

Ladybirds - the family Coccinellidae, comprising over 6000 known species, distributed throughout the world, is an important model group in the biological, ecological and genetic research. Most of them are predators, feeding mainly on aphids and scales, but their diet is much more diverse and includes other insects from the order Hemiptera (bugs, psyllids, whiteflies), beetle and moth larvae, as well as fungi, pollen and plant tissues. Many species are used for biological control of plant pests; some are invasive species, affecting the stability of ecosystems on the scale of entire continents (e.g. multicoloured Asian ladybird beetle, *Harmonia axyridis*).

However, it is still surprisingly little known about the evolution and relationship of ladybirds - a group so widely used in research, where the phylogenetic framework is particularly important. Previous attempts to reconstruct the phylogeny of the Coccinellidae were based on a small number of species and at most on several genes. Although current research confirms that the ladybirds form a natural taxon (monophyletic group), the relationships within this group, at the level of subfamilies and tribes remain largely unresolved. This situation - the lack of a credible hypothesis about family phylogeny - prevents comprehensive research on the most important aspects of ladybirds evolution (e.g., the evolution of food preferences or key morphological features) and significantly hinders taxonomic, systematic and ecological research of Coccinellidae.

Proposed research, through the analysis of phylogenomic data (transcriptomic and genomic sequences) and morphological characters, is aimed at a reconstruction of the reliable phylogenetic relationships within the ladybird family as well as the entire superfamily of Coccinelloidea and establishing a time frame for ladybird diversification. The obtained phylogenetic trees will be used to test hypotheses regarding the evolutionary history of Coccinellidae, differentiation, relationships, evolution of morphological traits and changes in food preferences in the course of evolution.

Using the resulting molecular time tree, (chronogram) and comparative phylogenetic methods, we want to specifically research (a) the absolute and relative time of differentiation of the evolutionary lines, (b) the presence of significant changes in the rate of differentiation, (c) the pattern of changes in food preferences, and (d) the origin and subsequent changes in the Coccinellidae defence mechanisms. We will also analyse the set of morphological characters of ladybirds and related groups, as an independent (from molecular data analysis) estimation of the phylogeny of this group. Morphological data will also be the basis for testing hypotheses on the evolution of morphology, both adults and larvae of Coccinellidae.

Based on a large-scale analysis of phylogenomic data, the proposed research, will lead to the first, reliable phylogenetic hypothesis and the molecular time tree of the ladybirds and the superfamily of Coccinelloidea based on fossil dating.

The resulting phylogenetic and evolutionary framework will enable the use of ladybirds as a model group to test more general theories concerning the co-evolution of predator-host systems, and the evolution of changes in food preferences (e.g., transitions from predation to herbivory). The parallel morphological analyses will provide an independent hypothesis about the phylogeny of this group of beetles. This will enable mutual testing of the results of analyses of different data sets and will expand knowledge about the suitability of morphological characters in the reconstruction of the phylogenies of rapidly evolving and diversifying groups of insects.

This research is also at the frontier of current work in phylogenetic systematics as it represents one of the first applications of combining transcriptomes and data from anchored hybrid enrichment.