Title : Functional Diversity of *Gilliamella* Strains in Honeybees

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ABSTRACT

Gilliamella, a key member of the honeybee gut microbiome, is essential for bee health by contributing to nutrient metabolism and pathogen defense. This study explored the relationship between host specificity and functional diversity in *Gilliamella* strains isolated from western honeybee (*Apis mellifera)* and eastern honeybee (*Apis cerana)*. Through comparative genomics and pathway analysis, we identified genes and metabolic pathways associated with specific host species, particularly those involved in carbohydrate and amino acid metabolism. The pathway analysis categorized *Gilliamella* strains into eight distinct functional groups, each with unique metabolic capabilities. For instance, Functional Group 1 synthesizes vitamin K but lacks the pathway for vitamin B1 biosynthesis. Additionally, functional groups linked to *A. cerana* were missing pathways for pentachlorophenol degradation, potentially reflecting differences in environmental exposure. These findings enhance our understanding of *Gilliamella*'s functional roles and provide a basis for future research on host-specific interactions, environmental detoxification, and pathogen defense in honeybees.

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