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Abstract

Determining abundance and diversity of fungi in the Harvester Ants (Genus: *Pogonomyrmex*)

Pathogens and their hosts are constantly evolving in response to one another. This coevolutionary process can lead to strong differences in pathogen impact among individuals and populations, as pathogens adapted to infect one genotype in particular may not be able to infect other genotypes. One possible mechanism to increase resistance to pathogens is interspecific hybridization, which creates novel genotypes unfamiliar to pathogens. Hybridization between two species of harvester ants, *Pogonomyrmex barbatus* and *Pogonomyrmex rugosus,* has given rise to two hybrid lineages ("H" and "J") that are highly ecologically successful, occurring across a wide range from southeastern Arizona to southwestern Texas. Southwestern Texas is a wetter region compare to southeastern Arizona that has a more arid region. Fungal growth is favored by high humidity, moisture and warm temperatures. We expected to see a higher diversity and abundance of fungi in populations of higher precipitation habitat than populations of lower precipitation habitat (*P.barbatus* > H, J> *P.rugosus*). To test for differences in abundance and diversity of fungi among habitats, we isolated fungi from soil samples and ant specimens of the two parent species and their hybrid lineages. Preliminary results suggest that *P. barbatus* has a higher abundance and diversity of fungi in its environment than the hybrid lineages and *P. rugosus*. We identified five entomopathogenic fungi in *Pogonomyrmex* species, which ranged in their geographic distribution from widespread to highly species-specific. Once we have identified differences in abundance and diversity in fungi, we will test experimentally whether hybridization increases pathogen resistance by comparing infection frequency at the individual and colony levels in the H and J hybrid lineages to the two parental species.