

OR389*The genetic basis of mutualism in Pseudomyrmex plant-ants***Benjamin Rubin, Corrie Moreau**

The obligate mutualism between ants in the genus *Pseudomyrmex* and acacia trees is one of the most well known of any ant-plant relationship. In this particular mutualism, ants nest in and feed on the hollow thorns, food bodies, and extra-floral nectar provided by the acacia. In exchange for these resources, resident ants aggressively protect their hosts by attacking herbivores, trimming encroaching plants, and removing pathogenic fungi. This ant defense is incredibly effective and their absence ensures plant death. In addition to the acacia specialists, the *Pseudomyrmex* ant genus includes two other obligate mutualistic clades that nest in trees from the genera *Triplaris* and *Tachigali*. These trees have hollow trunks and leaf petioles, respectively, instead of thorns and do not provide direct food rewards, as do acacias. Instead, ants feed on honeydew from plant-sucking insects cultivated inside the plants. Despite the differences in diet and nest structure, these ants behave in the same way as acacia-nesters, aggressively biting and stinging any intruders. Amazingly, these three groups of plant-ants evolved mutualistic behavior convergently. We present three newly sequenced *Pseudomyrmex* genomes representing species from each mutualistic clade as well as five genomes of closely related non-mutualistic *Pseudomyrmex* species. Using these genome sequences, we find a set of approximately 60 genes with consistent signatures of positive selection in all mutualists and no non-mutualists, suggesting their involvement in the evolution of mutualistic behavior. Several of these genes are involved in venom synthesis and carbohydrate digestion, reflecting the differences in life histories between mutualists and non-mutualists. On the whole, mutualistic genomes appear to evolve at a faster rate than closely related non-mutualists, an evolutionary difference possibly associated with their highly active lifestyles. Our findings provide a detailed understanding of the genetic features involved in the evolution of this complex behavior.