

Gene and genome duplication and phenotypic novelties – Insights from spiders and insects

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Phenotypic novelties, such as the wings in insects or silk glands in spiders, facilitate adaptations to changing environments and are thus a major driver for evolutionary diversification. Expansion of genomic information by small-scale gene duplications (tandem duplications) or large-scale duplications (chromosomal or whole genome duplications) are important prerequisites for such novelties. Recent genomic analyses of different arthropod groups revealed at least one large scale duplication event at the base of the arachnoplumonates (e.g. spiders and scorpions). This finding provides a unique opportunity to compare the consequences of large-scale duplication events to small-scale duplications commonly observed in insects. Since vertebrates (that underwent several rounds of whole genome duplications), have hitherto been the only animals to study the consequences of large-scale duplication events, new genomic resources in arthropods now facilitate the comparison of large-scale duplication events across different animal groups. Duplicated genes that are beneficial for the organism are usually retained in the genome and subsequent diversification of gene expression and function contributes to phenotypic innovations. A systematic genome-wide analysis of gene duplications and their impact on phenotypic novelties is missing in arthropods. Therefore, we will combine comparative genomics, functional genomics and functional genetics approaches to reveal gene retention and gene loss patterns in insects and spiders and to functionally test the impact of gene duplications on phenotypic novelties. We will assemble and annotate high-quality reference genomes for underrepresented spider lineages and analyze them together with existing high-quality insect and chelicerate genomes. We will study intron architecture, transposable element content, chromatin accessibility and transcript expression levels to gain insights into the molecular mechanisms underlying the diversification of expression of gene duplicates. For selected gene duplicates we will analyze spatial and temporal expression in developing spider novelties like breathing organs or the silk apparatus, and the function of a subset of genes will be functionally validated via RNA interference mediated gene knock-down. Our work will provide unique insights into the extent, nature and consequences of gene and genome duplications and their importance for the evolution and diversification of phenotypic novelties.