

Synteny-Based Identification of Genomic Innovations in Insects

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Genome architecture in insects varies notably within and between taxonomic groups in terms of size, intron distribution, repeat content, and patterns of ancient gene linkage structures. The relationship between these patterns of genome evolution and phenotypic and behavioral diversity of insects is, however, not well understood. Secondly increased or reduced genomes blurs the link between organismal complexity, and non-adaptive scenarios can explain the emergence of genomic complexity through population-genetic environments. Establishing a timeline of genome changes across a gradient of evolutionary distances, linked with a functional analysis of identified novelties, is thus essential to understand how genome innovation is linked to phenotypic sophistication.

In our SPP tandem project, we propose to systematically use syntenic conservation as a means of tracking orthology, local duplications, turn-over of repetitive elements, gains and losses of protein domains and coding capacity, and the emergence and decline of non-protein-coding genes. This synteny-based approach will go beyond the construction of reliable, unambiguous genomic alignments and thus overcome existing limits in classical methods of sequence-based gene phylogenies. This will, in particular, allow to unveil the evolutionary history of DNA elements that do not have 1-1 relationships across species, and to disentangle the evolutionary history also at phylogenetic distances that are too large to allow reliable sequence alignments.

To establish a scalable approach that can address innovation across a gradient of evolutionary distances, we will take advantage of the broad taxon sampling in the insect order Diptera (true flies) and its particularly deep sampling of the family Drosophilidae. Fly evolution has been previously characterized by distinct episodes of rapid increase in taxonomic diversity, and coarse comparisons of fly genomes have suggested fly specific innovations in patterning and signaling pathways. We will present the general outline of our project and comment on first results of our approach to catalogue signatures of innovation across 250+ fly genomes.