

**OR200***Biodiversity and life history adaptations of army ant myrmecophiles***Christoph von Beeren, Daniel Kronauer**

Over the last decades, biologists have begun to explore the last biological frontiers, from the deep sea to tropical rainforest canopies. Despite these efforts, such frontiers of largely unexplored biodiversity still exist today, albeit on a smaller scale. One example is the microcosm of myrmecophiles associated with tropical army ants. For instance, more than 300 myrmecophile species, primarily arthropods, are associated with a single species of Neotropical army ant, *Eciton burchellii*. It is clear, however, that this is only the tip of the iceberg and that many more species await scientific discovery and formal taxonomic description, especially because myrmecophiles of other army ant species are notoriously understudied. Furthermore, very little is known about the myrmecophiles' life cycles and basic life history adaptations. We study the myrmecophile communities associated with six *Eciton* army ant hosts at La Selva Biological Station, Costa Rica, by combining DNA barcoding for rapid species identification with detailed taxonomic descriptions. For each specimen, we provide species name, DNA barcode, digital voucher images, and detailed collection records. Such a reference database will form an essential baseline for further studies of these complex myrmecophile communities. A group of staphylinid beetles (genus *Vatesus*) exemplifies the benefits of our approach well. Our DNA-based species identification protocol uncovers cryptic species in this genus, and thereby provides evidence for unexpectedly high host specificity. Using DNA barcodes to match larval and adult stages, we demonstrate that both adults and larvae of all *Vatesus* species participate in colony emigrations, and that reproduction and larval development are remarkably well synchronized with the hosts' reproductive cycles. Besides revealing the biodiversity and life history adaptations of army ant myrmecophiles, a large-scale comparative analysis of different myrmecophile taxa will also unveil general evolutionary trends in such diverse multi-species networks.