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Fungal diversity in the gut of black soldier fly larvae (*Hermetia illucens* L.) from rearing farms in Thailand

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Abstract

The black soldier fly larvae (Hermetia illucens L.) are a saprotrophic insect that can decompose various types of waste and organic matter. The type of feeding waste influences the diversity of microorganisms in their gut, particularly fungi. This research aims to study the fungal community in the gut of black soldier fly larvae from rearing farms in different locations in Thailand Samples were collected from farms in four provinces Nakhon Pathom, Ratchaburi, Chonburi, and Roi Et The fungal community was identified using the non-culture method through metagenomics techniques. Analysis of the Internal Transcribed Spacer 1 gene region revealed a fungal diversity ranging from 119 to 611 Operational Taxonomic Units. The most abundant phylum was Ascomycota (90%). The most abundant classes were Saccharomycetes and Eurotiomycetes. Candida tropicalis, Talaromyces pratensis, Alternaria alstroemeriae, Sporopachydermia lactativora, and Wickerhamomyces anomalus were the most abundant species. For the culture method, the fungi were isolated from the dissected guts and cultured using three types of fungal growth media and incubated at 24°C for 4-7 days. Colony and hyphae characteristics were classified into 10 groups. The nucleotide sequences of the 5.8S-ITS gene region were analyzed for 38 isolates. The fungi belonged to the phyla Ascomycota (86.84%) and Basidiomycota (13.16%). The most abundant class was Eurotiomycetes, with the most abundant species—each found at more than 10%, including Aspergillus flavus, A. ruber, Schizophyllum commune, A. niger, and Talaromyces pinophilus. This obtained information provided data on fungal diversity in different locations and helped in selecting fungal species for future applications.

Keywords: Hermetia illucens L., Black soldier fly, Fungal diversity, Alimentary tract