

**Review of the doctoral thesis Phylogeny and Taxonomic Revision of
Subtribe Eurynotina (Coleoptera: Tenebrionidae) Filogeneza i rewizja
taksonomiczna chrząszczy z podplemienia Eurynotina (Coleoptera:
Tenebrionidae) of Ryan Lumen**

The thesis submitted for evaluation refers to the systematics, phylogeny, morphology, and taxonomy of darkling beetles (Coleoptera: Tenebrionidae), with particular emphasis on the poorly known subtribe Eurynotina within the tribe Platynotini (subfamily Blaptinae). The dissertation addresses a long-standing gap in the knowledge of this lineage, which had not undergone a comprehensive revision since its original establishment more than 70 years ago. The thesis integrates molecular and taxonomic evidence to reassess the phylogenetic relationships and classification of Eurynotina and provides a comprehensive revision of the group.

The thesis is structured around five scientific contributions, in leading journals in the field, published between 2023 and 2025, which are subsequently integrated into a comprehensive taxonomic and phylogenetic synthesis. The five publications are: Lumen & Kamiński (2023), a revision of the genus *Phylacastus*; Lumen & Kamiński (2024a), a revision of *Eurynotus* and the description of ovovivipary in Tenebrionidae; Lumen & Kamiński (2024b), addressing the generic boundaries of the *Schyzoschelus* group; Lumen et al. (2025), presenting a phylogenetic analysis of Eurynotina based on complementary genomic and morphological data; and Lumen & Kamiński (2025), providing a comprehensive revision of the subtribe Eurynotina. The sequence of these contributions is logical and reflects a progressive development from detailed taxonomic revisions toward an taxonomy integrative phylogenetic framework and, ultimately, a complete revision of the subtribe.

The research addresses an important and particularly challenging taxonomic group. Eurynotina comprises 95 species currently assigned to 16 genera, many of which are known from extremely limited material. More than 75% of the taxa are represented only

by their original type series, and many historical specimens are damaged or lack structures that are traditionally considered essential for taxonomic identification. These circumstances have severely limited previous attempts to evaluate the validity and relationships of the taxa included in the group. The thesis therefore addresses not only a taxonomic gap, but also, a methodological challenge, by combining historical material with and newly generated genomic data.

The principal objective of the thesis is to establish a robust phylogeny of Eurynotina and to test the monophyly and relationships of the subtribe, its genera, and its constituent species. To achieve this objective, the Ryan combines targeted enrichment of 499 nuclear loci, corresponding to 155,172 amino acids, with museomic data comprising 12 mitochondrial loci and 2,395 amino acids, together with extensive morphological examination of historical specimens in reference entomological collections. This integrative approach is essential for a group in which conventional taxonomy analyses are constrained by the scarcity and condition of available specimens.

The first contribution, within the *Eurynotus* group, Lumen & Kamiński (2023), presents a taxonomic revision of the genus *Phylacastus* Fairmaire using morphology. As a result, one synonym was proposed and two new species were described. This contribution represents an important foundation for the subsequent work within Tenebrionidae, by critically evaluating anatomical terminology and aedeagal homology, the authors establish a more consistent morphological framework for distinguishing taxa within the group. The paper demonstrates for the first time, Ryan's ability to combine detailed morphological examination within a taxonomic revision, providing an appropriate starting point for the broader reassessment of Eurynotina.

The second contribution, Lumen & Kamiński (2024a), focuses on the genus *Eurynotus* (*Biolus* and *Neosolenopistoma*) and includes new records of ovovivipary in Tenebrionidae with 3 species. Finally, *Neosolenopistoma* is becoming a junior synonym of *Biolous*, restoring one species, seven new combinations and two new species were described. The study represents a further detailed revision of one of the principal

lineages of Eurynotina and contributes both taxonomic and biological information. The incorporation of reproductive biology is particularly valuable, providing an additional biological dimension to the understanding of reproductive diversity within Tenebrionidae and confirming that all *Eurynotus* species possess elongate ovipositors

The third contribution, Lumen & Kamiński (2024b), addresses the generic boundaries within Eurynotina through a revision of the *Schyzoschelus* generic group. This study unresolves problems in the historical classification of the subtribe. By reassessing morphological characters and redefining generic boundaries, both authors provide a necessary basis for testing the traditional classification against the phylogenetic framework developed later in the thesis. The contribution also illustrates the progressive moved from individual generic revisions toward a broader evaluation of relationships within Eurynotina.

