

OR157*Microbiomes of Megalomyrmex social parasites and their fungus-growing ant hosts*

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Bacterial symbionts are important fitness determinants of insects. Some hosts have independently acquired microbes of the same lineage to meet similar challenges, but whether distantly related hosts that live in symbiosis can maintain similar microbial communities has not been investigated. The varying degrees of nest-sharing between *Megalomyrmex* social parasites (Solenopsidini) and their fungus-growing ant hosts (Attini) allowed us to address this question, as both ant lineages rely on the same fungal diet, interact through a variety of parasitic relationships, and are distantly related. We used tag-encoded FLX 454 pyrosequencing and diagnostic PCR to map bacterial symbiont diversity across the *Megalomyrmex* phylogenetic tree, which also contains clades of free-living generalist predators. We show that social parasites sharing the nest with their hosts or merely consuming host brood and fungus garden, harbour microbial communities that are partially overlapping with those of the attine species that they exploit. Particularly abundant were Entomoplasmatales, Bartonellaceae, *Acinetobacter*, *Wolbachia* and *Pseudonocardia*, in many cases co-infecting associated hosts and parasites with identical 16S rRNA genotypes. We further reconstructed population level infection dynamics for Entomoplasmatales and Bartonellaceae species in the particularly well sampled species-pair of *M. symmetochus* guest ants and *Sericomyrmex amabilis* hosts. Our results suggest that hosts and socially parasitic *Megalomyrmex* ants share a number of prevalent bacterial symbionts, as these bacteria may be transmitted via consumption of shared fungus gardens, predation on host brood by the social parasites, or parasite grooming by host workers.