

Description of a new species of *Lathrobium* Gravenhorst, 1802 (Staphylinidae: Paederinae) from Vietnam based on integrative taxonomy

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Abstract

The second species of the genus *Lathrobium* Gravenhorst, 1802 (Staphylinidae: Paederinae) from Vietnam, *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.**, is described. The COI fragments for five *Lathrobium* species from China and Vietnam are published for the first time. The distances between COI sequences of the new species, seven known *Lathrobium* species, and one species from a close genus are estimated. The new species is clearly distinct from all congeners examined, both morphologically and genetically. The COI sequence of *L. sapaensis* Tokareva & Bekchiev **sp. nov.** differs by 16–22% from those of related species, indicating a high level of genetic divergence. This finding extends the known distribution of *Lathrobium* in Southeast Asia and provides a valuable molecular reference for future studies of the genus.

Key words: barcoding, combined data, new species

Introduction

Only one species of *Lathrobium*, *L. austere* Assing, 2019, has so far been reported from Vietnam, where it occurs in the north and represents the southernmost record of the genus (Assing, 2019). In this study, we describe a new species of *Lathrobium* from northern Vietnam, providing further evidence that the region may host a higher diversity of the genus and that additional species may potentially be found farther south. Previous studies have shown that *Lathrobium* tends to undergo wide diversification in montane habitats compared to lowland areas (Haberski & Caterino, 2025; Assing, 2013; 2015; 2019). The mountainous habitats of northern Vietnam are partly ecologically similar to those of adjacent southern Yunnan, China, making comparisons with the Chinese montane endemic fauna particularly relevant. Interestingly, this type of habitat is also widespread across Myanmar, Laos, and Northern Thailand, but no *Lathrobium* species were reported from there yet. Therefore, we examined both morphology and COI sequence data of the new species in comparison with the most relevant neighbouring species, including *L. austere* (Vietnam), as well as *L. bifasciatum* Assing, 2013, *L. coadulum* Assing, 2015, and *L. daweanum* Assing, 2015 (southern Yunnan, China), as they were highlighted in the description of *L. austere* within the comparative notes section (Assing, 2019).

Materials and Methods

Specimen depositories

The holotype of the new species was discovered among unsorted ethanol-preserved material in the entomological collection of the National Museum of Natural History, Bulgarian Academy of Sciences, Sofia, Bulgaria (NMNHS).

It is now deposited in the main dry-pinned collection of the NMNHS and is available for further research under the specimen's unique number NMNHS-ST00001.

Additional material used for morphological comparison and DNA data acquisition was loaned from the Natural History Museum of Vienna (NHMW), Austria (curator: Dr. Harald Schillhammer) with permission for non-destructive DNA extraction from the loaned specimens. Four more COI barcodes for four widespread *Lathrobium* species and one species of *Tetartopeus* were downloaded from GenBank (NCBI) for COI distances comparison. Exact details for each specimen and data used are provided in the Table 1.

TABLE 1. Detailed information on the specimens examined for this study and NCBI-retrieved barcodes for reference species.

