 10A, 14A, *B. endophyticus* 12A, *B. halotolerans* 27A, *B. axarquiensis* 28A, *B. proteolyticus* 33S and *B. pumilus* 40S. IAA synthesis was examined at four NaCl concentrations: 0%, 3%, 5%, and 7%. Metabolite production was measured after 3, 5, and 7 days of cultivation. The experimental data obtained were used to comparatively assess the effects of salt stress and cultivation duration on the rate of IAA synthesis by the strains under study.

The results demonstrated that IAA synthesis depended on the sodium chloride concentration, the duration of cultivation, and the individual characteristics of the strains. Overall, extending the cultivation period from 3 to 7 days led to increased IAA production in the majority of the bacteria; however, the extent of this trend varied depending on the salt concentration.

On the third day of cultivation, the highest IAA synthesis levels were observed in *B. rugosus* 9A in the absence of NaCl (15.50 mg/L) and in *Brevibacillus fluminis* 1A at 5% NaCl (13.37 mg/L). No IAA synthesis was detected at 7% NaCl for several strains, including *B. rugosus* 8A, *B. rugosus* 10A, *B. endophyticus* 12A, *B. rugosus* 14A, *B. halotolerans* 27A, *B. axarquiensis* 28A, and *B. proteolyticus* 33S. This indicates a pronounced inhibitory effect of high salt concentrations during the early stages of cultivation for certain members of the studied group. Meanwhile, *B. pumilus* 40S showed no detectable IAA production on the third day in any of the experimental conditions.

By the fifth day, an increase in IAA synthesis was observed in the majority of strains. The maximum value in the absence of salt was recorded for *B. rugosus* 9A (30.44 mg/L), whereas at 3% NaCl, the highest level was observed in *B. rugosus* 8A (24.32 mg/L). Strain *B. proteolyticus* 33S also exhibited high IAA production at 3% NaCl (24.22 mg/L). At 5% NaCl, a relatively high level was noted for *Brevibacillus fluminis* 1A (18.22 mg/L), and at 7% NaCl, for *B. pumilus* 40S (16.86 mg/L). The results indicate that some strains retained the ability to synthesize IAA even under high salt stress, although production levels varied. On the seventh day, the highest rate of IAA synthesis

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in the absence of NaCl was recorded for *B. rugosus* 9A, amounting to 39.05 mg/L. High values were also observed for *Brevibacillus fluminis* 1A (30.34 mg/L) and *B. subtilis* 7A (29.92 mg/L). At 3% NaCl, the maximum level was observed in *B. rugosus* 9A (21.90 mg/L) and *B. rugosus* 10A (19.57 mg/L). At 5% NaCl, the highest IAA production was noted for *B. endophyticus* 12A, with a value of 18.80 mg/L. At 7% NaCl, relatively high values were recorded for *B. rugosus* 9A (17.25 mg/L), *B. subtilis* 7A (13.47 mg/L), and *Brevibacillus fluminis* 1A (12.89 mg/L).

Strain *B. rugosus* 9A is of particular interest, as it demonstrated the highest levels of IAA synthesis throughout the experiment. On the seventh day, its production at NaCl concentrations of 0%, 3%, 5%, and 7% was 39.05, 21.90, 15.79, and 17.25 mg/L, respectively. Although production decreased as salinity increased compared to the salt-free control, the strain retained its ability to synthesize IAA at all tested NaCl concentrations. This makes it a promising candidate for further study regarding growth-promoting potential under saline conditions.

Thus, the study revealed a marked dependence of indole-3-acetic acid production on sodium chloride concentration, cultivation duration, and the species of the soil bacteria. For most strains, the highest levels were observed on the seventh day of cultivation; however, high NaCl concentrations limited IAA synthesis in a number of isolates. *B. rugosus* 9A and *Brevibacillus fluminis* 1A appear the most promising in terms of IAA production levels and the retention of synthetic activity under saline conditions. These results may serve as a basis for the further selection of salt-tolerant bacteria – potential components of microbial inoculants for crops grown on saline soils.

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ЎЗБЕКИСТОННИНГ ҚУРҒОҚЧИЛ ҲУДУДЛАРИ ТУПРОҚЛАРИДАН АЖРАТИЛГАН БАКТЕРИЯЛАРНИНГ 16S rRNA ГЕНИ АСОСИДАГИ ТАКСОНОМИК ТАҲЛИЛИ

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Аннотация: Навоий, Бухоро ва Қашқадарё тупроқларидан ажратилган 18 та бактерия изолятининг 16S рРНК гени таҳлил қилинди. Изолятлар 9 та авлодга мансуб бўлиб, *Bacillus* улуши 38,89% ни ташкил этди. Таққослаш учун олинган кетма-кетликларга ўхшашлик 99,24-100% оралиғида бўлди.

Калит сўзлар: қурғоқчил тупроқ, бактерия, 16S рРНК, таксономик таркиб, *Bacillus*.

Аннотация: Проанализированы последовательности гена 16S рРНК 18 бактериальных изолятов из почв Навоийской, Бухарской и Кашкадарьинской областей. Изоляты отнесены к 9 родам; доля *Bacillus* составила 38,89%. Сходство с референсными последовательностями варьировало от 99,24 до 100%.

Ключевые слова: аридные почвы, бактерии, 16S рРНК, таксономический состав, *Bacillus*.

Abstract: The 16S rRNA gene sequences of 18 bacterial isolates from soils of Navoi, Bukhara and Kashkadarya regions were analysed. The isolates represented nine genera, with *Bacillus accounting* for 38.89%. Similarity to reference sequences ranged from 99.24 to 100%.

Keywords: arid soils, bacteria, 16S rRNA, taxonomic composition, *Bacillus*.

Кириш

Қурғоқчил ҳудудлар тупроқларидан ажратилган бактерияларнинг таксономик таркибини аниқлаш маҳаллий микроб ресурсларини тавсифлаш ва кейинги функционал тадқиқотлар учун изолятларни танлашда муҳимдир. 16S рРНК гени кетма-кетликларини қиёслаш бактерияларнинг таксономик яқинлигини баҳолаш имконини беради, бироқ яқин турларни фарқлашда мазкур маркернинг имконияти чекланган [1]. Тадқиқотнинг мақсади Навоий, Бухоро ва Қашқадарё вилоятлари қурғоқчил тупроқларидан ажратилган бактерияларнинг молекуляр идентификацияси ва авлодлар бўйича таркибини баҳолашдан иборат.

Материаллар ва методлар

Тадқиқотда Навоий вилояти Қизилқум чўлидан 6 та, Бухоро вилояти чўл ва ярим чўл ҳудудларидан 7 та ҳамда Қашқадарё вилоятидан 5 та, жами 18 та изолят таҳлил қилинди. Намуналар *Haloxylon aphyllum*, *Calligonum caput-medusae*, *Atriplex cana*, *Atriplex tatarica* ва *Artemisia terrae-albae* ўсимликлари билан боғлиқ тупроқлардан олинган. Изолятларнинг 16S рРНК гени нуклеотид кетма-кетликлари NCBI GenBank таққослаш учун олинган кетма-кетликлар билан қиёсланди. Авлодларнинг нисбий улуши тегишли авлодга мансуб изолятлар сонининг умумий изолятлар сонига нисбати асосида фоизда ҳисобланди.

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Натижалар

Қиёсий таҳлилда изолятлар таққослаш учун олинган кетма-кетликлар билан 99,24-100% ўхшашлик кўрсатди. Тақдим этилган идентификация маълумотларига кўра, 18 та изолят *Bacillus*, *Priestia*, *Peribacillus*, *Paenibacillus*, *Brevibacillus*, *Pseudomonas*, *Enterobacter*, *Burkholderia* ва *Stenotrophomonas* авлодларига мансуб бўлди. Энг катта улуш *Bacillus* авлодига тўғри келди: 7 та изолят, яъни 38,89%. *Pseudomonas* 3 та (16,67%), *Enterobacter* 2 та (11,11%) изолят билан ифодаланди. Қолган олтита авлоднинг ҳар бирига биттадан изолят (5,56%) тўғри келди. Навоий тупроқларидан ажратилган изолятлар *Bacillus vallismortis*, *Bacillus safensis*, *Bacillus sonorensis*, *Bacillus licheniformis*, *Bacillus subtilis* ва *Priestia megaterium* турларига яқинлиги билан тавсифланди. Уларнинг таққослаш учун олинган кетма-кетликларга ўхшашлиги 99,24-100% ни ташкил этди. Бухоро тупроқларидан ажратиб олинган изолятлар *Peribacillus frigoritolerans*, *Stenotrophomonas rhizophila*, *Burkholderia cepacia*, *Pseudomonas chlororaphis*, *Pseudomonas putida*, *Pseudomonas fluorescens* ва *Paenibacillus polymyxa* турларига яқин бўлиб, ўхшашлик 99,60-100% оралиғида қайд этилди. Қашқадарё тупроқларидан ажратиб олинган изолятлар *Bacillus amyloliquefaciens*, *Bacillus mojavensis*, *Brevibacillus brevis*, *Enterobacter cloacae* ва *Enterobacter ludwigii* турларига 99,67-100% ўхшашлик кўрсатди. Таҳлил қилинган кетма-кетликлар учун манбада PZ575044.1-PZ575061.1 GenBank кириш рақамлари келтирилган. Ҳудудлар кесимида Навоий тупроқларидан ажратиб олинган изолятлар 2 та, Бухоро тупроқларидан ажратиб олинган изолятлар 5 та ва Қашқадарё тупроқларидан ажратиб олинган изолятлар 3 та авлодни қамраб олди. Бу кўрсаткичлар тадқиқотда танланган изолятлар тўпламини тавсифлайди.

Муҳокама

Bacillus авлодининг кўпроқ учраши ажратилган культуралар таркибида ушбу гуруҳнинг устунлигини кўрсатади. Бироқ культивация қилинган 18 та изолят бўйича олинган улушларни бутун тупроқ микробиомидаги нисбий миқдор сифатида талқин қилиш мумкин эмас [2]. Худди шунингдек, ҳудудлардан турли сонда изолят олинганлиги сабабли мазкур натижалар уларнинг умумий микроб хилма-хиллигини бевосита қиёслаш учун етарли эмас. 16S рРНК гени бўйича юқори ўхшашлик таксономик яқинликни кўрсатса-да, айниқса яқин турлар гуруҳларида якуний тур идентификациясини ҳар доим ҳам таъминламайди [1,3]. Шу боис тур номлари мазкур маркер асосидаги дастлабки идентификация сифатида талқин қилинди. Изолятларнинг қурғоқчиликка чидамлилиги, ўсимлик ўсишини рағбатлантириши ёки антагонистик фаоллиги ушбу таҳлилда бевосита баҳоланмаган, бу хусусиятлар кейинги тажрибаларда текширилиши лозим.

Хулоса

Ўзбекистоннинг уч вилояти қурғоқчил тупроқларидан ажратилган 18 та бактерия изоляти 9 та авлодга мансуб бўлиб, тўпламда *Bacillus* авлоди энг катта улушни (38,89%) ташкил этди. Олинган маълумотлар маҳаллий бактериялар коллекциясини молекуляр тавсифлаш ҳамда кейинги функционал ва геномик тадқиқотлар учун изолятларни танлашга асос бўлади.

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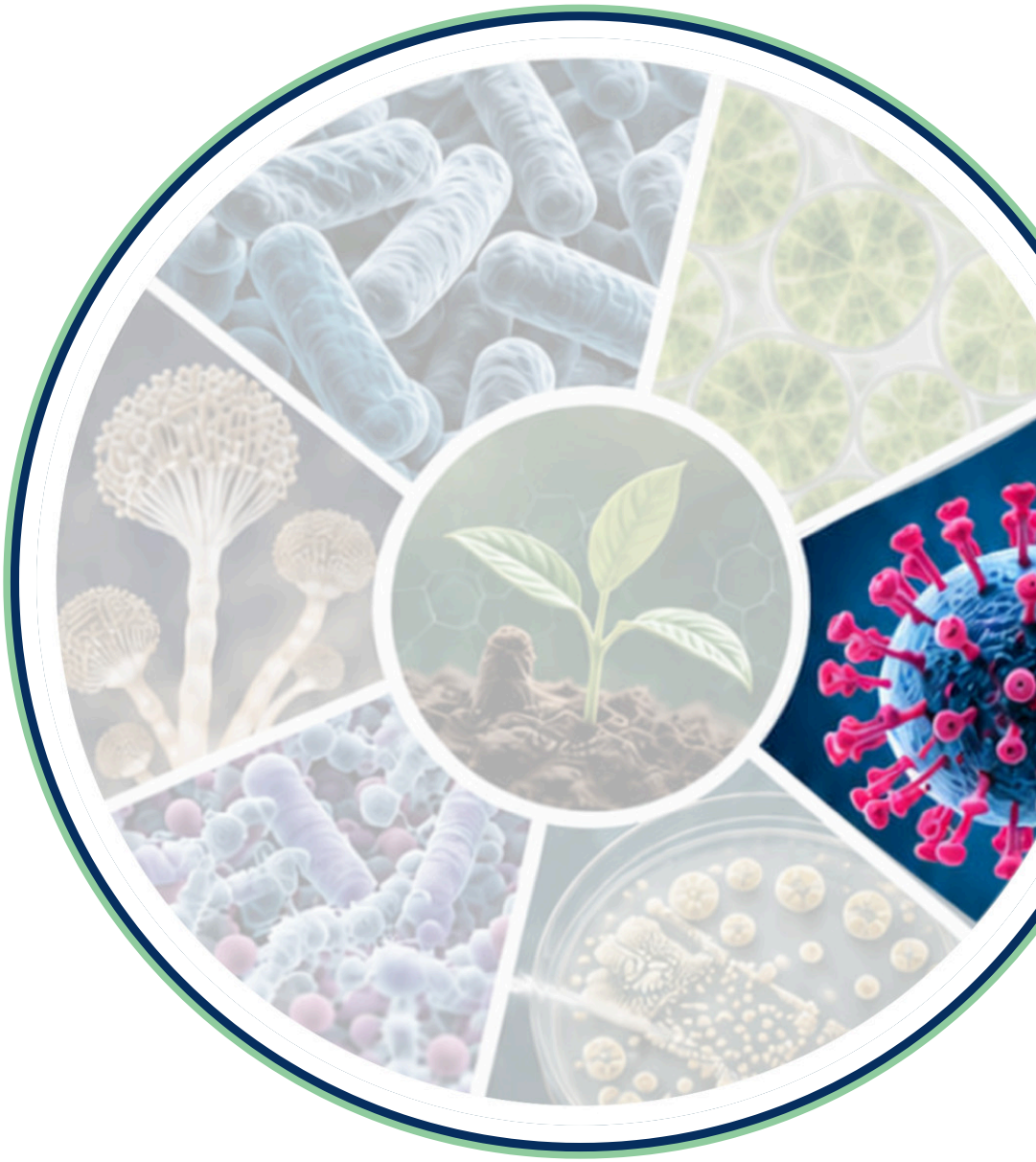
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INTERRELATIONSHIP BETWEEN HUMAN PAPILLOMAVIRUS (HPV) INFECTION AND DISTURBANCES OF THE CERVICAL MICROBIOCENOSIS

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Abstract: The article analyses evidence published in 2011–2025 on the interrelationship between human papillomavirus (HPV) infection and disturbances of the cervical microbiocenosis. A *Lactobacillus*-depleted anaerobic community state type (CST IV) is associated with HPV persistence and with the severity of cervical intraepithelial neoplasia (CIN): its share rises from 10% in normal cytology to 40% in invasive cancer. *Lactobacillus* dominance is linked to more frequent regression of CIN2 (70.0% vs 42.1%). The expediency of combining HPV screening with assessment of the microbiocenosis is substantiated.

Keywords: human papillomavirus, cervix uteri, microbiocenosis, vaginal dysbiosis, *Lactobacillus*, cervical intraepithelial neoplasia.

Annotatsiya: Maqolada odam papilloma virusi (OPV) infeksiyasi va bachadon bo‘yni mikrobiotsenozi buzilishi o‘rtasidagi bog‘liqlikka oid 2011–2025-yillarda chop etilgan ilmiy ma’lumotlar tahlil qilingan. Laktobatsillalar kamaygan va anaerob flora ustun bo‘lgan mikrob jamoasi (CST IV) OPV persistensiyasi hamda servikal intraepitelial neoplaziya (CIN) og‘irligi bilan bog‘liq: uning ulushi normal sitologiyada 10% bo‘lsa, invaziv saratonda 40% ga yetadi. *Lactobacillus* dominantligida CIN2 regressiyasi ko‘proq kuzatiladi (70,0% va 42,1%). OPV skriningini mikrobiotsenozni baholash bilan birga olib borish maqsadga muvofiqligi asoslandi.

Kalit so‘zlar: odam papilloma virusi, bachadon bo‘yni, mikrobiotsenoz, vaginal disbioz, *Lactobacillus*, servikal intraepitelial neoplaziya.

Аннотация: В статье проанализированы научные данные 2011–2025 гг. о взаимосвязи инфекции, вызванной вирусом папилломы человека (ВПЧ), и нарушений микробиоценоза шейки матки. Микробное сообщество с дефицитом лактобацилл и преобладанием анаэробной флоры (CST IV) ассоциировано с персистенцией ВПЧ и тяжестью цервикальной интраэпителиальной неоплазии (CIN): его доля возрастает с 10% при нормальной цитологии до 40% при инвазивном раке. При доминировании *Lactobacillus* регрессия CIN2 наблюдается чаще (70,0% против 42,1%). Обоснована целесообразность сочетания скрининга ВПЧ с оценкой микробиоценоза.

Ключевые слова: вирус папилломы человека, шейка матки, микробиоценоз, вагинальный дисбиоз, *Lactobacillus*, цервикальная интраэпителиальная неоплазия.

Introduction

Cervical cancer remains one of the most significant problems in women’s oncology: according to GLOBOCAN 2022, about 661,000 new cases and 348,000 deaths were registered worldwide [1]. HPV DNA is detected in 99.7% of invasive cervical carcinomas, and persistent infection with high-risk genotypes is regarded as a necessary cause of the disease [2]. However, most infections are cleared within one to two years, and only a small proportion persists and

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progresses through cervical intraepithelial neoplasia (CIN) to cancer. The natural history of the infection is therefore shaped by cofactors, among which the cervicovaginal microbiota attracts growing attention [3].

The healthy microbiocenosis of women of reproductive age is dominated by *Lactobacillus*. J. Ravel et al. described five community state types (CST): four are dominated by *L. crispatus*, *L. gasseri*, *L. iners* or *L. jensenii*, while CST IV contains few lactobacilli and a diverse anaerobic flora [4]. Lactobacilli maintain pH ≤ 4.5 through lactic acid production and compete with pathogens, whereas their replacement by *Gardnerella vaginalis*, *Fannyhessea vaginae*, *Prevotella*, *Sneathia* and other anaerobes corresponds to bacterial vaginosis (BV) and activates mucosal inflammation [3]. For Uzbekistan, where HPV vaccination began in 2019 and HPV testing is entering screening, this question is of practical importance.

The aim of the study was to systematise current evidence on the relationship between HPV infection and disturbances of the cervical microbiocenosis, to assess its dependence on lesion severity and to outline its clinical-laboratory implications.

Materials and methods

A structured literature review was performed following the principles of PRISMA 2020. PubMed/MEDLINE, Scopus, Web of Science and Google Scholar were searched for January 2011 – June 2025 using the terms “human papillomavirus”, “vaginal microbiota” and “cervical intraepithelial neoplasia”. Original studies and meta-analyses were included if the microbiota was characterised by 16S rRNA gene sequencing or Nugent/Amsel criteria and HPV status was determined by molecular methods. Owing to methodological heterogeneity, effect estimates were compared descriptively without pooling.

Results

In the cohort of 396 asymptomatic women studied by Ravel et al., CST III (*L. iners*) was the most frequent (34.1%), followed by CST IV (27.0%) and CST I (*L. crispatus*, 26.2%); thus about a quarter of clinically healthy women carried a *Lactobacillus*-depleted microbiota, with a mean pH of 5.3 versus 4.0 in CST I [4].

In the meta-analysis by Gillet et al. (12 studies, 6,372 women), BV was associated with cervical HPV infection (OR 1.43; 95% CI 1.11–1.84) [6]. Longitudinal studies showed that CST IV is associated with the slowest HPV clearance and with persistent infection [7, 8], and a network meta-analysis confirmed higher odds of HPV and dysplasia in *Lactobacillus*-depleted and, to a lesser degree, *L. iners*-dominated communities [9]. The key studies are summarised in the Table.

Table 1. Key studies of the cervicovaginal microbiota in HPV infection and cervical lesions

Study	Design, n	Main finding
Gillet et al., 2011 [6]	Meta-analysis, 6,372	BV and HPV: OR 1.43 (95% CI 1.11–1.84)
Brotman et al., 2014 [7]	Longitudinal, 32	CST IV-B – slowest HPV clearance
Di Paola et al., 2017 [8]	Cohort, 55	CST IV – persistence of hrHPV
Mitra et al., 2015 [10]	Cross-sectional, 169	CST IV: 10% (normal) → 40% (cancer)
Łaniewski et al., 2018 [11]	Cross-sectional, 100	Loss of lactobacilli, rise of inflammation towards cancer
Mitra et al., 2020 [12]	Cohort, 87	CIN2 regression: 70.0% vs 42.1%

A clear gradient was observed between dysbiosis and lesion severity: the prevalence of CST IV was 10% in normal cytology, 21% in LSIL, 27% in HSIL and 40% in invasive cancer (Figure 1) [10].

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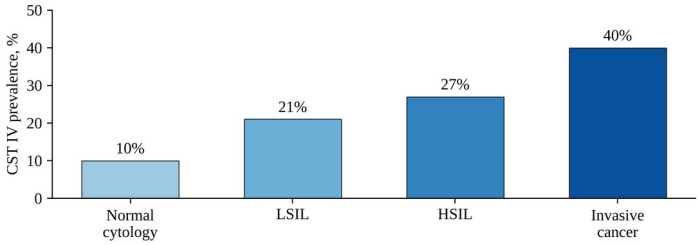


Figure 1. Prevalence of CST IV depending on the severity of cervical lesions, % (based on [10])

The microbiota also affects the outcome of established lesions. Among 87 women with untreated CIN2, regression at 12 months occurred in 70.0% with a *Lactobacillus*-dominant microbiota and in 42.1% with a depleted one (adjusted OR for non-regression 3.56; 95% CI 1.31–9.60) (Figure 2) [12].

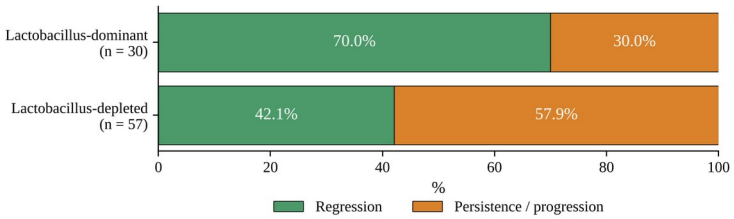


Figure 2. Outcome of untreated CIN2 at 12 months depending on the baseline microbiota, % (based on [12])

Discussion

The association between HPV and cervical dysbiosis concerns not only HPV prevalence but also its persistence and the course of CIN [7, 10, 12]. It is realised through loss of the acidic barrier, damage to mucus and epithelium by bacterial sialidases and cytolysins, chronic inflammation with oxidative DNA damage and genotoxic metabolites [3]. Causality is not proven: most studies are cross-sectional, and the relationship is likely bidirectional, since HPV oncoproteins E6 and E7 suppress local immunity [5]. Ethnic variation of CST IV [4] and the absence of regional data limit the transfer of results to women in Uzbekistan.

In practice, clinical diagnostic laboratories may supplement HPV genotyping with pH measurement, Nugent scoring and quantitative PCR of lactobacilli and anaerobic markers in women with persistent high-risk HPV or CIN. Evidence for probiotic prevention of cervical neoplasia is still insufficient outside clinical trials [13].

Conclusion

1. Depletion of *Lactobacillus* and predominance of anaerobic flora (CST IV) are consistently associated with HPV infection; BV increases the odds of HPV detection (OR 1.43).

2. The share of CST IV rises with lesion severity from 10% to 40%, and *Lactobacillus* dominance is linked to more frequent regression of CIN2 (70.0% vs 42.1%).

3. Assessment of the microbiocenosis may complement HPV screening in women at increased risk; its prognostic value requires prospective studies, including in Uzbekistan.

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TOSHKENT SHAHRIDA SARVDOSHLAR *(CUPRESSACEAE)* OILASI VAKILLARINING CHANGLANISH DINAMIKASINI O‘RGANISH

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O‘zbekiston Respublikasi Fanlar akademiyasi Xalqaro molekulyar allergologiya markazi
sh.akramjonova@gmail.com.

Annotatsiya: Mazkur matnda so‘nggi yillarda dolzarb muammoga aylanib borayotgan allergik kasalliklar, xususan, gul changi allergiyasi (pollinoz) va uning tarqalish ko‘rsatkichlari tahlil qilingan. Ma’lumotlarga ko‘ra, dunyo bo‘ylab millionlab odamlar, jumladan, Yevropa aholisining 40% i ushbu kasallikdan aziyat chekmoqda. Shuningdek, matnda Ochiq urug‘lilar bo‘limiga mansub Sarvdoshlar *(Cupressaceae)* oilasi va uning vakillari (sarv, archa, tuya, sekvoyya) haqida ma’lumot berilib, xalqaro tajribalar hamda Toshkent shahridagi holat yoritilgan. Xalqaro molekulyar allergologiya markazi ma’lumotlariga ko‘ra, Toshkent shahrida nafas olish yo‘llari allergiyasi alomatlari bor bolalarning 27% ida sarv molekulasi *Cup a 1* ga nisbatan sezuvchanlik aniqlangan.
Kalit so‘zlar: Sarvdoshlar *(Cupressaceae)*, pollinoz, aeropalinologiya, chang konsentratsiyasi, allergik kasalliklar, daraxt changlari.

Аннотация: В данном тексте анализируются аллергические заболевания, становящиеся все более актуальной проблемой в последние годы, в частности поллиноз (аллергия на пыльцу) и показатели его распространенности. Согласно данным, миллионы людей по всему миру, включая 40% населения Европы, страдают от этого заболевания. Кроме того, в тексте приводится информация о семействе Кипарисовые *(Cupressaceae)*, относящемся к отделу Голосеменных *(Gymnospermae)*, и его представителях (кипарис, можжевельник, туя, секвойя), освещаются международный опыт и ситуация в Ташкенте. По данным Международного центра молекулярной аллергологии, у 27% детей в Ташкенте с симптомами респираторной аллергии выявлена чувствительность к молекуле кипариса *Cup a1*.
Ключевые слова: Кипарисовые *(Cupressaceae)*, поллиноз, аэропалинология, концентрация пыльцы, аллергические заболевания, пыльца деревьев.

Abstract: This text analyzes allergic diseases, which have become an increasingly urgent problem in recent years, particularly pollinosis (pollen allergy) and its prevalence rates. According to data, millions of people worldwide, including 40% of the European population, suffer from this condition. Furthermore, the text provides information about the family *(Cupressaceae)* (cypress family) belonging to the division *(Gymnospermae)* and its representatives (cypress, juniper, thuja, sequoia), highlighting international experiences and the situation in Tashkent. Research by the International Center for Molecular Allergology shows that 27% of children in Tashkent with respiratory allergy symptoms exhibit sensitivity to the cypress molecule *Cup a1*.
Keywords: Cypress family *(Cupressaceae)*, pollinosis, aeropalynology, pollen concentration, allergic diseases, tree pollens.

Kirish

So‘nggi yillarda allergik kasalliklarning muttasil o‘sishi kuzatilmoqda, ular orasida pollinoz yetakchi o‘rinni egallaydi. Organizmlarning turli shamol yordamida changlanadigan o‘simliklar

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Akramjonova Sh.I., Djambekova G.S., Aymetova Sh.K., Rustamova S.R. va boshq. Toshkent shahrida Sarvdoshlar (Cupressaceae) oilasi vakillarining changlanish dinamikasini o‘rganish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 405–408.
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changiga nisbatan yuqori sezuvchanligi (sensibilizatsiyasi) tufayli kelib chiqadigan surunkali mavsumiy allergik kasallik pollinoz (lotincha pollen — «chang») yoki pichan isitmasi sifatida tanilgan.

Allergik rinit bo‘yicha rasmiy tibbiy ta’rifga ko‘ra, pollinoz shilliq qavatlarning, asosan nafas yo‘llari va ko‘zlarning IgE vositasidagi yallig‘lanishidir. Yevropa aholisining 40% pollinozdan — gul changiga allergiya kasalligidan aziyat chekadi. Butun dunyoda qayin changiga nisbatan allergiya alomatlari bo‘lgan bemorlar 100 milliondan ortiqni tashkil qiladi, Yevropada esa qayin changiga nisbatan klinik jihatdan muhim sezuvchanlik taxminan 19,6% ni tashkil qiladi.

Materiallar va metodlar

Lusitan va Arizona sarvlariga (kiparis) nisbatan pollinozni ilk bor 1945-yilda Janubiy Afrikada D. Ordman [1], doim yashil sarvga nisbatan esa 1986-yilda Janubiy Fransiyada R. Panzani [2] tavsiflab bergan. Qora dengiz va O‘rta yer dengizi mintaqasining bir qator xorijiy kurortlarida (Italiya, Fransiya, Ispaniya, Gretsiya, Turkiya, Isroil) doim yashil sarv changiga nisbatan pollinozlar qayd etilgan [3-4].

Toshkent shahrida nafas olish yo‘llari allergiya alomatlari bor va sarvga nisbatan IgE reaktivligi aniqlangan aholi o‘rtasidagi tadqiqotlar ilk bor Xalqaro molekulyar allergologiya markazi ishlarida keltirilgan [5]. Tadqiqotlar shuni ko‘rsatdiki, Arizona sarvi changi eng keng tarqalgan allergen chang turlaridan biriga kiradi va Toshkent shahridagi nafas yo‘llari allergiya alomatlari bo‘lgan tekshiruvdagi bolalarning 27 foizida (4–18 yoshdagilar) sarv changiga nisbatan sezuvchanlik (sarv molekulasi Cup a 1) aniqlangan.

Sarv Ochiq urug‘lilar bo‘limi, Sarvdoshlar *(Cupressaceae)* oilasiga mansub. Bu asosan doim yashil daraxtlar va yoyilib o‘sadigan butalarni o‘z ichiga olgan qadimiy va keng tarqalgan oilalardan biridir. Sarvdoshlar oilasi vakillari Yer yuzining deyarli barcha qit’alarida (Antarktidadan tashqari) tarqalgan bo‘lib, ularning eng katta xilma-xilligi Shimoliy yarimsharning mo‘tadil va iliq mintaqalarida kuzatiladi. Oila 30 ga yaqin turkum va 130–140 ga yaqin turni o‘z ichiga oladi. Ochiq urug‘lilar bo‘limining keng tarqalgan vakillari 1-jadvalda keltirilgan.

1-jadval. Ochiq urug‘li o‘simliklarning yer yuzida keng tarqalgan vakillari

№	Vakillari	Xususiyatlari
1	**Sarv / Kiparis** (*Cupressus*)	Tik o‘suvchi, manzarali daraxt.
2	**Archa / Junipyer** (*Juniperus*)	Tog‘li va quruq hududlarda o‘suvchi doimiy yashil vakil.
3	**Tuya / Biota** (*Thuja / Platycladus*)	Bog‘ va parklarda ko‘p ekiladigan manzarali turkum.
4	**Sekvoya** (*Sequoia*)	Dunyodagi eng ulkan va uzoq yashaydigan daraxtlar.

Ochiq urug‘lilar *(Gymnospermae)* bo‘limiga, jumladan, Sarvdoshlar *(Cupressaceae)* oilasiga mansub o‘simliklar uzluksiz va ommaviy shamol yordamida changlanish (anemofiliya) usuli, chang zarrachalarining yuqori aerobiologik konsentratsiyasi hamda tarkibida o‘ziga xos oqsil-allergenlarning (masalan, *Cup a1*) mavjudligi tufayli yuqori allergenlik faolligiga ega [6].

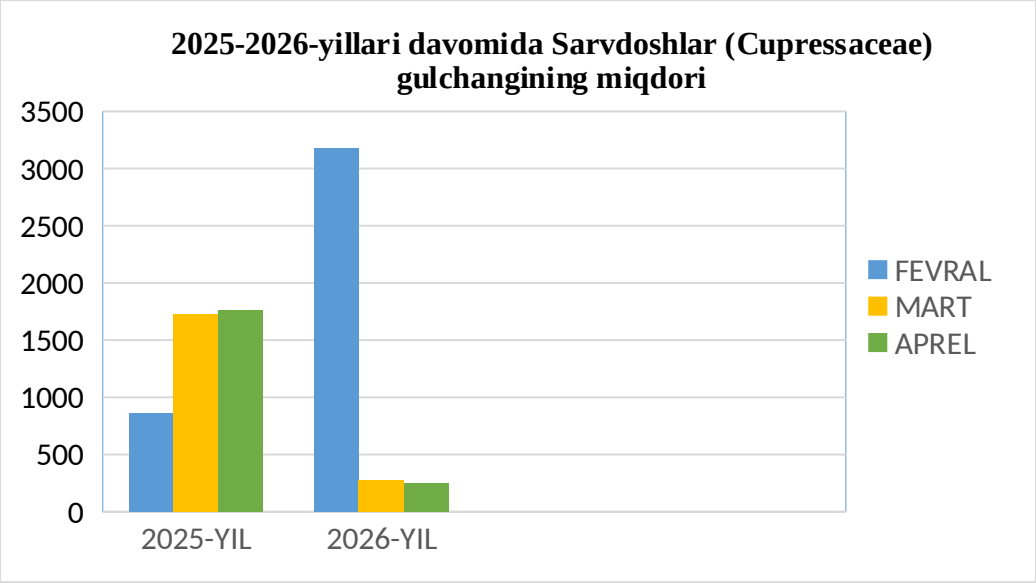
Changlanish davri asosan qishning oxiri va erta bahorda sodir bo‘lib, iqlim sharoitiga qarab fevral oyining oxiridan aprel oyining oxirigacha davom etadi. Changlanish vaqtida erkak qubechalaridan havoga juda ko‘p miqdordagi yengil chang ajralib chiqadi. Natijada havodagi chang hujayralari nafas yo‘llari orqali kirib, burunning shilliq qavatining nozik epiteliy to‘qimasini zararlashi va turli darajadagi allergik kasalliklarni keltirib chiqarishi mumkin. Shuning uchun sarv gullash va uning changi tarqalish davrida allergiyaga moyilligi bor bemorlarda turli darajadagi allergik alomatlar namoyon bo‘lishi mumkin [7].

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Natijalar va muhokama

Sarvdoshlar *(Cupressaceae)* changlanish dinamikasini o‘rganish maqsadida Toshkent shahrida va O‘zbekistonning boshqa hududlarida aerobiologik monitoring o‘tkazildi. Aerobiologik tadqiqotlar Xalqaro molekulyar allergologiya markazi tomonidan 2019-yildan beri olib borilmoqda.

Xalqaro molekulyar allergologiya markazining Aerobiologiya bo‘limida Lanzoni VPPS-2010 rusumidagi chang qopqoni yordamida 7 kun davomida havoda mavjud bo‘lgan barcha turdagi o‘simlik changlari va zamburug‘ sporalariga oid ma’lumotlar yig‘iladi. Shundan so‘ng, olingan chang qaysi o‘simlik yoki zamburug‘ turiga tegishli ekanligini aniqlash uchun maxsus usulda tadqiq qilinadi va uning miqdori hisoblab chiqiladi. Toshkent shahrining aeropalinologik monitoringi shuni ko‘rsatmoqdaki, ushbu o‘simliklar doimiy ravishda havo muhitiga ulkan miqdordagi chang zarrachalarini chiqaradi.



