



## **Dissonomini Medvedev, 1968: The Eighth Tribe of the Subfamily Blaptinae (Coleoptera: Tenebrionidae)**

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# DISSONOMINI MEDVEDEV, 1968: THE EIGHTH TRIBE OF THE SUBFAMILY BLAPTINAE (COLEOPTERA: TENEBRIONIDAE)

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**Abstract.**— The phylogenetic placement of the tribe Dissonomini Medvedev, 1968 (Coleoptera: Tenebrionidae) is investigated using sequences from a historical museum specimen of *Dissonomus tibialis* Reitter, 1904, along with representative sequences and specimens from the subfamilies Blaptinae (tribes Amphidorini, Blaptini, Dendarini, Opatrini, Pedinini, Platynotini), Tenebrioninae (Bolitophagini, Helopini), Pimeliinae (Adesmini, Sepidiini, Tentyriini, Zophosini), Alleculinae (Alleculini), and Lagriinae (Lagriini). Maximum likelihood and Bayesian analyses were performed on a multi-loci dataset (548 loci spanning 178,309 amino acids). The resulting trees render Dissonomini as sister to Blaptini within Blaptinae with high support. This phylogenetic relation is further supported by morphological traits (e.g., lack ancrae, tenebrionoid prothorax). As a result, Dissonomini is placed within Blaptinae.



**Key words.**— darkling beetles, museomics, classification, Blaptini, Platyscelidini

## INTRODUCTION

While assessing the polyphyletic subfamily Tenebrioninae Latreille, 1802, Kamiński *et al.* (2021) suggested the Central-Asian tribe Dissonomini Medvedev, 1968 (2 genera, 26 species, Iwan *et al.* 2020, Makhan 2018) as a potential member of the resurrected subfamily Blaptinae Leach, 1815. The inclusion of Dissonomini was suggested strictly based on morphological traits due to a lack of molecular data on the tribe at the time. Adult representatives in the tribe possess a reduced scutellar shield, aedeagal tegmen without ancorae (see Lumen & Kamiński 2023a), and ‘blaptoid’ habitus, all of which indicate a close morphological affiliation with the tribes Blaptini Leach, 1815 and Platyscelidini Lacordaire, 1859 (Medvedev 1968). Between these two tribes, Dissonomini appeared to share more adult morphological traits with Platyscelidini, such as widened pro- and mesotarsi (Medvedev 1968). However, when considering larval morphological characteristics, Dissonomini seemed to share more features in common with other Blaptinae, specifically Dendarini Mulsant & Rey, 1854, Pedinini Eschscholtz, 1829, and Platynotini Mulsant & Rey, 1853 (Medvedev 1968). Most larvae of those tribes are equipped with four enlarged apical spines on the terminal segment of the abdomen (Kamiński *et al.* 2019). As a result of conflicting morphology and the lack of molecular data, Kamiński *et al.* (2021) decided not to place Dissonomini within Blaptinae formally, pending additional data.

To investigate the phylogenetic position of Dissonomini, a historical museum specimen of *Dissonomus tibialis* Reitter, 1904 was sequenced using targeted enrichment with a hybridization capture probe set (after Swichtenberg *et al.* 2023). Phylogenetic analyses were then conducted using the recovered genetic loci for this species and representatives from the current Blaptinae tribes, as well as taxa representing four additional tenebrionid subfamilies.

## MATERIAL AND METHODS

### Newly sequenced material

Ethanol-preserved specimens used for extractions were collected by the authors (permits in acknowledgments) or contributed by collaborators (Table 1). Additionally, a single pinned museum specimen of *Dissonomus tibialis* (label data: “Turkest Ashabad” / “Tenebrionid Base Aaron D. Smith TB26594”) was acquired from the Entomological Collection of the Museum and Institute of Zoology PAS (MIZ PAN).

DNA was extracted from the head capsules and pronota of specimens using a Qiagen DNeasy Blood & Tissue Kit following the manufacturer’s protocols,

except pipetting was used to mix samples during incubation instead of vortexing to reduce DNA shearing. Grinding of the cuticle was also avoided to preserve specimens for future morphological examination. Extractions were performed in a sterilized laminar flow hood to minimize contamination from non-target DNA (see Kanda *et al.* 2015). After DNA extraction, voucher specimens were rearticulated and card-mounted. Unique identifiers (TB, KKRNA, and MEL#s) were assigned to each voucher specimen for linking back to sequence data in the Sequence Read Archive (Table 1). All voucher specimens are preserved in the Purdue Entomological Research Collection (PERC) and the Entomological Collection of MIZ PAN.

Extracts were sent to Daicel Arbor Biosciences for library preparation and targeted enrichment using a MyBaits probe kit designed to capture 618 protein-coding genetic loci (see Kanda 2017 and Swichtenberg *et al.* 2023). Libraries were sequenced on a NovaSeq 6000 system using 150 bp paired-end runs.

### Data acquired from NCBI-SRA

To increase the taxonomic coverage of Blaptinae and outgroups, additional sequences were downloaded from the Sequence Read Archive (NCBI-SRA) (Table 1). These additional data were generated and analyzed by Ragionieri *et al.* (2023) and Swichtenberg *et al.* (2023).

