

SCIENTIFIC REPORTS

OPEN

Comparison of intestinal bacterial and fungal communities across various xylophagous beetle larvae (Coleoptera: Cerambycidae)

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The microbial gut communities associated with various xylophagous beetles offer great potential for different biotechnologies and elaboration of novel pest management strategies. In this research, the intestinal bacterial and fungal communities of various cerambycid larvae, including *Acmaeops septentrionis*, *Acanthocinus aedilis*, *Callidium coriaceum*, *Trichoferus campestris* and *Chlorophorus herbstii*, were investigated. The intestinal microbial communities of these Cerambycidae species were mostly represented by members of the bacterial phyla Proteobacteria and Actinobacteria and the fungal phylum Ascomycota. However, the bacterial and fungal communities varied by beetle species and between individual organisms. Furthermore, bacterial communities' metagenomes reconstruction indicated the genes that encode enzymes involved in the lignocellulose degradation (such as peroxidases, alpha-L-fucosidases, beta-xylosidases, beta-mannosidases, endoglucanases, beta-glucosidases and others) and nitrogen fixation (nitrogenases). Most of the predicted genes potentially related to lignocellulose degradation were enriched in the *T. campestris*, *A. aedilis* and *A. septentrionis* larval gut consortia, whereas predicted genes affiliated with the nitrogenase component proteins were enriched in the *T. campestris*, *A. septentrionis* and *C. herbstii* larval gut consortia. Several bacteria and fungi detected in the current work could be involved in the nutrition of beetle larvae.

Insecta is the most diverse class of animals, living in multiple habitats and feeding on various substrates¹. Insects are colonized by different microorganisms, which are often beneficial or required by the hosts. Also, the intestinal systems of insects are excellent places for the growth of a wide variety of microorganisms²⁻⁴.

Cerambycidae (longhorned beetles or longicorns) is one of the largest families of beetles². All cerambycids are plant feeders, and most cerambycid larvae feed on healthy, dead, or decaying solid plant tissues or, less often, rotten softwoods. Cerambycid beetles can damage forest trees and dry structural wood timbers^{2,5}. Xylophagous beetles, which belong to one of the most important groups of arthropods, produce the enzymes necessary to digest many components of woody material by themselves; alternatively, these components can be degraded by the activity of xylophagous beetles' intestinal microbial communities^{3,6}. While the anatomy and physiology of many Cerambycidae species are well understood, little is known about the complex bacterial and fungal consortia associated with their gut systems.

The symbiotic relationships between prokaryotes/fungi and insects are one of the principal research areas of microbial ecology. One of the most promising examples of such symbiotic relationships is between xylophagous insects and their intestinal communities. According to previous research^{4,7}, symbiotic microbes can live in a variety of insect species, such as beetles, termites, cockroaches and others. The diet of the cerambycid larvae is poor in available nutrients but rich in fibers, which are hard to digest⁶. It was also reported that intestinal microorganisms can convert lignin in the gut systems of some cerambycid beetles⁸. Several bacterial species isolated from beetle guts can additionally metabolize terpenoid molecules, which helps the beetles to colonize the host trees⁹. In

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