

OR390*Comparative genomics of the attine fungus-growing ants*

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The attine fungus farming ants evolved in the Amazon Basin, spread across the (sub)tropical Americas and radiated into 15 extant genera with >250 currently described species. The attine lineage represents three major irreversible evolutionary transitions: (1) The ants becoming farmers ca. 50 MYA, (2) The mutual domestication of the ancestor of the higher attine ants and a single lineage of gongylidia-bearing crop fungus ca. 20 MYA and (3) The irreversibly committed symbiosis jointly adopting leaf-cutting herbivory and multiple queen mating, which resulted in extended worker caste differentiation, large colony size and substantial ecological footprints. After draft genomes of the leafcutting ants *Acromyrmex echinator* and *Atta cephalotes* were published in 2011, we decided to also obtain high-coverage reference genomes for *Trachymyrmex septentrionalis*, *T. cornetzi*, *T. zeteki* and *Cyphomyrmex costatus*, representing all genus-level branches of the higher attine ants, and a close lower attine outgroup. We also obtained an assembled reference genome of the dikaryotic fungal symbiont of *C. costatus* and transcriptomes of the functionally polyploid symbionts of the other species. I will present an update of the ongoing comparative analyses which so far indicate that: (1) Most significant genome-wise changes occurred when parties irreversibly committed to the mutualistic symbiosis, i.e. 50 MYA for the ants and 20 MYA for the fungal symbionts, (2) Significant additional change happened in the common ancestor of the leaf-cutting ants and their fungal symbiont and we confirm that the latter is a secondary later acquisition, (3) Signatures of selective change across the final two major evolutionary transitions in fungus farming indicate connections to metabolic pathways and mitochondrial function.