Species names	DNA voucher specimen	Full label data	Collection acronym
<i>Lathrobium sapaensis</i> sp. nov.	HT, ♀ NMNHS-LAT-001	Vietnam (North): Fansipan Mts; Hoang Lien National Park, near Sa Pa waterfall; Lao Cai Province; 1815 m, 22°21'43.1"N 103°46'40.6"E, 24.X.2023, leg. Bekchiev R., Simov N., Langourov M.	NMNHS
<i>Lathrobium austere</i> Assing, 2019	PT, ♂ NWM-LAT-001	Vietnam (North): Cao Bang Prov., Phia Oac-Phia Den Nat. Park, summit road, ca. 1800 m, 22°36'52.7"N 105°52'06.7"E, 17./18.V.2019, sifted, leg. Brunke A. & Schillhammer H.	NHMW
<i>Lathrobium bifasciatum</i> Assing, 2013	PT, ♀ NWM-LAT-002	China (N-Yunnan): Zhongdian Co., 51 km SSE Zhongdian, 2970 m, 27°25.3'N 99°56.5'E (creek valley, mixed conif. forest with shrubby veget., bamboo) 16.VIII.2003, leg. Wrase	NHMW
<i>Lathrobium coadulum</i> Assing, 2015	PT, ♀ NWM-LAT-003	China (Yunnan): SE Pingbian, primary forest, 22°54'31"N, 103°41'44"E, 2100 m, 27.VIII.2014, leg. Schülke M.	NHMW
<i>Lathrobium daweanum</i> Assing, 2015	PT, ♂ NWM-LAT-004	China (Yunnan): SE Pingbian, primary forest, 22°54'31"N, 103°41'44"E, 2100 m, 27.VIII.2014, leg. Assing V., Schülke M.	NHMW
<i>Lathrobium geminum</i> Kraatz, 1857	BC ZSM COLA 00055	See in GenBank at HQ948256.1	BC ZSM COLA
<i>Lathrobium brunnipes</i> (Fabricius, 1792)	ZFMK-TIS-2568232	See in GenBank at MW259940.1	ZFMK
<i>Lathrobium fovulum</i> Stephens, 1833	BC ZSM COLA 00110	See in GenBank at HQ953722.1	BC ZSM COLA
<i>Tetartopeus tetricus</i> Casey, 1905	CUAC000169031	See in GenBank at PQ046508.1	CUAC

Morphological examination and imaging

Habitus photographs of the dry specimen were taken with a Canon EOS 2000D attached to Zeiss Stemi 508 stereomicroscope. Close-up images of the specimen and its terminalia were taken with a Canon EOS 700D attached to Zeiss AxioScope 5 light microscope, under magnification up to x200, with the specimen placed onto a glass slide in a thick layer of alcohol-based disinfectant gel (C10-30 Alkyl Acrylate Crosspolymer, Triethanolamine, 65% EtOH, glycerin, water), and covered with a cover glass to avoid aberrations. Images were stacked using the Helicon Focus 5.3.14 software. Further processing and plates assembly was made with Adobe Photoshop CS5.1.

DNA data acquisition

DNA extraction was performed in the molecular laboratory of the Museum and Institute of Zoology, Polish Academy of Sciences, using a non-destructive protocol involving either a single detachment of the specimen's

abdomen from the thorax along the membrane, or in some cases no alteration at all. The exact details of the DNA extraction protocol, molecular libraries preparation and sequencing are described in a much larger study (Tokareva *et al.*, in prep), for which the genomic target capture data were obtained. In brief, the non-destructive DNA extraction was done using the QIAamp® DNA Micro kit on columns, with two series of 15 µL elution by EB-buffer warmed to 30–35°C. After obtaining the lysate of internal soft tissues, each specimen was carefully cleaned in distilled water, soaked in 70% EtOH, and then dried and re-mounted on cardboards. DNA libraries were prepared using an NEBNext DNA Ultra II FS Kit for Illumina (New England BioLabs) and dual-indexed with the NEBNext Multiplex Oligos for Illumina (Dual Index Primers Set 5) (New England BioLabs). Indexed libraries were pooled in portions, and target capture and enrichment was performed using the myBaits® Custom 1–20K 48 Rxn Kit (Arbor Biosciences) following the v5 protocol, with ~24-hour incubation. The final pool was sequenced on an Illumina NovaSeq 6000 (PE 2×150) by Genomed® (Poland) in pair-end mode, with 100 million reads per run. COI fragment sequences for *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.**, *L. austere*, *L. bifasciatum*, *L. coadulum*, and *L. daweanum* were mined from Illumina-sequenced genomic target capture data, using the PHYLUCE pipeline (Faircloth, 2016). Specifically, the script “*phyluce_assembly_match_contigs_to_barcode*” was used, with an alignment of four 658 bp COI barcodes for *Lathrobium* representatives downloaded from GenBank as the reference input barcode FASTA file for the PHYLUCE script. Due to poor DNA preservation in *L. coadulum* and *L. bifasciatum*, it was not possible to retrieve full-length barcode fragments for these species, and the matrix was cut down to 449 bp COI fragments to ensure equal sequence length.