1-rasm. Toshkent shahrida 2025-2026-yillarda Sarv o‘simligining changlanish dinamikasi

Yuqorida keltirilgan 1-rasmdan ko‘rinib turibdiki, 2025–2026-yillar davomida Sarv *(Cupressus)* o‘simligining chang zarrachalari 3 oy mobaynida (ya’ni bevosita changlanish davrida) turlicha darajada namoyon bo‘lgan. 2025-yilning mart va aprel oylarida nisbatan teng daraja kuzatildi, biroq u fevral oyiga nisbatan yuqoriroq bo‘lgan. 2026-yilga nazar tashlaydigan bo‘lsak, mutlaqo teskari ko‘rsatkichni ko‘rishimiz mumkin. Fevral oyida changlanish ikkala yil uchun eng yuqori darajaga yetgan va ikkala yil bilan taqqoslaganda eng yuqori cho‘qqini tashkil etgan. Ushbu yilda mart va aprel oylarida changlanish miqdori deyarli teng darajani, lekin ikkala yilga nisbatan ham eng kam darajani namoyon qilgan.

Xulosa

2025–2026-yillarda o‘tkazilgan aerobiologik kuzatuvlar natijasida Sarv *(Cupressus)* o‘simligining asosiy changlanish davri fevral–aprel oylariga to‘g‘ri kelishi aniqlandi. Ushbu davrda atmosferada sarv chang zarrachalari konsentratsiyasining ortishi allergiyaga moyil bo‘lgan kishilarda mavsumiy allergik rinit, rinokon’yunktivit, yo‘tal va bronxial astma alomatlarining kuchayishiga sabab bo‘lishi mumkin. Sarv changi bilan bog‘liq eng ko‘p uchraydigan klinik alomat allergik rinit, eng noqulay alomatlardan biri esa kon’yunktivit hisoblanadi. Lanzoni hajmiy chang qopqoni yordamida muntazam aerobiologik monitoring o‘tkazish sarv changlanish mavsumining boshlanish, cho‘qqi va tugash muddatlarini aniqlash imkonini beradi. Olingan ma’lumotlar aholini yuqori allergen xavfi mavjud kunlar haqida o‘z vaqtida xabardor qilish, mavsumiy allergik kasalliklarning oldini olish hamda profilaktika tadbirlarini rejalashtirishda muhim ahamiyat kasb etadi. Sarv changiga sezgir bo‘lgan bemorlarga fevral–aprel oylarida aerobiologik ma’lumotlarni muntazam kuzatib borish, chang miqdori yuqori bo‘lgan kunlarda ochiq havoda bo‘lish vaqtini cheklash,

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shuningdek, shifokor-allergolog tavsiyalariga muvofiq profilaktika va davolash choralarini ko‘rish tavsiya etiladi.

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KARPSIMON BALIQLAR PSEVDOMONOZINING PATOMORFOLOGIK DIAGNOSTIKASI VA QARSHI KURASH CHORALARI

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Annotatsiya: Psevdomonoz karpsimon baliqlarni sun’iy yetishtirish xo‘jaliklarida uchraydigan bakterial kasalliklardan biri bo‘lib, baliqlarning tashqi qoplamalari, jabralari va ichki a’zolarida turli darajadagi patologik o‘zgarishlarni yuzaga keltiradi. Kasallikning rivojlanishida Pseudomonas turkumiga mansub bakteriyalar bilan bir qatorda suv muhitining yomonlashuvi, yuqori zichlik, oziqlantirishdagi kamchiliklar va stress omillari muhim ahamiyatga ega. Mazkur maqolada karpsimon baliqlar psevdomonozida kuzatiladigan asosiy klinik va patomorfologik belgilar, ichki a’zolardagi gistologik o‘zgarishlar hamda ularning diagnostik ahamiyati tahlil qilindi. Shuningdek, kasallikning oldini olish va unga qarshi kurashishda sanitariya-gigiyena tadbirlari, suv sifatini nazorat qilish, karantin, xo‘jalik bioxavfsizligi va davolash yondashuvlari yoritildi.

Kalit so‘zlar: psevdomonoz, karpsimon baliqlar, patomorfologiya, diagnostika, Pseudomonas, bakterial kasalliklar, akvakultura, jabralar, lamellalar, nekroz, antibiotiklar.

Аннотация: Псевдомоноз относится к числу бактериальных заболеваний, встречающихся у карповых рыб в условиях искусственного выращивания, и сопровождается патологическими изменениями наружных покровов, жабр и внутренних органов различной степени выраженности. В развитии заболевания наряду с бактериями рода Pseudomonas важное значение имеют ухудшение качества воды, высокая плотность посадки, нарушения кормления и стрессовые факторы. В статье рассмотрены основные клинические и патоморфологические признаки псевдомоноза карповых рыб, гистологические изменения внутренних органов и их диагностическое значение. Освещены также основные подходы к профилактике и борьбе с заболеванием, включая санитарно-гигиенические мероприятия, контроль качества воды, карантин, биобезопасность рыбоводных хозяйств и рациональное применение антибактериальных препаратов с учетом результатов лабораторной диагностики.

Ключевые слова: псевдомоноз, карповые рыбы, патоморфология, диагностика, Pseudomonas, бактериальные болезни, аквакультура, жабры, ламеллы, некроз, антибиотики.

Abstract: Pseudomonosis is one of the bacterial diseases occurring in cyprinid fish under aquaculture conditions and is associated with pathological changes of the external integument, gills, and internal organs of varying severity. In addition to bacteria of the genus Pseudomonas, the development of the disease is influenced by poor water quality, high stocking density, inadequate feeding, and stress factors. This article examines the main clinical and pathomorphological signs of pseudomonosis in cyprinid fish, histological changes in internal organs, and their diagnostic significance. Particular attention is also given to preventive and control measures, including sanitary and hygienic practices, water-quality monitoring, quarantine, farm biosecurity, and the rational use of antibacterial drugs based on laboratory diagnostic results and antimicrobial susceptibility testing.

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Keywords: pseudomonosis, cyprinid fish, pathomorphology, diagnosis, Pseudomonas, bacterial diseases, aquaculture, gills, lamellae, necrosis, antibiotics.

Mavzuning dolzarbligi

Akvakultura oziq-ovqat xavfsizligini ta’minlash, aholini biologik qiymati yuqori bo‘lgan oqsil mahsulotlari bilan ta’minlash va qishloq xo‘jaligini diversifikatsiya qilishda muhim ahamiyatga ega bo‘lgan jadal rivojlanayotgan tarmoqlardan biridir. Baliq yetishtirish hajmining ortishi bilan bir qatorda, baliqchilik xo‘jaliklarida turli yuqumli va invazion kasalliklarning tarqalish xavfi ham ortib bormoqda. Ayniqsa, intensiv yetishtirish sharoitida yuqori zichlik, suv sifatining yomonlashuvi, organik moddalarning to‘planishi, oziqlantirishdagi nomutanosiblik va stress omillari baliqlarning tabiiy rezistentligini pasaytirib, opportunistik mikroorganizmlarning patogen xususiyatlarini namoyon etishiga sharoit yaratadi. Karpsimon baliqlar akvakulturada eng ko‘p yetishtiriladigan baliq guruhlaridan biri hisoblanadi. Sazan (Cyprinus carpio), oq amur (Ctenopharyngodon idella) va oq do‘ngpeshona (Hypophthalmichthys molitrix) kabi turlar turli bakterial kasalliklarga moyil bo‘lishi mumkin. Shular qatorida Pseudomonas turkumiga mansub bakteriyalar bilan bog‘liq infeksiyalar ham muhim o‘rin tutadi. Psevdomonozning rivojlanishida mikroorganizmlarning virulentlik xususiyatlari bilan bir qatorda xo‘jayin organizmining fiziologik holati va tashqi muhit omillari muhim ahamiyatga ega. Suvning fizik-kimyoviy ko‘rsatkichlarining me’yordan chetga chiqishi, kislorod tanqisligi, haroratning keskin o‘zgarishi, baliqlarning zich joylashtirilishi va mexanik shikastlanishlar infeksion jarayon rivojlanishi uchun qulay sharoit yaratishi mumkin. Kasallik klinik jihatdan teri qoplamalarining zararlanishi, gemorragik o‘choqlar, yaralar, tangachalarning tushishi, suzgichlarning shikastlanishi va umumiy holatning yomonlashuvi bilan namoyon bo‘lishi mumkin. Og‘ir kechgan hollarda infeksiya sistemali tus olib, ichki a’zolarda ham patologik o‘zgarishlar rivojlanadi. Shu sababli baliq kasalliklarini erta aniqlashda klinik, bakteriologik va patomorfologik tekshiruvlarni kompleks qo‘llash muhim ahamiyatga ega. Patomorfologik tekshiruvlar kasallik jarayonining xarakteri, tarqalish darajasi va asosiy nishon a’zolarini aniqlash imkonini beradi.

Baliqlarning bakterial kasalliklari, jumladan, Pseudomonas turkumiga mansub bakteriyalar bilan bog‘liq infeksiyalar veterinariya va ixtiopatologiya adabiyotlarida keng yoritilgan. V.F. Vanyatinskiy va hammualliflar tomonidan baliqlarning yuqumli kasalliklari, ularning klinik belgilari, patogenezi va diagnostikasiga oid ma’lumotlar keltirilgan [1]. O.N. Bauer va hammualliflar hovuz baliqlarining kasalliklari, jumladan, bakterial kasalliklarning rivojlanishiga ta’sir qiluvchi omillar hamda profilaktik tadbirlarning ahamiyatini yoritgan [2]. L.I. Grishchenko ma’lumotlariga ko‘ra, Pseudomonas turkumiga mansub mikroorganizmlar suv muhitida keng tarqalgan bo‘lib, noqulay ekologik va zoogigiyenik sharoitlarda baliqlarda kasallik jarayonlarini yuzaga keltirishi mumkin [6]. V.P. Mochalkin baliqlarning infeksion kasalliklarida teri, mushaklar va ichki a’zolarda kuzatiladigan patologik o‘zgarishlarga e’tibor qaratgan [7]. R.J. Roberts baliqlarning bakterial kasalliklarini tavsiflar ekan, sistemali infeksiya holatlarida gemorragik va nekrotik jarayonlar, shuningdek, ichki a’zolarning zararlanishi kuzatilishi mumkinligini qayd etadi [5]. B. Austin va D.A. Austin baliqlarda kasallik chaqiruvchi bakteriyalarning biologik xususiyatlari, virulentlik omillari va diagnostikasi masalalarini batafsil yoritgan [3]. E.J. Noga baliq kasalliklari diagnostikasida klinik, mikrobiologik va gistopatologik usullarni kompleks qo‘llash zarurligini ta’kidlaydi. Uning ma’lumotlariga ko‘ra, bakterial infeksiyalarda jabralarda epiteliy giperplaziyasi, shish, lamellalar tuzilishining buzilishi va nekrotik jarayonlar kuzatilishi mumkin [4]. Zamonaviy baliqchilik xo‘jaliklarida kasalliklarning rivojlanishi ko‘pincha bitta etiologik omil bilan emas, balki mikroorganizmlar, baliq organizmi va tashqi muhit o‘rtasidagi murakkab o‘zaro ta’sir bilan bog‘liq. Shu sababli psevdomonozning diagnostikasida faqat morfologik belgilar bilan cheklanib qolmasdan, bakteriologik yoki molekulyar-biologik tekshiruvlar bilan tasdiqlash maqsadga muvofiq.

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1-rasm. Psevdomonozga chalingan baliqning klinik belgilari

Tadqiqotning maqsadi

Tadqiqotning maqsadi karpsimon baliqlarda psevdomonoz bilan bog‘liq asosiy klinik va patomorfologik o‘zgarishlarni tahlil qilish, ularning diagnostik ahamiyatini baholash hamda baliqchilik xo‘jaliklarida kasallikning oldini olish va unga qarshi kurashishning samarali yondashuvlarini umumlashtirishdan iborat.

Tadqiqot materiallari va usullari

Psevdomonozni diagnostika qilishda klinik, patomorfologik, gistologik va bakteriologik usullardan kompleks foydalanish maqsadga muvofiq. Klinik tekshiruvda baliqlarning umumiy holati, harakatlanishi, ishtahasi, tana yuzasi, suzgichlari, jabralari va ko‘zlarining holati baholanadi.

Patomorfologik tekshiruv davomida baliqlarning tashqi qoplamalari, mushaklari, jabralari va ichki a’zolari makroskopik jihatdan tekshiriladi. Bunda gemorragiyalar, giperemiya, shish, nekroz, yara o‘choqlari, jigar va buyraklardagi patologik o‘zgarishlar qayd etiladi. Gistologik tekshiruv uchun patologik materialdan to‘qima namunalari olinib, standart usullar yordamida fiksatsiya qilinadi, parafin bloklariga joylashtiriladi, kesmalar tayyorlanadi va gematoksilin-eozin bilan bo‘yaladi. Mikroskopik tekshiruvda hujayralardagi distrofik va nekrotik o‘zgarishlar, yallig‘lanish infiltratsiyasi, qon tomirlaridagi o‘zgarishlar hamda to‘qima tuzilishining buzilishi baholanadi. Bakteriologik tekshiruv kasallik etiologiyasini aniqlash va ajratib olingan mikroorganizmlarning antibiotiklarga sezgirligini baholash uchun amalga oshiriladi. Zarurat bo‘lganda zamonaviy molekulyar-biologik usullar ham qo‘llanishi mumkin.

Tadqiqot natijalari

Psevdomonoz bilan kasallangan karpsimon baliqlarda tashqi va ichki a’zolarda turli darajadagi patologik o‘zgarishlar kuzatilishi mumkin. Kasallikning klinik ko‘rinishi baliq turi, yosh guruhi, immunologik holati, infeksion agentning xususiyatlari va tashqi muhit sharoitlariga bog‘liq. Makroskopik tekshiruvda tana yuzasida qizarish, qon quyilishlar, yara va eroziya o‘choqlari aniqlanishi mumkin. Ayrim hollarda tangachalarning tushishi, teri qoplamalarining yemirilishi va suzgichlar asosida gemorragik o‘zgarishlar kuzatiladi. Jarayon chuqurlashganda teri osti va mushak to‘qimalarida nekrotik o‘choqlar shakllanishi mumkin. Jabralarda giperemiya, shish, epiteliy qavatining qalinlashishi va ikkilamchi lamellalar tuzilishining buzilishi kuzatilishi mumkin. Og‘ir holatlarda lamellalarning bir-biriga yopishishi va nekrotik jarayonlar rivojlanishi nafas olish yuzasining kamayishiga olib keladi. Natijada baliqlarda nafas olishning qiyinlashuvi va suv yuzasiga yaqin joyda to‘planish kabi klinik belgilar paydo bo‘lishi mumkin. Ichki a’zolarda ham xarakterli o‘zgarishlar kuzatiladi. Jigarda giperemiya, rangning o‘zgarishi, shish va turli kattalikdagi nekrotik o‘choqlar aniqlanishi mumkin. Gistologik jihatdan gepatotsitlarda donador va yog‘li distrofiya, hujayralar nekrozi hamda yallig‘lanish reaksiyalari qayd etilishi mumkin. Buyraklarda gemopoetik to‘qimaning zararlanishi, buyrak kanalchalarida degenerativ o‘zgarishlar va yallig‘lanish

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infiltratsiyasi kuzatilishi mumkin. Taloqda esa qon dimlanishi, kattalashish va to‘qimaning rang o‘zgarishi kabi makroskopik belgilar aniqlanishi mumkin. Teri va mushak to‘qimalarining mikroskopik tekshiruvida nekrotik jarayonlar, hujayralar degeneratsiyasi, qon tomirlarining kengayishi va yallig‘lanish hujayralari infiltratsiyasi aniqlanishi mumkin. Shuni ta’kidlash lozimki, yuqoridagi patomorfologik o‘zgarishlar psevdomonoz uchun mutlaq spetsifik belgilar hisoblanmaydi. Shu sababli yakuniy etiologik tashxisni faqat makroskopik yoki gistologik o‘zgarishlarga asoslash to‘g‘ri emas. Tashxisni tasdiqlash uchun klinik va patomorfologik ma’lumotlarni bakteriologik yoki boshqa laboratoriya tekshiruvlari natijalari bilan birgalikda baholash zarur.

Psevdomonozga qarshi kurash va profilaktika choralari

Psevdomonozning oldini olishda asosiy e’tibor baliqlarni optimal saqlash sharoitlarini yaratish va xo‘jalik bioxavfsizligini ta’minlashga qaratilishi lozim.

Asosiy profilaktik tadbirlarga quyidagilar kiradi:

- suvning harorati, erigan kislorod miqdori, pH va boshqa muhim gidrokimyoviy ko‘rsatkichlarni muntazam nazorat qilish;
- baliqlarni me’yoriy zichlikda saqlash;
- hovuzlarda organik moddalarning ortiqcha to‘planishiga yo‘l qo‘ymaslik;
- sifatli va muvozanatlangan ozuqadan foydalanish;
- yangi keltirilgan baliqlarni karantin sharoitida saqlash;
- kasallik alomatlari kuzatilgan baliqlarni imkon qadar tez ajratish;
- hovuzlar va inventarlarni sanitariya ishlovidan o‘tkazish;
- nobud bo‘lgan baliqlarni o‘z vaqtida yig‘ish va belgilangan veterinariya-sanitariya talablariga muvofiq utilizatsiya qilish.

Kasallik aniqlanganda davolash strategiyasi laboratoriya diagnostikasi natijalariga asoslanishi kerak. Antibakterial preparatlarni qo‘llashdan oldin imkon qadar qo‘zg‘atuvchini aniqlash va uning antimikrob preparatlarga sezgirligini baholash maqsadga muvofiq. Antibiotiklardan nazoratsiz yoki profilaktik maqsadda foydalanish antimikrob rezistentlikning shakllanishiga olib kelishi mumkin.



2-rasm. Psevdomonozga gumon qilingan baliq tanasidagi yallig‘lanishlar

Suv havzalarida kimyoviy vositalardan foydalanish ham tegishli veterinariya-sanitariya me’yorlari, preparatning ruxsat etilgan qo‘llanish sohasi, baliq turi, suvning fizik-kimyoviy ko‘rsatkichlari va ekologik xavfsizlik talablari hisobga olingan holda amalga oshirilishi kerak.

Xulosa

Karpsimon baliqlarda psevdomonoz bilan bog‘liq infeksion jarayonlar tashqi qoplamalar, jabralar va ichki a’zolarning zararlanishi bilan kechishi mumkin. Kasallikning asosiy patomorfologik belgilariga gemorragik o‘zgarishlar, yallig‘lanish, nekrotik jarayonlar, jigar va buyraklardagi degenerativ o‘zgarishlar hamda jabra apparatining strukturaviy buzilishlari kiradi. Patomorfologik tekshiruv kasallik jarayonining tarqalishi va zararlangan a’zolarni aniqlashda muhim diagnostik ahamiyatga ega. Biroq aniqlangan morfologik o‘zgarishlar ko‘plab bakterial va boshqa kasalliklarda

uchrashi mumkinligi sababli etiologik tashxisni bakteriologik yoki boshqa laboratoriya usullari bilan tasdiqlash zarur. Psevdomonozning oldini olishda suv sifatini nazorat qilish, optimal zichlikni ta’minlash, to‘laqonli oziqlantirish, karantin, sanitariya-gigiyena va bioxavfsizlik tadbirlarini muntazam amalga oshirish muhim ahamiyatga ega. Davolashda antibakterial preparatlardan foydalanish esa laboratoriya diagnostikasi va antimikrob sezgirlik natijalariga asoslangan holda, amaldagi veterinariya talablari doirasida olib borilishi lozim.

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KARPSIMON BALIQLARDA BRONXIOMIKOZNING TARQALISHI VA OLDINI OLISH TADBIRLARI

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Annotatsiya: Ushbu maqolada karpsimon baliqlarda uchraydigan xavfli infeksion-mikotik kasalliklardan biri - bronxiomikozning tarqalishi, kasallik qo‘zg‘atuvchisining biologik xususiyatlari, epizootologik omillari, klinik belgilari, patologik o‘zgarishlari hamda oldini olish tadbirlari yoritilgan. Bronxiomikoz, ya’ni “jabra chirishi”, asosan Branchiomyces avlodiga mansub B. sanguinis va B. demigrans zamburug‘lari bilan bog‘liq bo‘lib, karpsimon baliqlarning jabra apparatini zararlaydi. Qo‘zg‘atuvchi jabraning qon tomirlarida rivojlanib, qon aylanishining buzilishi, tromboz, ishemiya va nekrotik jarayonlarning shakllanishiga sabab bo‘ladi. Kasallikning rivojlanishida suv haroratining ko‘tarilishi, organik moddalarning ko‘pligi, suv almashinuvining yetarli emasligi, baliqlarning zich joylashtirilishi, ortiqcha oziqlantirish, zoogigiyenik talablarning buzilishi va baliqlarning stress holati muhim ahamiyatga ega. Ayniqsa, suv harorati 20-25 °C dan yuqori bo‘lgan davrda kasallikning avj olishi kuzatilishi mumkin. Maqolada bronxiomikozni oldini olishda suv sifatini muntazam nazorat qilish, havzalarni quritish va dezinfeksiya qilish, kasal va o‘lgan baliqlarni tezda ajratish, yangi baliqlarni karantin qilish, inventar va ovlash jihozlarini dezinfeksiyalash, me’yoriy zichlikda baliq yetishtirish hamda suv almashinuvini yaxshilashning ahamiyati ko‘rsatib berilgan. Ilmiy manbalar tahlili kasallikni davolashdan ko‘ra profilaktik tadbirlarni muntazam tashkil etish iqtisodiy va veterinariya nuqtayi nazaridan samaraliroq ekanligini ko‘rsatadi.

Kalit so‘zlar: karpsimon baliqlar, bronxiomikoz, Branchiomyces sanguinis, Branchiomyces demigrans, jabra, zamburug‘, mikoz, infeksiya, baliq kasalliklari, karp, sazan, karas, nekroz, tromboz, gipoksiya, suv sifati, organik moddalar, harorat, aeratsiya, dezinfeksiya, profilaktika, epizootologiya, sun’iy suv havzasi, baliqchilik xo‘jaligi, sanitariya.

Аннотация: В статье представлены современные научные сведения о распространении бронхиомикоза у карповых рыб, биологии возбудителей, эпизоотологических факторах, клинических признаках, патологоанатомических изменениях и профилактических мероприятиях. Бронхиомикоз, или «жаберная гниль», является опасным инфекционным микозом рыб, поражающим жаберный аппарат. Основными возбудителями заболевания считаются грибы рода Branchiomyces, прежде всего B. sanguinis и B. demigrans. B. sanguinis преимущественно развивается в кровеносных сосудах жабр, вызывая нарушение кровообращения, тромбоз, ишемию и некроз жаберной ткани. B. demigrans способен развиваться как внутри кровеносных сосудов, так и в окружающих тканях.

Возникновению заболевания способствуют повышение температуры воды, накопление органических веществ, ухудшение гидрохимического режима, недостаточный водообмен, высокая плотность посадки, избыточное кормление и нарушение санитарно-гигиенических

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требований. При тяжелом течении поражение жаберной ткани приводит к нарушению газообмена и массовой гибели рыб вследствие асфиксии. Профилактика основывается на поддержании оптимального качества воды, своевременном удалении погибшей рыбы, соблюдении плотности посадки, карантинировании поступающего рыбопосадочного материала, дезинфекции инвентаря и регулярной санитарной обработке рыбоводных водоемов.

Ключевые слова: карповые рыбы, бронхиомикоз, Branchiomyces sanguinis, Branchiomyces demigrans, жабры, гриб, микоз, инфекция, карп, сазан, карась, некроз, тромбоз, гипоксия, вода, температура, органические вещества, аэрация, дезинфекция, профилактика, эпизоотология, рыбоводство, искусственный водоем, санитария.

Abstract: This article summarizes scientific information on the occurrence and prevention of branchiomycosis in cyprinid fish, including the biology of the causative agents, epidemiological factors, clinical signs, pathological changes and preventive measures. Branchiomycosis, commonly known as gill rot, is an important fungal disease affecting the gill apparatus of freshwater fish. The disease is mainly associated with fungi of the genus Branchiomyces, particularly B. sanguinis and B. demigrans. B. sanguinis is predominantly localized in the blood vessels of the gills, where fungal hyphae may obstruct blood flow and induce thrombosis, ischemia and necrosis. B. demigrans can develop both within and outside the blood vessels. The development of branchiomycosis is associated with elevated water temperature, high concentrations of organic matter, insufficient water exchange, excessive stocking density, overfeeding and poor sanitary management. Severe lesions of the gill tissue impair respiration and may result in rapid mortality. Preventive measures should include regular monitoring of water quality, adequate aeration and water exchange, removal of dead fish, quarantine of newly introduced fish, disinfection of equipment, proper stocking density and periodic sanitary treatment of ponds. Particular attention should be paid to prevention during warm periods when environmental conditions may favour disease development.

Keywords: cyprinid fish, branchiomycosis, Branchiomyces sanguinis, Branchiomyces demigrans, gills, fungus, mycosis, infection, carp, common carp, crucian carp, necrosis, thrombosis, hypoxia, water quality, temperature, organic matter, aeration, disinfection, prevention, epizootology, aquaculture, artificial pond, sanitation.

Kirish

Baliqchilik xo‘jaliklarida yetishtirilayotgan karpsimon baliqlar aholini sifatli oqsil mahsulotlari bilan ta’minlashda muhim biologik va iqtisodiy resurs hisoblanadi. Baliq yetishtirish texnologiyalarining intensivlashuvi bilan birga baliqlarda turli infeksion, invazion va mikotik kasalliklarning yuzaga kelish xavfi ham ortmoqda. Shunday kasalliklardan biri bronxiomikoz bo‘lib, u asosan baliqlarning jabra apparatini zararlashi bilan tavsiflanadi. Kasallikning asosiy xavfi shundaki, jabralar baliqlarda nafas olish, gaz almashinuvi va osmoregulyatsiyada muhim organ hisoblanadi. Jabra qon tomirlarida zamburug‘ giflarining rivojlanishi qon aylanishini buzib, tromboz, ishemiya va nekrozni keltirib chiqaradi. Natijada baliqning kislorodga bo‘lgan ehtiyoji qondirilmaydi va og‘ir holatlarda asfiksiya tufayli o‘lim kuzatiladi. Shu sababli karpsimon baliqlarda bronxiomikozning tarqalish sabablarini o‘rganish, xavf omillarini aniqlash va xo‘jaliklarda samarali profilaktik tizimni ishlab chiqish zamonaviy baliqchilikning dolzarb vazifalaridan biridir.

Mavzuning dolzarbligi

Bugungi kunda akvakultura dunyoning ko‘plab mamlakatlarida oziq-ovqat xavfsizligini ta’minlash, aholini sifatli hayvon oqsili bilan ta’minlash va qishloq xo‘jaligi ishlab chiqarishining samaradorligini oshirishning muhim yo‘nalishlaridan biri hisoblanadi. Baliqchilik xo‘jaliklarining rivojlanishi bilan baliqlarni yuqori zichlikda yetishtirish, ozuqa miqdorini oshirish, suv resurslaridan intensiv foydalanish va yopiq yoki yarim yopiq suv tizimlaridan foydalanish kengaymoqda. Bunday texnologiyalar ishlab chiqarish samaradorligini oshirishi bilan birga baliqlarning fiziologik stressini kuchaytirishi va yuqumli kasalliklarga moyilligini oshirishi mumkin. Intensiv yetishtirish sharoitida

suv sifati, organik yuklama, zichlik, harorat va boshqa omillar baliq sog‘lig‘ining asosiy determinantlariga aylanadi. Karpsimon baliqlar, xususan, karp, sazan, karas va ularning turli gibridlari sun’iy suv havzalarida keng yetishtiriladi. Ushbu baliqlarda uchraydigan kasalliklar orasida bronxiomikoz alohida epidemiologik va iqtisodiy ahamiyatga ega. Kasallik jabra apparatini zararlashi sababli uning klinik rivojlanishi juda tez kechishi mumkin. Jabra to‘qimalarining katta qismi zararlanganda baliqning nafas olish faoliyati keskin buziladi va qisqa muddat ichida yuqori o‘lim kuzatilishi mumkin. Ilmiy manbalarda og‘ir holatlarda kasallikdan nobud bo‘lish ko‘rsatkichi 50 foizgacha yetishi mumkinligi qayd etilgan. Bronxiomikozning dolzarbligi, avvalo, uning ekologik sharoit bilan chambarchas bog‘liqligidadir. Kasallikning rivojlanishiga suvda organik moddalarning ko‘payishi, suvning haddan tashqari “gullashi”, suv almashinuvining kamayishi va yuqori harorat qulay sharoit yaratadi. Ayniqsa, suv harorati 20 °C dan yuqori bo‘lganda kasallik rivojlanish xavfi ortadi. Issiq davrda suvdagi erigan kislorod miqdorining kamayishi bilan birga baliqlarning fiziologik zo‘riqishi kuchayadi. Bu esa jabra shilliq qavatining himoya xususiyatlarini pasaytirishi va qo‘zg‘atuvchining rivojlanishiga imkon yaratishi mumkin. Kasallikning yana bir muhim xususiyati uning ko‘pincha xo‘jalik boshqaruvidagi kamchiliklar bilan bog‘liq bo‘lishidir. Adabiyotlarda *Branchiomyces* infeksiyasi ayrim hollarda “bad-management disease”, ya’ni xo‘jalikni noto‘g‘ri boshqarish bilan bog‘liq kasallik sifatida tavsiflanadi. Bunga suv sifatining yomonlashuvi, organik chiqindining ortishi, ortiqcha oziqlantirish, suv almashinuvining yetarli emasligi va baliqlarning zich saqlanishi kiradi. Oziqlantirish masalasi ham alohida ahamiyatga ega.



1-rasm. Bronxiomikoz bilan zararlangan baliq jabrasining ko‘rinishi

Baliqlarga me’yoridan ortiq yem berilganda uning iste’mol qilinmagan qismi suv muhitida parchalanib, organik moddalar miqdorini oshiradi. Organik moddalar bakterial va zamburug‘ mikrofloraning rivojlanishi uchun qulay muhit yaratadi. Natijada suvning biokimyoviy ko‘rsatkichlari o‘zgaradi, kislorodga bo‘lgan biokimyoviy talab ortadi va baliqlarning umumiy rezistentligi pasayadi. Bronxiomikozning tarqalishida kasallangan baliqlar muhim infeksiya manbai hisoblanadi. Shuningdek, tashqi klinik belgilari hali namoyon bo‘lmagan baliqlar ham qo‘zg‘atuvchini tashishi va tashqi muhitga chiqarishi mumkin. Kasallikning suv va kontakt yo‘li bilan tarqalishi sababli bir havzada kasallik paydo bo‘lgandan keyin uning boshqa baliqlarga o‘tish ehtimoli yuqori bo‘ladi. Suv, loy, havza tubidagi tuproq, o‘lgan baliqlar, jabra to‘qimalari, yem, ovlash vositalari, to‘rlar va boshqa inventarlar mexanik yoki ekologik tashuvchi omillar bo‘lishi mumkin.

Shu nuqtayi nazardan baliqchilik xo‘jaliklarida bronxiomikozga qarshi faqat kasallik yuzaga kelgandan keyin kurashish yetarli emas.

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2-rasm. Bronxiomikoz bilan zararlangan baliq jabrasining marmar holatdagi ko‘rinishi

Profilaktika kasallikning oldini olishga yo‘naltirilgan kompleks veterinariya-sanitariya tizimi sifatida tashkil etilishi kerak. Birinchi navbatda, xo‘jalikka olib kiriladigan baliq materiallarini veterinariya nazoratidan o‘tkazish va karantin qilish talab etiladi. Yangi baliqlarni bevosita asosiy havzaga qo‘shib yuborish epizootik xavfni oshiradi. Ayniqsa, turli xo‘jaliklardan baliq ko‘chirilganda qo‘zg‘atuvchilarning yangi suv havzasiga kirib kelishi mumkin. Ikkinchidan, havzalar sanitariya holatini nazorat qilish zarur. Qish mavsumida imkon qadar suv havzalarini quritish, tubidagi organik qoldiqlarni kamaytirish, zarur hollarda dezinfeksiya tadbirlarini o‘tkazish muhim profilaktik chora hisoblanadi. Ilmiy manbalarda havzalarni quritish, ohaklash va sanitariya holatini yaxshilash bronxiomikoz xavfini kamaytiruvchi tadbirlar sifatida ko‘rsatiladi. Uchinchidan, suvning fizik-kimyoviy ko‘rsatkichlarini muntazam nazorat qilish lozim. Harorat, erigan kislorod, pH, ammiak, nitrit, organik moddalar va suvning tiniqligi xo‘jalikning kundalik veterinariya nazoratida bo‘lishi kerak. Ayniqsa yoz oylarida ertalabki va kechki kislorod ko‘rsatkichlarini kuzatish muhim, chunki suv o‘simliklari va fitoplanktonning tungi nafas olishi sababli tong oldidan kislorod miqdori pasayishi mumkin. To‘rtinchidan, baliqlarni ortiqcha zichlikda saqlamaslik kerak. Zichlik oshishi baliqlarning bir-biri bilan kontaktini kuchaytiradi, suvning organik yuklamasini oshiradi va stressni kuchaytiradi. Stress holatidagi baliqlarning immun fiziologik holati yomonlashishi natijasida infeksion kasalliklarga moyillik ortadi. Beshinchidan, aeratsiya va suv almashinuvini yaxshilash bronxiomikoz xavfi yuqori bo‘lgan davrlarda alohida ahamiyatga ega. Kasallik paydo bo‘lgan havzalarda suv almashinuvini kuchaytirish, organik ifloslanishni kamaytirish va o‘lik baliqlarni tezda olib tashlash tavsiya etiladi. Shuningdek, bronxiomikozni boshqa jabra kasalliklaridan farqlash diagnostik jihatdan muhim. Saprolegnioz, bakterial jabra kasalliklari, parazitar zararlanishlar va toksik shikastlanishlar ham jabralarda o‘xshash o‘zgarishlarni yuzaga keltirishi mumkin. Shu sababli faqat tashqi klinik belgilar asosida yakuniy tashxis qo‘yish maqsadga muvofiq emas. Mikroskopik tekshiruv, patologik materialni o‘rganish va imkoniyat bo‘lsa zamonaviy laboratoriya diagnostikasi qo‘llanishi kerak. Bronxiomikozda jabra to‘qimasining “marmarsimon” ko‘rinishga kelishi muhim klinik-patologik belgilaridan biridir. Qon tomirlarining zamburug‘ giflari bilan to‘silishi natijasida ayrim joylar to‘q qizil, jigarrang, kulrang yoki oqish rangga ega bo‘lishi mumkin. Keyinchalik qon aylanishining buzilishi natijasida nekroz rivojlanadi va jabra plastinkalarining ayrim qismlari yemiriladi. Kasallikning iqtisodiy zarari nafaqat nobud bo‘lgan baliqlar bilan, balki o‘sish sur’atining pasayishi, yemdan foydalanish samaradorligining kamayishi, davolash va dezinfeksiya xarajatlarining oshishi bilan ham belgilanadi. Shuning uchun bronxiomikozning oldini olish baliqchilik xo‘jaligining biologik xavfsizligi bilan bir qatorda iqtisodiy samaradorligini ham ta’minlaydi. Bizni sharoitda ushbu masala ayniqsa dolzarb. Respublikada karpsimon baliqlarni sun’iy suv havzalarida yetishtirishning kengayishi bilan suv havzalarining sanitariya holati, yuqori yozgi harorat, organik yuklama va suv almashinuvi bilan bog‘liq muammolar baliq kasalliklari uchun qulay sharoit yaratishi mumkin. Mutaxassislar tomonidan ham bronxiomikozning oldini olish, uni yuzaga keltiruvchi omillarni aniqlash va baliqchilik xo‘jaliklarida veterinariya-sanitariya tadbirlarini takomillashtirish bo‘yicha ilmiy ishlar olib borilmoqda. Demak, bronxiomikozga qarshi kurashda eng samarali yondashuv - kasallik paydo bo‘lishini kutmasdan, xavf omillarini oldindan bartaraf etish hisoblanadi.