### Sequence assembly and analysis

Read quality was assessed with FastQC v.0.11.9 (Andrews 2010). Reads with an average sequence quality across any 4 bases below 20 were removed with Trimmomatic (Bolger *et al.* 2014). HybPiper v. 2.0 pipeline (Johnson *et al.* 2016), operating in DIAMOND mode (Buchfink *et al.* 2015), was used to assemble reads using the set of orthologs designed by Kanda (2017). The implemented files contained sequence information for 618 protein-coding genetic loci acquired from transcriptomes of the following species: *Clamoris americana* (Horn, 1874) (voucher code: KKRNA00020) representing Phrenapatinae, *Eleodes delicata* Blaisdell, 1929 (KKRNA00086), and *Eulabis bicarinata* Eschscholtz, 1829 (KKRNA00037) both representing Tenebrioninae. This dataset is hereafter referred to as the Tenebrionidae bait probe markers (*Tps*). To ensure that mapped sequences of the museum sample were not biased by the reference (Smith *et al.* 2021), data acquired for *Dissonomus tibialis* were also mapped to a more phylogenetically distant probe-set designed for the subfamily Pimeliinae (for details see Kanda 2017) – referred hereafter as *Pps*. All data

Table 1. Characteristics of samples analyzed in the present study.

| Species   | Higher classification        | Voucher no. | NCBI-SRA no. | Reference                | Genotyping success rate* [%] |
|---|------------------------------|-------------|--------------|--------------------------|------------------------------|
| <b>Museum specimen</b>                                    |                              |             |              |                          |                              |
| <i>Dissonomus tibialis</i> Reitter, 1904                  | Blaptinae: Dissonomini       | TB26594     | SAMN40249083 | present paper            | 2.5                          |
| <b>Ethanol-preserved specimens</b>                        |                              |             |              |                          |                              |
| <i>Asiopus aciculatus</i> (LeConte, 1858)                 | Blaptinae: Platynotini       | MEL 147     | SAMN40249084 | present paper            | 35.6                         |
| <i>Blaps mucronata</i> Latreille, 1804                    | Blaptinae: Blaptini          | TB15113     | SAMN40249085 | present paper            | 62.8                         |
| <i>Blapstinus fortis</i> LeConte, 1878                    | Blaptinae: Opatrini          | KKRNA0060   | SAMN40249086 | present paper            | 97.9                         |
| <i>Byrsax</i> sp.   | Tenebrioninae: Bolitophagini | TB22621     | SAMN40249087 | present paper            | 58.4                         |
| <i>Eleodes nigrina</i> LeConte, 1858                      | Blaptinae: Amphidorini       | KKRNA0025   | SAMN40249088 | present paper            | 98.5                         |
| <i>Eurynotus capensis</i> (Fabricius, 1794)               | Blaptinae: Platynotini       | MEL 126     | SAMN40249089 | present paper            | 81.9                         |
| <i>Namibomodes</i> sp.                                    | Pimeliinae: Sepidiini        | TB23298     | SAMN40249090 | present paper            | 68.1                         |
| <i>Rhipidandrus paradoxus</i> (Palisot de Beauvois, 1818) | Tenebrioninae: Bolitophagini | TB16878     | SAMN40249091 | present paper            | 60.0                         |
| <b>Sequences acquired from previous studies</b>           |                              |             |              |                          |                              |
| <i>Allecula morio</i> (Fabricius, 1787)                   | Alleculinae: Alleculini      | na          | SRS15779361  | Ragionieri et al. 2023   | 97.9                         |
| <i>Archinamibia peezi</i> Koch, 1952                      | Pimeliinae: Tentyriini       | TB18861     | –            | Swichtenberg et al. 2023 | 68.3                         |
| <i>Blaps gibba</i> Laporte de Castelnau, 1840             | Blaptinae: Opatrini          | na          | SRR22314228  | Ragionieri et al. 2023   | 97.6                         |
| <i>Epiphysa flavicollis</i> (Fabricius, 1794)             | Pimeliinae: Adesmiini        | TB19082     | –            | Swichtenberg et al. 2023 | 70.1                         |
| <i>Lagria</i> sp.   | Lagriinae: Lagriini          | na          | SRS15779382  | Ragionieri et al. 2023   | 93.7                         |
| <i>Nalassus laevioctostriatus</i> (Goeze, 1777)           | Tenebrioninae: Helopini      | na          | SRS15779391  | Ragionieri et al. 2023   | 98.2                         |
| <i>Neoisocerus ferrugineus</i> (Fabricius, 1798)          | Blaptinae: Dendarini         | na          | SRS15779392  | Ragionieri et al. 2023   | 98.4                         |
| <i>Opatrum sabulosum</i> (Linnaeus, 1760)                 | Blaptinae: Opatrini          | na          | SRS15779401  | Ragionieri et al. 2023   | 98.4                         |
| <i>Pedinus</i> sp.  | Blaptinae: Pedinini          | na          | SRS15779402  | Ragionieri et al. 2023   | 98.4                         |
| <i>Stenolamus reichenspergeri</i> Koch, 1955              | Blaptinae: Opatrini          | TB26395     | PRJNA1016168 | Ragionieri et al. 2023   | 69.7                         |
| <i>Zophosis giessi</i> (Koch, 1962)                       | Pimeliinae: Zophosini        | TB19048     | –            | Kamiński et al. 2023     | 66.0                         |
| <i>Cis</i> sp.  | Ciidae (outgroup)            | na          | SRS15779349  | Swichtenberg et al. 2023 | 90.5                         |

