Apoidea Reloaded: Phylogenomic Relationships of Apoid Wasps and Bees, its Implications, and Future Perspectives

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Apoid wasps and bees (Apoidea) are an ecologically and morphologically diverse group of Hymenoptera. Major problems for our understanding of the evolutionary history of Apoidea have been the difficulty to trace the phylogenetic origin and to reliably estimate the geological age of bees. To address these issues, a comprehensive phylogenetic data set was compiled by simultaneously analyzing target DNA enrichment data and transcriptomic sequence data, comprising 195 single-copy protein-coding genes and covering almost all major lineages of apoid wasps and bee families. The comprehensive phylogeny allowed to trace the evolutionary origin of bees and revealed the Ammoplanidae as possibly the closest extant relatives of bees. In addition, the inferred phylogenetic relationships of apoid wasps require the implementation of a new classification to establish a natural system of Apoidea. To fill continuing gaps in our knowledge of the phylogeny of Apoidea I applied a genome skimming approach on key taxa that have not been considered in the previous phylogenetic study i.e. *Heterogyna, Eremiasphecium*, and *Entomosericus*. In my talk, I will present the results of the newly re-analyzed phylogenetic data set.

When studying the evolution of Hymenoptera reliable phylogenetic studies of representative groups are needed to provide new perspectives for future comparative and functional genomics, transcriptomics, and phylogenomics. The phylogenetic relationships of apoid wasps, for example, not only illuminate the most recent common ancestor of bees but also allow to trace the evolutionary origin of bees. The latter was accompanied by one of the most fundamental dietary transitions within the Hymenoptera, namely the shift from phyto-zoophagous to pollenivorous nutrition. The ammoplanids' biology thus indicates how the transition from a phyto-zoophagous to an exclusively pollenivorous nutrition could have taken place.

Finally, Hymenoptera are a highly suitable group to study dietary capabilities and adaptations to different food sources due to their two remarkable dietary transitions that have occurred during their evolution. On the one hand the switch from phytophagy to phyto-zoophagy which was concomitant with the evolution of parasitoidism, and the switch from phyto-zoophagy to pollenivory on the other, which mainly gave rise to the evolution of bees. In my talk, I will discuss new and future projects to study genomic adaptations and transcriptional versatility in representative Hymenoptera with specific food habits.