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Bunda suv sifati, baliqlar zichligi, oziqlantirish, karantin, dezinfeksiya, aeratsiya va muntazam veterinariya nazorati yagona profilaktik tizim sifatida qaralishi lozim.

Qo‘zg‘atuvchining biologiyasi

Bronxiomikozning asosiy qo‘zg‘atuvchilari *Branchiomyces* avlodiga mansub zamburug‘lardir. Ilmiy manbalarda karpsimon baliqlarda, ayniqsa, *Branchiomyces sanguinis* muhim qo‘zg‘atuvchi sifatida ko‘rsatiladi. *B. demigrans* esa ayrim boshqa baliq turlarida, jumladan tabiiy havza baliqlarida uchrashi mumkin; ayrim baliqlarda ikki tur birgalikda uchrashi ham qayd etilgan. *Branchiomyces sanguinis* giflari odatda septasiz, shoxlangan tuzilishga ega bo‘lib, jabraning qon tomirlarida joylashadi. Ilmiy tavsiflarda giflarning qalinligi taxminan 8-30 mkm diapazonda berilgan. Spora hosil bo‘lish jarayonida giflarning ayrim qismlari qalinlashishi va ichida sporalar shakllanishi kuzatiladi. Qo‘zg‘atuvchi jabra qon tomirlariga tushgach, giflar o‘sib, qon oqimini mexanik ravishda to‘sadi. Natijada tromboz va qon aylanishining buzilishi rivojlanadi. Jabraning ayrim qismlari kislorod bilan ta’minlanmay qoladi, ishemiya va keyinchalik nekroz paydo bo‘ladi. Shu sababli bronxiomikozda kasallikning asosiy patogenetik mexanizmi - jabra qon tomirlarining zamburug‘ giflari bilan zararlanishi va qon aylanishining buzilishidir. Infeksiya manbai kasallangan baliqlar, o‘lgan baliqlar va klinik belgilari bo‘lmagan, ammo qo‘zg‘atuvchini tashuvchi baliqlar bo‘lishi mumkin. Qo‘zg‘atuvchining tarqalishida suv, loy, havza tubi, o‘lgan baliq qoldiqlari, yem, to‘rlar va inventarlar muhim rol o‘ynaydi.

Tarqalish sabablari

Bronxiomikozning tarqalishiga quyidagi omillar asosiy ta’sir ko‘rsatadi:

- Suv haroratining ko‘tarilishi. 20 °C dan yuqori harorat kasallikning rivojlanishi uchun qulay sharoit yaratishi mumkin.
- Organik moddalar ko‘pligi. Chirigan o‘simliklar, baliq chiqindilari, ortiqcha yem va loyqa suv xo‘jalikdagi mikrobiologik yuklamani oshiradi.
- Suv almashinuvining yomonligi. Kam oqimli yoki turg‘un suvli havzalarda kasallik xavfi yuqorilaydi.
- Baliqlarning yuqori zichlikda saqlanishi. Bu stressni va suvning biologik yuklamasini oshiradi.
- Ortiqcha oziqlantirish. Iste’mol qilinmagan yemning parchalanishi suv sifatining yomonlashuviga olib keladi.
- Kasal baliqlarni boshqa havzalarga ko‘chirish. Bu qo‘zg‘atuvchining yangi hududga kirib kelishiga sabab bo‘lishi mumkin.
- Inventarlarning dezinfeksiya qilinmasligi. To‘r, chelak, nasos, transport idishlari va boshqa vositalar mexanik tashuvchi bo‘lishi mumkin.
- Havzalarni qishda quritmaslik. Uzoq vaqt foydalanilgan havzalarda organik qoldiqlarning to‘planishi epizootik xavfni oshiradi. O‘zbekistondagi ilmiy manbalarda ham havzalarni to‘g‘ri tashkil etmaslik, qishda quritmaslik, noto‘g‘ri oziqlantirish va yangi baliqlarni veterinariya nazoratisiz olib kirish bronxiomikoz xavf omillari sifatida qayd etilgan.

Klinik belgilari

Bronxiomikozning klinik belgilari kasallikning rivojlanish bosqichiga qarab farqlanadi. Dastlab baliqlar yemga qiziqishini kamaytiradi, sust harakat qiladi, tashqi ta’sirlarga javobi pasayadi, suvning yuzasiga yoki suv kiradigan joylarga to‘planadi, tez-tez va kuchli nafas oladi. Kasallik kuchayganda baliqlar suv yuzasida vertikal holatda yoki yonboshlab suzishi mumkin. Jabra qopqoqlarining harakati tezlashadi. Jabralarning tabiiy qizil rangi o‘zgarib, jigarrang, kulrang yoki oqish nekrotik o‘choqlar paydo bo‘ladi. Patologoanatomik tekshiruvda jabra yaproqlarining marmarsimon ko‘rinishi, qon quyilishlar, nekroz, eroziya, ayrim qismlarning tushib qolishi va tog‘ay asosining ochilib qolishi kuzatilishi mumkin.

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Oldini olish tadbirlari

Bronxiomikoz profilaktikasi quyidagi kompleks tadbirlarni o‘z ichiga olishi lozim:

1. Yangi olib kelingan baliqlar asosiy suv havzasiga darhol qo‘yilmasligi, veterinariya ko‘rigidan o‘tkazilishi va alohida karantin sharoitida kuzatilishi lozim.

2. Suv sifatini nazorat qilish-harorat, erigan kislorod, pH, ammiak va nitrit muntazam tekshirilishi kerak. Suv sifati yomonlashganda aeratsiya va suv almashinuvi kuchaytiriladi.

3. Organik yuklamani kamaytirish-ortiqcha yem berishdan saqlanish, suv o‘simliklarining chirigan qismlarini olib tashlash va havza tubida organik qoldiqlarning to‘planishiga yo‘l qo‘ymaslik kerak.

4. Baliqlarni me’yoriy zichlikda saqlash-haddan tashqari zichlik stress va kasallik tarqalishini kuchaytiradi.

5. Nobud bo‘lgan baliqlarni zudlik bilan olib tashlash baliq jasadlari suv havzasida qoldirilmasligi kerak. Ular infeksiya manbai bo‘lishi mumkin.

6. Havzalarni sanitariya qilish-havzalarni imkon qadar quritish, tubidagi organik qoldiqlarni tozalash va veterinariya mutaxassisi tavsiyasi asosida dezinfeksiya tadbirlarini o‘tkazish zarur.

7. Inventarlarni dezinfeksiya qilish-to‘r, chelak, transport idishlari va boshqa baliqchilik jihozlari har bir havza yoki xo‘jalik o‘rtasida foydalanilgandan keyin tegishli tartibda dezinfeksiya qilinishi lozim.

8. Issiq mavsumda kuchaytirilgan nazorat-suv harorati ko‘tarilgan davrda baliqlar har kuni kuzatilishi, ayniqsa suv yuzasida nafas olayotgan yoki sust harakatlanayotgan baliqlar bo‘lsa, jabralar tekshirilishi kerak.

9. Aeratsiya-kislorod tanqisligi kuzatilgan hollarda mexanik aeratorlardan foydalanish va suv almashinuvini yaxshilash kerak.

10. Laboratoriya diagnostikasi-bronxiomikozga gumon qilingan baliqlardan jabra namunalarini olib, mikroskopik tekshiruv o‘tkazish maqsadga muvofiq. Tashxis boshqa jabra kasalliklari bilan differensial diagnostika asosida tasdiqlanishi kerak.

Xulosa va tavsiyalar

Bronxiomikoz karpsimon baliqlarni yetishtirishda jiddiy veterinariya-sanitariya va iqtisodiy muammo tug‘dirishi mumkin bo‘lgan mikotik kasalliklardan biridir. Kasallikning asosiy xavfi uning jabra apparatini zararlashi bilan bog‘liq. *Branchiomyces sanguinis* va *B. demigrans* tomonidan hosil qilinadigan giflar jabraning qon tomirlarida rivojlanib, qon aylanishini buzadi, tromboz, ishemiya va nekrozga olib keladi. Natijada baliqlarda nafas olish faoliyati buzilib, og‘ir holatlarda asfiksiya va ommaviy o‘lim yuzaga kelishi mumkin. Kasallikning tarqalishida suv haroratining yuqoriligi, organik moddalarning to‘planishi, suv almashinuvining yetarli emasligi, baliqlarni yuqori zichlikda saqlash, ortiqcha oziqlantirish, stress va veterinariya-sanitariya qoidalarining buzilishi muhim ahamiyatga ega. Shu sababli bronxiomikozga qarshi kurashni faqat davolash vositalariga asoslash noto‘g‘ri. Eng maqbul strategiya - profilaktik tadbirlarni tizimli ravishda amalga oshirishdir. Baliqchilik xo‘jaliklariga yangi baliqlarni olib kirishda majburiy veterinariya ko‘rigi va karantin tashkil etish; suv havzalarining gidrokimyoviy holatini muntazam nazorat qilish; suvdagi erigan kislorod miqdorini, ayniqsa issiq mavsumda, doimiy kuzatish; baliqlarni me’yoriy zichlikda saqlash; ortiqcha oziqlantirishga yo‘l qo‘ymaslik tavsiya etiladi. Shuningdek, xo‘jaliklarda o‘lgan baliqlarni zudlik bilan yig‘ib olish, havzalarni mavsumiy sanitariya qilish, inventarlarni dezinfeksiya qilish, suv almashinuvini yaxshilash va zarur hollarda aeratsiyani kuchaytirish lozim. Kasallik belgilari paydo bo‘lganda baliqlarni boshqa havzalarga ko‘chirishni to‘xtatish va veterinariya mutaxassisiga murojaat qilish zarur.

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ONKOGEN VIRUSLAR VA ULARNING BOLALAR ONKOLOGIYASIDAGI ROLI

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Annotatsiya: Jahon sog‘liqni saqlash tashkiloti ma’lumotlariga ko‘ra, har yili dunyoda 0–19 yoshdagi taxminan 400 000 nafar bola va o‘smirda saraton kasalligi aniqlanadi [1].

Zamonaviy onkologiyada infeksion agentlar, xususan, onkogen viruslarning kanserogenez jarayonidagi roli tobora ko‘proq o‘rganilmoqda.

Odamda saraton bilan bog‘liqligi ishonchli isbotlangan viruslar qatoriga Epshteyn–Barr virusi (EBV), yuqori xavfli odam papilloma viruslari (HPV), gepatit B va C viruslari (HBV, HCV), odam T-hujayrali leykoz virusi 1 (HTLV-1), Kaposhi sarkomasi bilan bog‘liq gerpesvirus (HHV-8/KSHV), shuningdek Merkel hujayrali poliomavirusi (MCPyV) kiradi [2, 3].

Bolalar onkologiyasida ayniqsa EBV muhim bo‘lib, u Berkitt limfomasi, Xodjkin limfomasining ayrim shakllari va nazofaringeal karsinoma bilan bog‘liq.

HBV esa bolalik davrida infeksiyalangan bemorlarda keyinchalik gepatotsellyulyar karsinoma rivojlanishi xavfini oshiradi. Maqolada onkogen viruslarning molekulyar mexanizmlari, bolalardagi o‘smalar bilan bog‘liqligi, epidemiologik ahamiyati, dunyodagi bolalar onkologiyasi holati hamda virusga qarshi profilaktikaning ahamiyati tahlil qilingan.

Kalit so‘zlar: onkogen viruslar, bolalar onkologiyasi, Epshteyn–Barr virusi, HPV, HBV, Berkitt limfomasi, Xodjkin limfomasi, gepatotsellyulyar karsinoma, kanserogenez, virusli infeksiya, profilaktika.

Kirish

Bolalar onkologik kasalliklari zamonaviy tibbiyotning muhim muammolaridan biri hisoblanadi. Kattalardagi o‘smalardan farqli ravishda, bolalarda onkologik jarayonlar ko‘p hollarda embrional rivojlanish, genetik o‘zgarishlar, immun tizim xususiyatlari va ayrim infeksion omillar bilan bog‘liq bo‘ladi.

JSSTning 2026-yilda yangilangan ma’lumotlariga ko‘ra, har yili 0–19 yoshdagi taxminan 400 000 nafar bola va o‘smirda saraton kasalligi rivojlanadi [1]. Bolalarda eng ko‘p uchraydigan onkologik kasalliklar qatoriga leykozlar, markaziy asab tizimi o‘smalari, limfomalar, neyroblastoma va Vilms o‘smasi kiradi [1].

Xalqaro ma’lumotlarga ko‘ra, bolalar onkologik kasalliklarining tarkibi mamlakatlar va mintaqalar bo‘yicha sezilarli darajada farq qiladi. Bunga genetik va ekologik omillardan tashqari, infeksiyalar tarqalishi, immunitet holati, tibbiy yordamdan foydalanish imkoniyati va onkologik kasalliklarni qayd etish tizimi ta’sir ko‘rsatadi [4].

IARC ma’lumotlariga ko‘ra, odamda kanserogenligi isbotlangan viruslar qatoriga yuqori xavfli HPV turlari, HBV, HCV, EBV, HTLV-1, HHV-8/KSHV va HIV-1 kiradi. Infeksion agentlar bilan bog‘liq saratonlar ulushi dunyo miqyosida taxminan 20% atrofida baholanadi [2].

Shu nuqtai nazardan, onkogen viruslarni o‘rganish bolalar onkologiyasida nafaqat patogenezni tushunish, balki profilaktika, erta tashxis va xavf guruhlarini aniqlash uchun ham muhim ahamiyatga ega.

IQTIBOS UCHUN
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Dunyo bo‘yicha bolalar onkologik kasalliklari statistikasi

Onkologik bemorlarning qariyb 90%i past va o‘rta daromadli mamlakatlarda yashaydi [5]. Yuqori daromadli mamlakatlarda bolalar onkologik kasalliklarida davolanish va kompleks tibbiy yordam imkoniyatlari keng bo‘lgani sababli, bemorlarning 80%dan ortig‘i davolanishi mumkin. Past va o‘rta daromadli mamlakatlarda esa tirik qolish ko‘rsatkichi ko‘p hollarda 30%dan pastligicha qolmoqda [1, 5].

IARC va IACR hamkorligida tayyorlangan International Incidence of Childhood Cancer, Volume III (IICC-3) bolalar onkologiyasi bo‘yicha eng muhim xalqaro manbalardan biri hisoblanadi. Unda 82 mamlakat va hududdagi 308 ta aholiga asoslangan saraton qaydlaridan olingan ma’lumotlar jamlangan bo‘lib, 0–19 yoshdagi 770 000 dan ortiq bolalarning diagnostik ma’lumotlari qamrab olingan [6]. Ushbu ma’lumotlar bolalar onkologik kasalliklarini xalqaro miqyosda taqqoslash imkonini beradi.

O‘zbekistonda bolalar onkologiyasining epidemiologik holati

O‘zbekistonda ham bolalar onkologik kasalliklari sog‘liqni saqlash tizimi uchun dolzarb muammolardan biri hisoblanadi. JSSTning O‘zbekiston bo‘yicha Cancer Country Profile ma’lumotlarida 2020-yil uchun 0–14 yoshdagi bolalarda yillik onkologik holatlar soni 1028 ta deb ko‘rsatilgan. Ushbu ma’lumotlarda o‘tkir limfoid leykoz 306 ta, Xodjkin limfomasi 52 ta, Berkitt limfomasi 6 ta, markaziy asab tizimining past darajali o‘smalari 34 ta, retinoblastoma 33 ta, Vilms o‘smasi 49 ta holatni tashkil qilgan; qolgan 548 ga yaqin holat boshqa bolalar o‘smalari guruhiga kiritilgan [7]. IARC hisob-kitoblarida O‘zbekistonda 2022-yilda 15 yoshgacha bo‘lgan bolalarda saraton kasalliklarining taxminiy kasallanish ko‘rsatkichi 100 000 nafar bolaga 10,7 holatni tashkil etgan [8].

O‘zbekistonda bolalar onkologiyasi bo‘yicha 2017–2023-yillarni qamrab olgan milliy pediatrik onkologiya registriga asoslangan tadqiqotda 0–14 yoshdagi bolalar orasida jami 3909 ta yangi holat qayd etilgan. Tadqiqotda umumiy kasallanish 100000 nafar bolaga 5,6 holat, yoshga standartlashtirilgan ko‘rsatkich esa 5,62 ni tashkil qilgan. Qayd etilgan holatlarning taxminan 55%ini leykozlar, 8%dan kamrog‘ini markaziy asab tizimi o‘smalari tashkil etgan. Ushbu tadqiqotda 5 yillik umumiy tirik qolish 37% darajasida baholangan [9].

Onkogen viruslar tushunchasi

Onkogen viruslar — inson hujayralarida uzoq muddat saqlanib, hujayra proliferatsiyasi, apoptoz, immun nazorat, DNK reparatsiyasi va genom barqarorligini o‘zgartirish orqali malignizatsiya jarayonida ishtirok etishi mumkin bo‘lgan viruslardir.

IARC tomonidan inson uchun kanserogenligi yetarli darajada isbotlangan asosiy onkogen viruslar quyidagilardir [2]:

1. Odam papilloma viruslari — HPV;
2. Gepatit B virusi — HBV;
3. Gepatit C virusi — HCV;
4. Epshteyn–Barr virusi — EBV/HHV-4;
5. Odam T-limfotrop virusi 1 — HTLV-1;
6. Kaposhi sarkomasi bilan bog‘liq gerpesvirus — HHV-8/KSHV;
7. HIV-1;
8. Merkel hujayrali poliomavirusi — MCPyV [2,3].

Biroq ushbu viruslarning barchasi bolalarda bir xil ahamiyatga ega emas. Bolalar onkologiyasida EBV eng muhim viruslardan biri hisoblanadi.

Epshteyn–Barr virusining bolalar onkologiyasidagi roli

Epshteyn–Barr virusi (EBV) gerpesviruslar oilasiga mansub bo‘lib, asosan B-limfotsitlarni zararlaydi. Virusning odam onkologiyasidagi roli birinchi marta 1964-yilda Berkitt limfomasi hujayralarida aniqlanganidan keyin e’tiborga tushgan [10].

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EBV bilan bog‘liq eng muhim o‘smalardan biri — Berkitt limfomasi. Ayniqsa Afrikadagi endemik Berkitt limfomasi bolalarda uchraydi va EBV infeksiyasi hamda immunologik ta’sirlar bilan bog‘liq. Bezgak qo‘zg‘atuvchisi *Plasmodium falciparum* bilan birgalikdagi ta’sir EBV bilan infeksiyalangan B-limfotsitlarning nazoratsiz proliferatsiyasiga sharoit yaratishi mumkin [11].

EBVning kanserogen ta’siri bir nechta mexanizm orqali amalga oshadi. Virusning latent infeksiya davrida ekspressiyalanadigan EBNA va LMP oqsillari B-limfotsitlarning faollashuvi, proliferatsiyasi va apoptozdan himoyalanish jarayonlariga ta’sir qiladi [12]. EBV shuningdek, Xodjkin limfomasining ayrim variantlari, immuniteti susaygan bemorlardagi limfoproliferativ kasalliklar va nazofaringeal karsinoma bilan ham bog‘liq [12,13].

Gepatit B virusi va bolalarda jigar o‘smalari

HBV — DNK saqlovchi gepadnavirus bo‘lib, surunkali infeksiya holatida jigar hujayralarida uzoq muddatli yallig‘lanish va regeneratsiya jarayonlarini keltirib chiqaradi. Shu bilan birga, virus genomi hujayra genomiga integratsiyalanishi mumkin.

HBV infeksiyasining eng muhim onkologik asorati — gepatotsellyulyar karsinoma. Bolalarda jigar o‘smalari kattalarga nisbatan kam uchrasa-da, endemik hududlarda HBV bilan erta yoshda infeksiyalanish kelgusida jigar saratoni xavfini oshiradi [14]. HBV kanserogenezida surunkali yallig‘lanish, oksidlovchi stress, gepatotsitlarning doimiy regeneratsiyasi va virus genetik materialining hujayra genomi bilan o‘zaro ta’siri muhim ahamiyatga ega [3, 14]. Shu sababli chaqaloqlarni HBVga qarshi emlash nafaqat infeksion gepatitni, balki uzoq muddatda virus bilan bog‘liq jigar saratonini profilaktika qilishning ham muhim vositasidir.

Odam papilloma virusining onkologik ahamiyati

Yuqori xavfli HPV turlari, xususan HPV-16 va HPV-18, odamda bir qator epitelial o‘smalarning rivojlanishida muhim rol o‘ynaydi. HPVning kanserogen ta’siri asosan virusning E6 va E7 oqsillari bilan bog‘liq. E6 oqsili p53, E7 esa retinoblastoma oqsili (pRb) bilan bog‘liq hujayraviy nazorat mexanizmlarini buzadi [15]. HPV bilan bog‘liq saratonning eng yaxshi o‘rganilgan shakli bachadon bo‘yni saratonidir. Bundan tashqari, anogenital va ayrim orofaringeal o‘smalar ham HPV bilan bog‘liq [2,15].

Bolalarda HPV bilan bog‘liq invaziv o‘smalar nisbatan kam uchraydi. Biroq o‘smirlik davrida infeksiyalanish ehtimoli va keyinchalik HPV-assotsiatsiyalangan o‘smalar rivojlanish xavfi tufayli vaksinatsiya bolalar va o‘smirlar salomatligini uzoq muddatli himoya qilishda muhim profilaktik strategiya hisoblanadi.

HHV-8 va MCPyVning bolalar onkologiyasidagi o‘rni

HHV-8/KSHV Kaposhi sarkomasi, birlamchi effuzion limfoma va ayrim limfoproliferativ kasalliklar bilan bog‘liq [13]. Ushbu kasalliklar bolalarda juda kam uchraydi va asosan immuntanqislik bilan bog‘liq holatlarda ahamiyat kasb etadi.

Merkel hujayrali poliomavirusi esa Merkel hujayrali karsinomasi bilan bog‘liq bo‘lib, IARC uni odam uchun kanserogen virus sifatida baholagan [16]. Bu o‘sma asosan katta yoshda uchragani sababli, MCPyVning odatiy bolalar onkologiyasidagi klinik ahamiyati kam. Biroq virusning bolalik davrida yuqishi mumkinligi va organizmda persistensiya qilishi virusli kanserogenezning uzoq muddatli xususiyatini ko‘rsatadi [16].

Onkogen viruslar kanserogenezining asosiy mexanizmlari

Virusli kanserogenez murakkab ko‘p bosqichli jarayon bo‘lib, uni shartli ravishda quyidagi mexanizmlarga ajratish mumkin:

1. Hujayra proliferatsiyasining kuchayishi. Virus oqsillari hujayraning bo‘linish signallarini faollashtirib, nazoratsiz proliferatsiyaga olib kelishi mumkin.

2. Apoptozning susayishi. Ayrim virus oqsillari p53 kabi o‘sma supressorlari funksiyasini buzib, zararlangan hujayralarning yashab qolishiga imkon beradi [12, 15].

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3. Genom barqarorligining buzilishi. Virus infeksiyasi DNK reparatsiyasi va xromosomalar barqarorligiga ta’sir qilib, mutatsiyalar to‘planishiga sharoit yaratadi.

4. Immun nazoratning buzilishi. Immunitet tanqisligi virus bilan infeksiyalangan hujayralarning immun tizimi tomonidan yo‘q qilinishiga to‘sqinlik qiladi. Bu EBV va HHV-8 bilan bog‘liq limfoproliferativ kasalliklarda ayniqsa muhim [12,13].

5. Surunkali yallig‘lanish. HBV va HCV kabi viruslar uzoq muddatli yallig‘lanishni keltirib chiqarib, hujayralarning doimiy regeneratsiyasi va genetik shikastlanishiga sharoit yaratadi [3].

6. Virus genomining hujayra genomi bilan o‘zaro ta’sirlashuvi. Ayrim viruslarda virus DNKsining hujayra genomiga integratsiyalanishi kanserogenezga olib keluvchi molekulyar o‘zgarishlarni kuchaytirishi mumkin.

Onkogen viruslarni aniqlash bolalar onkologiyasida bir qator diagnostik usullar yordamida amalga oshiriladi. Ularga PZR, serologik, immunogistokimyoviy tekshiruvlar, in situ gibridizatsiya va virus genomini sekvenirlash kiradi.

EBV infeksiyasida EBV DNKni PZR orqali aniqlash, EBVga xos antitanalarni tekshirish hamda o‘sma to‘qimasida EBER in situ gibridizatsiyasidan foydalanish mumkin [12]. HBV infeksiyasida HBsAg, anti-HBc, HBeAg, anti-HBe va HBV-DNA aniqlanadi. HPV infeksiyasida esa yuqori xavfli HPV genotiplarini PZR asosida aniqlash muhim hisoblanadi.

Onkogen virusni aniqlash har doim ham o‘sma borligini anglatmasligini ta’kidlash lozim. Laboratoriya natijasi bemorning klinik holati, morfologik tekshiruvi va boshqa diagnostik ma’lumotlari bilan kompleks baholanishi kerak.

Profilaktika va istiqbolli yo‘nalishlar

Onkogen viruslar bilan bog‘liq saratonlarning bir qismi infeksiyaning oldini olish orqali profilaktika qilinishi mumkin. Bu jihat bolalar onkologiyasi uchun alohida ahamiyatga ega.

Birinchi muhim yo‘nalish — emlash. HBV vaksinatsiyasi surunkali HBV infeksiyasining oldini olish orqali keyinchalik gepatotsellyulyar karsinoma xavfini kamaytiradi.

Ikkinchi yo‘nalish — infeksiyalarni erta aniqlash. HBV va HCV infeksiyalarini aniqlash, immunitet tanqisligi holatlarini nazorat qilish va EBV bilan bog‘liq xavf guruhlarini monitoring qilish onkologik asoratlarni erta aniqlash imkonini beradi.

Uchinchi yo‘nalish — bolalar onkologik registrlarini takomillashtirish.

To‘rtinchi yo‘nalish — virusologiya va onkologiyaning integratsiyasi. Bolalarda virus-assotsiatsiyalangan o‘smalarning molekulyar profilini o‘rganish individual diagnostika va istiqbolda maqsadli davolash usullarini rivojlantirish uchun asos bo‘lishi mumkin.

Xulosa

Onkogen viruslar insondagi saratonlarning muhim qismi bilan bog‘liq bo‘lib, ularning ayrimlari bolalar va o‘smirlar onkologiyasida ham muhim ahamiyat kasb etadi. Bolalar onkologiyasi nuqtai nazaridan Epshteyn–Barr virusi eng muhim onkogen viruslardan biri bo‘lib, Berkitt limfomasi, Xodjkin limfomasining ayrim shakllari va boshqa limfoproliferativ kasalliklar bilan bog‘liq. HBV infeksiyasi esa erta yoshda yuqtirilganda uzoq muddatda gepatotsellyulyar karsinoma xavfini oshirishi mumkin. HPVning bolalardagi bevosita onkologik ta’siri cheklangan bo‘lsa-da, o‘smirlik davrida profilaktik vaksinatsiya keyingi hayotda HPV-assotsiatsiyalangan saratonlarning oldini olishda muhim ahamiyatga ega.

Milliy ma’lumotlarni to‘liq baholashda diagnostika va ro‘yxatga olish darajasidagi hududiy farqlarni hisobga olish zarur. Shuning uchun onkogen viruslar bilan bog‘liq kasalliklarni o‘rganish bilan bir qatorda, bolalar onkologiyasi registrini takomillashtirish, molekulyar virusologik diagnostika imkoniyatlarini kengaytirish, HBV va HPV vaksinatsiyasini yuqori qamrovda ta’minlash, immunitet tanqisligi holatlarini nazorat qilish va virus-assotsiatsiyalangan o‘smalar bo‘yicha ilmiy tadqiqotlarni kuchaytirish muhim vazifalardan hisoblanadi.

Shunday qilib, onkogen viruslarni o‘rganish zamonaviy bolalar onkologiyasida virusologiya, immunologiya, genetika va onkologiyani birlashtiruvchi muhim ilmiy yo‘nalishdir. Virusli

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infeksiyalarning kanserogenezdagi molekulyar mexanizmlarini chuqur o‘rganish kelajakda bolalarda saraton kasalliklarining bir qismini profilaktika qilish, xavf guruhlarini erta aniqlash va individual davolash strategiyalarini takomillashtirish imkonini beradi.

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СЕЗОННАЯ ДИНАМИКА КОНЦЕНТРАЦИИ СПОР ГРИБОВ В АТМОСФЕРНОМ ВОЗДУХЕ И ИХ ЗНАЧЕНИЕ ДЛЯ РИСКА РЕСПИРАТОРНЫХ АЛЛЕРГИЧЕСКИХ ЗАБОЛЕВАНИЙ (2023–2025 ГГ.)

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Аннотация: В статье рассматривается сезонная динамика концентрации спор микроскопических грибов в атмосферном воздухе в 2023–2025 гг. и её значение для оценки риска респираторных аллергических заболеваний. Проанализированы изменения концентрации грибковых спор в различные сезоны года, а также их взаимосвязь с температурой и влажностью воздуха. Установлено, что споры микромицетов присутствуют в атмосферном воздухе в течение всего года, характеризуются продолжительным периодом спороношения и высокой суммарной концентрацией. Наиболее выраженное увеличение количества спор наблюдалось в мае: 11591 спора в 2023 году и 28567 спор в 2024 году. В летне-осенний период концентрация спор сохранялась на относительно высоком уровне, составляя 7161–8825 спор в месяц. В 2024 году в октябре был отмечен повторный пик концентрации, тогда как в 2025 году наблюдались относительная стабильность показателей и отсутствие выраженных сезонных пиков. Полученные результаты подчёркивают важность круглогодичного мониторинга грибковых спор в атмосферном воздухе для оценки потенциальных рисков развития респираторных аллергических заболеваний.
Ключевые слова: аэробиологический мониторинг, микроскопические грибы, грибковые споры, сенсибилизация, сезонная динамика.

Abstract: This study examines the seasonal dynamics of airborne microscopic fungal spore concentrations during 2023–2025 and their significance for assessing the risk of respiratory allergic diseases. Changes in fungal spore concentrations across different seasons were analyzed, along with their relationship to air temperature and humidity. The findings indicate that fungal spores are present in the atmosphere throughout the year, with a prolonged sporulation period and high overall concentrations. The most pronounced increase in spore concentrations occurred in May, reaching 11,591 spores in 2023 and 28,567 spores in 2024. During the summer and autumn months, spore concentrations remained relatively high, ranging from 7,161 to 8,825 spores per month. A secondary peak was observed in October 2024, whereas 2025 was characterized by relatively stable concentrations without clearly defined seasonal peaks. These findings highlight the importance of year-round monitoring of airborne fungal spores for assessing potential risks associated with respiratory allergic diseases.
Keywords: Aerobiological monitoring, microscopic fungi, fungal spores, sensitization, seasonal dynamics.

ДЛЯ ЦИТИРОВАНИЯ
Айтметова Ш.К., Нармухамедова М.К., Акрамжонова Ш.И., Исмаилова Э.Н. и др. Сезонная динамика концентрации спор грибов в атмосферном воздухе и их значение для риска респираторных аллергических заболеваний (2023–2025 гг.) // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. – Ташкент, 2026. – С. 426–433.
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Введение

Изменения фенологии - сроков сезонной активности живых организмов в ответ на изменение климата очевидны и широко задокументированы в различных экосистемах, от полярных регионов до тропических океанов [1]. Большая часть фенологических исследований сосредоточена на заметных макроорганизмах, которые привлекли значительное внимание общественности. Например, исследования в Северной Америке и Европе показывают устойчивую тенденцию к более раннему наступлению биологических весенних событий, таких как миграция птиц, появление бабочек, нерест амфибий, а также распускание листьев и цветение растений, в ответ на потепление климата [2]. Однако соответствующим изменениям сезонности микроорганизмов, таким как фенология и интенсивность образования и выделения спор грибов, уделялось ограниченное внимание [3].

В работе Осмонбаевой К.Б. отмечена выраженная положительная корреляция: констатировано, что температура, осадки, относительная влажность и такие метеорологические параметры, как ветер, влияют на рост грибов, а также на концентрацию и распределение спор грибов в атмосфере. Повышение температуры, обеспечивая сухость окружающей среды, благоприятствует интенсивному выбросу спор и увеличению их концентрации в атмосфере [4].

Микроскопическая природа грибковых спор, переносимых по воздуху, приводит к неизбежному вдыханию, при этом более 80 родов грибов связаны с аллергической сенсибилизацией, которая характеризуется значительной вариабельностью в зависимости от таксономических родов и видов грибов, при этом *Alternaria*, *Cladosporium* и *Aspergillus* признаны наиболее важными сенсибилизаторами [1].

Вдыхание грибковых аэрозолей может оказывать воздействие на человека тремя основными способами: вызывать инфекционные заболевания; вызывать и усугублять аллергию; провоцировать развитие тяжелых токсических реакций, вызванных микотоксинами, иногда с летальным исходом у пациентов с ослабленным иммунитетом [5]. Микотоксины, продуцируемые грибами, токсичны как для человека, так и для животных; вызывают серьезные осложнения со стороны печени, почек, желудочно-кишечного тракта, сердца, центральной нервной системы и иммунной системы; некоторые считаются канцерогенными [6]. К числу распространенных респираторных заболеваний, вызываемых грибами у человека, относятся инвазивный легочный аспергиллез, аллергический бронхолегочный аспергиллез (АБЛА), аллергический грибковый синусит и грибковые аллергические инфекции уха [7]. В настоящее время доказано значение микогенной сенсибилизации в патогенезе аллергического ринита, бронхиальной астмы, экзогенного аллергического альвеолита и атопического дерматита [8,9].

Наибольшее число зарегистрированных грибковых аллергенов принадлежит к четырем родам микромицетов: *Aspergillus, Alternaria, Cladosporium, Penicillium* [10]. Сенсибилизирующая способность обусловлена микроскопическими размерами спор грибов (от 1 до 5 мкм), что позволяет им проникать в дыхательные пути человека, вызывая клинические симптомы респираторных аллергозов [11].

Alternaria alternata - повсеместно распространенный вид, который встречается преимущественно на растениях, в почве и на разлагающихся органических субстратах, при этом его высокая численность часто отмечается как на травянистых, так и на лесных растительных ассоциациях [12]. Известно, что поражает растения, вызывая «синдром пятнистости листьев»; является важным аллергеном, переносимым по воздуху; ассоциирован с развитием у людей ринита и астмы [13].

A. fumigatus - один из наиболее распространенных грибов, переносимых по воздуху, характеризуется обильным спорообразованием - каждая конидия этого гриба высвобождает тысячи спор в атмосферу; также широко присутствует в почве и разлагающихся органических веществах [14]. Сообщается, что люди ежедневно вдыхают не менее нескольких сотен спор *A.*

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fumigatus [15] и постоянное вдыхание этих спор людьми с ослабленным иммунитетом приводит к развитию инвазивного легочного аспергиллеза [16].

Cladosporium, широко известный гриб, вызывающий астму, считается одним из наиболее распространенных и обильно встречающихся в воздухе грибов по всему миру. При этом данные показывают, что *C. herbarium*, *C. macrocarpum* и *C. cladosporioides* являются наиболее часто встречающимися видами в окружающей среде [17]. Исследования, основанные на культивировании и проведенные для оценки концентрации *Cladosporium* в воздухе в различных регионах Европы и Северной Америки, показали круглогодичное присутствие *Cladosporium* в атмосферном воздухе [18].