\* Percentage of total targeted loci (n = 618) for which >50% of sequence was recovered. Tenebrionidae bait probe markers (Tps) were used.

used in the mapping process are available as supplementary material (see Kamiński *et al.* 2024). The resulting amino acid sequences were then aligned using MAFFT with the L-INS-I algorithm (Katoh *et al.* 2005). Low-quality amino acid sequence sites were masked, and sequences with over 50% gaps per locus were trimmed using trimAl (Capella-Gutiérrez *et al.* 2009). SendSketch script, as implemented in BMap/36.92, was used to characterize the metagenomic profile of assembled contigs. In the case of *Dissonomus tibialis*, data concerning two loci (OrthoMCL8004, OrthoMCL7212) were excluded from further analysis due to contamination detection. Surviving sequences were concatenated with FASConCAT (Kück and Meusemann 2010) into a single partitioned dataset including a total of 548 loci spanning 178,309 amino acids. All sequence assembly analyses were performed on Purdue University's Bell community cluster, within Rosen Center for Advanced Computing (McCartney *et al.* 2014).

### Phylogenetic analysis

IQ-TREE 2 (Minh *et al.* 2020) was used to run maximum likelihood (ML) analyses using an edge-unlinked partition model (-Q), with the dataset partitioned by loci and the models for each locus applied from ModelFinder (Kalyaanamoorthy *et al.* 2017). Support for the resulting topology was assessed using 10,000 Ultra-Fast Bootstrap (Hoang *et al.* 2018) iterations. The dataset, with the same partitions, was also analyzed using ExaBayes 1.5.1 (BI) (Aberer *et al.* 2014) run through the CIPRES portal (Miller *et al.* 2010). Two independent runs of 20 million generations, each with 1 cold chain and 2 heated chains, were performed with a burn-in fraction of 0.25.

### Morphological data

Additional pinned specimens loaned from the Národní Muzeum of Prague, Czech Republic (NMPC) representing *Dissonomus* Jacquelin du Val, 1861, and *Bradyus* Dejean, 1834, were included for morphological examination.

*Dissonomus* label data: "Turkmen.23.IV.81 BAL-RAM ALI Jelínek lgt.". "USSR Tadjikistan Aruk-Tau 20.4.(Garavuti) 1978 Mir. Dvořák lgt." / "ex coll. M. Dvořák National Museum Prague, Czech Republic". "USSR, Tadžikistan Aruk-Tau, 29.4. (Garavuti) 1978 Mir. Dvořák lgt." / "ex coll. M. Dvořák National Museum Prague, Czech Republic" (two specimens). "Kasakh SSR-8.V. UYUK NW Jambul Jelínek lgt, 1981". "USSR ARMENIA c. Garni-Gecharđ 24.-26.5.1982 Zd. Černý lgt."

*Bradyus* label data: "Uzbekistan Buchara, Kyzyl-Kyr 4-5.5.1977 J.Pradač leg." / "ex. coll. Pradač Nat. Mus. Prague" (9 specimens).

Additionally, specimens of *Blaps putrida* Motschulsky, 1845, *Oodoscelis tibialis* Ballion, 1878, and *Platyscelis striatia* Motschulsky, 1859 from MIZ PAN were included for morphological comparison. *Blaps putrida* label data: "Ciscaucasia Athsi Kulak" / QR label "MIZ PAN WARSZAWA 38/1947 99261". *Oodoscelis tibialis* label data: "Platyscelis tibialis Ball. H. Gebien det. 1939" / "Platyscelis tibialis Ball" / Mus. Zool. Polonicum Warszawa 12/45" / "MIZ PAN COL047871". *Platyscelis striatia* label data: "Turkistan" / "Platyscelis striata Mot. H.Gebien det.1939" / Mus. Zool. Polonicum Warszawa 12/45" / "Platyscelis striata Mot." / "striatus Motsch Turkest Faust" / QR label "MIZ PAN COL047854".

## RESULTS

Bioinformatic analysis did not reveal any obvious taxonomic sensitivity for the used probeset (Table 1). In particular, the genotyping success rates were relatively consistent between treated subfamilies, and seemed to be dependent on sample quality. This also included the outgroup (*Cis* sp.) for which more than 90% of targeted loci were at least partly (>50%) recovered (Fig. S1 in Kamiński *et al.* 2024). Furthermore, this study revealed a great degree of convergence between the molecular methodologies of Ragionieri *et al.* (2023) and Swichtenberg *et al.* (2023).

After sequence trimming and quality assessment, the final matrix contained a total of 548 loci (17,309 amino acids). Only a small portion of the total recovered loci for the matrix was recovered for *Dissonomus tibialis* (15 loci, 2047 amino acids) (Table S1 in Kamiński *et al.* 2024). The number of mapped reads for *Dissonomus tibialis* was similar regardless of the used bait probe markers in the bioinformatic analysis (Tps/Pps). In the case of the Tenebrionidae probes (Tps), 103,826 reads (12.0% of total recovered reads) were mapped, while 102,082 reads (11.8%) were mapped using Pimeliinae probes (Pps). Overlapping sequences obtained in both mapping approaches were identical, indicating that they were not subject to the mapping bias (Fig. 1).