The fourth contribution, Lumen et al. (2025), represents the central phylogenetic framework of the thesis. In this study, complementary genomic and morphological datasets are employed to elucidate the phylogeny of Eurynotina. The use of targeted enrichment data, together with mitochondrial data obtained from museum specimens, represents a particularly valuable methodological approach given the rarity and historical nature of much of the available material. The integration of molecular evidence with morphology is one of the principal strengths of the thesis, as it allows previously morphology-based hypotheses of relationships to be explicitly tested within a modern phylogenetic framework. The integrative approach provide the basis for reorganizing the subtribe Eurynotina into five principal lineages: *Eurynotus*, *Phylacastus*, *Schyzoschelus*, *Psectrapus*, and *Oncotus*. This provides a substantial contribution toward resolving the evolutionary relationships of this very unknown lineage of darkling beetles.

The fifth contribution, Lumen & Kamiński (2025), is the comprehensive revision of the subtribe Eurynotina. This monographic contribution represents the culmination of the research presented in the preceding studies. It integrates the taxonomic and phylogenetic evidence into a comprehensive classification and includes identification

keys to the five principal phylogenetic lineages, 19 genera, and 94 species. The precise monograph work also includes substantial nomenclatural changes required to stabilize the classification of the group.

The taxonomic contribution of the thesis is impressive. Accurate new genera and new species were described. In addition, several neotype and lectotype designations, new combinations, and redefinitions of genera are proposed. These actions are particularly important in a group in which many taxa are based on very limited historical material and where the absence of modern revisions has complicated the interpretation of generic and species boundaries.

The thesis therefore constitutes considerably more than a series of independent taxonomic contributions. The five publications constitute a coherent body of research, in which detailed morphological revisions provide the foundation for a broader phylogenetic analysis, while the resulting phylogenetic hypotheses are subsequently incorporated into a comprehensive taxonomic revision. This integrative taxonomy is one of the principal strengths of the dissertation.

A further strength of the thesis is the successful use of museum specimens for genomic analyses. The study demonstrates the potential of museomics and targeted enrichment approaches for obtaining molecular information from historically collected specimens, an approach that is particularly appropriate for Eurytomina because many species are extremely rare and difficult or impossible to obtain through contemporary field sampling. The combination of nuclear genomic data, mitochondrial data, and morphology therefore provides a particularly powerful framework for addressing taxonomic questions in groups where conventional approaches are constrained by specimen availability.

Together with as detailed above, with the revision of external and reproductive morphology, Ryan critically evaluates anatomical terminology and homology, particularly

concerning male genital structures. This aspect is important because morphological terminology can strongly influence the interpretation of character homology and consequently the resulting classification. His meticulous work increases the value of the thesis as a reference for future taxonomic work on Tenebrionidae.

The discovery and documentation of ovovivipary represents another interesting component of the work. This result illustrates the broader biological value of detailed taxonomic research and demonstrates that the examination of poorly known taxa may reveal biological traits that have remained undocumented.

One aspect that deserves mention is the inherent difficulty of working with scarce and often degraded historical museum material, which inevitably limits the availability of molecular data for some taxa. Despite these constraints, the candidate has successfully applied an integrative approach that substantially advances our understanding of the group.

Under such a robust framework, I only missed the inclusion of time-calibrated phylogeny and ancestral area reconstruction encompassing the five lineages, as these analyses would provide a more comprehensive view of their evolutionary history. Nevertheless, I am confident that these will constitute a natural and valuable continuation of this research.

In conclusion, the thesis presented by Mr. Ryan Lumen constitutes an original and substantial contribution to the systematics and evolutionary biology of Tenebrionidae. By combining classical morphology, detailed taxonomic revision, museomics, targeted genomic sequencing, and phylogenetic analyses, Ryan has successfully addressed longstanding problems in the classification of Eurynotina. The five publications included in the dissertation form a coherent and progressively developed body of work, culminating in a comprehensive revision of the subtribe.

In view of the above, I conclude that the doctoral dissertation submitted by MSc Ryan Lumen fully meets the requirements specified in Article 187 of the Act of 20 July 2018 – Law on Higher Education and Science (Journal of Laws of 2018, item 1668, as amended). I therefore request that the Scientific Council of the Museum and Institute of Zoology of the Polish Academy of Sciences admit MSc Ryan Lumen to the further stages of the doctoral proceedings.

In Madrid, on 6 August 2026.

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