Calculation of the COI barcodes distance matrix

To compare COI fragments of the new species with the representatives of the adjacent fauna, we calculated a matrix of genetic distances using the Kimura 2-parameter model of base substitution with MEGA12 (Kumar *et al.*, 2024). Additionally, COI barcodes from GenBank for four representatives of widespread lowland transpalearctic species and one species of a closely related genus *Tetartopeus* Czwalina, 1888 were included as references. The total alignment that includes both newly sequenced COI barcodes and the reference barcodes retrieved from the GenBank is provided in the Supplement File 1.

Results

Taxonomy

Lathrobium sapaensis Tokareva & Bekchiev **sp. nov.**

urn:lsid:zoobank.org:act:97EA96A2-9A5C-4C56-B68C-FBAC179A0C1A

(Figs 1–2)

Type material. Holotype ♀: “VIETNAM: Fansipan Mts; Hoang Lien National Park, near Sa Pa waterfall; Lao Cai Province; h = 1815 m, 22.36198N, 103.77795E, 24.X.2023, leg. Bekchiev R., Simov N., Langourov M./ DNA voucher 2024 NMNHS-LAT-001/ Holotypus ♀ *Lathrobium sapaensis* sp. nov., det. A. Tokareva 2025” (NMNHS).

Etymology. The specific epithet is an adjectival form derived from Sa Pa, the forest waterfall in mountainous Lao Cai Province, Vietnam, where nearby the species was discovered.

Diagnosis. Head round-triangular; epicranium with punctures slightly less dense in median dorsal portion; eyes small; antennae shorter than head and pronotum combined. Pronotum very elongate, nearly parallel-sided, slightly narrowed behind posterior angles. Elytra short, widening posteriorly; hind wings vestigial. Tergite VIII posteriorly produced at nearly right angle; sternite VIII conical, sides slightly concave, apex blunt. Paraprocts (tergite IX) anteriorly separated by membrane; proctiger (tergite X) elongate, conical. Coxites and valvifers of sternite IX separate.

Description. Body length 7.2 mm; length of forebody 3.4 mm. Habitus as in Fig. 1. Coloration: head, antennal bases, and tibial bases dark brown, rest of body brown to light brown.

Head (Fig. 1A) as long as wide, round-triangular, widest at posterior. Epicranium with moderately coarse and sparse punctation with punctures slightly less dense in median dorsal portion (Fig. 1A, B); punctures more than one diameter apart; dorsal integument with clear microreticulation (Fig. 1E); surface of head shiny; neck ½ as wide as

head. Eyes small, composed of 40 ommatidia (Fig. 1C), approximately one-sixth as long as postocular side of head in dorsal view. Ventral side of head with integument with clear microreticulation (Fig. 1F); gular sutures slightly concaved towards each other but completely separate, converging towards neck (Fig. 1D). Head setation prominent, setae distribution as in Fig. 1A–D. Antennae 2.6 mm long, moniliform, shorter than head combined with pronotum, scapus slightly longer than antennomeres II and III combined, antennomeres II and III elongate, antennomeres IV–X obconic, longer than wide but become progressively wider; antennomere XI elongate, subacute.

