



## **Comparative genomics of ant chemosensation: insights into the genomic evolution of sociality**

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Chemosensation is one of the dominant sensory modalities in insects, facilitating the detection of food, predators, mates, and social information. The chemosensory system plays a particularly important role in ant social evolution as it is responsible for the detection of the pheromones used for behavioral coordination within a colony. Indeed, it has been observed that the chemosensory gene repertoire in the ants is greatly expanded compared to all other insect, driven predominantly by expansions in a particular group of odorant receptors which were therefore hypothesized to play important roles in pheromone perception. We supported this hypothesis using a variety of comparative methods, and furthermore we found that this OR clade in particular evolves particularly rapidly, expanding from 3 genes in the ant ancestor to as many as 276 genes in extant ants. Intriguingly, the most rapid period of expansion was in the evolutionary lineage leading to extant ants, roughly concurrent with the evolution of eusociality. To assess the mechanisms of genome evolution facilitating this expansion, we re-sequenced the genome of the clonal raider ant with modern tools to provide a chromosome-level genome assembly. Using this highly contiguous assembly along with phylogenetics, we were able to map OR gene duplications in time and space. We showed that ORs mostly duplicate through local tandem array expansion, but the most rapid expansions happened after a genomic transposition event. Many clades of ORs have differentially expanded in specific ant lineages, likely due to the varying life histories of the species which have been sequenced. Analysis of the many high-quality ant genomes produced by GAGA will allow for investigation of the social and ecological pressures which drive OR gene family evolution. Combined with functional studies, such a research program would provide a complete picture of evolution from selective forces to genomic change to physiological adaptation.