

Core-project: Global patterns of genomic innovations

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New experimental and computational techniques provide exciting opportunities to study the evolutionary history of genomes and to reconstruct the emergence of new traits from an integrated, phylogenomic perspective, way beyond the limited perspective of model species. GEvol will exploit these opportunities by connecting researchers from complementary fields, including genomics, bioinformatics, evolutionary ecology, molecular evolution, and developmental biology to unravel the dynamics of major genomic innovations underlying novel traits in insects.

This project will knit together several strands of research from within the SPP and focus on the gain and loss of transcripts, genes, domains and regulatory motifs related to, e.g. sociality or mating systems; complex systems of communication and defence, developmental and morphological innovations and plasticity. The project will combine multiple genomic and other OMIC resources

(e.g., genomics, transcriptomics and epigenomics), allowing for comparative evolutionary genomic studies to delineate past events, even many million years ago. We will study the roles of coding vs. regulatory changes, transposable elements, epigenetics, gene family evolution, copy number dynamics and structural genomic rearrangements.

In first place we will focus on genomic innovations, comprising the expansion or contraction of gene families, including the de novo emergence of novel genes and the prevalence and effects of gene losses. We will study the frequency at which novel protein domains are gained or lost and how they are rearranged. Through collaborations, we will develop tools for automated integration of new data from annotation pipelines with the objective to compute selection signatures across the whole insect phylogeny and relate them to phenotypic innovations and transitions in gene regulation.