

A comprehensive genus-level reconstruction phylogeny of Paederinae (Coleoptera: Staphylinidae) based on combined genomic and morphological data

Abstract:

Beetles, despite being frequently overlooked in general discussions of the planet's biodiversity, represent the most diverse order within animals. Among them, Staphylinidae, or rove beetles, stand out as the most species-rich family, with over 67,000 extant species. Adapted to diverse ecological niches worldwide, rove beetles exhibit remarkable morphological and ecological diversity, from specialised environments like ant nests to generalists in forest leaf litter, playing crucial roles in ecosystem functioning.

Paederinae, a subfamily within Staphylinidae, ranks among the largest rove beetle groups, yet its phylogeny remains poorly understood due to historical taxonomic challenges and limited systematic studies. Numerous but disintegrated taxonomic works and revisions prevailed in the field until recent advancements in molecular techniques, which stimulated comprehensive DNA-based and total-evidence phylogenetic investigations to appear.

In this study, several significant advancements were made in the systematics and phylogeny of the Paederinae subfamily. A new set of morphological characters was identified, that is specific to Paederinae subtribes and provide a robust phylogenetic signal. Our total-evidence phylogeny targeting representatives from 180 genera, the first one to incorporate genomic data for Paederinae, demonstrated improved resolution at the subtribal level and allowed us to redefine subtribal classification. Systematic changes proposed include elevation of the subtribe Sphaeronina Casey, 1905 to the tribal level (Sphaeronini stat. rev.), designation of the new subtribe Scymbaliina subtrib. nov., and redefinition of subtribes Astenina sensu nov., Echiasterina sensu nov., Lathrobiina sensu nov., Lithocharina Casey 1905 sensu nov., Medonina sensu nov., Scopaeina sensu nov., and Stilicopsina sensu nov. with new genera compositions and updated diagnoses. The custom UCEs baits designed for this research was also proved effective in capturing genomic data from dry-pinned historical specimens, highlighting the significance of museum collections as unique molecular data repositories. These findings contribute to a deeper understanding of Paederinae evolution and taxonomy.