SPP 2349 (GEvol): Genomic basis of evolutionary innovations.

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# Recurrent genomic dynamics linked to parallel evolution of secondary phytophagy in Hymenoptera

**Abstract:**
The phytophagous lifestyle is a key innovation in insects and has, evolved in only one third of all insect orders. The evolution of, phytophagy likely involves fundamental behavioural and morphological changes accompanied by chemosensory and metabolic adaptations. To date, the genomic basis and genetic, innovations related to evolutionary dietary shifts are poorly understood. Here we focus on two monophyletic groups within the, order Hymenoptera, particularly Aculeata and Chalcidoidea, which, descend from zoophagous ancestors but exhibit repeated reversals towards secondary phytophagy. These lineages e.g., the gall-wasps and pollen-collecting bees, switched to phytophagy, while the sister lineages retained a zoophagous lifestyle. In order to contribute to our knowledge of the evolution of nutritional capabilities in insects, we propose to comparatively study the genomic architecture in representative Hymenoptera that are linked to transitions to secondary herbivory. To shed light on evolutionary processes that shaped the diversity of nutritional adaptations in Hymenoptera we
address the following main research questions: (1) Is parallel evolution at the phenotypic level reflected by parallel genome evolution? And (2), did similar genomic innovations appear when independent lineages realized convergent dietary transitions? Using comparative genomics and transcriptomics we aim to uncover genomic underpinnings of macroevolutionary dietary adaptations linked to e.g., the metabolism of plant secondary compounds, the composition of odorant receptors, gustatory receptor families, or carbon dioxide receptor genes. Further, we will study genomic changes underlying evolutionary dietary shifts, testing the repeatability of gene gain and loss, and rapid evolution in regulatory sequences, transposable element dynamics, and gene copy numbers. Results will be of major interest to scientists in the fields of functional genomics, systematic biology, and protein function analysis of insects, including those insects of economic importance.