Undergraduate Research, Innovation and Cooperative Education Symposium, Academic Year 2025

Faculty of Science, Chiang Mai University

Title : Bacterial communities in gut of Thai Bumblebee (*Bombus haemorrhoidalis*) and their potential metabolic expression

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Major : Microbiology

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ABSTRACT

Bumblebees are key pollinators in highland ecosystems. However, population declines driven by pesticide exposure and disease threaten their ecological roles. The gut microbiome also plays a critical role in their health. Despite its importance, information regarding the gut bacterial communities of Thai bumblebees remains limited. This study characterized the gut microbiome of the Thai bumblebee *Bombus haemorrhoidalis* across larval and adult developmental stages using 16S rRNA gene amplicon sequencing. Taxonomic profiling revealed developmental stage–associated differences in community composition. The larval gut microbiota was dominated primarily by the genus *Lactobacillus*, whereas adult guts exhibited greater taxonomic diversity, with dominant phyla including Proteobacteria, Firmicutes, and Bacteroidota. Core genera detected in adults included *Gilliamella*, *Snodgrassella*, and *Apibacter*. Predicted functional profiling suggested stage-associated metabolic differentiation. Larval microbiomes showed relative enrichment of pathways related to amino acid and nucleotide biosynthesis. In contrast, adult microbiomes exhibited greater representation of alternative carbohydrate degradation pathways, phosphotransferase system–associated sugar transport enzymes. These patterns are consistent with increased representation of Gram-negative symbionts and metabolic versatility associated with adult foraging behavior. Collectively, these findings provide foundational insight into the gut microbiome of *B. haemorrhoidalis* and

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highlight ontogenetic shifts in microbial community structure and functional capacity.

Keywords: *Bombus haemorrhoidalis*, gut microbiome, developmental stages

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