В журнале *Aerobiologia* (2026) опубликованы данные систематического обзора, включающего 94 исследования, в которых анализируется связь между концентрацией спор грибов в наружном воздухе и респираторными заболеваниями. Наиболее часто регистрируемыми таксонами грибов были *Alternaria sp*. и *Cladosporium sp*. В 77% этих исследований указывается на наличие четкой связи между концентрацией грибковых спор в воздухе и возникновением респираторных симптомов у сенсибилизированного населения. Значительный объем исследований указывает на связь между повышенным уровнем спор грибов в воздухе и увеличением числа госпитализаций и смертности от астмы [19].

Увеличение числа видов патогенных грибов связано с процессом глобального потепления в результате увеличения концентрации CO_2, закиси азота. Исследования в Новосибирске показали, что на формирование микобиоты оказывают влияние температура и влажность окружающей среды. При сухой, жаркой, безветренной погоде количество спор микромицетов постепенно увеличивалось (в основном, за счет грибов рода *Cladosporium*) [13]. Споры грибов - это постоянно присутствующий компонент воздуха, их концентрация и состав колеблются в зависимости от сложного взаимодействия биологических и экологических факторов, это: географическое положение, загрязнение воздуха, погодные условия, деятельность человека и местные источники растительности. Споры одних и тех же таксонов всегда обнаруживаются независимо от метода мониторинга [20].

В связи с климатическими изменениями и антропогенным воздействием, для выявления изменений в биоаэрозоле и прогнозирования их дальнейшей динамики, актуальным представляется необходимость проведения постоянного аэромониторинга, нового, но успешно развивающегося направления в Узбекистане [21].

Споры родов *Alternaria* и *Cladosporium* были впервые собраны с помощью гравиметрического пробоотборника Дюрама из атмосферы Эскишехира (Турция) в период с 1 января 2000 года по 31 декабря 2001 года. Были зафиксированы суточные, месячные и годовые колебания количества спор *Cladosporium* и *Alternaria* на см². За этот период было зарегистрировано в общей сложности 10231 спора, принадлежащих к родам *Cladosporium* и *Alternaria*. Из них 5103 были идентифицированы в 2000 году и 5128 — в 2001 году. При этом 63,09% от общего числа спор составляли споры *Cladosporium*, а 36,91% - споры *Alternaria*. Статистически исследована взаимосвязь между наличием спор грибов в воздухе и метеорологическими условиями [22].

В работе российских ученых изучалась концентрация спор плесневых грибов и причинно-значимых аллергенов пыльцы трав в городах юга России и частота мультисенсибилизации у пациентов с учетом определения специфических IgE к плесневым грибам. По результатам проведенных согласно международным методикам аэропалинологических исследований, установлено высокое содержание спор плесневых грибов в атмосферном воздухе изученных городов, которое сочеталось с ежесезонным ростом концентрации пыльцевых аллергенов в атмосферном воздухе. Также показано, что для южного региона РФ характерно круглогодичное присутствие аллергенов плесневых грибов с пиками спороношения в июле, августе и сентябре. Данные комплексной аллергодиагностики выявили превалирование (71%) полисенсибилизированных пациентов, чувствительных к пыльцевым аллергенам и спорам плесневых грибов [23].

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Учитывая вышеизложенное, целью настоящего исследования явилось изучение сезонной динамики концентрации спор микромицетов в атмосферном воздухе в 2023–2025 гг. и оценка её взаимосвязи с температурой и влажностью воздуха для определения потенциального риска развития респираторных аллергических заболеваний.

Методы исследования

Для проведения аэропалинологических исследований пыльцевые ловушки итальянской фирмы «Lanzoni» VPPS 2010 (рис.1) установлены в Ташкенте и в регионах республики (рис.2).



Рисунок 1. Пыльцевая ловушка «Lanzoni» VPPS 2010 (слева). Рисунок 2. Карта размещения ловушек в Ташкенте и регионах республики (справа)

Ловушка обеспечивает постоянный поток воздуха за счет работы помпы. Внутри ловушки находится барабан, на поверхность которого приклеена лента. Барабан вращается с постоянной скоростью относительно щели, через которую засасывается воздух. На ленту барабана ловушки собираются все микрочастицы из воздуха. Из этой ленты специалисты готовят препараты (рис.3) и под микроскопом определяют таксономическую принадлежность пыльцы или спор грибов, а также ведут их подсчет. На сегодняшний день идентифицируются пыльца 14 таксонов деревьев, 6 таксонов травянистых растений и 5 таксонов спор грибов.

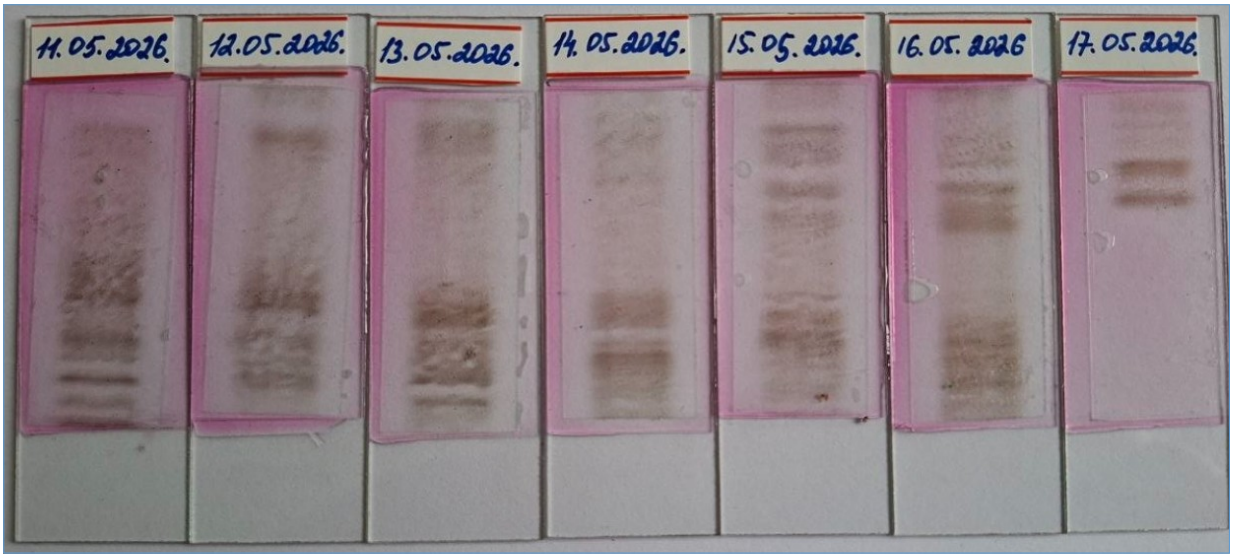


Рисунок 3. Препараты, приготовленные из ленты ловушки для микроскопического анализа

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Результаты и обсуждение

Споры микромицетов доминируют в составе аэропалинологического спектра круглогодично, характеризуются наиболее продолжительным сезоном спороношения и высокой суммарной концентрацией. Анализ динамики за 2023–2025 гг. выявил связь между пиками спороношения и ходом кривых температур и влажности.

В весенне-летний период наблюдается закономерное увеличение концентрации спор, достигающее максимума в мае (11591 спора в 2023 г. и 28567 спор в 2024 г.), что обусловлено оптимальным сочетанием суточных температур и уровня влажности. В летне-осенний период (июнь–сентябрь) концентрация спор стабильно высокая (7161–8825 спор в месяц) и формирует устойчивый аллергенный фон.

Особого внимания заслуживает межсезонная вариативность осенней динамики: если в 2023 году отмечалось постепенное снижение концентрации спор, то в октябре 2024 года зафиксирован повторный пик концентрации. В 2025 году, напротив, наблюдалась относительная стабильность концентрации спор (2471–6376 единиц) без отчетливо выраженных пиков, что, вероятнее всего, объясняется постепенным снижением влажности воздуха в осенний период. Независимо от сезонных колебаний, уровень концентрации спор в ноябре и декабре неизменно превышает концентрацию пыльцы растений, что позволяет рассматривать споры грибов как круглогодичный фактор риска для пациентов с респираторной аллергией. На графике (рис.4) отображена годовая динамика распространения в воздухе аллергенных спор двух основных родов микроскопических грибов *Alternaria* и *Cladosporium* за 2023 год. Сезон спороношения ярко выражен и приходится на теплое время года — с апреля по октябрь. Споры *Cladosporium* (оранжевая линия) демонстрируют значительно более высокие показатели концентрации в течение всего года по сравнению с *Alternaria* (синяя линия). Первый пик *Cladosporium* наблюдается в мае, а самый высокий пик активности зафиксирован в августе, когда концентрация спор достигает максимального значения за весь год. Концентрация *Alternaria* нарастает более плавно и достигает пика в летне-осенний период, при этом максимальное значение отмечено в сентябре.



Рисунок 4. Годовая динамика концентрации спор Alternaria и Cladosporium в атмосферном воздухе за 2023 год

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Полученные результаты свидетельствуют о выраженной сезонной изменчивости концентрации спор микромицетов в атмосферном воздухе в течение 2023–2025 гг. При этом сохранение спор в воздушной среде на протяжении всего года указывает на необходимость учитывать их потенциальное влияние на состояние здоровья людей не только в периоды максимального спороношения, но и в осенне-зимние месяцы.

Наиболее высокие показатели концентрации спор были зарегистрированы в мае 2023 и 2024 гг., составив 11591 и 28567 спор соответственно. Различия между этими показателями указывают на существенную межгодовую вариабельность спороношения. Одним из возможных объяснений такой динамики являются изменения метеорологических условий, включая температуру и влажность воздуха, которые могут влиять на развитие грибов, образование спор и их поступление в атмосферу. Однако для установления степени влияния отдельных метеорологических факторов необходим дополнительный статистический анализ.

В период с июня по сентябрь концентрация спор сохранялась на относительно высоком уровне, составляя 7161–8825 спор в месяц. Продолжительное сохранение повышенных показателей может способствовать формированию устойчивого фона воздействия грибковых биоаэрозолей. С учётом аллергенного потенциала ряда микромицетов, в частности представителей родов *Alternaria*, *Cladosporium* и *Aspergillus*, данные результаты представляют интерес для аэробиологических исследований и оценки потенциальных рисков развития респираторных аллергических заболеваний.

Сравнение осенней динамики за исследуемые годы выявило различия в характере изменения концентрации спор. В 2023 г. отмечалось постепенное снижение показателей, тогда как в октябре 2024 г. наблюдался повторный пик спороношения. В 2025 г. концентрация спор варьировала в пределах 2471–6376 единиц без выраженных пиков. Такая межгодовая изменчивость подчёркивает необходимость многолетних наблюдений, поскольку данные одного сезона не всегда позволяют достоверно охарактеризовать закономерности распространения грибковых спор в атмосферном воздухе.

Особое значение имеет сохранение высокой относительной представленности грибковых спор в конце календарного года. Превышение их концентрации над содержанием пыльцы растений в ноябре и декабре указывает на то, что после завершения основного сезона пыления растений грибковые споры могут оставаться значимым компонентом атмосферного биоаэрозоля. Вместе с тем оценка фактического риска для здоровья требует учёта таксономического состава спор, их аллергенного потенциала, индивидуальной сенсибилизации населения и клинических данных.

Таким образом, результаты исследования подтверждают важность круглогодичного аэробиологического мониторинга микромицетов и совместного анализа концентрации спор и метеорологических показателей. Полученные данные могут использоваться в качестве основы для дальнейшего изучения сезонных закономерностей распространения грибковых спор и их возможной связи с распространённостью респираторных аллергических заболеваний.

Заключение

По результатам исследования сезонной динамики спор микромицетов в атмосферном воздухе за 2023–2025 гг. установлено, что грибковые споры присутствуют в воздушной среде круглогодично и характеризуются выраженной сезонной и межгодовой изменчивостью концентрации. Максимальные показатели зарегистрированы в мае 2023 и 2024 гг. и составили 11591 и 28567 спор соответственно. В летне-осенний период (июнь–сентябрь) концентрация спор сохранялась на относительно высоком уровне, достигая 7161–8825 спор в месяц. Осенняя динамика различалась по годам: в октябре 2024 г. отмечен повторный пик концентрации, тогда как в 2025 г. наблюдались относительно стабильные показатели в диапазоне 2471–6376 единиц без выраженных пиков. Выявленные закономерности подчёркивают значимость метеорологических условий для дальнейшего изучения сезонного распространения грибковых спор и необходимость круглогодичного аэробиологического мониторинга. Учитывая

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аллергенный потенциал ряда микромицетов, полученные результаты представляют интерес для оценки потенциальных рисков развития респираторных аллергических заболеваний и обосновывают необходимость дальнейшего изучения взаимосвязи концентрации грибковых спор с метеорологическими показателями и клиническими данными.

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CERVICOVAGINAL DYSBIOSIS AS A COFACTOR OF PERSISTENT HUMAN PAPILLOMAVIRUS INFECTION AND PROGRESSION OF CERVICAL NEOPLASIA

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Abstract: Studies published in 2011–2025 on the role of cervicovaginal dysbiosis in the persistence of high-risk human papillomavirus (HPV) and the progression of cervical intraepithelial neoplasia (CIN) were analysed. The *Lactobacillus*-depleted community state CST IV, dominated by anaerobic bacteria, increases the odds of HPV detection, and its share rises from 10% in normal cytology to 40% in invasive cancer. Assessment of the microbiocenosis in HPV-positive women may improve risk stratification.

Keywords: human papillomavirus, cervicovaginal microbiota, dysbiosis, *Lactobacillus*, bacterial vaginosis, CIN.

Annotatsiya: Tezisda servikovaginal disbiozning yuqori onkogen xavfli inson papillomavirusi (HPV) persistensiyasi va bachadon bo‘yni intraepitelial neoplaziyasi (CIN) rivojlanishidagi o‘rni bo‘yicha 2011–2025-yillarda chop etilgan tadqiqotlar tahlil qilindi. Laktobatsillalar kamaygan va anaerob flora ustun bo‘lgan CST IV holati HPV aniqlanish ehtimolini oshirishi, uning ulushi normal sitologiyadan invaziv saratonga qadar 10% dan 40% gacha ortishi ko‘rsatildi. HPV-musbat ayollarda mikrobiotsenozni baholash xavfni tabaqalashtirishni yaxshilashi mumkin.

Kalit so‘zlar: inson papillomavirusi, qin mikrobiotasi, disbioz, *Lactobacillus*, bakterial vaginoz, CIN.

Аннотация: В тезисе проанализированы исследования 2011–2025 гг. о роли нарушения цервиковагинального микробиоценоза в персистенции вируса папилломы человека (ВПЧ) высокого онкогенного риска и прогрессировании цервикальной интраэпителиальной неоплазии (CIN). Показано, что состояние CST IV с дефицитом лактобактерий и преобладанием анаэробной флоры повышает вероятность выявления ВПЧ, а его доля возрастает с 10% при нормальной цитологии до 40% при инвазивном раке. Оценка микробиоценоза у ВПЧ-позитивных женщин может улучшить стратификацию риска.

Ключевые слова: вирус папилломы человека, вагинальная микробиота, дисбиоз, *Lactobacillus*, бактериальный вагиноз, CIN.

Introduction

Cervical cancer remains one of the leading causes of cancer death in women: according to GLOBOCAN 2022, about 661,000 new cases and 348,000 deaths were registered worldwide [1]. Almost all cases are initiated by persistent high-risk HPV infection, although most infections are cleared within one to two years and only a small proportion progresses through CIN to cancer [2]. In healthy women of reproductive age the cervicovaginal ecosystem is normally dominated by lactobacilli [3], and its disturbance is regarded as one of the cofactors that turn a transient infection into a persistent one. The aim was to summarise evidence on the contribution of cervicovaginal

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dysbiosis to HPV persistence and CIN progression and to substantiate microbiocenosis assessment in HPV-positive women.

Materials and methods

Cross-sectional, case-control and cohort studies and meta-analyses published in 2011–2025 and indexed in PubMed, Scopus and Web of Science were analysed. The search combined “HPV” with “vaginal microbiota”, “bacterial vaginosis”, “community state type” and “cervical intraepithelial neoplasia”. Studies were included if the microbiota was characterised by 16S rRNA gene sequencing or by Nugent/Amsel criteria and HPV status was determined by molecular methods (PCR, hybrid capture). Case reports, studies in pregnant women and animal studies were excluded; proportions and odds ratios with 95% CI were compared descriptively.

Results

Lactobacillus-dominated community state types (CST I, II, III, V) are distinguished from the polymicrobial state CST IV with predominance of *Gardnerella vaginalis*, *Fannyhessea vaginae*, *Prevotella*, *Sneathia* and *Megasphaera*; CST IV was found in 27.0% of 396 asymptomatic women [3]. A meta-analysis of 12 studies (6,372 women) showed that bacterial vaginosis increases the odds of cervical HPV detection (OR 1.43; 95% CI 1.11–1.84) [4]. The anaerobic state CST IV-B is associated with the slowest viral clearance [5], and *Lactobacillus*-depleted and *L. iners*-dominated communities carry higher odds of HPV infection and dysplasia than *L. crispatus* dominance [6]. The share of CST IV increases from 10% in normal cytology to 21% in LSIL, 27% in HSIL and 40% in invasive cancer [7]. In women with untreated CIN2, regression within 12 months was observed in 70.0% of those with a *Lactobacillus*-dominant microbiota and in only 42.1% of those with depletion of lactobacilli [8].

Discussion

Several mechanisms link dysbiosis with HPV-associated carcinogenesis. The fall in lactic acid production and the rise of vaginal pH above 4.5 weaken the virucidal and anti-inflammatory action of lactic acid [9]; sialidases and mucinases of *Gardnerella* and *Prevotella* degrade cervical mucus and damage the epithelium; anaerobic bacteria maintain chronic inflammation with production of IL-1β, IL-8 and TNF-α, which leads to oxidative stress and DNA damage [10]. HPV oncoproteins E6 and E7, in turn, suppress local immunity, so the relationship is bidirectional. For Uzbekistan, where HPV vaccination of girls began in 2019 and the adult female population remains unvaccinated, Gram-stain microscopy of vaginal smears already performed in clinical diagnostic laboratories allows microbiocenosis assessment without significant additional costs.

Conclusion

Depletion of lactobacilli and predominance of anaerobic flora in the cervicovaginal microbiocenosis act as a cofactor that favours HPV persistence and CIN progression. The share of the dysbiotic community state increases four-fold from normal cytology to invasive cancer, and *Lactobacillus* dominance is associated with more frequent regression of CIN2. Evaluating the microbiocenosis (pH, Nugent score, quantitative PCR of lactobacilli) alongside HPV genotyping may improve risk stratification in screening programmes.

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OVARIAN FIBROSIS IN POLYCYSTIC OVARY SYNDROME: TRANSLATIONAL PERSPECTIVES ON MOLECULAR BIOMARKERS AND CHALLENGES IN NON-INVASIVE DIAGNOSIS

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Introduction

Polycystic ovary syndrome (PCOS) is a complex endocrine and metabolic disorder characterized by hyperandrogenism, insulin resistance, chronic inflammation, and oxidative stress. The convergence of these factors activates profibrotic pathways, including transforming growth factor-beta (TGF-β)/Smad, Wnt/β-catenin, and PI3K/Akt signaling pathways, resulting in fibroblast activation, extracellular matrix (ECM) remodeling, collagen deposition, and ovarian stiffening [1]. Experimental studies have consistently demonstrated ovarian fibrosis mediated by these profibrotic pathways, including increased expression of TGF-β and connective tissue growth factor (CTGF), collagen deposition, and myofibroblast activation, ultimately contributing to progressive ovarian fibrosis and stiffening [1,2]. While human studies have primarily investigated non-invasive imaging and circulating biomarkers, evidence from histological evaluation remains limited and is largely restricted to surgically obtained ovarian specimens. Consequently, the assessment of ovarian fibrosis remains challenging because of the lack of standardized diagnostic criteria and the limited accessibility of ovarian tissue [3]. This highlights the need to understand the translational barriers that currently prevent the development of a clinically validated, non-invasive, fibrosis-specific diagnostic standard despite promising molecular biomarkers and elastographic techniques. This review aims to summarize the current evidence on non-invasive approaches to assessing ovarian fibrosis in women with PCOS and to highlight the major translational gaps between animal evidence and human clinical application.

Keywords: PCOS, ovarian fibrosis, extracellular matrix, shear wave elastography, and biomarkers.

Methods

A narrative review of human and animal studies published between 2020 and 2026 was conducted. Relevant literature was identified using databases including PubMed, Google Scholar, and other peer-reviewed sources.

Results and discussion

Animal studies: In DHEA-induced PCOS rat models, ovarian fibrosis was found to be mediated by the TGF-β signaling pathway. Fibrotic markers, including TGF-β, CTGF, fibronectin (FN), collagen, and α-SMA, were investigated following treatment with the TGF-β receptor I inhibitor SB431542 and were found to be upregulated [4]. An imbalance between matrix metalloproteinases (MMPs) and their tissue inhibitors (TIMPs), whose intricate interplay plays an important role in ECM turnover, further contributed to abnormal ECM remodeling. Similar findings were reported in another experimental study in which molecular analyses of rats with PCOS demonstrated increased CTGF expression and elevated protein levels. In addition, the study reported

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increased ovarian stiffness in PCOS rats using transabdominal two-dimensional ultrasound and shear wave elastography (SWE), which corresponded with extensive collagen deposition demonstrated by Masson's trichrome staining [2]. These findings suggest that ovarian fibrosis contributes to increased ovarian stiffness. Therefore, animal models provide strong evidence for the existence of ovarian fibrosis in PCOS through combined histological and molecular evidence.

Human studies: In women diagnosed with PCOS, increased ovarian stiffness has been detected using transvaginal ultrasound and SWE [2]. Although SWE demonstrates potential diagnostic utility in PCOS, its role as a surrogate marker for ovarian fibrosis remains unvalidated because ovarian stiffness has not yet been correlated with ovarian fibrosis using an accepted histological reference standard in humans. Furthermore, stiffness measurements can be influenced by several factors, including patient heterogeneity, the stage of PCOS progression, and differences in hormonal therapy. Circulating biomarkers are also promising because they offer a non-invasive approach; however, they lack ovarian specificity and may be influenced by systemic conditions. Consequently, the absence of validated diagnostic cut-off values, lack of standardization, and limited longitudinal evidence mean that these methods should currently be regarded as potential indicators rather than validated fibrosis-specific diagnostic tools for ovarian fibrosis in women with PCOS.

Conclusion

These limitations highlight the need for further research to establish appropriate diagnostic cut-off values. Future studies should include larger sample sizes and multicenter data collection to reduce bias and improve the reliability of findings. Particular emphasis should be placed on developing standardized diagnostic criteria and validating their accuracy against an accepted reference standard. Longitudinal studies are needed to determine whether these markers accurately reflect the progression of ovarian fibrosis. Studies should also evaluate the generalizability of these approaches for diagnosing ovarian fibrosis and their feasibility for routine clinical practice. Addressing these gaps could facilitate the development of clinically applicable, non-invasive approaches for assessing ovarian fibrosis and provide a foundation for more precise and targeted therapeutic approaches.

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VABO QO‘ZG‘ATUVCHISINING TARQALISHINING OLDINI OLISH ISTIQBOLLARI

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Annotatsiya: vabo qo‘zg‘atuvchisining tarqalishining oldini olish, davolash va tashxis qo‘yish bilan bog‘liq ko‘plab muammolarni hal etish bugungi kunning o‘ziga xos muammolaridan biri hisoblanadi. Suv havzalarida genetik jihatdan bog‘liq turlarning ko‘payishi va/yoki mamlakatga tashqaridan kirib kelishi natijasida *Vibrio cholerae* populyatsiyasining tanlanishi aholi salomatligiga iqtisodiy zarar yetkazadi, bu esa salbiy oqibatlarga olib keladi. Vabo qo‘zg‘atuvchisini o‘rganishda olingan ma’lumotlarning ishonchliligi, o‘tkazilgan chora-tadbirlar va e’tibor qaratish lozim bo‘lgan jihatlar keltirilgan.

Kalit so‘zlar: vabo qo‘zg‘atuvchisi, *Vibrio cholerae*, oldini olish, chora-tadbirlarni o‘tkazish.

ПЕРСПЕКТИВЫ ПРЕДОТВРАЩЕНИЯ РАСПРОСТРАНЕНИЯ ВОЗБУДИТЕЛЯ ХОЛЕРЫ

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Аннотация: решение многих проблем, связанных с предотвращением распространения, лечением и диагностикой возбудителя холеры, является одной из специфических проблем современности. Выбор популяции *Vibrio cholerae* в результате размножения генетически связанных видов в водоемах и/или их проникновения в страну извне наносит экономический ущерб здоровью населения, что приводит к негативным последствиям. Приведены достоверность полученных данных при изучении возбудителя холеры, проведенные мероприятия и аспекты, на которые следует обратить внимание.

Ключевые слова: возбудитель холеры, Vibrio cholerae, профилактика, проведение мероприятий

PROSPECTS FOR PREVENTING THE SPREAD OF CHOLERA PATHOGENS

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Abstract: solving many problems related to preventing the spread, treatment, and diagnosis of the cholera pathogen is one of the specific problems of our time. The selection of *Vibrio cholerae* populations as a result of the reproduction of genetically related species in water bodies and/or their penetration into the country from outside causes economic damage to public health, leading to negative consequences. The reliability of the data obtained during the study of the cholera pathogen, the measures taken, and aspects to be considered are presented.

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Keywords: cholera pathogen, *Vibrio cholerae*, prevention, implementation of measures

Kirish

Jahonda vabo bo‘yicha epidemiologik vaziyatning tahlili va O‘zbekistonda uzoq yillardan buyon vaboga qarshi kurash amaliyotining keng qamrovli materiallari shuni ko‘rsatadiki, ushbu o‘ta xavfli infeksiyaning oldini olish XXI asrda ham davlatimiz uchun dolzarb bo‘lib qolmoqda. Bu, birinchi navbatda, respublikaning barcha hududlariga taalluqlidir. Respublikaning jadal rivojlanayotgan eng obod shaharlari, sifatli suv, kanalizatsiya, sanitariya-tozalash vositalari, davolash-profilaktika, sanitariya-epidemiologiya, ilmiy-tibbiyot muassasalarining qudratli tarmog‘i bilan boshqalardan yaxshiroq ta’minlangan bo‘lsa-da, gidrosferaning ekologik nosozligini boshdan kechirmoqda. Bu esa suv arteriyalarining korxonalarning ishlab chiqarish oqovalari, avtomobillarga yoqilg‘i quyish shoxobchalarining neft mahsulotlari, shaharlar atrofidagi va qishloqdagi kanalizatsiya qilinmagan xonadonlar, chorvachilik xo‘jaliklari, tabiiy chiqindixonalarning maishiy oqovalari bilan ifloslanishi bilan bog‘liqdir.

Metodologiya

Vabo qo‘zg‘atuvchisining epidemiologik tekshirish usullaridagi populyatsiyaning tarqalish usullarining holatiga e’tibor qaratilgan.

Natijalar va muhokama

Natijada, yer usti suv havzalari tabiiy suv biotsenozlarini buzuvchi va shu bilan birga patogen mikrofloraning, shu jumladan vabo vibrionlarining ko‘payishiga yordam beruvchi moddalar bilan to‘yinadi. Shunday qilib, mamlakatimizning yer usti suv havzalaridan tekshiruv natijalarida 600 dan ortiq 01 El-Tor vabo vibrionlari shtammlari ajratib olindi, bu respublikaning barcha ma’muriy tumanlarida ajratib olingan bunday shtammlarning umumiy sonining deyarli 10 foizini tashkil etdi. Ularning aksariyati vabo qo‘zg‘atuvchisining kuchsiz virulentli va avirulentli variantlariga mansub hisoblanadi, ammo ba’zi shtammlar o‘z xususiyatlariga ko‘ra epidemik xavfli turlarga tegishliligi ham aniqlangan. Bemorlar va vibrion tashuvchilarni o‘z vaqtida aniqlash, tegishli epidemiyaga qarshi chora-tadbirlar infeksiya tarqalishiga yo‘l qo‘ymadi. Biroq ushbu soha bo‘yicha mutaxassislarni tayyorlash, malakasini oshirish, ular tanqisligini bartaraf etish zarurdir – bu esa faktligicha qolmoqda. Vabo epidemiyasi rivojlanishi mumkinligining yana bir muhim sababi qo‘zg‘atuvchining chet eldan kirib kelishidir. Buning oldini olish uchun chet eldan mamlakatimizga kirib kelish chegara tekshiruv punktlarida nazoratni kuchaytirishni talab qiladi. Klassik vabo og‘ir o‘tadi, bemor yotib qoladi, kasallik belgilari (tez-tez ich ketishi, qusish, buning oqibatida organizmning suvsizlanishi, shuningdek, haroratning pasayishi, mushaklarning taranglashishi va intoksikatsiyaning boshqa belgilari, yurak urishining susayishi va h.k.) aksariyati aniq ko‘rinadi, shunga ko‘ra kasallik vabo boshlanishi bilanoq tez aniqlanganda, uning tarqalishi cheklanadi. Vaboning El-Tor turi aksariyat hollarda yengil kechadi. Kasallik belgilari bo‘lmagan holda vibrionlarni tashib yuruvchi odamlar ko‘proq uchraydi, shu sababli El-Tor vabosini aniqlash klassikani aniqlashga nisbatan qiyinroq, shuning uchun El-Tor vibrionida bir mamlakatdan ikkinchisiga o‘tish va keng tarqalish imkoniyatlari katta. Ushbu belgilarni doimo inobatga olish zarurdir.

Xulosa

Demak, barcha hududlar bo‘yicha epidemiologik nazoratni samarali tashkil etish uchun yetarlicha chora-tadbirlar ishlab chiqish, kasallik qo‘zg‘atuvchilarini tezroq aniqlash uchun zamonaviy laboratoriyalar tashkil etish, kerakli ingrediyentlar bilan ta’minlashni markazlashgan holatga erishish, malakali kadrlar tanqisligini bartaraf etish hamda mutaxassislar malakasini oshirish bugungi kunning dolzarb talabi ekanligini ta’kidlash zarurdir.

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FARG‘ONA VILOYATI SHAROITIDA post-COVID-19 ASSOTSIATSIYALANGAN OVQAT HAZM QILISH TIZIMI KASALLIKLARI EPIDEMIOLOGIYASINING HUDUDIY JIHATLARINI BAHOLASH

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Annotatsiya: Farg‘ona viloyatida COVID-19 ni boshdan o‘tkazgan 18-60 yoshli 1605 nafar aholi orasida post-COVID-19 assotsiatsiyalangan ovqat hazm qilish tizimi kasalliklari (OHTK) epidemiologiyasi o‘rganildi. Kasallik tuzilmasida gastroduodenit (19,9%), ezofagit (15,7%) va o‘n ikki barmoqli ichak yara kasalligi (12,6%) yetakchilik qildi. Xavf omillari eng ko‘p 18-29 yoshli guruhda (50,9%) qayd etildi, erkaklarda esa 40-49 yoshda ustunlik ko‘rsatdi. Olingan ma’lumotlar hududiy profilaktika dasturini shakllantirish uchun ilmiy asos bo‘lib xizmat qiladi.

Kalit so‘zlar: post-COVID-19; ovqat hazm qilish tizimi kasalliklari; epidemiologiya; gastroduodenit; Farg‘ona viloyati.

Аннотация: Изучена эпидемиология заболеваний органов пищеварения (ЗОП), ассоциированных с post-COVID-19, среди 1605 жителей Ферганской области в возрасте 18-60 лет, перенёсших COVID-19. В структуре заболеваний преобладали гастродуоденит (19,9%), эзофагит (15,7%) и язвенная болезнь двенадцатиперстной кишки (12,6%). Факторы риска чаще всего регистрировались в возрастной группе 18-29 лет (50,9%), у мужчин — в группе 40-49 лет. Полученные данные служат научной основой для формирования региональной программы профилактики.

Ключевые слова: post-COVID-19; заболевания органов пищеварения; эпидемиология; гастродуоденит; Ферганская область.

Abstract: The epidemiology of post-COVID-19-associated digestive system diseases (DSD) was studied in 1,605 residents of the Fergana region aged 18-60 years with a history of COVID-19. Gastroduodenitis (19.9%), esophagitis (15.7%) and duodenal ulcer disease (12.6%) predominated in the disease structure. Risk factors were recorded most often in the 18-29-year age group (50.9%), and in men in the 40-49-year group. The data obtained provide a scientific basis for a regional prevention program.

Keywords: post-COVID-19; digestive system diseases; epidemiology; gastroduodenitis; Fergana region.

Kirish

SARS-CoV-2 infeksiyasi nafas yo‘llari bilan cheklanmaydi. Virus angiotenzin-konvertaza fermenti-2 (ACE2) retseptorlari orqali oshqozon-ichak trakti epiteliysiga kirib boradi va shilliq qavatda uzoq davom etuvchi yallig‘lanish jarayonini qo‘zg‘atadi [2, 5]. AQSh faxriylarining 154 068 nafarlik kohortida o‘tkir infeksiyadan keyingi bir yil davomida dispepsiya, gastroezofageal reflyuks, peptik yara kasalligi, o‘tkir pankreatit hamda jigar va o‘t yo‘llari kasalliklari xavfi nazorat guruhlariga nisbatan yuqori bo‘lib qolgan [1]. Ichak mikrobiotasi tarkibidagi buzilishlar esa virus organizmdan

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yo‘qolganidan keyin ham 30 kungacha saqlanadi va post-COVID simptomatikasining davom etishiga hissa qo‘shadi [4].

O‘zbekistonda, xususan Farg‘ona vodiysida, post-COVID-19 assotsiatsiyalangan ovqat hazm qilish tizimi kasalliklarining (OHTK) epidemiologiyasi aholi darajasida ilgari o‘rganilmagan.

Tadqiqot maqsadi — Farg‘ona viloyati sharoitida post-COVID-19 assotsiatsiyalangan OHTK tarqalishining hududiy, gender va yosh xususiyatlarini baholash.

Metodlar

Bir vaqtli epidemiologik tadqiqot Jahon sog‘liqni saqlash tashkilotining epidemiologik tekshiruvlarni tashkil etish talablariga muvofiq o‘tkazildi. Tadqiqotga 2022-2024-yillarda Farg‘ona shahri poliklinikalarida ro‘yxatga olingan va nazoratda turgan, COVID-19 infeksiyasini boshdan o‘tkazgan 18-60 yoshli 1605 nafar aholi tasodifiy tanlov yo‘li bilan jalb qilindi. Ulardan 853 nafarini (53,1%) ayollar, 752 nafarini (46,9%) erkaklar tashkil etdi.

Tekshiruvda so‘rovnomali, umumklinik, biokimyoviy, fizikaviy va instrumental usullar qo‘llanildi. So‘rovnomali usulda “Yuqumli bo‘lmagan surunkali kasalliklarni aniqlash uchun anketa” hamda bemorning klinik holatini baholash shkalasi ishlatildi. Biokimyoviy tekshiruvlarda xolesterin, triglitseridlar, kaliy va magniy konsentratsiyasi aniqlandi. Instrumental usullarda antropometrik o‘lchovlar, ultratovush, rentgenologik va elektrokardiografik tekshiruvlar bajarildi. OHTK tashxisi xalqaro “Sidney tizimi” mezonlari asosida shakllantirildi.

Statistik tahlil Microsoft Excel va IBM SPSS Statistics 27.0 dasturlarida bajarildi: deskriptiv statistika, xi-kvadrat (χ^2) testi, nisbiy xavf (RR), 95% ishonch intervali (II) va korrelyatsion tahlil.

Natijalar

Tekshirilgan katta yoshdagi populyatsiyada post-COVID-19 assotsiatsiyalangan OHTK ayollarda 53,1% va erkaklarda 46,9% chastotada qayd etildi (RR = 1,58; II = 2,01-1,12; χ^2 = 2,54; r++ = 0,98; P > 0,05).

