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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.

References

1. Ali H.R.K., Hemeda N.F., Abdelaliem Y.F. Symbiotic cellulolytic bacteria from the gut of the subterranean termite Psammotermes hypostoma Desneux and their role in cellulose digestion // AMB Express. – 2019. – Vol. 9, No. 1. – Art. 111. – DOI: 10.1186/s13568-019-0830-5.
2. Dar M.A., Xie R., Pandit R.S. et al. Exploring the region-wise diversity and functions of symbiotic bacteria in the gut system of wood-feeding termite, Coptotermes formosanus,

toward the degradation of cellulose, hemicellulose, and organic dyes // Insect Science. – 2022. – Vol. 29, No. 5. – P. 1414–1432. – DOI: 10.1111/1744-7917.13012.
3. Salgado J.F.M., Hervé V., Vera M.A.G. et al. Unveiling lignocellulolytic potential: a genomic exploration of bacterial lineages within the termite gut // Microbiome. – 2024. – Vol. 12, No. 1. – Art. 201. – DOI: 10.1186/s40168-024-01917-7.
4. Togaev U., Mathur V., Rakhmonkulova A. et al. Comparative metagenomic analysis of gut microbiota in Anacanthotermes turkestanicus and A. ahngerianus reveals diet- and habitat-driven functional divergence // Frontiers in Insect Science. – 2026. – Vol. 6. – Art. 1807673. – DOI: 10.3389/finsc.2026.1807673.