

## **Genomic, morphological, and paleontological data in reconstructing the taxonomic structure and evolutionary history of the hyperdiverse Staphylinidae genus *Lathrobium* Gravenhorst, 1802**

Taxonomy is a field of biological study, which is responsible for keeping organisms' nomenclature in order corresponding to their evolutionary relationships. These relationships are a matter of intensive research and reevaluation, which often brings a lot of taxonomical changes, such as new species names, or transfer of an organism from one group to another. In large groups (taxa) of organisms, especially poorly studied ones, the problem of taxonomic impediment arise quite often. It means that the taxon includes so many species described, that taxonomists are not able to handle its classification in order. Thus, different issues appear there, e.g., when the same species are described twice under different names or when species which belong to another lineage artificially is placed in non-related taxon, etc.

Rove beetles (Staphylinidae), the largest family of not only beetles but all animals, are a great example of the taxonomically challenged taxon. It includes 64 000 known recent species occurring on every continent, except Antarctica. As with many megadiverse groups, the taxonomic impediment for rove beetles is challenging. The genus *Lathrobium*, which belongs to one of Staphylinidae subfamily Paederinae, includes almost 900 species is a prime example of a lineage with such a complex taxonomy that it makes studies of the group problematic. Data on *Lathrobium* species are scarce although this genus is one of the most typical representatives of forest leaf litter. Biased descriptions, evidence for unnatural grouping, and numerous non-valid species names are not a full list of problems in the group.

The reason of taxonomic impediment is often connected with the fact that the classical taxonomic work with reexamination of the types, careful dissections of thousands of specimens and nomenclature decisions made with bare eye and life experience would take years with such large genus. Integrative approach with the use of genomic data may help the situation, but was never yet applied for taxonomic revisions in Paederinae.

Based on this, my project aims to reconstruct relationships of *Lathrobium* sensu stricta (the "original" genus) with closely related genera via phylogenetic method, build a comprehensive morphological matrix for the genus, provide a new concept of *Lathrobium* s. str. species composition based on three types of data, and estimate the time and ways of *Lathrobium*'s evolution and distribution.

The main novelty of the approach is to analyze two types of genomic data together with morphological data of both recent and extinct species of *Lathrobium* and allied. This will let me tackling the problem from the new angle and disclose species relationships of the group with cost and time efficient methods. The project will result in a number of papers in peer-reviewed journals.

Completion of this project will provide the necessary background for further research in taxonomy, evolution, and environmental studies of *Lathrobium* and similarly challenging taxa. Accumulation of novel DNA-based methods, bioinformatic tools, and fine-grained morphology would allow moving considerably beyond the current understanding of species delimitation in target taxa by using a sustainable workflow uniting the best current practices of integrative taxonomy. Also, the details of early evolution and dispersion of such a widespread genus will help to understand its current distribution and ecological preferences.