Regardless of the used bait probe markers and phylogenetic inference method (ML/BI), *Dissonomus tibialis* was recovered sister to both analyzed *Blaps* species, and clustered with *Eleodes nigrina* (Fig. 1). The *Dissonomus*+*Blaps*+*Eleodes* clade (*i.e.* 'blaptinoid clade') constitutes a sister grouping to the opatrinoid clade composed of members of Dendarini (*Neoisocerus ferrugineus*), Opatrini (*Opatrum sabulosum*, *Stenolamus reichenspergeri*), Pedinini (*Pedinus* sp.), and Platynotini (*Asiopus aciculatus*, *Eurynotus capensis*). All taxa above represent the subfamily Blaptinae, and statistical support for the majority of recovered clades was absolute (Fig. 1).

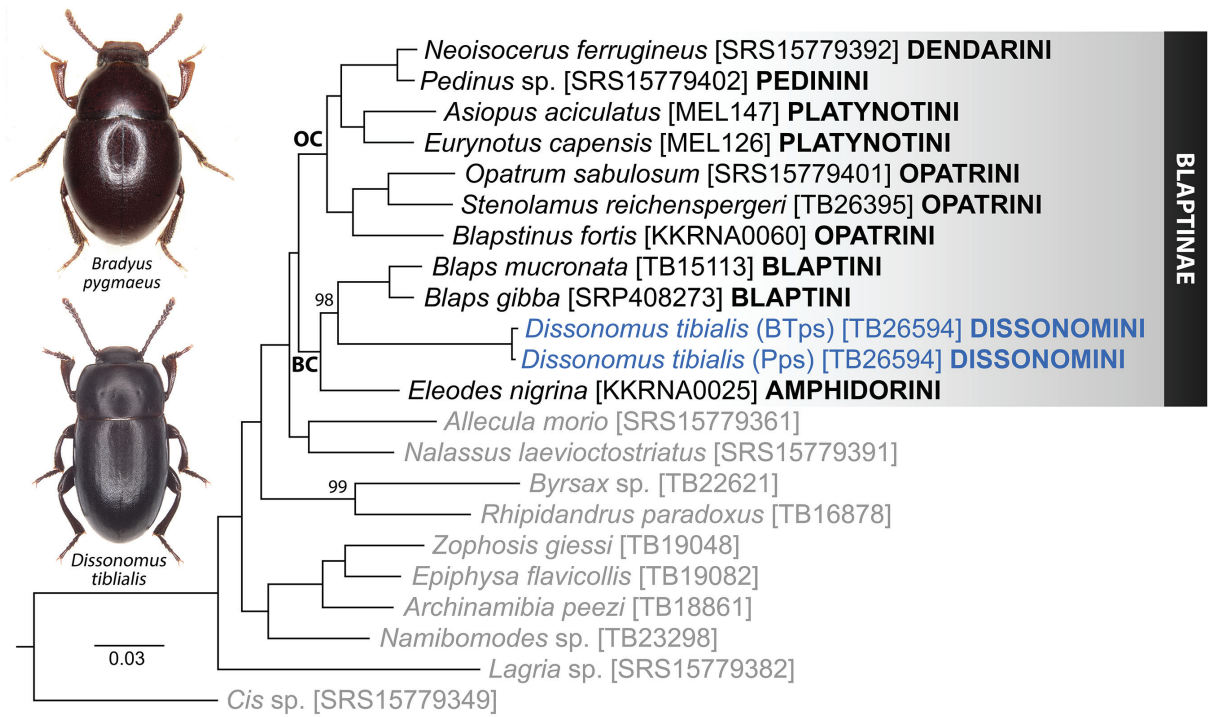


Figure 1. Phylogenetic placement of Dissonomini within the subfamily Blaptinae. Strict consensus tree derived from the maximum likelihood analysis of the concatenated matrix. Gray taxon names represent subfamilies outside Blaptinae, and Dissonomini representatives are blue. Branch support is displayed as an ultrafast bootstrap (above). Missing values indicate full branch support. All displayed nodes were fully supported in the Bayesian analysis (Posterior probability = 1.0). *Dissonomus tibialis* samples: Tps – sample mapped to Tenebrionidae probeset; Pps – sample mapped to Pimeliinae probeset. Abbreviations: BC – ‘blaptinoid clade’, OC – ‘opatrinoide clade’.

