

Metagenomics of Shipworm (*Spathoteredo obtusa*) and Its Essential Bioactive Compounds

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Abstract

Shipworms (*Spathoteredo obtusa*) are marine bivalves known for their wood-boring abilities and pivotal ecological role in decomposing submerged wood and produce secondary metabolites with potential applications in aquaculture and marine biotechnology. Despite their ecological importance, the microbial symbionts and bioactive compounds associated with *S. obtusa* remain poorly understood. This study aimed to explore the microbial diversity and secondary metabolite composition of *S. obtusa* collected from Sidoarjo East Java to evaluate microbial diversity and metabolite composition. The 18S rRNA gene was amplified using PCR for molecular identification, and the species identity was verified by sequencing and phylogenetic analysis. Metagenomic profiling was performed using Nanopore GridION sequencing. The metabolite profiles was identified with compound identification conducted through mzCloud matching. LCHRMS was done to identified the bioactive compounds in shipworms extract. All specimens were confirmed as *S. obtusa* with more than 99% sequence similarity. Microbial community analysis revealed a diverse array of bacterial taxa, with dominant genera including *Aequoribacter fuscus*, *Agarilytica rhodophyticola*, and *Aristaeella*. Analysis identified multiple bioactive compounds—implicated in bioremediation, probiotics, anti-inflammatory agent for marine bioproduct development.

Index Terms

Metagenomics, Microbial Symbiosis, Secondary Metabolism, Anti-Inflammatory