

Genomic changes during the evolution of increasing specialization in fungus-farming ants

Ants are an ecologically important group of insects with a vast array of specialized lifestyles and symbioses. One of the most spectacular ant symbioses is fungus farming, found in a single clade of New World (attine) ants, a mutualism to which the ants contribute plant material in exchange for food provided by the fungal crops. Since this mutualism evolved in the Amazon basin from hunter-gatherer like ancestors some 50 mya, it has undergone a series of evolutionary transitions of which the use of specialized rather than generalist fungal strains, active herbivory rather than using dead plant parts, polymorphic rather than monomorphic worker castes, and multiple rather than single mating of queens are the most important. The advent of high-throughput sequencing techniques now allows these questions to also be addressed at the molecular evolutionary level. In a recent study, we showed that the genome sequence of the leafcutter ant *Acromyrmex echinatior*, a representative of the most highly derived leaf-cutting fungus-farming ants, has characteristic changes in detoxification pathways, loss of function in arginine metabolism pathways, and expansion of specific peptidase gene-families relative to other ant genomes. We have now sequenced and partly analyzed the genomes of five additional fungus-farming ant species, representing all phylogenetic branches of the higher attine ants and a lower attine outgroup, and thus most of the major evolutionary transitions. Here I will discuss the results from our first genome study, and what insights we have gained from the (preliminary) analyses of the additional genomes.

