

## **Understanding and Modulating Nutrition Competition between Two *Apis mellifera* Gut Symbionts**

Competition plays a crucial role in shaping microbial communities, occurring primarily through interference or exploitative mechanisms (Ghoul and Mitri 2016). Exploitative competition, the struggle to acquire limited resources, is especially prominent in dense, surface-attached microbial communities. Exploitative competition can be tuned via modulating resource availability, offering insights into the principles governing microbial interactions and potential environmental applications. Increasing competition through resource depletion may allow one species to dominate, while reducing competition through resource partitioning can promote coexistence (Zhou et al. 2002; Wilson and Lindow 1994).

The honeybee gut microbiome serves as a simple yet powerful model for studying host-microbe and microbe-microbe interactions. Among its symbionts, *Frischella perrara* and *Gilliamella apicola* engage in strong competition within the pylorus, a gut region where both species are thought to rely on similar carbon sources (Engel, Bartlett, and Moran 2015). Both bacteria exhibit overlapping metabolic traits, including reliance on fermentation and limited TCA cycle activity, suggesting nutrient competition is central to their interactions (Engel, Vizcaino, and Crawford 2015). Their close taxonomic relationship further reinforces the likelihood of overlapping metabolic needs, suggesting nutrient competition is a key factor.

This project aims to uncover the mechanisms regulating *F. perrara* and *G. apicola* competition, focusing on nutrient competition. We will characterize their metabolic potentials and carbon utilization profiles *in vitro* and *in vivo*, identifying carbon sources that influence their interactions. Building on these findings, we will modulate competition at the colony level by manipulating honeybee diets. This study will provide a proof-of-concept for modulating microbial competition through dietary interventions, with potential applications for improving microbiome management. 259 words

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