18 yoshdan katta aholida OHTKning ayrim turlari quyidagi chastotalarda aniqlandi: gastroduodenit — 19,9%, ezofagit — 15,7%, oshqozon yara kasalligi — 9,8%, o‘n ikki barmoqli ichak yara kasalligi — 12,6%, enterokolit — 8,4%, pankreatit — 5,9%, surunkali gepatit — 6,6%, jigar sirrozi — 3,2%, surunkali xoletsistit — 10,1% va surunkali toshli xoletsistit — 7,9%. Eng yuqori chastotada gastroduodenit, ezofagit va o‘n ikki barmoqli ichak yara kasalligi tasdiqlandi, jigar sirrozi, pankreatit, surunkali gepatit va enterokolit esa sezilarli kam uchradi. Sanab o‘tilgan kasalliklarning chastotasi ayollar va erkaklar orasida farqlandi.

O‘rganilgan xavf omillarining taqsimoti yoshga bog‘liq holda ham o‘zgardi. Umumiy post-COVID-19 populyatsiyasida ularning aniqlanish darajasi 18-29 yoshda 50,9%, 30-39 yoshda 3,0%, 40-49 yoshda 19,8%, 50-59 yoshda 26,2% va 60 yoshdan katta guruhda 0,1% ni tashkil etdi. Yoshga bog‘liq tafovutlanish 50,0% ni tashkil qilib, eng yuqori ko‘rsatkich 18-29 yoshli guruhda kuzatildi (RR = 0,64; II = 0,404-1,015; χ^2 = 3,3; r++ = 0,995; P > 0,05).

Gender bo‘yicha qiyosiy tahlilda xavf omillarining aniqlanish darajasi 18-29 yoshda ayollarda 52,8% va erkaklarda 49,1%; 30-39 yoshda mos ravishda 6,0% va 0,0%; 40-49 yoshda 14,8% va 24,7%; 50-59 yoshda 26,3% va 26,1%; 60 yoshdan katta guruhda 0,2% va 0,1% ni tashkil qildi. Barcha taqqoslashlarda P > 0,05. Har ikkala jinsda ham xavf omillari eng ko‘p 18-29 yoshda to‘plandi. Ko‘pchilik yosh guruhlarida ko‘rsatkichlar ayollarda yuqori bo‘ldi, 40-49 yoshli guruhda esa erkaklar ustunlik qildi.

Muhokama

Gastroduodenit, ezofagit va o‘n ikki barmoqli ichak yara kasalligining yetakchi o‘rin egallashi xorijiy kohort ma’lumotlariga mos keladi: Xu va hammualliflari ham post-COVID davrda aynan kislotaga bog‘liq kasalliklar va motorika buzilishlari xavfi oshganini ko‘rsatgan [1]. Bunday manzaraning patofiziologik asosi sifatida ACE2 retseptorlari orqali virusning shilliq qavatga bevosita ta’siri hamda ichak mikrobiotasi muvozanatining buzilishi ko‘rib chiqiladi [4, 5].

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Xavf omillarining 18-29 yoshli guruhda to‘planishi ko‘p jihatdan tadqiqot tanlanmasining yosh tarkibini aks ettiradi, shu sababli uni nisbiy taqsimot sifatida talqin qilish lozim. Erkaklarda 40-49 yoshda kuzatilgan ustunlik mehnat sharoiti va murojaat faolligining pastligi bilan bog‘liq bo‘lishi mumkin, ammo mazkur dizayn bu farazlarni ajrata olmaydi. Barcha gender taqqoslashlarida $P > 0,05$ bo‘lgani uchun topilgan farqlar tendensiya darajasida baholanadi.

Xulosa

Farg‘ona viloyatida post-COVID-19 assotsiatsiyalangan ovqat hazm qilish tizimi kasalliklari tasodifiy asorat emas, balki tuzilmasi aniq ko‘rinib turgan hududiy muammodir: har beshinchi bemorda gastroduodenit, har oltinchisida ezofagit qayd etiladi, xavf omillari esa eng mehnatga layoqatli 18-29 yoshli guruhda jamlanadi. Infeksiyani boshdan o‘tkazgan aholini faol dispanser kuzatuviga olish, gastroenterologik skriningni yosh va gender xususiyatlariga moslashtirish hamda ichak mikrobiotasini tiklashga qaratilgan chora-tadbirlarni profilaktika dasturiga kiritish zarur. Pandemiya tugadi, uning hazm tizimidagi izi esa hamon davolanishni kutmoqda.

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YIRINGLI-YALLIG‘LANISH JARAYONLARIDAN AJRATILGAN PIOGEN KOKKLARNI PROTEOMIK VA MOLEKULYAR-GENETIK USULLAR ASOSIDA IDENTIFIKATSIYA QILISH

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Annotatsiya: Mazkur tadqiqotda yiringli-yallig‘lanish jarayonlaridan ajratilgan piogen kokklarni zamonaviy mikrobiologik, proteomik va molekulyar-genetik usullar yordamida identifikatsiya qilish natijalari o‘rganildi. Bakterial kulturalarning morfologik xususiyatlari Gram usulida bo‘yash, MALDI-TOF MS tahlili, 16S rRNK geni sekvensiyasi va polimeraza zanjir reaksiyasi (PZR) yordamida baholandi. Olingan nukleotid ketma-ketliklari NCBI BLAST ma’lumotlar bazasi orqali taqqoslandi hamda filogenetik tahlil o‘tkazildi. Natijalar bakterial izolyatlarni aniqlashda proteomik va molekulyar-genetik usullarni birgalikda qo‘llash muhimligini ko‘rsatdi.

Kalit so‘zlar: piogen kokklar, *Staphylococcus aureus*, *Streptococcus pyogenes*, *Granulicatella adiacens*, MALDI-TOF MS, 16S rRNK, PZR, filogenetik tahlil.

Kirish

Piogen kokklar insonlarda turli yiringli-yallig‘lanish kasalliklarini keltirib chiqaruvchi muhim bakterial guruh hisoblanadi. Ular orasida *Staphylococcus* va *Streptococcus* avlodlariga mansub bakteriyalar alohida klinik ahamiyatga ega. Ushbu mikroorganizmlarni to‘g‘ri identifikatsiya qilish infeksion kasalliklarni tashxislash, qo‘zg‘atuvchilarni aniqlash va epidemiologik monitoringni takomillashtirishda muhim o‘rin tutadi. An’anaviy mikrobiologik tekshiruvlarda bakteriyalarning morfologik, kultural va biokimyoviy xususiyatlari o‘rganiladi. Zamonaviy laboratoriya amaliyotida esa MALDI-TOF MS va molekulyar-genetik usullar bakteriyalarni tezkor hamda aniqroq identifikatsiya qilish imkonini beradi. Shu sababli ushbu usullar natijalarini o‘zaro taqqoslash dolzarb ilmiy-amaliy ahamiyatga ega.

Tadqiqotning maqsadi. Yiringli-yallig‘lanish o‘choqlaridan ajratilgan bakterial izolyatlarni MALDI-TOF MS, 16S rRNK geni sekvensiyasi va PZR yordamida identifikatsiya qilish hamda filogenetik tahlil asosida ularning taksonomik mansubligini baholash.

Materiallar va tadqiqot usullari

Tadqiqotda Sanitariya-epidemiologik nazorat boshqarmasi bakteriologiya laboratoriyasidan olingan namunalar asosida ajratilgan bakterial kulturalardan foydalanildi. Namunalar tegishli ozuqa muhitlariga ekilib, hosil bo‘lgan koloniyalardan sof kulturalar ajratib olindi. Bakteriyalarning morfologik xususiyatlari Gram usulida bo‘yash va mikroskopik tekshiruv orqali o‘rganildi. Mikroskopik kuzatuvlarda stafilokokklarga xos to‘p-to‘p joylashish va *streptokokklarga* xos zanjirsimon tuzilish belgilari baholandi.

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Iskandarova Y.N., Fayziyev V.B., Adilkhonova N.A. Yiringli-yallig‘lanish jarayonlaridan ajratilgan piogen kokklarni proteomik va molekulyar-genetik usullar asosida identifikatsiya qilish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 445–446.
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Dastlabki identifikatsiya MALDI-TOF MS usulida amalga oshirildi. Molekulyar tekshiruvlarda bakterial DNK ajratilib, 16S rRNK geni sekvensiyasi hamda PZR tahlillari bajarildi. *Staphylococcus aureus* uchun *nuc* va *coa*, *Streptococcus pyogenes* uchun esa *emm* genlari nishon sifatida belgilandi. Olingan 16S rRNK ketma-ketliklari National Center for Biotechnology Information (NCBI) ma'lumotlar bazasining BLAST dasturi yordamida taqqoslandi. Filogenetik shajaralar MEGA dasturida Maximum Likelihood usuli asosida tuzildi.

Natijalar va muhokama

MALDI-TOF MS tahlilida uchta tekshiruv natijasi uchun moslik koeffitsiyentlari mos ravishda 2,38; 2,18 va 2,14 ni tashkil etdi. Keltirilgan mezon bo‘yicha 2,0 va undan yuqori ko‘rsatkichlar ishonchli identifikatsiyani qo‘llab-quvvatlaydi. Biroq uchinchi namuna nomi dastlabki ma'lumotlarda *Streptococcus aureus* shaklida berilganligi sababli, uning aniq taksonomik nomini laboratoriya bayonnomasi bilan solishtirish zarur. 16S rRNK geni ketma-ketliklarini NCBI BLAST bazasida taqqoslash natijasida Y1 izolyati *Staphylococcus aureus* bilan 100% o‘xshashlik ko‘rsatdi. Y2 izolyati esa *Granulicatella adiacens* va ma'lumotlar bazasida *Uncultured bacterium* sifatida qayd etilgan ketma-ketliklar bilan 99,65% o‘xshashlikka ega bo‘ldi. Y1 izolyatining filogenetik tahlili MEGA4 bioinformatik dasturida Maximum Likelihood usuli yordamida amalga oshirildi. Filogenetik daraxtda Y1 izolyati *Staphylococcus aureus* turiga mansub ketma-ketliklar bilan yaqin joylashdi. Ushbu natija NCBI BLAST orqali aniqlangan 100% o‘xshashlik ko‘rsatkichi bilan mos kelib, izolyatning taksonomik mansubligini qo‘llab-quvvatladi. Y2 izolyatining filogenetik shajarasi *Granulicatella adiacens*, *Streptococcus pyogenes* va *Streptococcus pneumoniae* ketma-ketliklari bilan taqqoslandi. Natijada Y2 izolyati *Streptococcus* turlaridan farqli guruhga joylashdi va NCBI BLAST natijasiga mos ravishda *Granulicatella adiacens* bilan yaqinlik ko‘rsatdi. Shu sababli Y2 izolyatini *Streptococcus pyogenes* deb belgilashdan oldin qo‘shimcha tasdiqlovchi tekshiruvlar talab etiladi. Olingan natijalar MALDI-TOF MS va molekulyar-genetik usullarni birgalikda qo‘llash bakterial izolyatlarni identifikatsiya qilishda muhimligini ko‘rsatadi. Bunda har bir usulning natijasi alohida baholanib, yakuniy identifikatsiya o‘zaro mos keladigan laboratoriya dalillari asosida amalga oshirilishi lozim.

Xulosa

Tadqiqot davomida piogen kokklarni mikrobiologik, proteomik va molekulyar-genetik usullar yordamida identifikatsiya qilish natijalari tahlil qilindi. MALDI-TOF MS tekshiruvlarida moslik koeffitsiyentlari 2,0 dan yuqori bo‘ldi. 16S rRNK geni ketma-ketligini NCBI BLAST bazasida taqqoslash natijasida Y1 izolyati *Staphylococcus aureus* bilan 100% o‘xshashlik ko‘rsatdi. Filogenetik tahlil ushbu natijani qo‘llab-quvvatladi. Y2 izolyatining *Granulicatella adiacens* bilan 99,65% o‘xshashligi esa uning taksonomik mansubligini qo‘shimcha usullar bilan aniqlashtirish zarurligini ko‘rsatdi. Shunday qilib, MALDI-TOF MS, 16S rRNK sekvensiyasi va filogenetik tahlilni uyg‘unlashtirish bakterial izolyatlarni identifikatsiya qilish imkoniyatlarini kengaytiradi. Ushbu yondashuv klinik mikrobiologik diagnostika va epidemiologik monitoringda muhim ahamiyatga ega.

Foydalanilgan adabiyotlar

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3. Bakteriyalarning 16S rRNK sekvensiyasi va filogenetik tahliliga oid ilmiy manbalar.

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HOMILADORLIKDA INTRAGEPATIK XOLESTAZNING YUZAGA KELISHINING PATOGENETIK JIHATLARI

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Annotatsiya: Homiladorlikdagi jigar ichi xolestazi (HJIX) — II–III trimestrda o‘t kislotalari almashinuvi buzilishi bilan kechadigan, ona va homila uchun xavfli holat. 2013–2023-yillarda HJIX asoratlaridan vafot etgan 51 nafar ayol va 12 nafar nazorat materiali morfologik, morfometrik hamda immunogistokimyoviy usullarda o‘rganildi. Oshqozon osti bezida dimlanishli pankreatit va steatonekroz ustunlik qildi. Natijalar patogenezda ichak mikrobiotasining dekonyugatsiyalovchi faolligi muhim bo‘g‘in bo‘lishi mumkinligini ko‘rsatadi.

Kalit so‘zlar: jigar ichi xolestazi, o‘t kislotalari, ichak mikrobiotasi, o‘t tuzlari gidrolazasi (BSH), FXR, oshqozon osti bezi, steatonekroz.

Аннотация: Внутрипечёночный холестаз беременных (ВХБ) — состояние II–III триместров с нарушением обмена жёлчных кислот, опасное для матери и плода. Изучены материалы 51 женщины, умершей от ВХБ в 2013–2023 гг., и 12 случаев контроля морфологическими, морфометрическими и иммуногистохимическими методами. В поджелудочной железе преобладали застойный панкреатит и стеатонекроз. Результаты указывают на роль деконъюгирующей активности кишечной микробиоты в патогенезе ВХБ.

Ключевые слова: внутрипечёночный холестаз, жёлчные кислоты, кишечная микробиота, гидролаза солей жёлчных кислот (BSH), FXR, поджелудочная железа, стеатонекроз.

Abstract: Intrahepatic cholestasis of pregnancy (ICP) is a second- and third-trimester disorder of bile acid homeostasis hazardous to both mother and fetus. Archival material from 51 women who died of ICP complications between 2013 and 2023 and from 12 controls was examined morphologically, morphometrically and immunohistochemically. Congestive pancreatitis and steatonecrosis predominated in the pancreas. The findings implicate the deconjugating activity of the gut microbiota in ICP pathogenesis.

Keywords: intrahepatic cholestasis of pregnancy, bile acids, gut microbiota, bile salt hydrolase, FXR, pancreas, steatonecrosis.

Kirish

HJIX teri qichishishi hamda zardobda umumiy o‘t kislotalari (UO‘K) va aminotransferazalar darajasining ortishi bilan kechadi. Individual ma’lumotlar meta-tahliliga ko‘ra, o‘lik tug‘ilish HJIX da 0,83 %, nazorat homiladorliklarida 0,32 % ni tashkil etadi; UO‘K ≥ 100 μmol/l bo‘lganda bu ko‘rsatkich 3,44 % gacha ko‘tariladi (HR 30,50; 95 % IO 8,83–105,30) [1]. 21 ta tadqiqotni qamragan meta-tahlilda HJIX muddatidan oldin tug‘ilish (OR 2,64), preeklampsiya (OR 2,64) va neonatal

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intensiv terapiyaga yotqizish (OR 2,10) xavfini oshirgani aniqlangan [2]. Etiopatogenez hanuz to‘liq ochilmagan: gormonal, genetik va mexanik omillar bilan bir qatorda ichak mikrobiotasining o‘t kislotalari almashinuvidagi roli alohida ahamiyat kasb etmoqda [3]. Oshqozon osti bezining HJIX dagi morfologik holati esa kam o‘rganilgan.

Tadqiqot maqsadi

HJIX patogenezining morfologik asoslarini, xususan oshqozon osti bezidagi o‘zgarishlarni aniqlash va ularni «o‘t kislotalari — ichak mikrobiotasi» o‘qi nuqtai nazaridan baholash.

Material va metodlar

Respublika patologik anatomiya markazi arxivi asosida retrospektiv tadqiqot o‘tkazildi. Asosiy guruh — 2013–2023-yillarda HJIX asoratlaridan vafot etgan 51 nafar fertil yoshdagi ayol; nazorat guruhi — o‘tkir miokard infarktidan vafot etgan shu yoshdagi 12 nafar ayol. Material 10 % neytral formalinda fiksatsiya qilinib, gematoksilin-eozin, Van Gizon va PAS-reaksiyasi bilan bo‘yaldi; immunogistokimyoda CK19, α-SMA va CD68 markerlari qo‘llanildi. Morfometriya ImageJ muhitida bajarildi. Statistik tahlil STATA 19.5 da Styudent t-mezoni va χ^2 mezoni yordamida o‘tkazildi; $p < 0,05$ ahamiyatli hisoblandi.

Natijalar

Asosiy guruhda bez to‘qimasi barcha kuzatuvlarda o‘zgargan: interstitsial shish va to‘laqonlik 44 (86,3 %), atsinar hujayralar distrofiyasi 39 (76,5 %), duktal ektaziya va sekret dimlanishi 31 (60,8 %), steatonekroz o‘choqlari 27 (52,9 %) holatda qayd etildi (1-jadval). Duktal dimlanish darajasi xoledoxdagi dimlanish bilan parallel kechdi. Morfometrik tahlilda atsinuslarning o‘rtacha diametri asosiy guruhda 38,6 ± 4,2 µm, nazoratda 46,1 ± 3,8 µm ni tashkil etdi ($p < 0,001$); steatonekroz maydonining nisbiy ulushi o‘rtacha 12,4 ± 3,1 % ga yetdi. Duktal epiteliyda CK19 ekspressiyasi kuchaygan, CD68-pozitiv makrofaglar infiltratsiyasi ortgan.

1-jadval. HJIX da oshqozon osti bezidagi morfologik o‘zgarishlarning guruhlar bo‘yicha taqsimlanishi

Morfologik belgi	Asosiy guruh (n = 51)	Nazorat (n = 12)	p
Interstitsial shish va to‘laqonlik	44 (86,3 %)	3 (25,0 %)	< 0,001
Atsinar hujayralar distrofiyasi	39 (76,5 %)	2 (16,7 %)	< 0,001
Duktal ektaziya, sekret dimlanishi	31 (60,8 %)	2 (16,7 %)	0,006
Steatonekroz o‘choqlari	27 (52,9 %)	1 (8,3 %)	0,004

Muhokama

Natijalar HJIX da o‘t dimlanishi jigar bilan cheklanmasligini, oshqozon osti bezi sekretsiyasi ham parallel ravishda tormozlanishini ko‘rsatadi. Bu jarayonning muhim bo‘g‘ini — ichak mikrobiotasi: bakterial o‘t tuzlari gidrolazasi (bile salt hydrolase, BSH) konyugatsiyalangan o‘t kislotalarini dekonyugatsiyalab, ikkilamchi o‘t kislotalari hovuzini o‘zgartiradi va FXR signalizatsiyasini susaytiradi. Tang va hammualliflar HJIX bilan kasallangan ayollar mikrobiotasida Bacteroides fragilis ustunligini aniqlab, uning BSH faolligi FXR signalini to‘sishi orqali o‘t kislotalari sintezini oshirishi va gepatik ekskretsiyani buzishini isbotladilar; bemorlar mikrobiotasi ko‘chirilgan sichqonlarda xolestaz rivojlangan [4]. Zhan va hammualliflar kasallikning og‘ir kechishida Escherichia–Shigella, Olsenella va Turicibacter avlodlari ko‘payishini ko‘rsatdi [5]. Disbioz homilaga ham ta’sir qiladi: bunday chaqaloqlarda yallig‘lanishga moyillik ortishi va Lactobacillus rhamnosus bilan korreksiya imkoniyati tajribada tasdiqlangan [6]. Shundan kelib chiqib, bizda qayd etilgan duktal dimlanish va steatonekroz manzarasi o‘t kislotalari hovuzining sifat o‘zgarishi — gidrofob, sitotoksik fraksiyalar ulushining ortishi bilan izohlanishi mumkin. Ursodezoksixol kislotasi terapiyasining o‘lik tug‘ilishga ta’siri meta-tahlilda ishonchli bo‘lmagani [7] mikrobiota–o‘t

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kislotalari o‘qiga qaratilgan qo‘shimcha strategiyalar zarurligini ko‘rsatadi. Cheklov — retrospektiv dizayn va mikrobiologik materialning yo‘qligi.

Xulosa

1. HJIX da oshqozon osti bezida dimlanishli pankreatit, atsinar distrofiya va steatonekroz ko‘rinishidagi barqaror morfologik o‘zgarishlar shakllanadi; ularning ifodalanishi xoledoxdagi dimlanish darajasiga mutanosib. 2. Patogenezning markaziy bo‘g‘ini o‘t kislotalari hovuzining miqdoriy va sifat o‘zgarishi bo‘lib, bunda ichak mikrobiotasining BSH faolligi hamda FXR signalizatsiyasi muhim o‘rin tutadi. 3. HJIX ni erta aniqlash va prognozlashda zardob o‘t kislotalari monitoringini 16S rRNK sekvenlash va mikrobiota metabolitlari profili bilan birgalikda qo‘llash istiqbolli yo‘nalishdir.

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TOVUQLAR KOLIBAKTERIOZINI ANIQLASHDA BAKTERIOLOGIK VA MOLEKULAR USULLARNING AHAMIYATI

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Annotatsiya: Tovuqlar kolibakteriozini aniqlashda bakteriologik tekshiruv va bakteriyaning irsiy belgilarini o‘rganish usullarining ahamiyati yoritildi. Ilmiy manbalar asosida namuna olish, kasallik qo‘zg‘atuvchisini aniqlash va laboratoriya natijalarini to‘g‘ri baholash masalalari ko‘rib chiqildi.
Kalit so‘zlar: tovuq, kolibakterioz, *Escherichia coli*, bakteriologik tekshiruv, PCR, tashxis.

Аннотация: На основе научных источников рассмотрены бактериологические и молекулярные методы диагностики колибактериоза кур, особенности отбора проб и совместной оценки результатов исследований.
Ключевые слова: куры, колибактериоз, *Escherichia coli*, бактериологическое исследование, ПЦР.

Abstract: The importance of bacteriological and molecular methods in diagnosing avian colibacillosis is reviewed. Particular attention is paid to sample selection and the combined interpretation of laboratory findings.
Keywords: chickens, colibacillosis, *Escherichia coli*, bacteriology, PCR, diagnosis.

Parrandachilikda yuqumli kasalliklar tovuqlarning o‘sishi, tuxum berishi va saqlanishiga salbiy ta’sir ko‘rsatadi. Shunday kasalliklardan biri kolibakterioz bo‘lib, uni *Escherichia coli* bakteriyasining ayrim kasallik qo‘zg‘atuvchi shtammlari keltirib chiqaradi. Kasallangan parrandalarda holsizlik, ishtahaning pasayishi va nafas olishning qiyinlashishi kuzatiladi. Ayrim hollarda yurak va jigar atrofidagi pardalar, shuningdek havo xaltachalarida yallig‘lanish yuz beradi [1, 2].

Kolibakteriozni aniqlashda e’tibor berilishi kerak bo‘lgan jihat shuki, *E. coli* sog‘lom tovuqlarning ichagida ham uchraydi. Shuning uchun ichak yoki kloakadan ushbu bakteriyani topishning o‘zi kasallikni tasdiqlamaydi. Bakteriyaning qaysi a’zodan ajratilgani, parrandadagi kasallik belgilari va laboratoriya tekshiruvi natijalari bir-biriga mos kelishi zarur. Ushbu ishning maqsadi kolibakteriozni aniqlashda an’anaviy bakteriologik hamda zamonaviy molekular usullarning ahamiyatini qiyosiy yoritishdan iborat.

Ushbu tadqiqot materialini tayyorlashda tovuqlar kolibakteriozi bo‘yicha chop etilgan tadqiqotlarda namuna olish, bakteriyani oziqa muhitida o‘stirish, biokimyoviy xususiyatlarini aniqlash, serologik tekshiruv hamda PCR usullaridan foydalanish holatlari ko‘rib chiqildi. Xususan, ushbu usullarning qanday ma’lumot berishi va qaysi hollarda qo‘shimcha tekshiruv talab etishi taqqoslandi.

Ilmiy manbalarga ko‘ra, tashxisning ishonchliligi, avvalo, namunaning to‘g‘ri olinishiga bog‘liq. Kasallangan yoki yaqinda nobud bo‘lgan tovuqlarning jigar, taloq, yurak qoni va kasallik belgilari kuzatilgan ichki a’zolaridan namuna olish maqsadga muvofiq. Odatda bakteriya uchramasligi kerak bo‘lgan a’zolardan *E. coli* ajratilishi uning kasallikka aloqadorligini baholashda muhimroq dalil bo‘ladi. Bunda foydalaniladigan asboblarning tozaligi, namunaning boshqa

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mikroblar bilan aralashib ketmasligi hamda laboratoriyaga yetkazish sharoiti e’tibordan chetda qolmasligi kerak [1].

Bakteriologik tekshiruvda namunalar MacConkey va EMB kabi maxsus oziqa muhitlariga ekiladi. O‘sib chiqqan koloniyalar tashqi ko‘rinishi, mikroskopdagi shakli va biokimyoviy belgilariga qarab tekshiriladi. Masalan, *E. coli* ning laktozani parchalashi va ayrim biokimyoviy reaksiyalari uni boshqa bakteriyalardan farqlashda yordam beradi. Ushbu usulning eng katta ustunligi tirik bakteriya kulturasini olish imkoniyatidir. Ajratilgan bakteriyani keyinroq boshqa testlarda ham tekshirish mumkin. Shunga qaramay, bakteriya *E. coli* ekanligi aniqlanishi uning albatta kasallik qo‘zg‘atganini anglatmaydi.

Serologik tekshiruv bakteriyalarning ayrim guruhlarini ajratishga xizmat qiladi. Ilmiy adabiyotlarda tovuqlar kolibakteriozi bilan O1, O2 va O78 guruhlari ko‘p bog‘langan [2]. O‘zbekistonning Farg‘ona viloyatida o‘tkazilgan tadqiqotlarda esa O1, O26 va O78 serotiplari qayd etilgan [5]. Bunday ma’lumotlar xo‘jaliklarda uchraydigan bakteriya guruhlarini kuzatishda foydali. Ammo bir guruhdagi barcha bakteriyalar bir xil darajada kasallik keltirib chiqarmaydi. Shu bois serologik natija yakuniy tashxis uchun yolg‘iz o‘zi yetarli emas.

PCR usuli bakteriya DNKsining ma’lum qismlarini aniqlashga asoslanadi. Parrandalarda kasallik bilan bog‘liq *E. coli* shtammlarini o‘rganishda iutA, hlyF, iss, iroN va ompT genlaridan foydalanish taklif etilgan [3]. Ushbu genlar bakteriyaning yashab qolishi va organizmga moslashishiga aloqador belgilar haqida ma’lumot beradi. Bir nechta genni bir vaqtda tekshiruvchi multiplex PCR usuli bitta genni aniqlashga qaraganda ko‘proq ma’lumot beradi. Biroq ayrim genlar sog‘lom tovuqlardan ajratilgan *E. coli* da ham uchrashi mumkin. Shu sababli gen aniqlanganining o‘zi kasallikka yakuniy tashxis qo‘yish uchun yetarli emas.

Bakteriyalarni tez aniqlashda MALDI-TOF MS usulidan foydalanish mumkin. U bakteriyaning oqsil belgilari orqali qaysi turga mansubligini ko‘rsatadi, ammo kasallik qo‘zg‘atish xususiyatini to‘liq baholamaydi. DNKni chuqurroq o‘rganishga asoslangan usullar esa turli xo‘jaliklardan ajratilgan bakteriyalarning o‘xshashligi va ulardagi ayrim chidamlilik belgilarini taqqoslashga yordam beradi [4]. Bunday tekshiruvlar ko‘proq ilmiy izlanishlar va kasallik tarqalishini o‘rganishda foydalidir.

Umuman olganda, amaliyot uchun eng to‘g‘ri yo‘l bir nechta tekshiruvni izchil qo‘llashdir. Dastlab kasallik belgilari va ichki a’zolardagi o‘zgarishlar baholanadi, so‘ng kerakli a’zodan namuna olinib, bakteriya ajratiladi. Shundan keyin zaruratga qarab PCR o‘tkaziladi. Antibiotik tanlash masalasida esa bakteriyaning dorilarga sezgirligini alohida tekshirish muhim: ma’lum bir gen aniqlanishi bakteriyaning dori vositasiga amalda qanday javob berishini har doim ham ko‘rsatmaydi. Bu yondashuv har bir testning imkoniyatidan o‘z o‘rnida foydalanishga yordam beradi.

Xulosa qilib aytganda, tovuqlar kolibakterioziga tashxis qo‘yishda faqat *E. coli* aniqlanganiga asoslanish mumkin emas. Bakteriologik tekshiruv kasallik qo‘zg‘atuvchisini ajratib olishga, PCR esa uning ayrim irsiy belgilarini o‘rganishga yordam beradi. Ularning natijalari kasallik belgilari va ichki a’zolardagi o‘zgarishlar bilan birgalikda baholansa, xulosa ancha asosli bo‘ladi. Shu sababli parrandachilik laboratoriyalarida namuna olish tartibiga qat’iy rioya qilish, bakteriologik tekshiruvni to‘g‘ri tashkil etish va zarur hollarda molekular usullarni qo‘llash maqsadga muvofiqdir.

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VI

BO‘LIM · SECTION · СЕКЦИЯ

YOSH OLIMLAR TADQIQOTLARI VA INNOVATSION ISHLANMALAR

Research of Young Scientists and Innovative Developments

Исследования молодых учёных и инновационные разработки



10
ta maqola va tezis

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RESPIRATION INTENSITY OF BEAN SEEDS STORED UNDER VARIOUS CONDITIONS

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Abstract: This article highlights the respiration intensity of common bean (Phaseolus vulgaris L.) seeds stored under various conditions and the effect of storage conditions on the physiological and biochemical processes occurring in seeds. The main objective of the research is to evaluate the changes in the respiration intensity of bean seeds under different storage conditions and to analyze the physiological state of seeds in relation to storage conditions.
Keywords: Common bean, Phaseolus vulgaris L., seed, respiration intensity, storage conditions, temperature, moisture, metabolism, physiological processes, seed viability.

Annotatsiya: Ushbu maqolada turli sharoitlarda saqlangan oddiy loviya (*Phaseolus vulgaris L.*) urug‘larining nafas olish intensivligi va saqlash sharoitlarining urug‘larda kechadigan fiziologik-biokimyoviy jarayonlarga ta’siri yoritiladi. Urug‘larning nafas olishi ularning hayotchanligi, unuvchanligi va saqlanish davridagi fiziologik holatini tavsiflovchi muhim ko‘rsatkichlardan biridir. Saqlash jarayonida harorat, namlik va saqlash muddati kabi omillar urug‘larda moddalar almashinuvi jadalligiga ta’sir ko‘rsatishi mumkin. Mazkur omillarni o‘rganish loviya urug‘larini uzoq muddat davomida sifatini saqlagan holda saqlash usullarini takomillashtirishga xizmat qiladi.
Kalit so‘zlar: Oddiy loviya, *Phaseolus vulgaris L.*, urug‘, nafas olish intensivligi, saqlash sharoiti, harorat, namlik, moddalar almashinuvi, fiziologik jarayonlar, urug‘ hayotchanligi.

Аннотация: В данной статье освещается интенсивность дыхания семян фасоли обыкновенной (Phaseolus vulgaris L.), хранящихся в различных условиях, и влияние условий хранения на физиолого-биохимические процессы, происходящие в семенах. Основной целью исследования является оценка изменений интенсивности дыхания семян фасоли при различных условиях хранения и анализ физиологического состояния семян в связи с условиями хранения.
Ключевые слова: Фасоль обыкновенная, Phaseolus vulgaris L., семена, интенсивность дыхания, условия хранения, температура, влажность, обмен веществ, физиологические процессы, жизнеспособность семян.

Introduction

The respiration intensity of seeds is a key physiological indicator that characterizes their physiological state, metabolic rate, and level of vital activity. During respiration, the oxidation of carbohydrates, lipids, and other reserve substances generates energy (ATP), which sustains the minimal metabolic processes essential for life within the seed tissues. However, high respiration intensity during storage leads to the rapid depletion of nutrient reserves, an increase in the production of reactive oxygen species (ROS), and an acceleration of the physiological aging process. Consequently, assessing respiration intensity serves as an important physiological criterion for determining the storability and quality of seeds.

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Research results indicate that respiration intensity is influenced by a combination of factors: seed moisture content, storage temperature, and storage duration. While a sharp increase in respiration intensity was observed at the beginning of the storage period—correlating with higher seed moisture and temperature—a gradual decline was noted across all experimental variants in the subsequent months. This trend is attributed to the aging of physiologically active tissues, a reduction in mitochondrial activity, and a slowdown in energy metabolism during the storage period. Under the optimal storage conditions—8% seed moisture content and a temperature of +5 °C—the respiration intensity was 19.9 µmol CO_2/g dry mass/hour during the first month, decreasing to 11.9 µmol CO_2/g dry mass/hour after 13 months. This represents a 40.2% reduction compared to the initial value. Due to the restricted activity of respiratory enzymes at low temperatures, reserve substances were consumed more slowly, and the physiological condition of the seeds was relatively well preserved.

When the temperature was increased to +15 °C (at the same moisture level), the respiration intensity was 25.2 µmol CO_2/g dry mass/hour in the first month, falling to 13.1 µmol CO_2/g dry mass/hour after 13 months. At +25 °C, this figure decreased from 30.5 to 15.0 µmol CO_2/g dry mass/hour. Thus, while higher temperatures intensified metabolism during the initial stage of storage, the respiratory system declined more rapidly over the course of long-term storage. An increase in seed moisture content further intensified respiration. For instance, at +25 °C during the first month, the respiration rate was 30.5 µmol CO_2/g dry mass/hour at 8% moisture, 35.5 at 10% moisture, 40.6 at 12% moisture, and 45.2 at 14% moisture. These values are linked to the fact that as seed moisture increases, the amount of free water within the cells rises, hydrolytic enzymes become activated, and metabolic processes accelerate.

Methods

Seeds of the common bean (Phaseolus vulgaris L.) were used as the research subject. The seeds were stored under laboratory conditions at varying moisture levels (8%, 10%, 12%, and 14%) and temperatures (+5 °C, +15 °C, and +25 °C) for a period of 13 months [4]. Throughout the storage period (at 1, 4, 7, 10, and 13 months), the respiration intensity of the seeds was determined using standard methodologies accepted in seed science [2, 3], with the amount of carbon dioxide released calculated in units of µmol CO_2/g dry mass/hour. Furthermore, to assess the impact of the respiration process on seed aging, the content of malondialdehyde (MDA) and the activity of the antioxidant enzymes catalase and peroxidase were analyzed in parallel [1, 6]. The obtained numerical data were subjected to statistical analysis to determine mean values and standard errors.

Results

The research findings indicated that seed moisture content, storage temperature, and storage duration collectively influenced respiration intensity [4, 5]. While a sharp increase in respiration intensity was observed at the beginning of the storage period as seed moisture content and temperature rose, a gradual decline was recorded across all experimental variants in the subsequent months (Table 1).