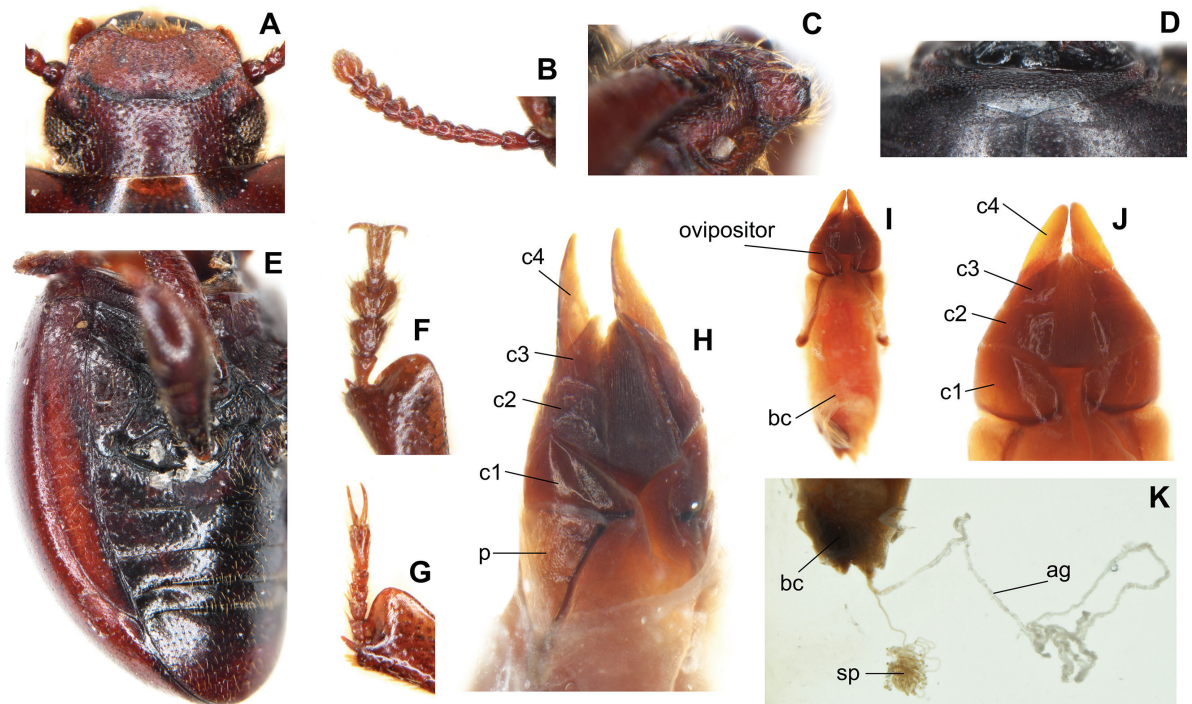


Figure 2. Morphology of species representing Dissonomini. (A–H) *Bradyus pygmaeus*, (I–K) *Dissonomus tibialis*. (A) dorsum of head, (B) antenna, (C) prosternal process in lateral view, (D) scutellum, (E) epipleuron, (F) male protarsus, (G) female protarsus, (H–J) ovipositor, (K) genital tubes. Abbreviations: bc – bursa copulatrix, c1–4 – coxites, p – paraproct, sp – spermatheca, ag – accessory gland.

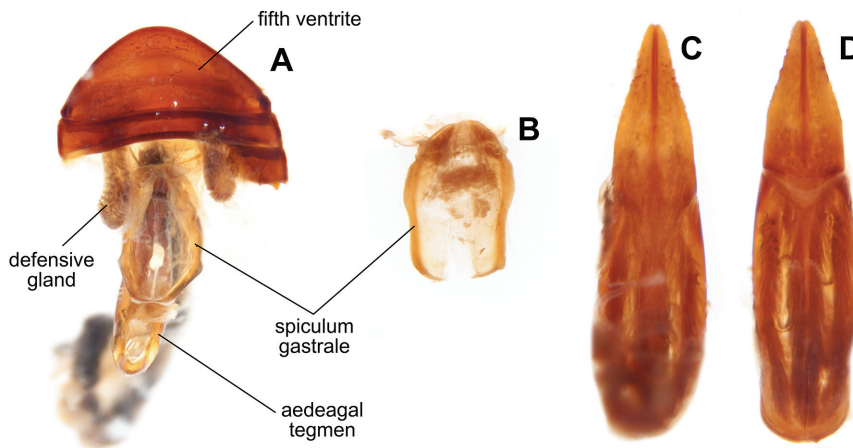


Figure 3. Male terminalia of (A) *Dissonomus tibialis* and (B, C, D) *Bradyus pygmaeus*. (B) Spiculum gastrale, (C) ventral and (D) dorsal views of tegmen.

## DISCUSSION

The analyses here provide novel data necessary to address the neglected phylogenetic position of Dissonomini, which were recovered deeply embedded within Blaptinae (Fig. 1). Their position close to Blaptini within the ‘blaptinoid clade’ appears to be morphologically justified, as representatives of Dissonomini lack

ancorae (Lumen & Kamiński 2023a) and opatrinoid trochanters (Iwan & Kamiński 2016) – precluding a closer relationship with Dendarini, Pedinini, Platynotini, and Opatrini (Iwan & Kamiński 2016, Kamiński & Iwan 2017, Kamiński *et al.* 2021, Lumen & Kamiński 2023b). The lack of ancorae also distinguishes Dissonomini from the Nearctic tribe Amphidorini (Johnston *et al.* 2022), which also clustered within the ‘blaptinoid clade’

