

## Abstract:

Despite a growing number of contributions concerning their taxonomic diversity, many studies of darkling beetles (Coleoptera: Tenebrionidae) still rely on classic morphology that remains untested in modern phylogenetic contexts. Consequently, many taxa have eluded additional scrutiny beyond alpha taxonomic additions. To complicate matters further, specimens unobserved in the wild or represented in collections by scant few specimens compound issues for taxonomists working on classification. New analyses using molecular and morphological methodologies and data are presented here to fill in gaps left by historical contributions, as well as to reevaluate previous classification based solely on morphology. The darkling beetle tribe Platynotini (subfamily Blaptinae) is a grouping with one well-studied lineage (subtribe Platynotina) alongside one which is contrastingly obscure and rare (Eurynotina). Eurynotina has undergone no revisionary work since its original inception over 70 years ago, and includes species described nearly 200 years ago. Originally classified within three informal groupings (*Eurynotus*, *Schyzoschelus*, and *Oncotus*), the 95 species and 16 genera of Eurynotina are largely based upon small series of specimens (>75% of taxa represented only by original type series). To date, specimens remain uncommon in collections and are often damaged or missing important parts that can preclude morphological or molecular analysis. This study focused on leveraging large genomic data sets obtained from next-generation sequencing in tandem with morphology to address gaps in analyses of the phylogenetic status and examine the monophyly of the subtribe, genera, and species of subtribe Eurynotina. Specifically, targeted enrichment (499 nuclear loci / 155,172 amino acids) with museomics (12 mitochondrial loci / 2,395 amino acids) are used alongside classic morphological data from historical specimens to produce a comprehensive, phylogenetically informed backbone classification. As a result of the analyses presented in this thesis, the subtribe is reorganized into five lineages supported by morphological and molecular data: *Eurynotus*, *Phylcastus*, *Schyzoschelus*, *Psectrapus*, and *Oncotus*. Two new genera (*Colophonexsula* Lumen & Kamiński, *Muelleropsectropus* Lumen & Kamiński) and 13 new species (*Eurynotus brunoi* (Lumen & Kamiński), *E. privisolum* Lumen & Kamiński, *Isoncophallus ovanullum* Lumen & Kamiński, *I. crispiformus* Lumen & Kamiński, *Ograbies calumnus* Lumen & Kamiński, *Phaleriderma iwani* Lumen & Kamiński, *Phylcastus ancoralium* Lumen & Kamiński, *Phy. makskacymirowi* Lumen & Kamiński, *Psectrapus byki* Lumen & Kamiński, *Ps. distaticum* Lumen & Kamiński, *Ps. latimentulum* Lumen & Kamiński, *Ps. simplicimentulum* Lumen & Kamiński, *Schyzoschelus aetheculus* Lumen &

Kamiński) are described along with several neotype and lectotype designations to stabilize the taxonomy of the group, as well as new combinations and redefinitions of genera over five published manuscripts. Non-target subjects such as ovovivipary and new revised terminology for reproductive morphology are also described. Finally, a total revision is presented in the form of an exhaustive monograph including keys to all five phylogenetic lineages, 19 genera, and 94 species. As a result of the body of work presented in this thesis, the subtribe Eurynotina now has a well-documented and tested phylogenetic background upon which future work can scaffold.