Table 1. Respiration intensity of bean seeds stored under various conditions (µmol CO_2/g dry mass/hour)

№	Seed moisture, %	Temperature, °C	Shelf life, months				
			1	4	7	10	13
1	8	+5	19,9±2,19	18,0±1,98	16,0±1,56	13,9±1,59	11,9±1,08
2		+15	25,2±2,21	22,2±1,89	19,2±1,73	16,0±1,53	13,1±1,45
3		+25	30,5±2,86	26,2±2,20	22,3±2,14	18,2±1,82	15,0±1,63
4	10	+5	25,3±2,43	22,4±2,30	19,0±1,97	16,1±1,64	14,1±1,38
5		+15	30,4±2,74	26,3±2,36	22,5±2,27	18,3±1,96	15,1±1,60
6		+25	35,5±3,09	30,0±3,04	25,3±2,46	20,3±1,94	17,2±1,79

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7	12	+5	30,6±2,95	26,3±2,35	21,9±2,06	18,4±1,72	16,1±1,78
8		+15	35,4±2,83	30,0±2,87	25,3±2,38	20,5±2,05	17,0±1,70
9		+25	40,6±3,66	34,4±3,15	28,2±2,64	23,2±2,15	20,5±2,03
10	14	+5	35,3±3,22	30,3±286	26,0±1,26	21,4±2,22	18,2±1,72
11		+15	40,3±3,80	34,1±3,46	28,2±2,66	23,5±2,13	20,3±2,06
12		+25	45,2±4,36	38,2±3,58	32,0±2,92	27,3±2,49	23,4±2,19

In the variant with 14% moisture content and a temperature of +25 °C—where the highest respiration intensity was recorded during the storage period—this indicator decreased from 45.2 to 23.4 µmol CO_2/g dry mass/hour, representing a relative reduction of 48.2%. Nevertheless, even after 13 months, the respiration intensity in this variant remained higher than in the others. This indicates that metabolism remained active for an extended period under high-moisture conditions, though this process occurred at the cost of a rapid depletion of energy reserves.

A slower rate of respiration under low-temperature conditions is considered physiologically optimal for seeds. For instance, in the variant with 14% moisture content and a temperature of +5 °C, respiration intensity decreased from 35.3 to 18.2 µmol CO_2/g dry mass/hour. This demonstrates a more economical consumption of energy resources compared to conditions at higher temperatures. The results obtained regarding respiration intensity were found to be closely correlated with the previously analyzed levels of malondialdehyde (MDA) and the activities of catalase and peroxidase. Under storage conditions characterized by high temperature and high humidity, respiration intensity reached its peak; simultaneously, MDA levels also reached their highest values, while the activities of catalase and peroxidase declined sharply. This indicates that the accelerated respiration process leads to an increased production of reactive oxygen species (ROS) within the mitochondria—which the antioxidant enzyme system fails to fully neutralize—thereby intensifying lipid peroxidation.

From a physiological perspective, this process can be explained as follows: as seed moisture content increases, the degree of cytoplasmic hydration rises, activating the enzymes of the respiratory chain. A rise in temperature further accelerates enzymatic reactions, intensifying electron transport within the mitochondria. Along with ATP synthesis, this also enhances the production of reactive oxygen species, such as superoxide anions and hydrogen peroxide. If the antioxidant system (comprising catalase, peroxidase, and other enzymes) is unable to completely neutralize these free radicals, lipid peroxidation within cell membranes intensifies, the selective permeability of the membranes is compromised, and the physiological aging process is accelerated. At the same time, a decrease in respiration intensity during prolonged storage is not always a positive development. This condition often arises from a decline in the functional activity of mitochondria, the inactivation of respiratory enzymes, and the disruption of energy metabolism. Consequently, a sharp drop in respiration intensity during long-term storage serves as a significant indicator of the physiological aging of seeds and a reduction in their viability.

Overall, research findings indicate that the primary factors influencing respiration intensity during the storage of bean seeds are seed moisture content, temperature, and the duration of storage. A seed moisture content of 8–10% combined with a temperature of +5°C maintains the respiration process at a physiologically optimal level; this ensures the economical consumption of reserve substances and allows for the long-term preservation of seed viability. Conversely, under conditions of 12–14% moisture and a temperature of +25°C, high respiration intensity leads to the rapid depletion of energy resources, increased oxidative stress, reduced activity of antioxidant enzymes, and accelerated lipid peroxidation—all of which hasten the physiological aging of the seeds.

Thus, when the results obtained for respiration intensity are evaluated in conjunction with indicators for catalase, peroxidase, and MDA (malondialdehyde), they provide a comprehensive characterization of the mechanisms—such as oxidative stress, energy metabolism, and physiological aging—that occur during the storage of bean seeds. Furthermore, these findings serve as an important scientific basis for improving seed storage technology.

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Conclusion

The results of the study indicate that the respiration intensity of common bean (Phaseolus vulgaris L.) seeds stored under various conditions depends on seed moisture content, storage temperature, and the duration of storage.

An increase in respiration intensity was observed as seed moisture content rose from 8% to 14% and storage temperature increased from +5 °C to +25 °C. Specifically, under conditions of 14% seed moisture and a temperature of +25 °C, respiration intensity reached its peak during the first month of storage, measuring 45.2 ± 4.36 µmol CO_2/g dry mass/hour. In contrast, for seeds with 8% moisture stored at +5 °C, this value was 19.9 ± 2.19 µmol CO_2/g dry mass/hour.

As the storage period extended from 1 month to 13 months, respiration intensity decreased across all experimental variants. For instance, in the variant with 14% moisture content and a temperature of +25 °C, this value decreased from 45.2 to 23.4 µmol CO_2/g dry mass/hour, while in the variant with 8% moisture content and a temperature of +5 °C, it dropped from 19.9 to 11.9 µmol CO_2/g dry mass/hour.

Overall, the results obtained demonstrate the importance of controlling moisture and temperature conditions when storing bean seeds. Storage at lower moisture levels and temperatures can help limit the respiration rate of the seeds. However, to fully evaluate the quality of seeds during long-term storage, it is necessary to assess indicators of germination capacity and viability, in addition to respiration intensity.

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MIKROBIOLOGIYA VA VIRUSOLOGIYA FANINI O‘QITISHDA MENTAL XARITA METODIDAN FOYDALANISH

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Annotatsiya: Mazkur maqolada oliy ta’lim muassasalarida Mikrobiologiya va virusologiya fanlarini o‘qitishda mental xarita texnologiyasidan foydalanishning didaktik va metodik imkoniyatlari yoritilgan. Shuningdek, mental xaritalarni ta’lim jarayoniga integratsiya qilishning tayyorgarlik, yaratish, tahlil va muhokama, baholash bosqichlari hamda ularni tashkil etish metodikasi bayon etilgan. Mental xaritalardan foydalanish orqali ta’lim oluvchilarning mustaqil, mantiqiy, tahliliy va ijodiy fikrlashini, axborotni tizimlashtirish, umumlashtirish va amaliy kompetensiyalarini rivojlantirish imkoniyatlari asoslangan.

Kalit so‘zlar: mental xarita, Mikrobiologiya, virusologiya, pedagogik texnologiya, ta’lim jarayoni, vizual ta’lim, biologik tushunchalar, bilimlarni tizimlashtirish, mustaqil fikrlash, tahliliy fikrlash, kompetensiya, interfaol ta’lim, baholash.

Аннотация: В данной статье рассматриваются дидактические и методические возможности использования технологии ментальных карт в преподавании микробиологии и вирусологии в высших учебных заведениях. Также описываются этапы подготовки, создания, анализа, обсуждения и оценки интеграции ментальных карт в образовательный процесс, а также методология их организации. Использование ментальных карт основано на возможности развития самостоятельного, логического, аналитического и творческого мышления студентов, систематизации, обобщения информации и практических компетенций.

Ключевые слова: ментальная карта, микробиология, вирусология, педагогическая технология, образовательный процесс, наглядное образование, биологические концепции, систематизация знаний, самостоятельное мышление, аналитическое мышление, компетентность, интерактивное обучение, оценивание.

Abstract: This article highlights the didactic and methodological possibilities of using mind mapping technology in teaching Microbiology and Virology at higher education institutions. It also outlines the stages of integrating mind maps into the educational process — preparation, creation, analysis and discussion, and assessment — as well as the methodology for implementing them. The article substantiates the potential for developing students' independent, logical, analytical, and creative thinking, as well as their skills in systematizing and synthesizing information and their practical competencies, through the use of mind maps.

Keywords: mind map, microbiology, virology, pedagogical technology, educational process, visual learning, biological concepts, systematization of knowledge, independent thinking, analytical thinking, competence, interactive learning, assessment.

Kirish

Bugungi kunda oliy ta’lim tizimida ta’lim mazmunini zamonaviy pedagogik texnologiyalar asosida tashkil etish, talabalarning mustaqil fikrlashi, tahliliy yondashuvi va amaliy kompetensiyalarini rivojlantirish muhim pedagogik vazifalardan biri hisoblanadi. Ayniqsa, Mikrobiologiya va virusologiya fanlarini o‘qitishda katta hajmdagi nazariy ma’lumotlar, ko‘plab

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biologik atamalar, mikroorganizmlarning morfologik, fiziologik va biologik xususiyatlari, ularning tasnifi hamda o‘zaro bog‘liq jarayonlarini izchil o‘zlashtirish talab etiladi. Mazkur holat o‘quv materiallarini an’anaviy bayon qilish bilan bir qatorda, ularni vizual, tizimli va mantiqiy shaklda ifodalashga imkon beruvchi zamonaviy ta’lim texnologiyalaridan foydalanishni taqozo etadi. Mikrobiologiya va virusologiya fanlarining o‘ziga xosligi shundaki, unda ko‘z bilan bevosita kuzatish imkoniyati cheklangan biologik obyektlar, murakkab tuzilish va jarayonlar hamda ko‘plab o‘zaro bog‘liq tushunchalar o‘rganiladi. Masalan, mikroorganizmlarning morfologik shakllari, bakteriyalarning tasnifi, spora hosil bo‘lishi, mikroorganizmlarning ko‘payishi, oziqlanishi, patogenligi, viruslarning tuzilishi va replikatsiyasi kabi mavzularni o‘zlashtirishda tushunchalar o‘rtasidagi mantiqiy bog‘lanishlarni ko‘rsatish muhim ahamiyatga ega. Shu jihatdan Mental xarita texnologiyasi o‘quv materiallarini markaziy va ikkilamchi tushunchalarga ajratish, ularning o‘zaro aloqadorligini grafik tarzda ifodalash hamda bilimlarni tizimlashtirish imkonini beradi.

Fanlarni o‘qitishda Mental xaritalardan foydalanishning dolzarbligi, shuningdek, ta’lim jarayonini talabaning faol ishtirokiga asoslangan holda tashkil etish zarurati bilan ham belgilanadi. Ushbu texnologiya orqali talaba tayyor ma’lumotni qabul qiluvchi subyekt emas, balki ma’lumotlarni izlash, saralash, tahlil qilish, umumlashtirish va ular o‘rtasidagi bog‘lanishlarni aniqlash jarayonining faol ishtirokchisiga aylanadi. Natijada mustaqil, mantiqiy va ijodiy fikrlash, axborotni tizimlashtirish hamda o‘zlashtirilgan bilimlarni yangi vaziyatlarda qo‘llash ko‘nikmalarini rivojlantirish uchun imkoniyat yaratiladi.

Mavzuning yana bir muhim jihati — mental xaritalardan bilimlarni nazorat qilish va kompetensiyalarni baholash vositasi sifatida foydalanish imkoniyatidir. Talabaning tuzgan mental xaritasi orqali uning mavzuning asosiy tushunchalarini qay darajada o‘zlashtirgani, tushunchalar o‘rtasidagi mantiqiy bog‘lanishlarni to‘g‘ri aniqlay olishi, bilimlarni umumlashtirish va amaliy jihatdan qo‘llay olishi haqida tasavvur hosil qilish mumkin. Shu sababli mental xarita texnologiyasi nafaqat yangi bilimlarni o‘zlashtirish, balki takrorlash, mustahkamlash, umumlashtirish, nazorat qilish va baholash bosqichlarida ham metodik vosita sifatida qo‘llanishi mumkin.

Shuningdek, raqamli ta’lim vositalarining rivojlanishi mental xaritalarni elektron shaklda yaratish va ulardan interaktiv ta’lim jarayonida foydalanish imkoniyatlarini kengaytirmoqda. Raqamli mental xaritalar yordamida o‘quv materiallarini tezkor ravishda tahrirlash, tushunchalar o‘rtasidagi aloqalarni vizual ifodalash, guruhiy ishlash va natijalarni taqdim etish mumkin.

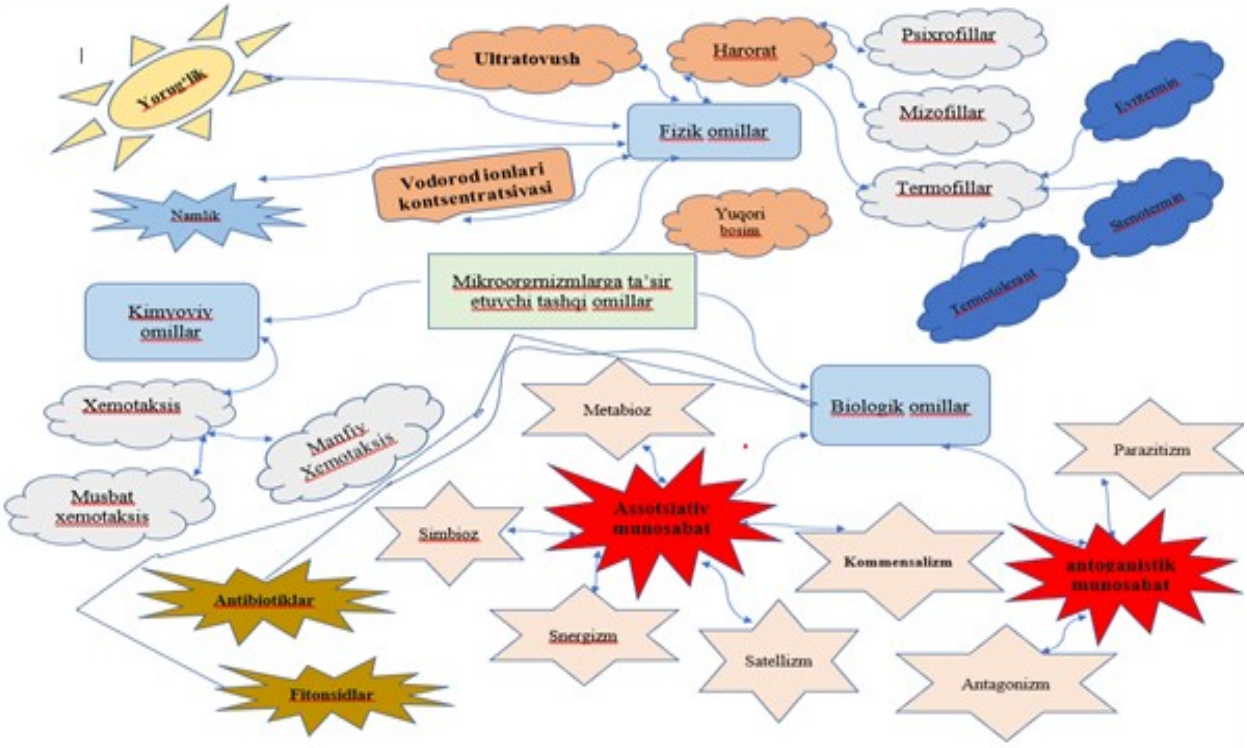
Shu nuqtai nazardan, Mikrobiologiya va virusologiya fanini o‘qitishda mental xarita texnologiyasining didaktik va metodik asoslarini ishlab chiqish, undan ta’limning turli bosqichlarida foydalanish imkoniyatlarini aniqlash hamda uning o‘quvchilarning bilim, ko‘nikma va kompetensiyalarini shakllantirishdagi pedagogik imkoniyatlarini asoslash dolzarb ilmiy-metodik masalalardan biridir.

Mental xaritalar texnologiyasini ta’lim jarayoniga samarali integratsiya qilish metodik jihatdan puxta asoslangan yondashuvni talab etadi. Mazkur metodni faqat vizual axborotni ifodalash vositasi sifatida emas, balki o‘quvchilarning kognitiv faolligini oshirish, mustaqil va mantiqiy fikrlashini rivojlantirish, bilimlarni tizimlashtirish hamda o‘zlashtirilgan ma’lumotlar o‘rtasidagi bog‘liqlikni anglashga xizmat qiluvchi pedagogik texnologiya sifatida baholash mumkin. Shu nuqtai nazardan, mental xaritalardan foydalanishda uning didaktik maqsadlari, qo‘llash bosqichlari, metodik tamoyillari va baholash mezonlarini aniq belgilash muhim ahamiyat kasb etadi.

Mental xaritalarni qo‘llash metodikasi izchil bosqichlarda tashkil etiladi.

Birinchi bosqich — tayyorgarlik bosqichi bo‘lib, unda o‘qituvchi o‘quv maqsadini belgilaydi, mavzuning asosiy tushunchalarini aniqlaydi, ularni mazmuniy va mantiqiy jihatdan tartibga soladi hamda mental xaritani shakllantirish uchun zarur bo‘lgan asosiy elementlarni belgilab oladi. Shu bilan birga, o‘quvchilarga mental xarita tuzishning asosiy qoidalari, markaziy tushuncha, asosiy va ikkilamchi tarmoqlar, kalit so‘zlar, ranglar va grafik belgilarni qo‘llash tartibi tushuntiriladi. Mazkur bosqich o‘quvchilarning keyingi faoliyatini to‘g‘ri tashkil etish uchun metodik asos vazifasini bajaradi.

Ikkinchi bosqich — mental xaritani yaratish bosqichi hisoblanadi. Ushbu bosqichda o‘quvchilar mavzuning markaziy tushunchasi aniqlanadi. Mikroorganizmlarga tashqi muhit omillarining ta’siri va undan kelib chiqadigan asosiy g‘oyalar fizik, kimyoviy va biologik omillar tarmoqlar shaklida joylashtiradi. Keyinchalik asosiy tarmoqlar kichik tushunchalar bilan to‘ldiriladi. Mental xaritada qisqa va mazmunli kalit so‘zlardan, ranglar, shartli belgilar, rasmlar va boshqa vizual elementlardan foydalanish mumkin. Bunday yondashuv o‘quv materialini ixcham va tizimli tarzda ifodalash hamda asosiy tushunchalarni ajratib ko‘rsatishga yordam beradi.



1-rasm. Mikroorganizmlarga tashqi omillarning ta’siri mavzusiga mantiqiy mazmundagi mental xarita

Uchinchi bosqich — tahlil va muhokama bosqichidir. Unda talabalar tomonidan tuzilgan mental xaritalar taqdim etiladi, o‘zaro tahlil qilinadi va muhokama qilinadi. O‘quvchilar o‘zlari tanlagan tushunchalar, ularning joylashuvi va o‘zaro bog‘liqligini izohlaydilar. Guruhiy muhokama jarayonida ular o‘z fikrlarini asoslash, boshqa o‘quvchilarning qarashlarini tinglash va tahlil qilish, mavjud farqlarni aniqlash hamda umumiy xulosaga kelish imkoniyatiga ega bo‘ladilar. Shu jihatdan mazkur bosqich kommunikativ, tahliliy va refleksiv ko‘nikmalarni rivojlantirishga xizmat qiladi.

To‘rtinchi bosqich — baholash bosqichi bo‘lib, unda o‘quvchilarning mental xarita bilan ishlash jarayoni va yakuniy natijasi belgilangan mezonlar asosida baholanadi. Baholashda xaritaning mazmuniy to‘liqligi, mantiqiyligi, strukturaviy tuzilishi, tushunchalar o‘rtasidagi bog‘lanishlarning to‘g‘ri ifodalanganligi, vizual elementlardan maqsadga muvofiq foydalanish va ijodiy yondashuv kabi mezonlar hisobga olinishi mumkin. Shuningdek, o‘z-o‘zini baholash va o‘zaro baholash elementlaridan foydalanish o‘quvchilarning refleksiv ko‘nikmalarini rivojlantirishga yordam beradi.

Xulosa qilib aytganda, mikrobiologiya va virusologiya fanlarini o‘qitishda Mental xarita texnologiyasidan foydalanish o‘quv materiallarini tizimlashtirish, murakkab biologik tushunchalar o‘rtasidagi mantiqiy bog‘lanishlarni aniqlash hamda ta’lim oluvchilarning mustaqil, mantiqiy va ijodiy fikrlashini rivojlantirishga xizmat qiladi. Mental xaritalar orqali katta hajmdagi nazariy ma’lumotlarni ixcham va ko‘rgazmali shaklda ifodalash, mavzuning asosiy mazmunini ajratib ko‘rsatish va bilimlarni yaxlit holda o‘zlashtirish imkoniyati yaratiladi. Yangi bilimlarni o‘zlashtirish, bilimlarni mustahkamlash va umumlashtirish, takrorlash, muammoli vaziyatlarni tahlil qilish,

mustaqil va guruhiy faoliyatni tashkil etish, shuningdek, bilim va kompetensiyalarni nazorat qilish hamda baholash jarayonlarida qo‘llash mumkinligi aniqlandi. Ayniqsa, mikrobiologiya va virusologiya fanidagi tasniflar, mikroorganizmlarning tuzilishi, morfologik shakllari, ko‘payishi, spora hosil qilishi, viruslarning tuzilishi va biologik xususiyatlarini o‘rganishda mental xaritalar samarali metodik vosita bo‘la oladi.

Shuningdek, mental xaritalarni muammoli, loyiha va kooperativ ta’lim texnologiyalari bilan integratsiya qilish ta’lim oluvchilarning bilish faolligi va fan bo‘yicha amaliy kompetensiyalarini rivojlantirish uchun qo‘shimcha imkoniyat yaratadi. Nazariy mazmundagi, mantiqiy, kompetensiyalarni nazorat qilish va baholashga yo‘naltirilgan mental xaritalardan maqsadga muvofiq foydalanish ta’lim jarayonining mazmunini yanada tizimli tashkil etishga yordam beradi.

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MIKROBIOLOGIYA, VIRUSOLOGIYA VA IMMUNOLOGIYA FANINI O‘QITISHDA INTERFAOL PEDAGOGIK TEXNOLOGIYALARDAN FOYDALANISH

ИСПОЛЬЗОВАНИЕ ИНТЕРАКТИВНЫХ ПЕДАГОГИЧЕСКИХ ТЕХНОЛОГИЙ ПРИ ПРЕПОДАВАНИИ МИКРОБИОЛОГИИ, ВИРУСОЛОГИИ И ИММУНОЛОГИИ

THE USE OF INTERACTIVE PEDAGOGICAL TECHNOLOGIES IN TEACHING MICROBIOLOGY, VIROLOGY, AND IMMUNOLOGY

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Annotatsiya: Ushbu maqolada tibbiyot oliy ta’lim muassasalarida mikrobiologiya fanini o‘qitishda interfaol pedagogik texnologiyalardan foydalanishning nazariy va amaliy jihatlari yoritilgan. Mikrobiologiya fanining katta hajmdagi nazariy materialni klinik vaziyatlar, laboratoriya diagnostikasi va kasalliklarning etiologiyasi bilan bog‘lab o‘zlashtirishni talab qilishi an’anaviy ma’ruza usulidan tashqari talaba faol ishtirokini ta’minlovchi ta’lim texnologiyalaridan foydalanish zaruratini yuzaga keltiradi. Maqolada case-study, muammoli ta’lim, kichik guruhlarda ishlash, brainstorming, klaster, Venn diagrammasi va vizual ta’lim elementlaridan foydalanish imkoniyatlari tahlil qilinadi. Ilmiy adabiyotlar tahlili interfaol va faol ta’lim yondashuvlari talabalarning bilimni qo‘llash, klinik fikrlash, muammoli vaziyatlarni tahlil qilish hamda kommunikativ ko‘nikmalarini rivojlantirishda samarali ekanligini ko‘rsatadi. Mikrobiologiya mashg‘ulotlarida nazariy bilimni klinik vaziyat bilan integratsiya qilish talabaning mikroorganizmlar haqidagi bilimlarini amaliy tibbiy tafakkur bilan bog‘lash imkonini beradi.

Kalit so‘zlar: mikrobiologiya, tibbiy ta’lim, interfaol ta’lim, faol ta’lim, case-study, muammoli ta’lim, klinik fikrlash, kichik guruh, pedagogik texnologiya.

Аннотация: В статье рассматриваются теоретические и практические аспекты применения интерактивных педагогических технологий при преподавании микробиологии в медицинских вузах. Поскольку освоение микробиологии требует интеграции обширного теоретического материала с клиническими ситуациями, методами лабораторной диагностики и этиологией заболеваний, возникает необходимость использования образовательных технологий, стимулирующих активное участие студентов и выходящих за рамки традиционных лекционных методов. В статье анализируются возможности применения таких методов, как анализ конкретных ситуаций (кейс-метод), проблемно-ориентированное обучение, работа в малых группах, «мозговой штурм», кластерный метод, диаграммы Венна и элементы визуализации учебного материала. Анализ научной литературы свидетельствует об эффективности интерактивных и активных подходов к обучению для формирования у студентов навыков применения знаний, развития клинического мышления, умения анализировать проблемы и коммуникативных компетенций. Интеграция теоретических знаний с клиническими сценариями в ходе занятий по микробиологии позволяет студентам связать представления о микроорганизмах с практическим врачебным мышлением.

IQTIBOS UCHUN
Mirhomidov A.A. Mikrobiologiya, virusologiya va immunologiya fanini o‘qitishda interfaol pedagogik texnologiyalardan foydalanish // Fundamental va amaliy mikrobiologiyaning bugungi holati va rivojlanish istiqbollari: yosh olimlar nigohi: Respublika ilmiy-amaliy anjumani materiallari. – Toshkent, 2026. – B. 462–466.
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Ключевые слова: микробиология, медицинское образование, интерактивное обучение, активное обучение, кейс-метод, проблемно-ориентированное обучение, клиническое мышление, малая группа, педагогическая технология.

Abstract: This article examines the theoretical and practical aspects of using interactive pedagogical technologies in teaching microbiology at higher medical education institutions. Because mastering microbiology requires integrating a vast amount of theoretical material with clinical scenarios, laboratory diagnostics, and disease etiology, there is a need to employ educational technologies that foster active student participation beyond traditional lecture methods. The article analyzes the potential application of case studies, problem-based learning, small-group work, brainstorming, clustering, Venn diagrams, and visual learning elements. An analysis of scientific literature indicates that interactive and active learning approaches are effective in developing students' knowledge application, clinical reasoning, problem analysis, and communication skills. Integrating theoretical knowledge with clinical scenarios during microbiology classes enables students to connect their understanding of microorganisms with practical medical thinking.

Keywords: microbiology, medical education, interactive learning, active learning, case study, problem-based learning, clinical reasoning, small group, pedagogical technology.

Kirish

Mikrobiologiya tibbiyot ta’limining fundamental fanlaridan biri bo‘lib, mikroorganizmlarning morfologiyasi, fiziologiyasi, patogenlik xususiyatlari, laboratoriya diagnostikasi, antibiotiklarga sezgirligi va yuqumli kasalliklar patogenezini o‘rganishni o‘z ichiga oladi. Shu sababli ushbu fanni o‘zlashtirish faqat termin va tasniflarni yodlash bilan cheklanmasligi, balki olingan bilimlarni klinik vaziyatlarda qo‘llash qobiliyatini ham shakllantirishi kerak.

Mikrobiologiya ta’limida an’anaviy ma’ruza usuli muhim o‘rin tutsa-da, faqat o‘qituvchi markazidagi yondashuv talabaning mustaqil fikrlashi va bilimni amaliy vaziyatga ko‘chirish imkoniyatlarini yetarlicha rivojlantirmasligi mumkin. Faol ta’limga bag‘ishlangan yirik meta-tahlilda 225 ta tadqiqot natijalari tahlil qilinib, faol ta’lim qo‘llanilgan guruhlarda o‘quv natijalari an’anaviy ma’ruzaga nisbatan yaxshiroq bo‘lgani ko‘rsatilgan.

Tibbiy mikrobiologiyaga bevosita oid tadqiqotlarda ham interfaol va case-based yondashuvlarning samaradorligi qayd etilgan. Xususan, mikrobiologiya fanida case-based learning qo‘llangan tadqiqotda talabalarning bilimni o‘zlashtirishi va uzoqroq muddat saqlab qolishi an’anaviy didaktik ma’ruzaga nisbatan yaxshiroq bo‘lgan.

Shuningdek, mikrobiologiya bo‘yicha interfaol case-based mashg‘ulotlar talabalar tomonidan ijobiy baholangan va bunday mashg‘ulotlar case-based imtihon savollarini yechishdagi natijalar bilan bog‘liq ijobiy ko‘rsatkichlarni namoyon qilgan.

Bugungi tibbiy ta’limda mikrobiologiya bilimlarini klinik amaliyot, infeksion nazorat va antimikrob preparatlardan oqilona foydalanish bilan bog‘lash alohida ahamiyatga ega. Jahon sog‘liqni saqlash tashkiloti 2024-yilda tibbiy ta’lim uchun antimikrob rezistentlik bo‘yicha o‘quv dasturlarini baholash vositasini e’lon qilgan va AMR kompetensiyalarini tibbiyot ta’limiga integratsiya qilish zarurligini ta’kidlagan.

Mazkur tadqiqotning maqsadi — tibbiyot oliy ta’lim muassasalarida mikrobiologiya fanini o‘qitishda interfaol pedagogik texnologiyalardan foydalanishning metodik imkoniyatlarini asoslash hamda ularni nazariy va amaliy mashg‘ulotlarga integratsiya qilish bo‘yicha tavsiyalar ishlab chiqish.

Tadqiqot vazifalari: Mikrobiologiyani o‘qitishda faol va interfaol ta’limning ilmiy-pedagogik asoslarini tahlil qilish.

Mikrobiologiya mashg‘ulotlarida case-study metodidan foydalanish imkoniyatlarini aniqlash.

Muammoli ta’lim va kichik guruhlarda ishlash metodlarining mikrobiologik bilimlarni amaliy vaziyatlarga tatbiq etishdagi ahamiyatini ko‘rsatish.

Vizual materiallar va grafik-organayzerlardan foydalanish imkoniyatlarini ishlab chiqish.

Interfaol metodlarni mikrobiologiyaning klinik yo‘naltirilgan mavzulariga moslashtirish bo‘yicha metodik tavsiyalar berish.

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Material va metodlar

Mazkur maqola mikrobiologiya fanini o‘qitishda faol va interfaol ta’lim metodlaridan foydalanishga oid ilmiy adabiyotlarni tahlil qilish asosida tayyorlandi. Tadqiqot materiallari sifatida tibbiy ta’limda faol ta’lim, klinik vaziyatga asoslangan o‘qitish (case-based learning), muammoli ta’lim hamda kichik guruhlarda ishlash metodlariga bag‘ishlangan ilmiy maqolalar va Jahon sog‘liqni saqlash tashkilotining tegishli metodik hujjatlaridan foydalanildi.

Tahlil jarayonida adabiyotlarni qiyosiy o‘rganish, ilmiy ma’lumotlarni umumlashtirish va mikrobiologiya fanining mazmuniga mos pedagogik tavsiyalarni ishlab chiqish usullaridan foydalanildi. Interfaol metodlarni qo‘llash imkoniyatlari mikroorganizmlarning morfologiyasi, biologik xususiyatlari, patogenligi, laboratoriya diagnostikasi va klinik ahamiyatini o‘rgatish misolida ko‘rib chiqildi.

Mikrobiologiya, virusologiya, immunologiya fani mashg‘ulotlarida quyidagi interfaol metodlardan foydalanish taklif etiladi: case-study, muammoli savollar, kichik guruhlarda ishlash, brainstorming, klaster, Venn diagrammasi, savol-javob va tezkor test, vizual mikroskopik tasvirlarni tahlil qilish, laboratoriya diagnostikasi algoritmlarini tuzish.

Mazkur metodlarning asosiy pedagogik tamoyili talabani tayyor ma’lumotni passiv qabul qiluvchi emas, balki muammoni tahlil qiluvchi va yechim ishlab chiquvchi faol ishtirokchiga aylantirishdan iborat.

Mikrobiologiya mashg‘ulotlarida case-study metodidan foydalanish. Case-study mikrobiologiyani klinik vaziyat bilan bog‘lash uchun ayniqsa qulay metod hisoblanadi. Masalan, stafilokokklar mavzusida talabalarga quyidagi vaziyat berilishi mumkin:

Klinik vaziyat: bemorda teri va yumshoq to‘qimalarda yiringli yallig‘lanish kuzatilgan. Laboratoriya tekshiruvida Gram-musbat kokklar aniqlangan. Mikroorganizmlar uzum shingiliga o‘xshash guruhlar hosil qilgan.

Talabalarga quyidagi savollar beriladi:

1. Ushbu mikroorganizm qaysi guruhga mansub?
2. Uning asosiy morfologik va tinktorial xususiyatlari qanday?
3. Qaysi laboratoriya tekshiruvlari tashxisni tasdiqlashga yordam beradi?
4. Mikroorganizmning asosiy virulentlik omillari nimalardan iborat?
5. Antibiotiklarga rezistentlik masalasi qanday baholanadi?
6. Infeksiya profilaktikasida qanday choralar muhim?

Bunday yondashuvda talaba bir vaqtning o‘zida mikroorganizmning morfologiyasi, biologik xususiyatlari, patogenligi, diagnostikasi va davolash prinsiplari o‘rtasidagi bog‘liqlikni izlaydi. Mikrobiologiya bo‘yicha o‘tkazilgan tadqiqotlarda aynan shunday klinik case-based yondashuv talabalarning bilimni qo‘llash va saqlab qolish ko‘rsatkichlarini yaxshilashi qayd etilgan.

Muammoli ta’limdan foydalanish. Muammoli ta’limda talabaga tayyor javob berilmaydi. O‘qituvchi muammoni shakllantiradi va talaba mavjud bilimlari asosida yechim topishga harakat qiladi. Masalan: “Nima sababdan Mycoplasma spp. beta-laktam antibiotiklarga tabiiy ravishda chidamli?”

Talaba ushbu savolga javob berish uchun:

hujayra devori → peptidoglikan → beta-laktamlarning nishoni → Mycoplasma hujayra devorining yo‘qligi → antibiotik ta’sir mexanizmi ketma-ketligini tahlil qiladi.

Shunday qilib, bitta muammoli savol bir nechta alohida faktlarni mexanik yodlashdan ko‘ra, ularni sabab-oqibat munosabatida tushunishga yordam beradi.

Kichik guruhlarda ishlash. Kichik guruhlarda ishlash mikrobiologiyaning murakkab mavzularini jamoaviy tahlil qilish imkonini beradi. Masalan, “Gram-musbat va Gram-manfiy bakteriyalar” mavzusida ikki guruhga topshiriq berilib, ular quyidagi mezonlar asosida taqqoslash jadvalini tuzishi mumkin: hujayra devori, peptidoglikan qavati, tashqi membrana, lipopolisaxarid, Gram bo‘yash natijasi, toksinlar, klinik ahamiyati, antibiotiklarga sezgirlik xususiyatlari. Keyinchalik guruhlar o‘z natijalarini himoya qiladi va o‘qituvchi yakuniy ilmiy xulosani beradi.

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Vizual ta’lim texnologiyalaridan foydalanish. Mikrobiologiya ko‘plab mikroskopik va morfologik obyektlarni o‘rganishni talab qilgani sababli vizual materiallar muhim ahamiyatga ega.

Mashg‘ulotlarda:

-Gram bo‘yalgan surtma tasvirlari;

-bakteriyalarning morfologik shakllari;

-zamburug‘larning mikroskopik ko‘rinishlari;

-parazitlarning rivojlanish bosqichlari;

-laboratoriya diagnostikasi sxemalari;

-antibiotik rezistentlik mexanizmlari;

-mikroorganizmlarning patogenlik omillari kabi materiallardan foydalanish mumkin.

