

Metagenomic Study of the Black-winged Subterranean Termite (*Odontotermes formosanus*) and its Ecological Function in Lignocellulose Degradation

Overview: This study aims to unveil the metagenome of microbial communities within the nest of the Black-winged Subterranean Termite (*Odontotermes formosanus*) and investigate the roles of these microorganisms in lignocellulose decomposition and ecosystem functions. By combining second and third-generation sequencing data, we conducted a comprehensive analysis of the microbial community in the nests of these termites, with particular emphasis on microorganisms potentially involved in lignocellulose degradation. Our results highlight the critical importance of diverse microbial communities under different environmental conditions in facilitating lignocellulose degradation by Black-winged Subterranean Termites. We have identified various genes associated with lignocellulose degradation, including enzyme genes and metabolic pathways, providing vital clues on how microorganisms efficiently degrade lignocellulose. Furthermore, our study sheds light on the intricate interactions between the microbial community of Black-winged Subterranean Termites and soil ecosystem functions. This work offers essential insights into understanding the lignocellulose decomposition process, advancing sustainable utilization of biomass resources, and maintaining soil ecological balance.

Background: The Black-winged Subterranean Termite (*Odontotermes formosanus*) is a fungus-growing termite that typically nests underground and is a significant pest in agriculture, forestry, and water resources. Its ability to control fungal growth within the nest using microorganisms makes it a potential candidate for biocontrol. However, a comprehensive metagenomic study of the microbial community within the nest of the Black-winged Subterranean Termite has not been conducted. Lignocellulose is one of the most abundant organic compounds on Earth, and its decomposition and degradation hold significant implications for carbon cycling, soil ecosystems, and the sustainable utilization of biomass resources. Despite extensive attention to lignocellulose degradation, the microbial communities and molecular mechanisms still need to be understood. Therefore, this study employs metagenomic approaches to analyze in detail the microbial communities within the nests of Black-winged Subterranean Termites. The metagenomes of lignocellulose-degrading microorganisms reveal how these microorganisms collaborate under various environmental conditions to degrade lignocellulose efficiently. By identifying critical genes associated with lignocellulose degradation, we provide foundational knowledge for future biomass resource utilization and the maintenance of soil ecological balance. Moreover, our research underscores the close relationship between microbial community diversity and lignocellulose degradation efficiency, offering valuable insights into ecosystem functions and sustainable development. This work helps unravel how microorganisms tackle complex carbon waste and provides strategic guidance for the efficient conversion of biomass resources and the health of soil ecosystems.