

OR150*Hidden diversity in the gut microbiota of Apis mellifera***Philipp Engel**, Ramunas Stepanauskas, Nancy A. Moran

Honeybees (*Apis sp.*) and bumblebees (*Bombus sp.*) harbor characteristic gut communities composed of only a small number of bacterial species. This contrasts the immense diversity found in the guts of other animals and renders these social insects simple model systems for gut microbiology. Yet, only little is known about the functions and evolution of these communities. We sequenced a metagenome of the gut microbiota of the Western honeybee to gain insights into the functional gene repertoire of these bacteria. Our comparative analyses showed that different species of the bee gut microbiota harbor distinct functional capabilities linked to adhesion, biofilm formation, and carbohydrate breakdown. These functions are likely to be involved in symbiosis with the host, affecting immunity, pathogen colonization, and nutrient utilization. We further detected marked degrees of genetic diversity within species of the bee gut microbiota. We examined the extent of this intraspecific diversity by sequencing genomes from single bacterial cells of two species: *Snodgrassella alvi* and *Gilliamella apicola*. In both species, we found striking variation in genome divergence, despite uniform levels of 16S rRNA similarity. Some genotypes revealed genome cohesion indicated by high levels of recombination and low levels of sequence divergence. Other genotypes were highly divergent, constituting distinct and irreversibly separated lineages. Gene repertoires differed markedly among strains in both species, suggesting functional differences, which could be important for symbiosis with the host. Our findings from the honeybee parallel observations from mammals, suggesting that in situ diversification of a few bacterial lineages is a common pattern in the evolution of gut communities. In the future, we want to understand which factors drive this diversification and how it affects the interaction with the host.