Bunda o‘qituvchi tasvirni shunchaki ko‘rsatib qo‘ymasdan, talabaga “Nimani ko‘ryapsiz?”, “Qaysi diagnostik belgi muhim?”, “Bu belgiga asoslanib qanday xulosa qilish mumkin?” kabi savollarni beradi.

1-jadval. Interfaol metodlarni mikrobiologiya mavzulariga moslashtirish

Stafilokokklar	Case-study
Streptokokklar	Venn diagrammasi
Gram-musbat va Gram-manfiy bakteriyalar	Klaster
Mycoplasma	Muammoli savol
Antibiotik rezistentlik	Brainstorming + case
Zamburug‘lar	Vizual tahlil
Viruslar	Konseptual xarita

Muhokama

Ilmiy adabiyotlar tahlili mikrobiologiya ta’limida case-based va boshqa faol ta’lim shakllaridan foydalanishning istiqbolli ekanligini ko‘rsatadi. Xususan, mikrobiologiyada CBL qo‘llangan tadqiqotlarda talabalar natijalari an’anaviy ma’ruza bilan taqqoslaganda yuqoriroq bo‘lgan va uzoq muddatli bilimni saqlashda ham ijobiy natijalar kuzatilgan.

2025-yilda e’lon qilingan sistematik sharhda sog‘liqni saqlash yo‘nalishidagi talabalar orasida case-based learning an’anaviy ma’ruzaga nisbatan tanqidiy fikrlash va muammolarni hal qilish ko‘nikmalarida afzallik bergani ko‘rsatilgan, biroq bilim va tushunish natijalaridagi barcha farqlar bir xil darajada ishonchli emasligi ham qayd etilgan. Shu sababli CBLni an’anaviy ta’limni to‘liq almashtiruvchi emas, balki maqsadga muvofiq integratsiya qilinadigan metod sifatida ko‘rish ma’qul.

2026-yilgi meta-tahlil esa CBL va PBL kombinatsiyasini an’anaviy ma’ruza bilan taqqoslab, nazariy bilim, amaliy ko‘nikma, klinik fikrlash va o‘quvchilarning qoniqish ko‘rsatkichlarida ijobiy natijalarni bildirgan.

Bundan tashqari, JSSTning tibbiy ta’lim uchun antimikrob rezistentlik bo‘yicha 2024-yilgi vositasi AMR bo‘yicha bilim va kompetensiyalarni tibbiyot ta’limi dasturlariga tizimli ravishda kiritish zarurligini ko‘rsatadi. Bu mikrobiologiya mashg‘ulotlarini klinik fikrlash, antibiotiklardan oqilona foydalanish va infeksiya nazorati bilan bog‘lashning dolzarbligini oshiradi.

Xulosa (Conclusion)

Mikrobiologiya fanini tibbiyot oliy ta’lim muassasalarida o‘qitishda interfaol pedagogik texnologiyalardan foydalanish talabalarni o‘quv jarayonining faol ishtirokchisiga aylantirish imkonini beradi. Case-study, muammoli ta’lim, kichik guruhlarda ishlash va vizual ta’lim usullarining mikrobiologiya mashg‘ulotlariga integratsiyasi nazariy bilimlarni klinik vaziyatlar bilan bog‘lash uchun qulay sharoit yaratadi.

Ayniqsa, mikroorganizmning morfologik xususiyatidan boshlab uning patogenligi, laboratoriya diagnostikasi va klinik ahamiyatigacha bo‘lgan mantiqiy zanjirni shakllantirish talabaning mikrobiologik bilimlarini amaliy tibbiy tafakkur bilan integratsiya qilishga yordam beradi.

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Shu bilan birga, interfaol metodlarning samaradorligini aniq baholash uchun kelgusidagi tadqiqotlarda pretest-posttest natijalari, bilimni uzoq muddat saqlash ko‘rsatkichlari, talabalar fikri va klinik vaziyatlarni yechish qobiliyatini standartlashtirilgan mezonlar asosida baholash maqsadga muvofiq.

Foydalanilgan adabiyotlar

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ZUBTURUM (*PLANTAGO MAJOR L.*) O‘SIMLIGIDAN AJRATIB OLINGAN MIKROORGANIZMLAR VA ULARNING BIOLOGIK FAOLLIGI

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Annotatsiya: Ushbu tadqiqotda katta zubturum (*Plantago major L.)* o‘simligining barg va ildiz to‘qimalaridan endofit zamburug‘larni ajratib olish va ularning biologik salohiyatini o‘rganish maqsad qilindi. Jizzax viloyati Zomin tumanidan olingan o‘simlik namunalari yuza sterilizatsiyasidan so‘ng PDA ozuqa muhitida 25–28 °C haroratda 7 kun inkubatsiya qilindi. Natijada sog‘lom o‘simlik to‘qimalaridan endofit zamburug‘ kulturalari ajratib olindi. Adabiyotlar tahlili ushbu mikroorganizmlar antimikrob metabolitlarning istiqbolli manbai bo‘lishi mumkinligini ko‘rsatdi. Olingan natijalar izolyatlarning biologik faolligini kelgusida chuqur o‘rganish uchun asos bo‘lib xizmat qiladi.

Kalit so‘zlar: *Plantago major*, zubturum, endofit zamburug‘lar, biologik faol metabolitlar, antimikrob salohiyat.

Аннотация: Целью данного исследования было выделение эндофитных грибов из тканей листьев и корней подорожника большого (*Plantago major* L.) и изучение их биологического потенциала. Образцы растений, собранные в Зааминском районе Джизакской области, после поверхностной стерилизации инкубировали на питательной среде PDA при температуре 25–28 °C в течение 7 суток. В результате из здоровых тканей растения были выделены культуры эндофитных грибов. Анализ научной литературы показал, что данные микроорганизмы могут служить перспективными источниками антимикробных метаболитов. Полученные результаты создают основу для дальнейшего углублённого изучения биологической активности выделенных изолятов.

Ключевые слова: *Plantago major*, подорожник большой, эндофитные грибы, биологически активные метаболиты, антимикробный потенциал.

Abstract: This study aimed to isolate endophytic fungi from the leaf and root tissues of *Plantago major* L. and investigate their biological potential. Plant samples collected from the Zomin district of the Jizzakh region were surface-sterilized and incubated on potato dextrose agar (PDA) at 25–28 °C for 7 days. As a result, endophytic fungal cultures were isolated from healthy plant tissues. A review of the scientific literature indicated that these microorganisms may serve as promising sources of antimicrobial metabolites. The obtained results provide a basis for further investigation of the biological activity of the isolated strains.

Keywords: *Plantago major*, broadleaf plantain, endophytic fungi, bioactive metabolites, antimicrobial potential.

Kirish

Dorivor o‘simliklar to‘qimalarida kasallik alomatlarini keltirib chiqarmasdan yashovchi mikroorganizmlar — endofitlar yangi biologik faol birikmalarning istiqbolli manbai hisoblanadi.

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Katta zubturum (*Plantago major L.*) *Plantaginaceae* oilasiga mansub ko‘p yillik o‘t o‘simlik bo‘lib, tarkibida iridoid glikozidlar, flavonoidlar, polisaxaridlar va oshlovchi moddalar mavjudligi aniqlangan; ushbu biologik faol muhit o‘simlik ichida o‘ziga xos ikkilamchi metabolitlar sintez qiluvchi mikrobial jamoa shakllanishiga sharoit yaratadi [1]. Antibiotiklarga chidamli shtammlarning (xususan MRSA) tarqalishi va kimyoviy pestitsidlardan voz kechish zaruriyati endofit mikroorganizmlarni o‘rganishni dolzarb qilmoqda [2,4,5]. Tish kariesi global sog‘liqni saqlash muammosi bo‘lib, JSST ma’lumotlariga ko‘ra, maktab yoshidagi bolalarning taxminan 60–90 foizida va kattalarning deyarli barchasida uchraydi [1]. Kariesning rivojlanishida tish biopardasi, xususan *Streptococcus mutans* muhim rol o‘ynaydi. An’anaviy vosita — xlorgeksidin yuqori samarali bo‘lsa-da, uzoq qo‘llanganda ta’m buzilishi, tishlarning bo‘yalishi kabi nojo‘ya ta’sirlar chaqiradi, unga nisbatan bakteriyalar chidamliligi haqida ham ma’lumotlar mavjud [8]. Shu sababli xavfsizroq o‘simlik asosidagi vositalarga qiziqish ortmoqda. Zubturum (*P. major L.*) tarkibida flavonoidlar, terpenoidlar, iridoid glikozidlar va yog‘ kislotalari mavjud bo‘lib, antibakterial, yallig‘lanishga qarshi va antioksidant xossalarga ega [1]. Braziliyada o‘tkazilgan tadqiqotda uning ekstrakti *S. mutans* o‘sishini to‘xtatgan (MIK 25 mg/ml; bakteriostatik ta’sir), ingibitsiya zonasi o‘rtacha 9,95 mm bo‘lgan, ammo bu ko‘rsatkich xlorgeksidinnikidan (12,35–14,98 mm) past bo‘lgan [8].

Tadqiqotning maqsadi — zubturum tarkibidagi endofit zamburug‘larni ajratib olish, olingan mavjud ilmiy ma’lumotlarni tahlil qilish va umumlashtirishdan iborat.

Material va metodlar

Tadqiqot uchun Jizzax viloyati Zomin tumani Duoba qishlog‘idan olingan sog‘lom *Plantago major* L. o‘simligining barg va ildiz namunalari tanlandi. Namunalar yuvilib, mayda bo‘laklarga ajratildi va 70% etanol hamda 1–3% NaOCl eritmalari yordamida yuza sterilizatsiyasidan o‘tkazildi. Steril suvda uch marta chayilgan to‘qima bo‘laklari PDA ozuqa muhitiga ekilib, 25–28 °C haroratda 7 kun inkubatsiya qilindi. O‘sib chiqqan zamburug‘ gifalari yangi PDA muhitiga ko‘chirilib, sof kulturalar ajratib olindi.

Natija va muhokama

2026-yil 23-martda Jizzax viloyati Zomin tumani Duoba qishlog‘idan olib kelingan sog‘lom *Plantago major* L. o‘simligining 4 ta bargi va 4 ta ildizi tadqiq qilindi (1-rasm). Yuza sterilizatsiyasidan so‘ng to‘qima bo‘laklari PDA muhitiga ekilib, 25–28 °C da 7 kun inkubatsiya qilindi. Nazorat sifatida ekilgan oxirgi chayish suvida mikroorganizmlar o‘smadi, bu sterilizatsiya sifatli o‘tganini va o‘sgan kulturalar yuza kontaminantlari emas, endofitlar ekanini ko‘rsatadi. Tadqiqotda zubturumning sog‘lom barg va ildiz to‘qimalaridan endofit zamburug‘lar ajratib olindi. Bizning ishimizda ham shunga o‘xshash yondashuv qo‘llanib, barg va ildiz to‘qimasidan izolyat olindi. Buni organlarning namlik va ozuqa moddalari bilan ta’minlanishi hamda mikroorganizmlar kolonizatsiyasi uchun ekologik sharoitidagi farq bilan izohlash mumkin.

Ishning cheklovlari: namuna bitta joydan va bitta vaqtda olingan, namunalar soni kam (4 ta barg, 4 ta ildiz), izolyatlar faqat morfologik jihatdan tavsiflangan, molekulyar identifikatsiya (ITS sekvenslash) va antimikrob faollik sinovlari o‘tkazilmagan. Shuning uchun turlar aniqlanmagan va faollik haqida xulosa berilmaydi.

Xulosa

Tadqiqot natijasida katta zubturum (*Plantago major* L.) o‘simligining sog‘lom barg va ildiz to‘qimalaridan endofit zamburug‘ kulturalari ajratib olindi. Olingan natijalar ushbu dorivor o‘simlik endofit mikroorganizmlar uchun tabiiy yashash muhiti ekanligini ko‘rsatdi. Ilmiy adabiyotlar tahliliga ko‘ra, zubturum endofitlari biologik faol, xususan, antimikrob metabolitlarning istiqbolli manbai hisoblanadi. Kelgusida ajratilgan izolyatlarni molekulyar identifikatsiya qilish, antimikrob faolligini baholash va biologik faol metabolitlarini aniqlash maqsadga muvofiqdir.

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НАУЧНЫЕ ПРЕДПОСЫЛКИ РАЗРАБОТКИ ОРГАНОМИНЕРАЛЬНЫХ УДОБРЕНИЙ НА ОСНОВЕ САПРОПЕЛЕЙ С УЧЁТОМ УГЛЕРОДНО-АЗОТНОГО БАЛАНСА, ГУМУСОВОГО СОСТАВА И МИКРОБИОЛОГИЧЕСКОЙ АКТИВНОСТИ

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Аннотация: В данной работе приведены результаты процессов компостирования, где в качестве исходного сырья рассматривается сапропель рыбных хозяйств Сырдарьинской и Хорезмской областей. В ходе исследований наблюдаются процессы трансформации органического вещества (ОВ) этих компонентов в гуминовые соединения с различными C/N.

Найдено, что с увеличением соотношения сапропеля к навозу, и срока выдержки 1-150 суток привело к повышению степени гумификации и снижению потери веществ в газовую фазу. Определены оптимальные условия компостирования: Сапропель: Навоз равной 70:30 и срок созревания 90 суток.

Ключевые слова: Органо-минеральное удобрение, сапропель, навоз, компостирование, трансформация органического вещества, гумификация

Annotatsiya: Ushbu maqolada Sirdaryo va Xorazm viloyatlaridagi baliqchilik xo‘jaliklaridan olingan sapropeldan asosiy xomashyo sifatida foydalangan holda kompostlash jarayonlari natijalari keltirilgan. Tadqiqotda ushbu tarkibiy qismlardagi organik moddalarning (OM) C/N nisbati turlicha bo‘lgan gumusli birikmalarga aylanish jarayoni o‘rganilgan. Aniqlanishicha, sapropelning go‘ngga nisbatini oshirish hamda 1–150 kun davomida yetiltirish jarayoni gumuslanish darajasining ortishiga va moddalarning gaz fazasiga yo‘qolishining kamayishiga olib keladi. Kompostlash uchun eng maqbul sharoitlar sifatida sapropelning go‘ngga nisbati 70:30 bo‘lishi hamda yetiltirish davri 90 kunni tashkil etishi belgilandi.

Kalit so‘zlar: organik-mineral o‘g‘it, sapropel, go‘ng, kompostlash, organik moddalarning o‘zgarishi, gumifikatsiya

Abstract: This paper presents the results of composting processes using sapropel from fish farms in the Syrdarya and Khorezm regions as a primary feedstock. The research examines the transformation of organic matter (OM) from these components into humic compounds with varying C/N ratios. It was found that increasing the ratio of sapropel to manure, combined with a maturation period of 1–150 days, led to a higher degree of humification and reduced loss of material to the gas phase. The optimal composting conditions were determined to be a sapropel-to-manure ratio of 70:30 and a maturation period of 90 days.

Keywords: organic-mineral fertilizer, sapropel, manure, composting, transformation of organic matter, humification

Сапропели представляют собой природную органоминеральную основу для удобрений, сочетающих питательное и почвоулучшающее действие. Их ценность определяется происхождением органического вещества, гумусовыми фракциями и минеральным составом. K. Stankevica и соавт. [1] на материале пяти озёр Латвии показали,

ДЛЯ ЦИТИРОВАНИЯ
Исаев Г.Я., Мамасалиева Л.Э., Мячина О.В., Пулатов Б.А. и др. Научные предпосылки разработки органоминеральных удобрений на основе сапропелей с учётом углеродно-азотного баланса, гумусового состава и микробиологической активности // Состояние и перспективы развития фундаментальной и прикладной микробиологии: точка зрения молодых учёных: материалы Республиканской научно-практической конференции. ...
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что содержание гуминовых веществ существенно зависит от типа сапропеля. Разработка твёрдых и жидких удобрений на сапропелевой основе, описанная L. Agafonova и соавт. [2], подтверждает возможность технологической переработки сырья. Однако для компостируемых композиций необходимо учитывать взаимосвязь химического состава с микробным преобразованием органического вещества.

Углеродно-азотный баланс определяет обеспеченность микроорганизмов энергетическим и азотным субстратами. Для исходной смеси при аэробном компостировании распространённым ориентиром служит C:N около 25–30:1 [3, 6]. Метаанализ B. Shen и соавт. [6], включивший 192 исследования, подтверждает значение этого диапазона, одновременно выявляя различия между видами сырья. При избытке доступного углерода недостаток азота замедляет разложение; при недостатке углерода относительно азота возрастает риск накопления аммонийных форм и потерь аммиака. Следовательно, подбор соотношения сапропеля, навоза и растительных добавок должен опираться на анализ компонентов, а не только на их массовые доли.

При оценке готового удобрения следует отличать оптимум компостирования от условий его действия в почве. Для зрелых компостов практическим ориентиром является C:N порядка 10–20:1; Clemson University указывает диапазон 10–15:1 [3]. Более широкое отношение, особенно выше 25–30:1 при наличии легкоразлагаемого углерода, повышает риск временного связывания почвенного азота микробной биомассой. Вместе с тем одно значение C:N не определяет удобрительную эффективность: важны устойчивость органического вещества и содержание доступного азота. Для карбонатных сапропелей необходимо отдельно учитывать органический углерод. Добавление минерального азота может арифметически сузить C:N, не обеспечивая биологической зрелости продукта; её следует подтверждать самостоятельными показателями.

Гумусовый состав характеризует способность сапропелевой основы удерживать элементы питания и участвовать в формировании почвенной структуры. Гуминовые кислоты (ГК) и гумины связаны со стабилизацией органического вещества и катионообменными свойствами, а более растворимые фульвокислоты (ФК) участвуют в комплексообразовании и переносе элементов [1]. Поэтому существенны содержание обеих кислотных фракций на сухое вещество и отношение их углерода С(ГК)/С(ФК). Универсального оптимума ГК:ФК для всех сапропелевых удобрений нет. По данным S. M. Tiquia [5], динамика гуминовых фракций связана с микробными показателями компостирования. Для доказательства накопления ГК и ФК необходимо учитывать убыль сухой массы, поскольку увеличение их процентного содержания может частично отражать концентрирование при минерализации других компонентов.

Микробиологические свойства исходного сапропеля определяют его участие в совместном компостировании, однако должны оцениваться применительно к аэробным условиям процесса. G. Isayev и соавт. [4] обнаружили в сапропеле Сырдарьинской области культивируемую бактериальную и актиномицетную микрофлору. На мясопептонном агаре численность составляла $1{,}06\times10^5$ КОЕ/г в исходном сапропеле, $7{,}61\times10^5$ КОЕ/г в навозе и $7{,}20\times10^5$ КОЕ/г в зрелом компосте при соотношении сапропель:навоз 70:30. Эти результаты подтверждают присутствие жизнеспособной микрофлоры, но сами по себе не доказывают скорость разложения, видовую принадлежность или полезные функции всех обнаруженных микроорганизмов.

Для отбора сапропелей, предназначенных для компостирования, целесообразно сочетать посевы на питательные среды с измерением дыхания и ферментативной активности. Исследование S. M. Tiquia [5] показало информативность потребления кислорода, дегидрогеназной активности и микробной биомассы при оценке гумификации и зрелости компоста. При разработке сапропелевых смесей такие показатели следует отслеживать вместе с температурой, влажностью и аэрацией. Высокая активность полезна на стадии разложения, тогда как её снижение при созревании необходимо отличать от подавления

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микрофлоры неблагоприятными условиями. Вывод о зрелости надёжнее делать по совокупности биологической стабильности, химических показателей и отсутствия фитотоксичности.

В мировой научно-технической литературе имеются сведения о получении органических удобрений (ОУ), ОМУ, стимуляторов роста растений и других агрохимических средств, позволяющих повысить плодородие и обеспечить рекультивацию деградированных почв, а также получение высокого и качественного урожая. Однако нет сведений по использованию донных отложений с низким содержанием органического вещества (менее 20%) и высоким минеральным составом для получения на их основе ОМУ методом совместного компостирования сапропелей (СП) с навозом (НЗ), пшеничной соломой и минеральными солями, не изучены процессы трансформации (гумификации и минерализации), а также их состав и свойства.

Целью данных исследований являлась разработка ресурсосберегающей технологии получения ОМУ на основе сапропелей, органических отходов и минеральных компонентов, определение питательных и пролонгированных свойств, полученных ОМУ, оценка их влияния на плодородие почвы, а также развитие и урожайность сельскохозяйственных растений.

В задачи наших исследований входило изучение состава, физико-химических и физико-механических свойств сапропелей из водоемов рыбных хозяйств Сырдарьинского и Хорезмского вилоятов; исследование степени гумификации органического вещества в зависимости от массовых соотношений компонентов компостирования, с различными показателями C/N и времени компостирования; а исследование агрохимической эффективности удобрений и экологической безопасности их применения.

Объектом исследования являются сапропели 2 водных источников рыбных хозяйств «Gayrat fayzli dalasi» Сырдарьинской области (СП-С), «Yangiboy boyovulli» Хорезмской области (СП-Х), продукты компостирования, навоз КРС, солома пшеничная.

Процесс компостирования изучался при различных массовых соотношениях СП и НЗ = от 90:10 до 10:90 с различными соотношениями C / N. С целью уравновешивания ОВ в СП была использована солома пшеницы (СО). Компостирование проводилось в условиях аэробного режима при комнатной температуре (25 °C) в течение 150 суток инкубации. Учитывая влагоудерживающие свойства сапропеля, в смеси дополнительно добавляли воду для достижения оптимальной влажности в пределах 30-50 %, необходимой для протекания процессов гумификации ОВ. Отбор проб для анализа химического состава проводили каждые 15 суток. В качестве вариантов сравнения был также изучен процесс компостирования исходного сырья - сапропеля и навоза по отдельности. В образцах сапропеля и навоза КРС, а также в компостах после 150 дней компостирования определяли общую численность гетеротрофных микроорганизмов методом серийных десятикратных разведений и чашечного посева.

Следует отметить, что данная работа была выполнена в рамках плана научно-исследовательских работ Института общей и неорганической химии «Новые полифункциональные гуминовые удобрения: агрохимическая и агроэкологическая оценка, разработка научно-практических рекомендаций по применению», и содержит большой объем научных результатов. Однако в данной статье будет приведена лишь часть полученных результатов, затрагивающих разработки органоминеральных удобрений на основе сапропелей с учётом углеродно-азотного баланса, гумусового состава и микробиологической активности.

Как показали исследования, снижение массовой доли сапропеля и увеличение количества навоза количество углерода, азота, органического вещества (ОВ), гуминовых кислот (ГК) и фульвокислот (ФК), водорастворимых органических веществ (ВОВ) при компостировании, соотношение углерода к азоту увеличиваются. При этом с увеличением сроков инкубации, через 15 суток, наблюдается снижение органического вещества, а с

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другой стороны, повышение содержания ГК и ФК, ВОВ. Так при использовании сапропелей из Сырдарьинской области (СП-С) к навозу (НЗ) при соотношении 90:10 и 10: 90 после 1 сутки ОУ содержит ОВ, ГУ, ФК, ВОВ в порядке 16,17; 1,85; 1,91, 1,80% и 45,45; 5,20; 5,38; 5,08% соответственно, то через 15 суток эти показатели достигают 15,86; 1,97; 2,03; 1,92% и 45,04; 5,32; 5,51; 5,08%. Такая же закономерность наблюдается с увеличением продолжительности от 30 до 150-суток, что для ОВ, ГУ, ФК, ВОВ варьируются от 15,57; 2,08; 2,15; 2,03% и 44,85; 5,43; 5,62; 5,30% до 14,82; 2,43; 2,51; 2,37% и 44,17; 5,83; 6,03; 5,69 % соответственно для СП-С: НЗ =90: 10 и 10: 90. В случае применения сапропеля из Хорезмской области (СП-Х), где количество ОВ, ГУ, ФК, ВОВ варьируют от 21,35; 3,06; 3,16; 3,00% и 47,44; 6,25; 6,47; 6,10% до 19,24; 4,04; 4,16; 3,93% и 42,86; 7,23; 7,46; 7,04 % соответственно при указанных сутках и соотношений СП-К: НЗ.

Кроме того исследованиями было выявлено, что с увеличением соотношений СП-С: НЗ повышается степень гумификации и снижение потерь газовой фракции. Однако с увеличением массовой доли навоза по отношению к сапропелю наблюдается снижение степени гумификации (СГ). Независимо от массового соотношения СП:НЗ повышение продолжительности сроков компостирования способствует увеличению степени гумификации. Например, при СП-С: НЗ = 90: 10 и СП-С: НЗ = 10: 90 СГ увеличивается от 37,72 до 49,32% и от 35,30 до 39,73% соответственно от 15 до 150 суток компостирования. Однако снижаются потери в газовой фракции от 1,82 до 1,71 и от 3,43 до 3,31% соответственно при указанных условиях. Что касается СП-К: НЗ = 90: 10 и СП-К: НЗ = 10: 90 степень гумификации увеличивается от 38,46 до 63,04% и от 36,90 до 50,70% соответственно от 15 до 150 суток компостирования.

Результаты микробиологического анализа экспериментальных вариантов выявили принципиальные различия в численности и структуре микробных сообществ, что напрямую определяет направленность процессов трансформации органического вещества. Как показали исследования по численности и качественному составу микрофлоры в варианте с НЗ содержится в 7 раз больше жизнеспособных микроорганизмов, чем в варианте СП-С. Такой высокий титр микрофлоры в НЗ обусловлен внесением лабильного органического вещества, служащего легкодоступным источником питания и энергии для гетеротрофов. Однако ключевые различия кроются не только в количестве, но и в качественном составе микробиома, так в варианте НЗ, микрофлора данного объекта преимущественно представлена спорообразующими бактериями рода *Bacillus*. Эти микроорганизмы обладают мощным набором экзоферментов, способных стремительно расщеплять белки, простые углеводы и аминокислоты. Тогда как в вариантах с СП, напротив, зафиксирована существенно более высокая доля актиномицетов (лучистых грибов). Как известно, актиномицеты развиваются медленнее бактерий, но играют незаменимую роль на более поздних стадиях деструкции, так как способны разрушать труднорастворимые и устойчивые полимеры (хитин, лигнин, целлюлозу).

Разница в архитектонике микробного ценоза предопределяет противоположную биохимическую направленность процессов в компостах. Быстрая минерализация в варианте с НЗ происходит за счёт доминирования бактерий рода *Bacillus* обеспечивая при этом бурную и быструю минерализацию субстрата. Так происходит активный распад органических соединений до конечных продуктов (углекислого газа, воды, аммиака), что приводит к быстрому высвобождению доступных для растений элементов питания (азота, фосфора, калия). Однако интенсивная минерализация сопряжена с риском повышенных газообразных потерь азота и углерода. Тогда как стабилизация процессов гумификации в вариантах с применением высокого содержания сапропеля и соломы в сочетании с активностью актиномицетов замедляет деструкцию. Мы считаем, что данный вариант обеспечивает стабилизацию и гумификацию органического вещества. Медленная ферментация лигноцеллюлозных остатков соломы и специфических гуминовых комплексов

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сапропеля способствует процессам ресинтеза — формированию новообразованных зрелых гуминовых и фульвокислот.

Таким образом, по проведенным исследованиям можно сделать следующее заключение: увеличение массовой доли сапропеля и продолжительности компостирования способствует повышению степени гумификации и накоплению гуминовых и фульвокислот при одновременном снижении содержания органического вещества вследствие его трансформации. Установлено, что сапропель Хорезмской области обладает более высоким потенциалом гумификации по сравнению с сапропелем Сырдарьинской области. Микробиологический анализ выявил, что преобладание бактерий рода *Bacillus* в навозе способствует интенсивной минерализации органических соединений, тогда как высокая доля актиномицетов в сапропеле обеспечивает более медленное разложение устойчивых органических компонентов и способствует их гумификации. Таким образом, применение сапропеля в сочетании с навозом позволяет регулировать процессы минерализации и гумификации, повышать устойчивость органического вещества и снижать газообразные потери углерода и азота.

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XORAZM VILOYATI POMIDOR AGROTSENOZI HASHAROTLARINING HUDUDIY TARQALISHI VA EKOLOGIK JOYLASHUV XUSUSIYATLARI

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Annotatsiya: Mazkur tezisda Xorazm viloyati Urganch tumani sharoitida pomidor (*Solanum lycopersicum* L.) agrotsenozida uchraydigan hasharotlarning hududiy tarqalishi, o‘simlik organlari bo‘yicha ekologik joylashuvi hamda fitofag va entomofag turlarning funksional ahamiyati tahlil qilindi. Tadqiqotlar 2023–2025-yillarda “Davlat Rahmatulla” va “Yakubboy Zarifboy” fermer xo‘jaliklarida olib borildi. Kuzatuvlar davomida 9 turkumga mansub 28 tur hasharot qayd etildi. Hasharotlarning hududlar bo‘yicha tarqalishida agroekologik sharoitlar, sug‘orish rejimi, begona o‘tlar va o‘simlikning vegetatsiya bosqichlari bilan bog‘liq farqlar kuzatildi. Fitofaglar asosan barg, poya va generativ organlarda, entomofaglar esa zararkunandalar uchraydigan mikrobiotoplarda tarqalganligi aniqlandi. Natijalar pomidor agrotsenozida ekologik monitoring va integratsiyalashgan himoya tadbirlarini takomillashtirishda muhim ahamiyatga ega.

Kalit so‘zlar: pomidor, agrotsenoz, entomofauna, fitofag, entomofag, hududiy tarqalish, ekologik joylashuv, biologik nazorat.

Аннотация: В тезисе проанализированы территориальное распространение, распределение по органам растений и экологическое значение насекомых агроценоза томата (*Solanum lycopersicum* L.) в Хорезмской области. Исследования проводились в 2023–2025 годах в фермерских хозяйствах «Davlat Rahmatulla» и «Yakubboy Zarifboy» Ургенчского района. Зарегистрировано 28 видов насекомых, относящихся к 9 отрядам. Выявлены различия в распространении фитофагов и энтомофагов, связанные с агроэкологическими условиями и фазами развития растений. Полученные результаты имеют значение для экологического мониторинга и интегрированной защиты томата.

Ключевые слова: томат, агроценоз, энтомофауна, фитофаги, энтомофаги, территориальное распространение, экологическое распределение, биологический контроль.

Abstract: This thesis examines the spatial distribution, plant-organ associations, and ecological significance of insects in tomato (*Solanum lycopersicum* L.) agrocenosis in Khorezm region. Field observations were conducted from 2023 to 2025 at the Davlat Rahmatulla and Yakubboy Zarifboy farms in Urgench district. A total of 28 insect species belonging to 9 orders were recorded. Differences in the distribution of phytophagous and entomophagous insects were observed in relation to agroecological conditions and plant developmental stages. The findings provide information for ecological monitoring and integrated pest management in tomato cultivation.

Keywords: tomato, agrocenosis, entomofauna, phytophagous insects, entomophagous insects, spatial distribution, ecological distribution, biological control.

Pomidor (*Solanum lycopersicum* L.) agrotsenozi turli ekologik guruhlarga mansub hasharotlarning yashashi, oziqlanishi va rivojlanishi uchun muhim agroekologik muhit hisoblanadi. Hasharotlarning tur tarkibi va tarqalishi o‘simlikning fenologik bosqichlari, mikroiqlim sharoiti, sug‘orish rejimi, agrotexnik tadbirlar hamda begona o‘tlar tarkibiga bog‘liq holda o‘zgaradi.

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Ayniqsa, fitofag va entomofag hasharotlarning agrotsenozdagi joylashuvini aniqlash zararkunandalar populyatsiyasini nazorat qilish va ekologik xavfsiz himoya tizimini ishlab chiqishda muhim ilmiy-amaliy ahamiyatga ega.

Tadqiqotlar 2023–2025-yillar davomida Xorazm viloyati Urganch tumanidagi “Davlat Rahmatulla” va “Yakubboy Zarifboy” fermer xo‘jaliklarining ochiq pomidor maydonlarida olib borildi. Kuzatuvlar natijasida 9 turkumga mansub 28 tur hasharot aniqlanib, ularning agrotsenozda hududiy tarqalishi va o‘simlik organlari bilan bog‘liq ekologik xususiyatlari o‘rganildi. Hasharotlarning uchrash darajasi agroekologik sharoitlarga muvofiq farqlanishi qayd etildi.

“Davlat Rahmatulla” fermer xo‘jaligida Hemiptera turkumiga mansub fitofag hasharotlar, ayniqsa *Aphis gossypii*, *Myzus persicae* va *Bemisia tabaci* barglar hamda yosh novdalarda muntazam uchradi. Mazkur turlar o‘simlik hujayra shirasi bilan oziqlanib, barglarning deformatsiyalanishi, fotosintetik faollikning susayishi va vegetativ rivojlanishning sekinlashishiga sabab bo‘lishi mumkin. Shuningdek, *Helicoverpa armigera* va *Agrotis segetum* lichinkalarining pomidorning meva va poya qismlariga zarar yetkazishi kuzatildi.

“Yakubboy Zarifboy” fermer xo‘jaligida fitofaglar bilan bir qatorda foydali entomofag hasharotlar ham nisbatan keng tarqalganligi qayd etildi. *Coccinella septempunctata*, *Hippodamia variegata*, *Chrysoperla carnea* va *Episyrphus balteatus* kabi yirtqich turlar shiralar va boshqa mayda fitofaglar bilan oziqlanishi sababli agrotsenozda biologik nazoratning muhim tabiiy agentlari hisoblanadi. *Bracon hebetor* va *Campoletis chlorideae* parazitoidlarining uchrashi ham zararkunandalar populyatsiyasini tabiiy cheklash imkoniyatlarini ko‘rsatadi.

1-jadval. Pomidor agrotsenozi hasharotlarining tadqiqot hududlari bo‘yicha tarqalishi

Turkum	**Davlat Rahmatulla F/X**	**Yakubboy Zarifboy F/X**
Coleoptera	+++	+++
Lepidoptera	+++	++
Hemiptera	+++	+++
Thysanoptera	++	++
Orthoptera	++	+++
Neuroptera	++	+++
Diptera	++	+++
Hymenoptera	++	+++
Mantodea	+	++

Izoh: +++ — keng tarqalgan; ++ — o‘rtacha tarqalgan; + — kam uchraydi. Belgilar kuzatuv natijalarining sifat jihatidan baholanishini ifodalaydi.

Jadval ma’lumotlariga ko‘ra, Coleoptera va Hemiptera turkumlari har ikkala fermer xo‘jaligida keng tarqalgan. Lepidoptera vakillari “Davlat Rahmatulla” xo‘jaligida, Orthoptera, Neuroptera, Diptera va Hymenoptera turkumlari esa “Yakubboy Zarifboy” xo‘jaligida nisbatan kengroq uchradi. Bunday farqlar agroekologik sharoitlar, sug‘orish tizimi va begona o‘tlar tarkibining o‘ziga xosligi bilan bog‘liq bo‘lishi mumkin.

Hasharotlarning o‘simlik organlari bo‘yicha tarqalishida ham muayyan ekologik qonuniyatlar kuzatildi. Hemiptera va Thysanoptera turkumlari vakillari asosan barg apparatida, Lepidoptera lichinkalari esa barg, gul va meva qismlarida uchradi. Tuproq va maydon chetlari ayrim Orthoptera vakillari uchun muhim mikrobiotop hisoblanadi. Entomofag hasharotlar esa ko‘proq fitofaglar uchraydigan barg va generativ organlar atrofida qayd etildi.

