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# Comparative metagenomic analysis of gut microbiota in *Anacanthotermes turkestanicus* and *A. ahngerianus* reveals diet- and habitat-driven functional divergence

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The gut microbiome of termites plays a crucial role in lignocellulose degradation and nutrient recycling. This study presents the first metagenomic characterization of the gut microbiota in two lower termite species, *Anacanthotermes ahngerianus* and *Anacanthotermes turkestanicus*, collected from distinct ecological habitats. In Uzbekistan, the first lives in building a mound in nature in the West part while the second mainly lives in contact with human constructions in the East part without building a proper mound. Both species showed similar bacterial dominance (~53%) in their guts but *A. ahngerianus* exhibited higher overall microbial diversity (Shannon index: 4.046 vs. 3.363; Simpson's index: 0.927 vs. 0.776). Moreover, both termite species showed differences in microbial profiles, including bacterial taxa and eukaryotic groups relevant to lower-termite gut symbiosis. Protist-associated eukaryotic reads were retained because flagellated protists are essential symbionts of lower termites, whereas unexpected non-protist eukaryotic assignments were interpreted cautiously and were not used as evidence of functional gut symbionts or host adaptation. Functional profiling revealed enrichment of pathways related to carbohydrate metabolism, amino acid transport, and energy production in both species. However, *A. turkestanicus* exhibited stronger bacterial dominance associated with lignocellulose degradation and nitrogen cycling, while *A. ahngerianus* maintained a more balanced representation of bacteria, fungi, and viruses. These findings suggest that species identity and ecological habits may be associated with differences in gut microbiome structure and predicted functional potential.

##### KEYWORDS

archaea, bacteria, lignocellulose, metagenome, microbes, shotgun sequencing, termites