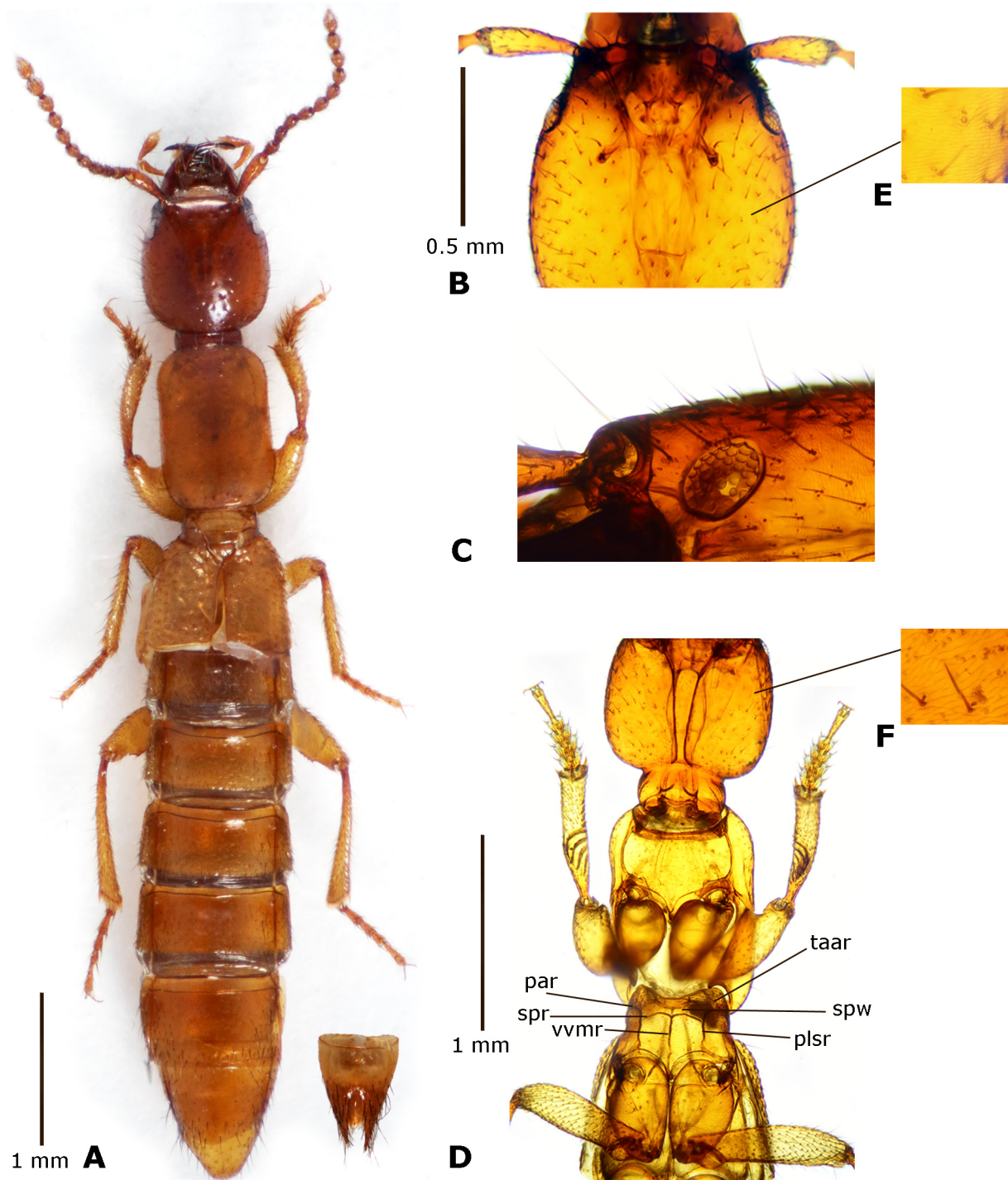


FIGURE 1. *Lathrobium sapaensis* sp. nov., holotype specimen. A—habitus of the dry-pinned holotype specimen; B—close-up photo of head, dorsal view; C—close-up photo of eye, lateral view; D—close-up photo of forebody, ventral view, par: posterior anepisternal ridge, plsr: paired longitudinal secondary ridges, spr: secondary prepectal ridge, spw: single prepectal window, taar: transversal anterior anepisternal ridge, vvmr: vertical ventral median ridge; E—head, microreticulation of integument on dorsal side; F—head, microreticulation of integument on ventral side.

Pronotum (Fig. 1A, D) significantly longer than wide, narrower than head and elytra, slightly narrowed after posterior angles, posterior edge as wide as anterior edge; punctation sparse, less coarse than that of epicranium; punctures more than one diameter apart; midline impunctate; integument with no to very shallow interrupted microsculpture; surface of pronotum shiny.