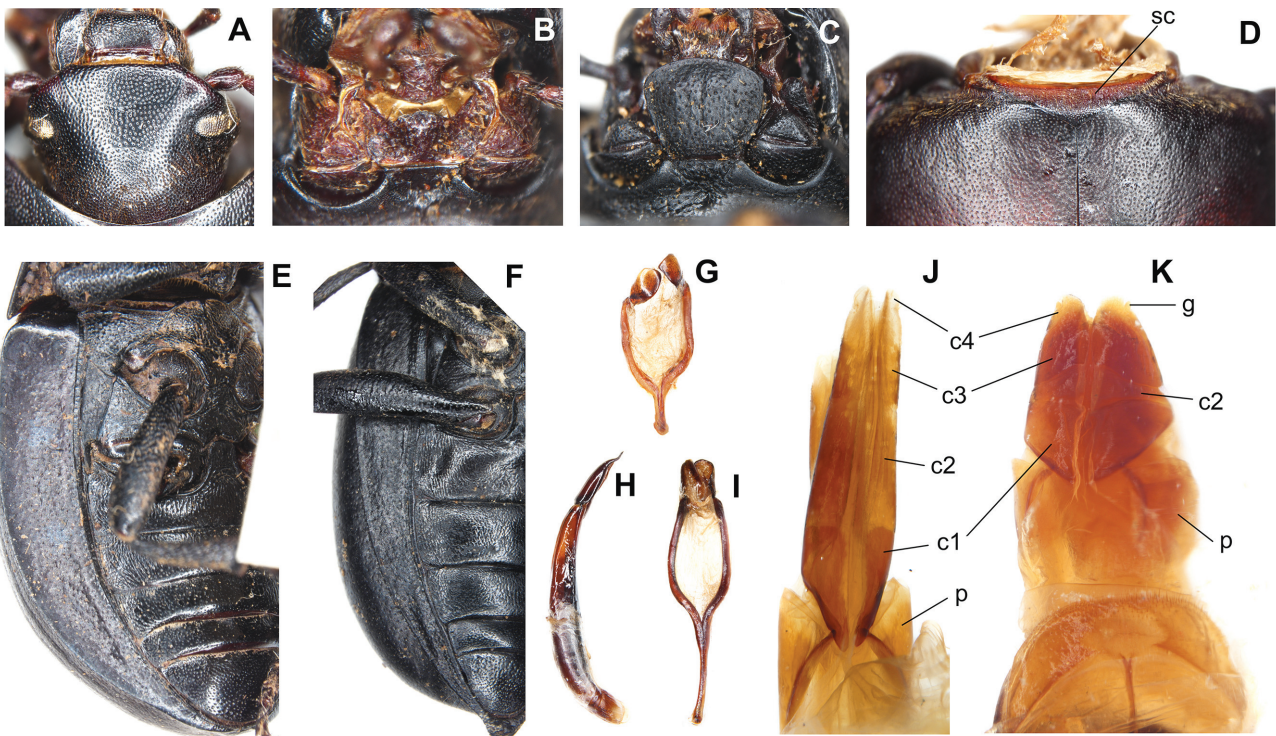


Figure 4. Morphology of selected representatives of Blaptini and Platyscelidini. (C, F) *Blaps putrida*, (A, B, D, I, J) *Oodoscelis tibialis*, and (E, G, H, K) *Platyscelis striata*. (A) Head in dorsal view, (B, C) mentum, (D) scutellum, (E, F) epipleura, (G, I) spiculum gastrale, (H) aedeagal tegmen, (J, K) ovipositor. Abbreviations: c1–4 – coxites, g – gonostylus, p – paraproct, sc – scutellum.

in these (Fig. 1), and previous analyses (Kamiński *et al.* 2021). Both tribes can be further separated by the ovipositor structure, which in Amphidorini is composed of fused apical coxites (4-lobed in Dissonomini, Fig. 2H–J).

Dissonomini is easily distinguished from Blaptini by the widened protarsi in males (Medvedev 1968, Chigray *et al.* 2020) (Fig. 2F). While this study lacked sequences of Platyscelidini, Dissonomini is morphologically separable *inter alia* by the notched epistoma (Fig. 2A). Dissonomini is also distinct from both Blaptini and Platyscelidini by their sharply keeled menta (flat in Blaptini or broadly keeled at most in Platyscelidini, Fig. 4B and C) and epipleura terminating at abdominal ventrite V (epipleura ending later in Platyscelidini and continuing to apex in Blaptini) (Figs 2E and 4E and F) (see also Egorov 2004).

Although the monophyly of Dissonomini was not tested here by molecular data, several unique morphological features strongly suggest that *Bradysus* and *Dissonomus* are linked (Figs 2, 3, Medvedev 1968): concealed scutellum (Figs. 1 and 2D), antennal shape (short, robust, with apical antennomeres forming a loose club (Fig. 2B); longer in Blaptini and Platyscelidini where the third antennomere is often also elongated,) termination of the epipleura (reaching the level of the base of fifth ventrite) (Fig. 2E), notched epistoma (Fig. 2A), configuration of the aedeagi (ventrally without clear opening for the penis) (Fig. 3C), formation of the spiculum gastrale (weakly sclerotized, U-shaped with reduced ‘stem’ (Fig. 3A and B); Platyscelidini and Blaptini both have strongly sclerotized spiculae with or without a long stem and large, paddle-shaped terminations of the ‘arms’) (Fig. 4G and I) (see also Chigray *et al.* 2020), and the structure of the ovipositor (4-lobed coxities, lack of gonostyli, and overlapping coxites 3 and 4) (Fig. 2I and J).