2-jadval. Pomidor agrotsenozi hasharotlarining o‘simlik organlari bo‘yicha tarqalishi

Turkum	**Barg**	**Poya**	**Gul**	**Meva**	**Tuproq**
Hemiptera	+++	++	+	–	–
Lepidoptera	++	++	+++	+++	+
Coleoptera	++	+	–	+	++
Thysanoptera	+++	+	++	+	–

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Orthoptera	+	++	–	+	+++
Neuroptera	++	+	++	+	–
Diptera	++	–	++	+	–
Hymenoptera	++	+	++	+	–
Mantodea	+	++	+	+	–

Izoh: +++ — keng tarqalgan; ++ — o‘rtacha tarqalgan; + — kam uchraydi; – — kuzatuvlarda qayd etilmagan.

Fitofag hasharotlarning asosiy qismi barg va generativ organlarda to‘plangan. *Aphis gossypii*, *Myzus persicae*, *Bemisia tabaci*, *Trialeurodes vaporariorum* va *Thrips tabaci* barg qatlamida uchraydigan turlar sifatida qayd etildi. Ular o‘simlikning fotosintetik faoliyatiga salbiy ta’sir ko‘rsatishi mumkin. *Helicoverpa armigera* lichinkalari esa mevalarga zarar yetkazish salohiyati bilan ajralib turadi.

Tuproq va poya asosiga yaqin mikrobiotoplarda *Gryllotalpa gryllotalpa* uchrashi kuzatildi. *Locusta migratoria*, *Calliptamus italicus* va *Dociostaurus maroccanus* kabi chigirtkalar esa asosan ochiq maydonlar hamda begona o‘tlar mavjud uchastkalar bilan bog‘liq bo‘ldi.

Foydali entomofauna vakillaridan *Coccinella septempunctata*, *Hippodamia variegata*, *Chrysoperla carnea*, *Episyrphus balteatus*, *Bracon hebetor*, *Campoletis chlorideae* va *Mantis religiosa* agrotsenozdagi fitofag hasharotlar bilan trofik aloqaga ega muhim turlar hisoblanadi. Ushbu turlarning mavjudligi tabiiy biologik nazoratni rivojlantirish imkoniyatlarini ko‘rsatadi.

Tadqiqot natijalari pomidor agrotsenozida hasharotlarning hududiy tarqalishi va ekologik joylashuvi bir xil emasligini ko‘rsatdi. Bunda barg qatlami so‘ruvchi fitofaglar, generativ organlar kemiruvchi lichinkalar, tuproq va maydon chetlari esa yer usti hamda tuproq bilan bog‘liq hasharotlar uchun muhim yashash muhiti vazifasini bajaradi.

Xulosa

Xorazm viloyati Urganch tumanidagi pomidor agrotsenozlarida 2023–2025-yillar davomida qayd etilgan 28 tur hasharotning tarqalishi fermer xo‘jaliklari va o‘simlik organlari bo‘yicha farqlanishi aniqlandi. “Davlat Rahmatulla” fermer xo‘jaligida ayrim fitofag hasharotlar, “Yakubboy Zarifboy” xo‘jaligida esa bir qator entomofaglar nisbatan kengroq uchradi. Fitofaglar asosan barg va generativ organlarda, foydali hasharotlar esa zararkunandalar uchraydigan mikrobiotoplarda tarqaldi. Mazkur natijalar pomidor agrotsenozida ekologik monitoringni takomillashtirish, foydali entomofaunani saqlash va integratsiyalashgan himoya tadbirlarini ishlab chiqish uchun ilmiy-amaliy asos bo‘lib xizmat qiladi.

Foydalanilgan adabiyotlar

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A RESEARCH STATUS OF LIBYOSTRONGYLUS GENUS IN OSTRICHES (*STRUTHIO CAMELUS*): A REVIEW

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Abstract: This paper outlines the current state of research regarding three nematode species belonging to the genus Libyostrongylus.
Keywords: Libyostrongylus douglassii, Libyostrongylus dentatus, Libyostrongylus magnus, distribution.

Annotatsiya: Ushbu tezisda Libyostrongylus avlodiga mansub 3 ta turdagi nematoda haqida olimlar tomonidan o‘rganilganlik holati bayon etilgan.
Kalit so‘zlar: Libyostrongylus douglassii, Libyostrongylus dentatus, Libyostrongylus magnus, tarqalish.

Аннотация: В данной статье представлен обзор современного состояния исследований трех видов нематод, относящихся к роду Libyostrongylus.
Ключевые слова: Libyostrongylus douglassii, Libyostrongylus dentatus, Libyostrongylus magnus, распространение.

According to the data given by Ederli N. B. some ostrich-specific nematodes were determined for the first time by Arthur Douglass who gathered small nematodes from a proventriculus of an ostrich in South Africa in 1880 and these nematodes were sent to Cobbold who determined the worms and called this new species as *Strongylus douglassii* in the honor of their collector and announced this in the paper published under the name “New entozoon from the ostriches” in 1882. Later, Lane laid the foundation of the Libyostrongylus genus for some African Trichostrongylidae, where *Libyostrongylus douglassii* is the type species from ostriches, and *Libyostrongylus hebrenicutus* (Lane, 1923), is the type species for gorillas [3].

Gilbert described a new species *Libyostrongylus magnus*, being defined solely in ostriches in the African continent, without recent reports in the world. Ortlepp established the genus Paralibyostrongylus; being *Paralibyostrongylus vondwei* Ortlepp, 1939, the type species and *Paralibyostrongylus hebrenicutus*, and *Paralibyostrongylus nigeriae* Baylis, 1928 included in this new genus. Hoberg E.P. et al. reported a third species, called *Libyostrongylus dentatus* (Hoberg, Lloyd, and Omar, 1995), because of the existence of prominent esophageal teeth [3,4]. The original geographical distribution of Libyostrongylus sp. is Africa; however, *Libyostrongylus douglassii* and *Libyostrongylus dentatus* have been documented from several non-African countries, thus having been introduced with ostriches imported for farming [1,2,3]. In ostriches, the trichostrongylid nematodes *Libyostrongylus douglassii* (most common), *Libyostrongylus dentatus*, and *Libyostrongylus magnus* are found in the openings of the deep proventricular glands and under the koilin layer of the proventriculus and the gizzard [3]. All of these can infect the proventriculus of ostriches [3]. The most usual species is *Libyostrongylus douglassii*, which has been recorded by Reinecke (1983) [3], Fockema et al. (1985) [3], Pintori et al. (2000) in Italy; Paliy A.P. et al. (2020) in Ukraine [3]. *Libyostrongylus dentatus* was recorded by Hoberg E.P. et al. (1995) in North America [4], Bonadimon et al. (2006) in Brazil [3], Ederli, N.B. and Oliveira, F.C.R. (2015) in

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Brazil [69], Andrade J.G. et al. (2013, 2018) in Ethiopia [2]. *Libyostrongylus magnus* was reported only in South Africa [3], *Libyostrongylus magnus* was described in the Ukraine in ostriches originating from Ethiopia [1]. Hoberg et al. (1995) [4] were able to re-examine some specimens deposited in the International Institute of Parasitology which was previously identified as *Libyostrongylus douglassii* in 1933 in Ethiopia. They identified those nematodes as *Libyostrongylus magnus*. *Libyostrongylus magnus* (Gilbert, 1937) [1] was described as having long ovejector, but it can be distinguished from *Libyostrongylus dentatus* by the larger number of eggs inside. Based on the data by Reinecke (1983), Libyostrongylus spp. is considered the most pathogenic nematode, responsible for 50% of the mortality of juvenile birds and occasionally killing adults [5]. Differentiation of these species has become possible because of studies conducted by Ederli et al., which describe the infective larvae of these nematodes. According to the data by Ederli, N.B.; Oliveira, F.C.R, *Libyostrongylus douglassii* is distributed worldwide and has been found in several countries on five continents, excluding Asia and Antarctica nematodes [3]. Fockema A. et al. (1985) determined *Libyostrongylus douglassii* (L_4 larvae of the nematode) in the proventriculus of ostriches in South Africa in the year of 1985 and treated ostriches with Fenbendazole at dosage rate of 15 mg/kg [3,4]. Hoberg E.P. et al. (1995) gathered specimens of Libyostrongylus sp. at the time of the necropsy from 2 adult ostriches on farms in North Carolina and Texas and made comparisons. During the necropsy of the ostriches, two species of Libyostrongylus sp. were defined; one of them was gravid female specimens of *Libyostrongylus douglassii* [4]. Sotiraki S.T. et al. (2001) recorded nematode eggs looking like strongylid-type eggs that were characterized as *L. douglassii* or *C. struthionis* in fecal samples in Greece, researchers informed that it was not possible to differentiate them at this stage and larval cultures were not performed [3]. Ponce G. F. et al. (2002) also determined the eggs of Libyostrongylus sp. in the feces of ostriches from the Spanish, Netherlands, Belgium and Portuguese. According to the scholar, eggs found in the feces were similar to those of *Codiostomum struthionis*, a non-pathogenic roundworm. According to the data offered by Cork S.C. (2005), it was not clear how Libyostrongylus spp. arrived in New Zealand, and it was probably entered with live ostrich imports in the 1990s. The nematode, *Libyostrongylus douglassii* was determined in samples from debilitated ostriches on the North Island farm in May 2004 using in-vitro larval culture and examination of adult parasite morphology [3,4]. British researchers, Ederli N.B. et al. (2008, 2015), examined the proventriculus of 10 ostriches too, and there were both species of Libyostrongylus sp. in all analyzed proventriculus [3]. In 2013, Andrade J.G. et al. focused on investigating the genetic characterization supporting a different evolutionary history of blood-sucking nematodes, including *Libyostrongylus douglassii* and *Libyostrongylus dentatus*, for the first time in Brazil [2]. After several years, fecal samples were gathered from wild ostriches (*Struthio molybdophanes*) in Ethiopia by Andrade J.G. et al. (2018) to verify Libyostrongylus spp. infections. To perform this duty, researchers did a coproculture, and to identify infective larvae, general morphology and morphometry were done [1].

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STEVIA REBAUDIANA AGROTSENOZI HASHAROTLARINING EKOLOGIK XUSUSIYATLARI VA FUNKSIONAL AHAMIYATI

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Annotatsiya: Maqolada *Stevia rebaudiana* agrotsenozida aniqlangan hasharotlarning ekologik tarkibi, oziqlanish xususiyatlari, mavsumiy faolligi va funksional ahamiyati tahlil qilingan. Tadqiqotlarda 23 tur hasharot qayd etilib, ulardan 19 turi fitofag, 4 turi parazitoid ekanligi aniqlangan. Fitofaglar orasida so‘ruvchi turlar ustunlik qilgan. Zararkunandalarning o‘simlik organlariga ta’siri va parazitoidlarning biologik nazoratdagi ahamiyati yoritilgan.
Kalit so‘zlar: *Stevia rebaudiana*, agrotsenoz, entomofauna, fitofag, parazitoid, ekologik xususiyatlar, biologik nazorat.

Аннотация: В статье рассмотрены экологический состав, особенности питания, сезонная активность и функциональное значение насекомых агроценоза *Stevia rebaudiana*. Выявлено 23 вида насекомых, из которых 19 относятся к фитофагам и 4 к паразитоидам. Среди фитофагов преобладают сосущие виды. Рассмотрены их вредоносность и роль паразитоидов в биологическом контроле.
Ключевые слова: *Stevia rebaudiana*, агроценоз, энтомофауна, фитофаги, паразитоиды, экологические особенности, биологический контроль.

Abstract: The article examines the ecological composition, feeding characteristics, seasonal activity, and functional significance of insects recorded in *Stevia rebaudiana* agrocenosis. A total of 23 insect species were identified, including 19 phytophagous species and 4 parasitoids. Sap-feeding species predominated among phytophagous insects. Their potential damage and the role of parasitoids in biological control are discussed.
Keywords: *Stevia rebaudiana*, agrocenosis, entomofauna, phytophagous insects, parasitoids, ecological characteristics, biological control.

Stevia rebaudiana agrotsenozida uchraydigan hasharotlarning ekologik xususiyatlarini o‘rganish ularning oziqlanish biologiyasi, rivojlanish davri va agroekotizimdagi funksional ahamiyatini aniqlashda muhim hisoblanadi. Hasharotlar populyatsiyasining shakllanishi o‘simlikning fenologik bosqichlari, iqlim omillari va trofik munosabatlar bilan chambarchas bog‘liq. Ayniqsa, steviya barglari xo‘jalik jihatidan qimmatli bo‘lganligi sababli fitofag hasharotlarning zararlilik xususiyatlarini baholash va biologik nazorat imkoniyatlarini aniqlash dolzarbdir.

Tadqiqotlarda steviya agrotsenozida jami 23 tur hasharot aniqlanib, ularning 19 turi (82,6 %) fitofag va 4 turi (17,4 %) parazitoid ekologik guruhga mansubligi qayd etildi. Fitofaglar orasida 14 tur (73,7 %) so‘ruvchi va qirib-so‘ruvchi, 5 tur (26,3 %) esa kemiruvchi oziqlanish tipiga ega bo‘ldi. Mazkur natijalar agrotsenoz entomofaunasida o‘simlik shirasi bilan oziqlanuvchi turlar ustunlik qilishini ko‘rsatadi.

1-jadval. *Stevia rebaudiana* agrotsenozi hasharotlarining ekologik tarkibi

Ekologik guruh	Turlar soni	Ulushi, %	Oziqlanish xususiyati

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So‘ruvchi va qirib-so‘ruvchi fitofaglar	14	60,9	Barg, novda, poya shirasi va to‘qimalari
Kemiruvchi fitofaglar	5	21,7	Barg, gul, poya va ildiz bo‘g‘zi
Parazitoidlar	4	17,4	Boshqa hasharotlar hisobiga rivojlanadi
Jami	**23**	**100,0**	

Fitofaglarning asosiy qismini Aphididae oilasi vakillari tashkil etdi. Jumladan, *Aphis urticata*, *A. verbasci*, *A. fabae*, *Brachycaudus helichrysi*, *Cavariella aegopodii*, *C. theobaldi*, *Eucarazzia elegans*, *Macrosiphum euphorbiae*, *Myzus persicae* va *Rhopalosiphum padi* barg hamda yosh novdalar shirasi bilan oziqlanadi. Ularning ta’sirida barglarning deformatsiyalanishi, xloroz, fotosintetik faollikning susayishi va vegetativ o‘sishning sekinlashishi kuzatilishi mumkin. Ayniqsa, *Aphis fabae* va *Myzus persicae* yuqori zararlilik darajasiga ega turlar sifatida ajralib turdi.

Miridae oilasiga mansub *Lygus pratensis*, *Adelphocoris lineolatus* va *Asciodema obsoleta* o‘simlikning barg, poya hamda generativ organlarini zararlaydi. *Lygus pratensis* gullash davrida nisbatan faol uchrashi bilan tavsiflandi. *Thrips tabaci* esa barg epidermisini qirib-so‘rib oziqlanib, barg yuzasida kumushsimon dog‘lar paydo bo‘lishiga sabab bo‘lishi mumkin.

Lepidoptera turkumiga mansub *Helicoverpa armigera*, *Chloridea peltigera*, *Heliothis viriplaca*, *Agrotis segetum* va *Mamestra brassicae* kemiruvchi fitofaglar sifatida qayd etildi. Ularning lichinkalari barg, gul, yosh poya va ildiz bo‘g‘zini zararlaydi. Ayniqsa, *Helicoverpa armigera* va *Mamestra brassicae* barg apparatiga zarar yetkazish salohiyati bilan, *Agrotis segetum* esa ko‘chatlarning ildiz bo‘g‘zini zararlashi bilan ajralib turadi.

Hasharotlarning mavsumiy faolligi aprel–oktabr oylarini qamrab oldi. Fitofaglarning ayrim turlari aprel oyidan, boshqalari esa may oyidan boshlab faol uchradi. Vegetativ o‘sish va gullash bosqichlari zararkunandalar rivojlanishi uchun muhim davr sifatida qayd etildi.

Steviya agrotsenozida foydali hasharotlardan *Encarsia formosa*, *Encarsia partenopea*, *Eretmocerus mundus* va *Trichogramma evanescens* parazitoidlari aniqlandi. Ushbu turlar iyun–oktabr oylarida faol bo‘lib, fitofag hasharotlar populyatsiyasini tabiiy cheklashda muhim ahamiyatga ega. *Encarsia* va *Eretmocerus* vakillari asosan oqqanotlilarda, *Trichogramma evanescens* esa Lepidoptera tuxumlarida parazitlik qilishi bilan tavsiflanadi. Ularning mavjudligi agrotsenozda biologik nazorat imkoniyatlarini ko‘rsatadi.

Xulosa

Stevia rebaudiana agrotsenozida aniqlangan 23 tur hasharotning 82,6 % ini fitofaglar, 17,4 % ini parazitoidlar tashkil etdi. Fitofaglar orasida so‘ruvchi va qirib-so‘ruvchi turlar ustunlik qilib, *Aphis fabae*, *Myzus persicae*, *Thrips tabaci*, *Lygus pratensis*, *Helicoverpa armigera*, *Agrotis segetum* va *Mamestra brassicae* yuqori zararlilik salohiyati bilan ajralib turdi. Parazitoidlarning mavjudligi zararkunandalar sonini tabiiy boshqarish imkoniyatlarini ko‘rsatadi. Olingan natijalar steviya agrotsenozida ekologik xavfsiz va integratsiyalashgan himoya tizimini ishlab chiqish uchun ilmiy-amaliy asos bo‘lib xizmat qiladi.

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BIOLOGIK FAOL MODDALAR VA MINERAL OZIQLANISHNING KUZGI BUG‘DOYNING MORFOFIZIOLOGIK KO‘RSATKICHLARI, FOTOSINTETIK APPARATI VA HOSILDORLIGIGA TA’SIRI

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Annotatsiya: Tezisda biologik faol moddalar va mineral oziqlanishning kuzgi bug‘doy navlarida morfofiziologik jarayonlar, fotosintetik pigmentlar tizimi va mahsuldorlik shakllanishiga ta’siri yoritilgan. Grom, Kuma, Asr va Zvezda navlari bo‘yicha olib borilgan tajribalarda gumat preparatlarining fotosintetik apparatga ta’siri baholangan. Grom navida 0,45 % kaliy gumat qo‘llanilganda xlorofill a, xlorofill b, umumiy xlorofill va karotinoidlar miqdorining eng yuqori ko‘rsatkichlari qayd etilgan.
Kalit so‘zlar: kuzgi bug‘doy, biologik faol moddalar, kaliy gumat, natriy gumat, mineral oziqlanish, xlorofill, karotinoidlar, fotosintetik apparat, hosildorlik.

Аннотация: В тезисе рассмотрено влияние биологически активных веществ и минерального питания на морфофизиологические процессы, систему фотосинтетических пигментов и формирование продуктивности сортов озимой пшеницы. В опытах с сортами Grom, Kuma, Asr и Zvezda оценено действие гуматных препаратов на фотосинтетический аппарат. У сорта Grom применение 0,45 % гумата калия обеспечило наиболее высокие показатели содержания хлорофилла a, хлорофилла b, общего хлорофилла и каротиноидов.
Ключевые слова: озимая пшеница, биологически активные вещества, гумат калия, гумат натрия, минеральное питание, хлорофилл, каротиноиды, фотосинтетический аппарат, урожайность.

Abstract: The thesis examines the effects of biologically active substances and mineral nutrition on morphophysiological processes, the photosynthetic pigment system, and productivity formation in winter wheat cultivars. Experiments with Grom, Kuma, Asr, and Zvezda evaluated the influence of humate preparations on the photosynthetic apparatus. In the Grom cultivar, 0.45% potassium humate produced the highest values of chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids.
Keywords: winter wheat, biologically active substances, potassium humate, sodium humate, mineral nutrition, chlorophyll, carotenoids, photosynthetic apparatus, yield.

Fotosintez o‘simliklarda organik moddalarning hosil bo‘lishini ta’minlovchi asosiy fiziologik jarayonlardan biri bo‘lib, uning samaradorligi barg yuzasi, xloroplastlarning funksional holati, pigmentlar miqdori hamda mineral oziqlanish bilan uzviy bog‘liq. Kuzgi bug‘doyda fotosintetik apparatning shakllanishi navning genetik xususiyatlari, tashqi muhit sharoiti va oziqa elementlari bilan ta’minlanganlik darajasiga bog‘liq holda kechadi. Shu jihatdan biologik faol moddalarni mineral oziqlanish bilan uyg‘un qo‘llash o‘simlikning o‘sishi, barg apparatining faoliyat muddati va assimilatsiya jarayonlarini boshqarishning istiqbolli usullaridan hisoblanadi [1, 2].

Gumin moddalar o‘simlik hujayralaridagi metabolik jarayonlarga ta’sir etib, ildiz tizimi faolligini va oziqa elementlarining o‘zlashtirilishini yaxshilashi mumkin. Mineral oziqlanishda azot xlorofill molekulasi va fotosintetik oqsillar shakllanishida, fosfor energiya almashinuvida, kaliy esa fermentlar faolligi, suv rejimi va stomatalar ishining boshqarilishida muhim ahamiyatga ega. Shu

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sababli gumat preparatlari va NPK oziqlanishining birgalikdagi ta’siri fotosintetik apparatning strukturaviy hamda funksional holatini yaxshilashi mumkin [1–3].

Tadqiqotlarda biologik faol moddalar va mineral oziqlanishning kuzgi bug‘doyning Grom, Kuma, Asr va Zvezda navlarida fotosintetik apparat shakllanishiga ta’siri o‘rganildi. Asosiy e’tibor xlorofill a, xlorofill b, umumiy xlorofill (a+b) va karotinoidlar miqdorining o‘zgarishiga qaratildi. Pigmentlar tizimidagi o‘zgarishlar barg yuzasi va biomassa to‘planishi kabi morfofiziologik ko‘rsatkichlar bilan kompleks ravishda baholandi. Bunday yondashuv biologik faol moddalarning o‘simlikdagi ta’sirini faqat tashqi o‘sish ko‘rsatkichlari orqali emas, balki fotosintetik va biokimyoviy jarayonlar bilan bog‘liq holda izohlash imkonini beradi.

Grom navida nazorat variantida xlorofill a miqdori 1,62 mg/g, xlorofill b 0,58 mg/g, umumiy xlorofill 2,20 mg/g va karotinoidlar 0,46 mg/g ni tashkil etdi. Biologik faol moddalar qo‘llanilganda ushbu ko‘rsatkichlarning barchasida o‘sish kuzatildi. Kaliy gumatning 0,15 % konsentratsiyasida umumiy xlorofill 2,42 mg/g, 0,30 % da 2,67 mg/g gacha oshdi. Eng yuqori natija 0,45 % kaliy gumat variantida qayd etilib, xlorofill a 2,18 mg/g, xlorofill b 0,79 mg/g, umumiy xlorofill 2,97 mg/g va karotinoidlar 0,58 mg/g ni tashkil etdi. Bu nazoratga nisbatan mos ravishda 34,6; 36,2; 35,0 va 26,1 % ga yuqori bo‘ldi.

Kaliy gumat konsentratsiyasini 0,60 % gacha oshirishda umumiy xlorofill miqdori 2,87 mg/g gacha biroz pasaydi. Ushbu natija biologik faol modda konsentratsiyasini oshirish har doim ham fiziologik samaradorlikning mutanosib ortishiga olib kelmasligini ko‘rsatadi. Natriy gumat variantlarida ham pigmentlar miqdori nazoratga nisbatan yuqori bo‘lib, 0,45 % konsentratsiyada umumiy xlorofill 2,89 mg/g va karotinoidlar 0,57 mg/g ni tashkil etdi. Shunga qaramay, Grom navida kaliy gumatning 0,45 % konsentratsiyasi eng samarali variant sifatida ajralib turdi.

Tajriba davomida Chl a/Chl b nisbati 2,75–2,79 oralig‘ida saqlanib qoldi. Bu biologik faol moddalar pigmentlarning mutlaq miqdorini oshirgan bo‘lsa-da, fotosistemalar tarkibidagi funksional muvozanatni keskin o‘zgartirmaganini ko‘rsatadi. Karotinoidlar miqdorining ko‘payishi esa fotosintetik apparatning himoya imkoniyatlari kuchayganidan dalolat beradi, chunki ushbu pigmentlar ortiqcha yorug‘lik energiyasini so‘ndirish va oksidlovchi stressni cheklashda ishtirok etadi. Natijada barglarning funksional faoliyati barqarorlashib, vegetatsiya davomida assimilatsion yuzaning samarali ishlashi uchun qulay sharoit yuzaga keladi.

Olingan ma’lumotlar biologik faol moddalar ta’sirining dozaga bog‘liqligini ko‘rsatadi. Gumatlarning mo‘tadil konsentratsiyalari pigmentlar biosintezi va fotosintetik apparat faoliyatini rag‘batlantirgan, yuqori konsentratsiyada esa samaradorlikning biroz pasayishi kuzatilgan. Bu holat amaliy dehqonchilikda preparat turini va me’yorini nav xususiyatlari hamda mineral oziqlanish foniga mos holda tanlash zarurligini ko‘rsatadi. Xalqaro tadqiqotlarda ham biostimulyatorlar, jumladan, gumin va fulvo kislotalarning ildiz o‘sishi, oziqa moddalarini o‘zlashtirish hamda stressga chidamlilikka ijobiy ta’siri qayd etilgan [1, 2].

Fotosintetik pigmentlar miqdori va barg apparatining funksional davomiyligi don hosilini shakllantirishda muhim fiziologik omillardir. Shuning uchun tajribada qayd etilgan xlorofill va karotinoidlar miqdorining ortishi, shuningdek morfofiziologik ko‘rsatkichlarning yaxshilanishi hosildorlik elementlari shakllanishi uchun qulay fiziologik zamin yaratadi. Biroq biologik faol moddalar ta’sirining yakuniy agronomik samaradorligini baholashda hosildorlik ko‘rsatkichlari, donning strukturaviy elementlari va iqtisodiy samaradorlikni fotosintetik ko‘rsatkichlar bilan birgalikda tahlil qilish maqsadga muvofiq.

Xulosa qilib aytganda, biologik faol moddalar va mineral oziqlanishning uyg‘un qo‘llanilishi kuzgi bug‘doyning fotosintetik apparatini faollashtirishning samarali omili hisoblanadi. Grom navida 0,45 % kaliy gumat varianti pigmentlar miqdori bo‘yicha eng yuqori natijani berdi. Mazkur konsentratsiya xlorofill a va b, umumiy xlorofill hamda karotinoidlarning to‘planishini sezilarli rag‘batlantirdi. Olingan natijalar gumat preparatlaridan ilmiy asoslangan me’yorlarda foydalanish kuzgi bug‘doyning fiziologik holatini yaxshilash, assimilatsion jarayonlarni kuchaytirish va yuqori mahsuldorlik shakllanishi uchun qulay sharoit yaratishda muhim ahamiyat kasb etishini ko‘rsatadi.

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TURLI SOYA NAVLARIDAN AJRATILGAN TUGANAK BAKTERIYA IZOLYATLARINING TURLI XIL NaCl TUZI KONSENTRATSIYALARIGA CHIDAMLILIGI

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Soya (*Glycine max* (L.) Merr.) oqsil va o‘simlik moyiga boy muhim qishloq xo‘jaligi ekinlaridan biri hisoblanadi. Uning hosildorligini oshirishda o‘simlik va tuganak bakteriyalar o‘rtasidagi simbiotik munosabatlar muhim o‘rin tutadi. O‘zbekistonning ayrim hududlarida tuproq sho‘rlanishi qishloq xo‘jaligi ekinlarining o‘sishi va hosildorligini cheklovchi muhim abiotik omillardan biridir. Tuproqda NaCl miqdorining ortishi bakteriya hujayralarida osmotik stressni yuzaga keltirishi, ionlar muvozanatini buzishi va hujayra metabolizmiga salbiy ta’sir ko‘rsatishi mumkin. Natijada tuganak bakteriyalarning yashovchanligi, ildizlarni kolonizatsiyalash xususiyati hamda o‘simlik bilan simbiotik munosabatlarni shakllantirish qobiliyati pasayishi mumkin.

Soya yetishtiriladigan maydonlarni kengaytirish va hosildorlikni oshirishda sho‘rlangan va sho‘rlangan-ishqorli tuproqlardan foydalanish muhim hisoblanadi. Kimyoviy azotli o‘g‘itlarni ko‘p qo‘llash tuproqning kislotalashishiga va oziq elementlari balansining buzilishiga olib keladi. Shuning uchun tuproqning sho‘rlanishiga (NaCl), kislota va ishqorga chidamli tuganak bakteriya izolyatlarini ajratib olish va ularning turli soya navlari bilan simbiotik mosligini aniqlash biologik azot fiksatsiyasini rivojlantirishda amaliy ahamiyatga ega.

Shu sababli, mahalliy soya navlari tuganaklaridan ajratilgan bakteriya izolyatlarining sho‘rlanishga chidamliligini aniqlash, ularning yuqori NaCl konsentratsiyalarida o‘sish xususiyatlarini baholash va istiqbolli izolyatlarni tanlab olish ilmiy hamda amaliy ahamiyatga ega.

Tadqiqotning maqsadi mahalliy soya navlari tuganaklaridan ajratilgan bakteriya izolyatlarining turli NaCl konsentratsiyalariga chidamliligini o‘rganish hamda sho‘rlanish stressiga yuqori darajada bardosh bera oladigan istiqbolli izolyatlarni aniqlashdan iborat.

Tadqiqot obyekti sifatida To‘maris, Orzu, Nafis va Ehtiyoj soya navlari tuganaklaridan ajratilgan tuganak bakteriya izolyatlari olindi. Izolyatlarning sho‘rlanishga chidamliligini aniqlash uchun tarkibiga 100, 200, 300, 400, 600, 800, 900, 1000, 1200 va 1500 mM NaCl qo‘shilgan no‘xatli agar ozuqa muhitidan foydalanildi.

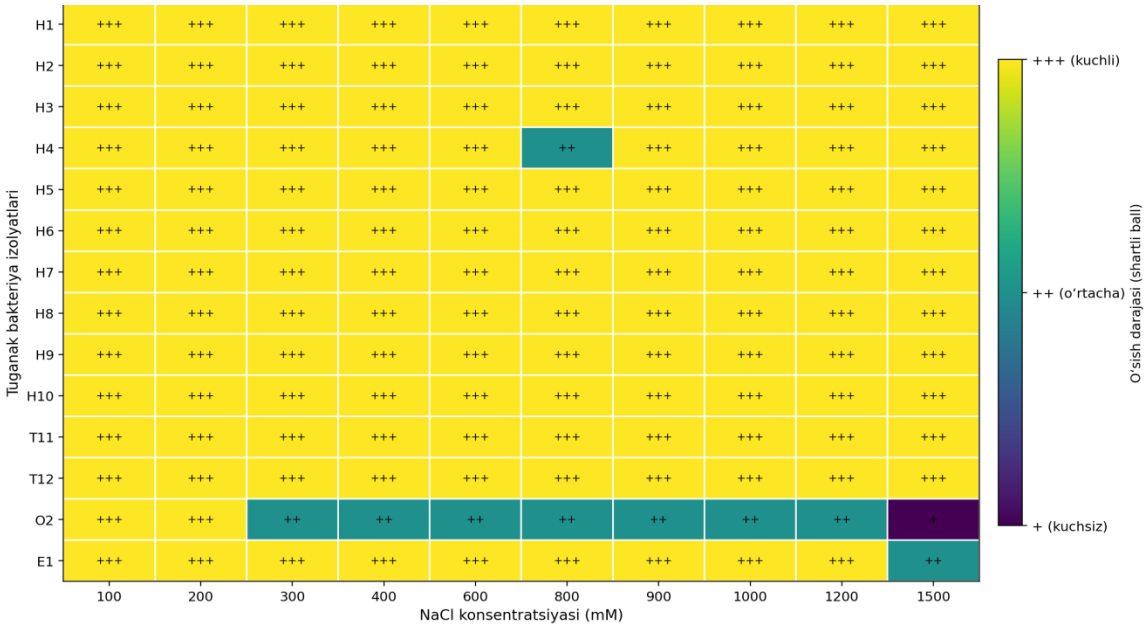
Bakteriya izolyatlarining o‘sish faolligi inkubatsiyaning uchinchi kunida vizual baholandi. O‘sish darajasi shartli ravishda “+++” – kuchli o‘sish, “++” – o‘rtacha o‘sish va “+” – kuchsiz o‘sish ko‘rinishida ifodalandi. Olingan natijalar izolyatlarning turli tuz konsentratsiyalariga nisbatan o‘sish reaksiyalarini taqqoslash asosida tahlil qilindi.

Tadqiqot natijalari soya tuganaklaridan ajratilgan bakteriya izolyatlarining NaCl ta’siriga javobi bir xil emasligini ko‘rsatdi (1-rasm). Olingan natijalarga ko‘ra, H1–H11 va T12 izolyatlarida 100–1500 mM NaCl konsentratsiyalari oralig‘ida, H4 izolyatida esa 800 mM konsentratsiyada kuchli o‘sish qayd etildi. Ushbu izolyatlarda yuqori tuz konsentratsiyalarida ham o‘sish faolligining saqlanishi ularning sho‘rlanish stressiga nisbatan yuqori chidamlilik salohiyatiga ega ekanligini ko‘rsatdi. E1 izolyatida 100–1200 mM NaCl sharoitida kuchli o‘sish kuzatildi, biroq 1500 mM

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konsentratsiyada o‘sish o‘rtacha darajaga tushdi. O2 izolyatida esa tuz konsentratsiyasi oshishi bilan o‘sishning izchil pasayishi aniqlandi: 100–200 mM NaCl da kuchli, 300–1200 mM oralig‘ida o‘rtacha, 1500 mM da esa kuchsiz o‘sish qayd etildi. Bu holat O2 izolyatining yuqori sho‘rlanish sharoitlariga nisbatan boshqa izolyatlarga qaraganda sezgirroq ekanligini ko‘rsatdi.

Umuman olganda, 13 ta izolyatdan 11 tasida 1500 mM NaCl sharoitida kuchli o‘sish, E1 izolyatida o‘rtacha, O2 izolyatida esa kuchsiz o‘sish qayd etilgan. Ushbu natijalar ayrim mahalliy soya navlari tuganaklaridan ajratilgan bakteriyalar yuqori osmotik stress sharoitida ham o‘sish qobiliyatini saqlab qolishi mumkinligini ko‘rsatdi.



1-rasm. Turli soya navlaridan ajratilgan tuganak bakteriya izolyatlarining NaCl tuzi turli konsentratsiyalariga chidamliligi (inkubatsiyaning 3-kuni)

Turli mahalliy soya navlari tuganaklaridan ajratilgan bakteriya izolyatlarining NaCl konsentratsiyalariga chidamliligini o‘rganish natijasida ularning sho‘rlanish stressiga javobi farqlanishi aniqlandi. Nafis (H1–H10) va To‘maris (T11, T12) navlaridan ajratilgan izolyatlar 1500 mM NaCl sharoitida ham kuchli o‘sishni saqlab qolganligi bilan ajralib turdi. Ehtiyoj navidan ajratilgan E1 izolyatida ushbu konsentratsiyada o‘sishning o‘rtacha darajagacha pasayishi, Orzu navidan ajratilgan O2 izolyatida esa kuchsiz o‘sish kuzatildi.

Olingan natijalar yuqori tuz konsentratsiyalariga chidamli izolyatlarni dastlabki saralash imkonini berdi. Keyingi tadqiqotlarda istiqbolli izolyatlarni molekulyar-genetik usullar yordamida identifikatsiya qilish, ularning turli soya navlari bilan simbiotik mosligini baholash hamda sho‘rlangan tuproq sharoitidagi samaradorligini o‘rganish rejalashtirilgan. Mazkur tadqiqot natijalari mahalliy tuproq-iqlim sharoitlariga mos, biologik azot fiksatsiyasida samarali ishtirok etuvchi bakteriya shtammlari asosida mikrobiologik preparatlar yaratish uchun ilmiy asos bo‘lib xizmat qilishi mumkin.

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