Mesoventral plate (Fig. 1D) typical for type 12 for Lathrobiina (see details in Tokareva & Żyła, 2025, figs. 4F, 10G), nearly as long as wide; anepisternal ridges (taar) reaching anterior margin of mesoventrite; posterior anepisternal ridge (par) has additional short acute angle on each lateral side curved posteriad on ventrite; prepectal window wide, rectangular, shield-shaped, shorter than posterior portion of ventrite; posterior median portion of ventrite nearly as long as wide, flat, with prominent secondary ridge (vvmr) protruding vertically from posterior acute process of ventrite reaching acute angle formed by prepectal window.

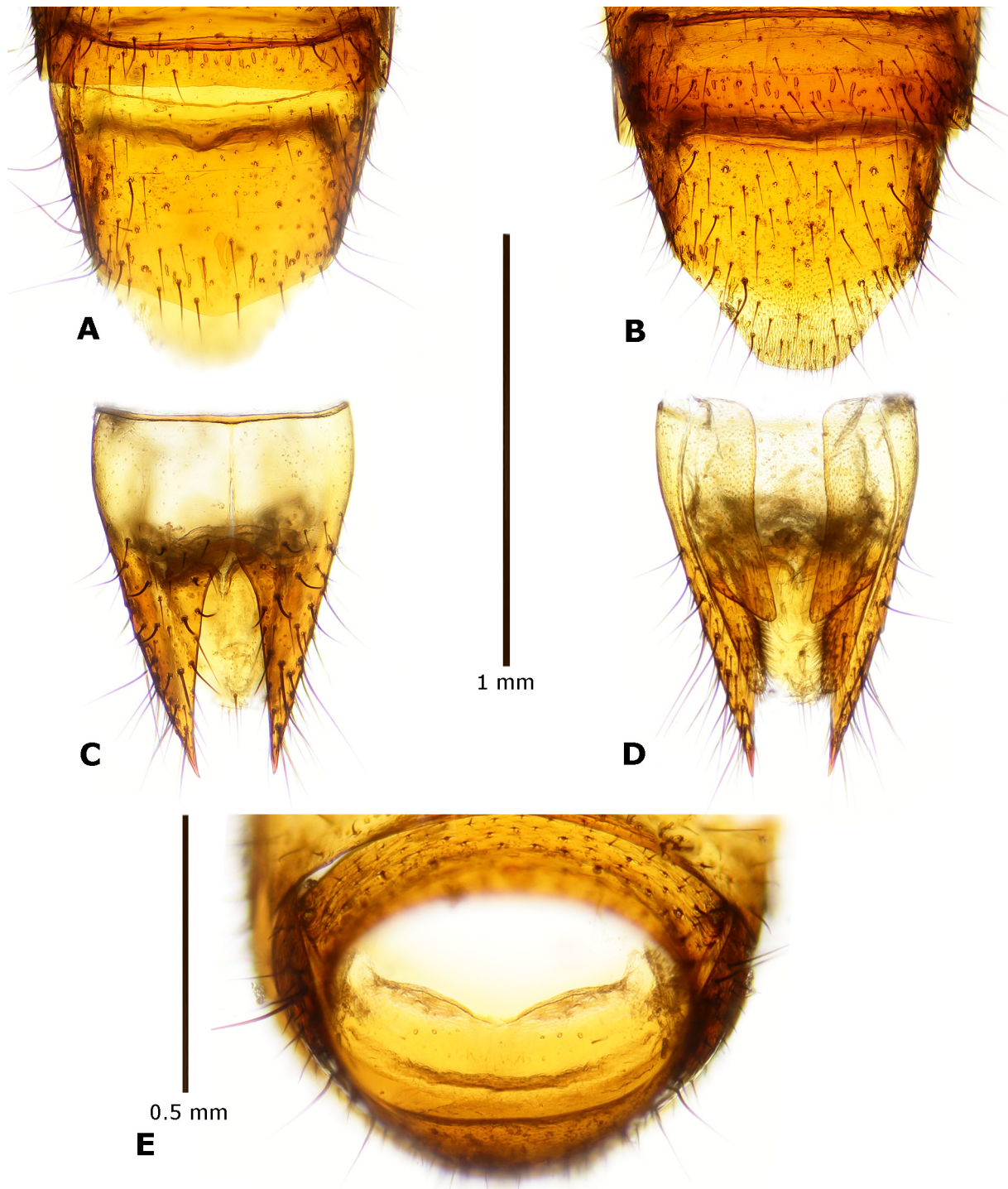


FIGURE 2. *Lathrobium sapaensis* sp. nov., terminal abdominal sclerites, holotype specimen. A—female tergite VIII; B—female sternite VIII; C—female tergites IX (paraprocts) and X (proctiger); D—female sternite IX; E—subgenital plate.

Elytra (Fig. 1A) approximately 1.6 of length of pronotum, widening posteriorly; punctation fine, sparse, shallow; setation sparse, with medium-length setae; integument without microsculpture, surface shiny; posterior edge without fringe of microsetae. Hind wings vestigial.

Abdomen (Fig. 1A) broader than elytra; punctation dense and fine; setation sparse, with short and medium-length setae on tergite and sternite plates and long macrosetae close to edges of each plate and on paratergites; integument with fine microsculpture.

♀: Tergite VII with posterior edge straight, sternite VII with posterior edge straight, without modifications or fringes of wide microsetae; tergite VIII with posterior edge produced in straight angle in middle (Fig. 2A), sternite VIII conical, with posterior edges slightly concaved towards each other and blunt apex with slightly ragged edge bearing light short micropubescence (Fig. 2B), but without any fringe of wide microsetae; paraprocts separated by membrane anteriorly, apices acute, slightly curved upwards (Fig. 2C), longer than basal portion; proctiger conical; sternite IX with coxites and valvifers separate and free (Fig. 2D); subgenital plate largely membranous, elongate, slightly rectangular (Fig. 2E).

♂: Unknown.

Comparative notes. *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.** is distinguished from the other species known from this area (Vietnam, Southern China (Yunnan)) by the following combination of characters: head round-triangular, epicranium with punctures slightly less dense in median dorsal portion; pronotum very elongate, slightly narrowed after posterior angles, of even width throughout; elytra short, widening posteriorly; shape and proportions of female terminalia.