In conclusion, the molecular data recovered here are consistent with morphological data revealed for adult forms (Figs 1–4). The taxonomic distinctiveness of Dissonomini appears well-grounded, and its phylogenetic position regarding Platyscelidini should be investigated further (for recent treatments within Platyscelidini see Bai *et al.* 2019a, b, Bai & Ren 2019). Based on the results presented here, Dissonomini is incorporated within the borders of Blaptinae where it becomes the eighth tribe of the subfamily. The definition of Blaptinae remains unmodified (Kamiński *et al.* 2021): Adults: antennae lacking compound/stellate sensoria (except *Stenolamus* Gebien, 1920 – Kamiński *et al.* 2023); procoxal cavities externally and internally closed, intersternal membrane of abdominal ventrites 3–5 visible; paired abdominal defensive glands present, elongate, not annulated. Larvae: prolegs enlarged (adapted for digging); ninth tergite lacking urogomphi.

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## REFERENCES

- Aberer, AJ, Kobert, K, A. Stamatakis. 2014. ExaBayes: massively parallel Bayesian tree inference for the whole-genome era. *Molecular Biology and Evolution*, 31: 2553–2556.
- Andrews, S. 2010. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>.
- Bai, XL, GD Ren. 2019. Revision of the genus *Platyscelis* Latreille, 1818 from China (Coleoptera: Tenebrionidae: Platyscelidini). *Zootaxa*, 4609: 101–126.
- Bai, XL, Li, XM, GD Ren. 2019a. A review of the genus *Oodescelis* Motschulsky, 1845 (Coleoptera: Tenebrionidae: Platyscelidini) from China. *Zootaxa*, 4656(3): 401–430.
- Bai, XL, Merkl, O, GD Ren. 2019b. Revision of the genus *Bioramix* Bates, 1879 from Nepal (Coleoptera, Tenebrionidae: Platyscelidini). *Entomological Review*, 99: 898–905. <https://doi.org/10.1134/S0013873819070030>.
- Bolger, AM, Lohse, M, B Usadel. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*, 30: 2114–2120.
- Buchfink, B, Xie, C, D Huson. 2015. Fast and sensitive protein alignment using DIAMOND. *Nature Methods*, 12: 59–60. <https://doi.org/10.1038/nmeth.3176>.
- Capella-Gutiérrez, S, Silla-Martínez, JM, T Gabaldón. 2009. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics*, 25: 1972–1973.
- Chigray, I, Nabozhenko, M, Abdurakhmanov, G, B Keskin. 2020. A systematic review of the genus *Dila* Fischer von Waldheim 1844 (= *Caenoblaps* König, 1906, syn.n.) (Coleoptera: Tenebrionidae) from the Caucasus, Turkey and boundary territories of Iran. *Insect Systematics & Evolution*, 51: 753–783.
- Egorov, LV. 2004. The classification of the tenebrionid beetles of the tribe Platyscelidini (Coleoptera, Tenebrionidae) of the world fauna. *Entomological Review*, 84(6): 641–666.
- Hoang, DT, Chernomor, O, Von Haeseler, A, Minh, BQ, LS Vinh. 2018. UFBoot2: improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution*, 35: 518–522. <https://doi.org/10.1093/molbev/msx281>.
- Iwan, D, MJ Kamiński. 2016. Toward a natural classification



