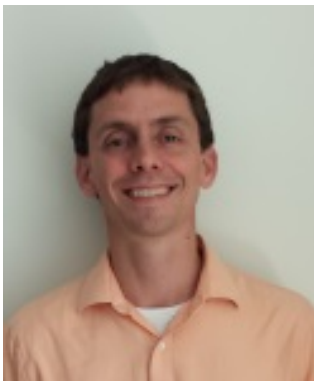




INSTITUTE FOR GENOMICS AND EVOLUTIONARY MEDICINE

## Hotspots for bacterial symbiosis across the ants



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While several ants invest in specialized symbioses with bacteria, we know little about symbiont function across these insects. Also limited is our understanding of how ant phylogeny and ecology predict the composition and functional roles of internally housed symbionts. To address this, we studied ant symbionts using both 16S rRNA amplicon sequencing and shotgun metagenomics. The resulting data were analyzed using a phylogenetic and ecological framework derived from a multi-gene host phylogeny and from trophic placement via stable isotope ratios. Many ants in our study harbored low biomass symbiont communities. Among those with detectable symbionts, we found several recurring bacteria with broad distributions. Several formed ant-specific lineages, suggesting some degree of specialization. Related, ant-specific symbionts often colonized related ant hosts, revealing the ant phylogeny as a predictor of symbiont composition. But such related symbionts were also found in unrelated ants from comparable trophic levels, suggesting an impact of host ecology. Metagenomic assessments reinforce the importance of host ecology, revealing functionally similar symbionts among unrelated ants from similar trophic levels. Bacteria from herbivorous ants possess genes enabling nitrogen recycling and the provisioning of recycled nitrogen to their ant hosts. Symbiotic microbes from carnivorous ants encode few genes from such pathways, investing in a divergent set of metabolisms. To conclude, life at trophic extremes is frequently associated with specialized symbioses between ants and bacteria. Signatures in symbiont genomes suggest that independent co-option of "functionally attuned" bacteria may have facilitated the origins or maintenance of disparate diets across a diverse range of ants.

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