

Impact of the Paleocene-Eocene Thermal Maximum on diversification dynamics in Paederinae rove beetles

Climate is one of the main factors driving the evolution of life on Earth and thus reconstructing past biological and geological processes is important for studying its effects on recent biodiversity. Eocene is a truly unique time in Cenozoic era in terms of the magnitude of climatic and related biotic changes, and many recent plant and animal lineages stem from this epoch. However, the impact of the most rapid and significant climatic warming event of the last 65 million years, the Paleocene-Eocene Thermal Maximum (PETM) on the evolution of recent groups is still very little understood. Moreover, the majority of studies omit the highly diverse organismal groups such as insects and all of the few studies in this topic on insects have been focused on phytophagous groups only. **Predators or groups that are not directly dependent on plant diversity are still unexplored in this context.**

Rove beetles (Staphylinidae), the largest family of animals, are a great example of the amazing evolutionary success with ca. 64 000 known recent species occurring on every continent, except Antarctica. One of the most diverse groups among them, in terms of the number of species and worldwide distribution are Paederinae, a subfamily of only predatory species. At the same time, a significant increase in their fossil record after the PETM event has been observed, which could mean that it had a significant impact on evolution of the group perhaps leading to the current mega-diversity. Such subfamily makes a very promising 'model group' for studying the effect of past climatic events and thus **Paederinae rove beetles are chosen as a study group** in the proposed project.

The main goal of the proposed project is to investigate the evolutionary response of predatory beetles from the subfamily Paederinae to the Paleocene-Eocene Thermal Maximum event.

Unfortunately, the subfamily Paederinae is also among the examples of a mega-diverse group where we know very little to nothing about their phylogeny. The species-richness makes this group extremely challenging for phylogenetics and thus has never been a subject in broader evolutionary studies. The proposed project will help to overcome this obstacle by building the first genus-level phylogeny of the subfamily and will allow introducing them to macroevolutionary research.

I intend to achieve this goal by applying a set of innovative methods, such as machine learning for species identification, Next Generation Sequencing approaches, and Bayesian statistical phylogenetics. The first such large-scale phylogeny of Paederinae rove beetles will be built based on their morphology and information contained in their genomes (ultraconserved elements) and further used for exploration of evolutionary processes. I will apply a recently developed method for dating phylogenies, which uses fossils directly included into data matrix. Dated phylogeny and testing different diversification models will allow to assess the impact of PETM on diversification dynamics of the group and will answer the question if the event has been one of the main causes of their current mega-diversity.

The project will result in a number of papers in peer-reviewed journals. It will contribute to increasing the knowledge about the evolutionary driving forces and provide an insight into the role of climate changes in the evolution of predatory insects like rove beetles. One of the intermediate results of the project would be the first genus-level phylogeny using genomic data in the whole family Staphylinidae. Last, but not least, machine-learning methods will be applied to two taxonomically difficult genera and for the first time used in larger-scope evolutionary studies.