OR188

Utilizing genotyping-by-sequencing to elucidate Neotropical army ant evolution

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As keystone predators in Neotropical forests, hundreds of vertebrate and invertebrate organisms associate with the 12 known species of *Eciton*, which exert strong top-down effects on community structure in the leaf litter. Despite their clear ecological importance and strong history of research, a comprehensive phylogenetic and biogeographic study is lacking for the important clade. This absence of phylogenetic resolution has been a substantial impediment to determining ecological and evolutionary dynamics, and presents an opportunity to investigate broader mechanisms of diversification in the Neotropics. Using the high-throughput method genotyping-by-sequencing (GBS), we harvested SNPs from across the Eciton genome to infer the clade's phylogenetic history and their colonization of Neotropical habitats. This work contributes both to a better understanding of the ecological impact of Neotropical army ants as well as the significance of biogeographic processes in macroevolutionary dynamics.