- of opatrine darkling beetles: comparative study of female terminalia. *Zoomorphology*, 135: 453–485. <https://doi.org/10.1007/s00435-016-0328-5>.
- Iwan, D, Löbl, I, Bouchard, P, Bousquet, Y, Kamiński, M, Merkl O, Ando, K, W Schawaller. 2020. Family TENEBRIONIDAE Latreille, 1802 in Catalogue of Palaearctic Coleoptera Volume 5, Tenebrionoidea Revised and Updated Second Edition by Iwan, D., Löbl, I. Brill NV, Leiden, The Netherlands, 969pp [ISBN: 978-90-04-43498-1] <https://brill.com/view/title/59110>.
- Johnson, MG, Gardner, EM, Liu, Y, Medina, R, Goffinet, B, Shaw, AJ, Zerega, NJC, NJ Wickett. 2016. HybPiper: extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. *Applications in Plant Sciences*, 4(7): 1600016. <https://doi.org/10.3732/apps.1600016>.
- Johnston, MA, Smith, AD, Kanda, K, Kamiński, MJ, Naverette, P, Sanchez, LA, Aalbu, RL, Miller, KB, Wheeler, QD, NM Franz. 2022. Testing the taxonomy of Amphidorini LeConte (Coleoptera: Tenebrionidae): a molecular phylogeny leveraging museum sequencing. *Annales Zoologici*, 72: 49–68.
- Kalyanamoorthy, S, Minh, BQ, Wong, TKF, Von Haeseler, A, LS Jermini. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14(6): 587–589. <https://doi.org/10.1038/nmeth.4285>.
- Kamiński, MJ, D Iwan. 2017. Revision of the subtribe Pedinina (Tenebrionidae: Pedinini). *Annales Zoologici*, 67: 585–607.
- Kamiński, MJ, Lumen, R, Kubicz, M, Steiner, W, Kanda, K, D Iwan. 2019. Immature stages of beetles representing the 'Opatrinoid' clade (Coleoptera: Tenebrionidae): an overview of current knowledge of the larval morphology and some resulting taxonomic notes on Blapstinina. *Zoomorphology*, 138: 349–370. <https://doi.org/10.1007/s00435-019-00443-7>.
- Kamiński, MJ, Lumen, R, Kanda, K, Iwan, D, Johnston, MA, Kergoat, G, Bouchard, P, Bai X-L, Li, X-M, Ren G-D, AD Smith. 2021. Reevaluation of Blapimorpha and Opatrinae: addressing a major phylogeny-classification gap in darkling beetles (Coleoptera: Tenebrionidae: Blaptinae). *Systematic Entomology*, 46(1): 140–156. <https://doi.org/10.1111/syen.12453>.
- Kamiński, MJ, Lumen, R, Smith, AD, D Iwan. 2023. Welcome home: phylogenetic placement and taxonomy of an enigmatic subtribe Stenolamina Koch, 1956 (Tenebrionidae: Blaptinae: Opatrini). *Annales Zoologici*, 73: 513–523. <https://doi.org/10.3161/00034541ANZ2023.73.3.013>.
- Kamiński, MJ, Rork, AM, Drake, ME, Replogle, CR, Lumen, R, Wirth, CC, Kanda, K, AD Smith. 2024. Supplementary data for the paper entitled: Dissonomini Medvedev, 1968: the eighth tribe of the subfamily Blaptinae (Coleoptera: Tenebrionidae). *Harvard Dataverse*, online. <https://doi.org/10.7910/DVN/UVJ6VP>.
- Kanda, K. 2017. Phylogenetic Studies in Tenebrionidae (Coleoptera) and Related Families. Unpublished Ph.D. Dissertation Thesis, Oregon State University.
- Kanda, K, Pflug, JM, Sproul, JS, Dasenko, MA, DR Maddison. 2015. Successful recovery of nuclear protein-coding genes from small insects in museums using illumina sequencing. *PLoS ONE*, 10: e0143929. <https://doi.org/10.1371/journal.pone.0143929>.
- Katoh, K, Kuma, KI, Toh, H, T Miyata. 2005. MAFFT version 5: Improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research*, 33: 511–518.
- Kück, P, K Meusemann. 2010. FASconCAT: Convenient handling of data matrices. *Molecular Phylogenetics and Evolution*, 56(3): 1115–1118.
- Lumen, R, MJ Kamiński. 2023a. Taxonomic revision of the genus *Phylacastus* Fairmaire (Tenebrionidae, Eurynotina): shortfalls of anatomical nomenclature with notes on aedeagal homology. *Zookeys*, 1138: 1–27. <https://doi.org/10.3897/zookeys.1138.95968>.
- Lumen, R, MJ Kamiński. 2023b. Revision of the darkling beetle genus *Eurynotus* (Blaptinae: Platynotini) and new records of ovovivipary in Tenebrionidae. *Zoological Journal of the Linnean Society*, zlad146, <https://doi.org/10.1093/zoolinnean/zlad146>.
- Makhan, D. 2018. *Dissonomus aschmae* sp. nov. (Tenebrionidae: Dissonomini) from Kandovan, the Central District of Osku County, East Azerbaijan Province, Iran. *Calodema*, 638: 1–3.
- McCartney, G, Hacker, T, B Yang. 2014. Empowering faculty: a campus cyberinfrastructure strategy for research communities. USA: Educational Review.
- Medvedev, GS. 1968. Coleoptera. Darkling-beetles (Tenebrionidae), subfamily Opatrinae, tribes Platynotini, Dendarini, Pedinini, Dissonomini, Pachypterini, Opatrini (part) and Heterotarsini. Leningrad: Fauna of USSR, Zhestkokrylye, 19.
- Miller, MA, Pfeiffer, W, T Schwartz. 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. In: Gateway Computing Environments Workshop (GCE), USA, p. 1–8.
- Minh, BQ, Schmidt, HA, Chernomor, O, Schrempf, D, Woodhams, MD, von Haeseler, A, R Lanfear. 2020. IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, 37: 1530–1534. <https://doi.org/10.1093/molbev/msaa015>.
- Ragionieri, L, Zúñiga-Reinoso, A, Bläser, M, R Predel. 2023. Phylogenomics of darkling beetles (Coleoptera: Tenebrionidae) from the Atacama Desert. *PeerJ*, 11: e14848. <https://doi.org/10.7717/peerj.14848>.
- Smith, AD, Kamiński, MJ, Kanda, K, Sweet, AD, Betancourt, JL, Holmgren, CA, Hempel, E, Alberti, F, M Hofreiter. YEAR? Recovery and analysis of ancient beetle DNA from subfossil packrat middens using high-throughput sequencing. *Scientific Reports*, 11: 12635. <https://doi.org/10.1038/s41598-021-91896-8>.
- Swichtenberg, KL, Kamiński, MJ, Gearner, OM, Lumen, R, Kanda, K, AD Smith. 2023. Preliminary phylogenomic analyses reveal multiple reversions to nocturnal behavior and morphology within the primarily diurnal tribe Adesmiini (Coleoptera: Tenebrionidae). *Insect Systematics and Diversity*, 7: 1–9. <https://doi.org/10.1093/isd/ixad013>.