Compared to the only other species known from Vietnam, *L. austere*, the new species is slightly larger, lighter in coloration, with narrowing area after posterior angles of pronotum, anteriorly separated paraprocts (tergite IX), and conical, longer proctiger (tergite X).

In comparison with *L. coadulum*, the new species has another shape of pronotum (more rectangular, of even width throughout), less tapering median process of tergite VIII, different shape of sternite VIII, nothing comparable to the segments IX and X modification as in *L. coadulum*.

Compared to *L. daweianum*, the new species is much larger, its head is wider than pronotum, it has different shape of tergite and sternite VIII and anteriorly separated paraprocts (tergite IX).

In comparison with *L. bifasciatum*, the new species is larger, has bigger eyes, different shape of pronotum and structure of female terminalia.

Along with that, *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.** COI barcode fragment sequence differs from that of *L. austere*, *L. coadulum*, and *L. bifasciatum* in numerous positions (see the sequences alignment as the Supplement 1).

Distribution and natural history. *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.** is the second species of the genus to be described from Vietnam. The type locality is situated near a forest waterfall, in the mountains of the Northern part of Vietnam, ~100 km from the border with Southern China (Yunnan). This locality is almost at the same latitude as the type locality of *L. austere*, but the latter formally remains the southernmost species of *Lathrobium* described.

Barcodes distance matrix

According to the distance matrix, presented in the Table 2, the compared COI fragment of the barcoding region for *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.** has unique sequence that drastically differs from all species brought to comparison. The estimated evolutionary divergence between *Lathrobium sapaensis* Tokareva & Bekchiev **sp. nov.** and the only other species known from Vietnam, *L. austere*, turned out to be slightly larger (0.17 base substitutions per site between sequences) than between the new species and *L. coadulum* from China (0.16 base substitutions per site between sequences).

At the same time, the estimated evolutionary divergence between the new species and *L. bifasciatum*, another similarly looking species from China, is nearly as large (0.20 base substitutions per site between sequences) as between the new species and the single representative of another genus, *Tetartopeus* (0.22 base substitutions per site between sequences).

TABLE 2. Pairwise nucleotide distance matrix of the barcoding COI region for nine *Lathrobium* species and a single *Tetartopeus* species. Genetic distances given in terms of the number of base substitutions per site between sequences.

Species	Voucher ID	GenBank accession number	1	2	3	4	5	6	7	8
<i>Lathrobium sapaensis</i> sp. n. (Vietnam)	NMNHS-LAT-001	PX279351	1							
<i>Lathrobium austere</i> (Vietnam)	NWM-LAT-001	PX279352	0.20	2						
<i>Lathrobium bifasciatum</i> (China)	NWM-LAT-002	PX279353	0.23	0.15	3					
<i>Lathrobium coadulum</i> (China)	NWM-LAT-003	PX279354	0.17	0.16	0.19	4				
<i>Lathrobium daweanum</i> (China)	NWM-LAT-004	PX279355	0.20	0.18	0.20	0.20	5			
<i>Lathrobium geminum</i> (Germany)	BC ZSM COLA 00055	HQ948256.1	0.21	0.17	0.20	0.16	0.16	6		
<i>Lathrobium brunnipes</i> (Germany)	ZFMK-TIS-2568232	MW259940.1	0.21	0.15	0.15	0.18	0.20	0.14	7	
<i>Lathrobium fovulum</i> (Germany)	BC ZSM COLA 00110	HQ953722.1	0.20	0.11	0.14	0.14	0.16	0.12	0.10	8
<i>Tetartopeus tetricus</i> (USA: NC)	CUAC000169031	PQ046508.1	0.25	0.28	0.30	0.29	0.29	0.28	0.26	0.27

Discussion

The genus *Lathrobium*, which currently comprises nearly 800 described species (Newton, 2025) and continues to grow with the description of several new taxa each year, is in clear need of a modern revision. Considering such an overwhelming genus diversity, molecular data would play an essential role in making such an ambitious task feasible. Our trials with COI sequences suggest, however, that this marker may be of limited utility for reconstructing species relationships within the genus. In deeply diversified endemic lineages, COI appeared to be too variable to yield robust phylogenetic signal. While this indicates that traditional single-locus approaches may be insufficient for *Lathrobium*, recent advances in sequencing technology now provide access to genome-wide markers suitable for phylogenomic analyses, and ongoing work is expected to address these questions more comprehensively (Tokareva *et al.*, in prep.). Nevertheless, COI barcodes remain useful for species-level identification and for certain intrageneric comparisons.

The discovery of an additional *Lathrobium* species in northern Vietnam highlights the continuing underestimation of the genus' diversity within the Oriental region. The pattern of localised, often mountain-associated endemism observed here supports the idea that the complex topography and ecological heterogeneity of the region have promoted local diversification. This finding, together with comparable cases in adjacent parts of southern China, underscores the likelihood that montane areas across continental Southeast Asia harbor many yet-undescribed *Lathrobium* lineages. Continued sampling in the adjacent areas, including Vietnam, Laos, Myanmar, Thailand and with similar habitats and integrative taxonomic efforts are therefore essential for clarifying the true extent and evolutionary structure of Oriental *Lathrobium* diversity.

Acknowledgements

This work was supported by the Bulgarian Ministry of Education and Science under the National Research Programme “Young scientists and postdoctoral fellows—2” approved by DCM 206/07.04.2022.

Acquisition of DNA data was made in advance with the funds of the National Science Center (NCN), Poland, grant UMO-2022/45/N/NZ8/04096 (PRELUDIUM-21).

The authors are very grateful to the curator of the Coleoptera collection, Natural History Museum of Vienna, Dr. Harald Schillhammer, for the provided material.

References

- Assing, V. (2013) On the *Lathrobium* fauna of China V. New species and additional records from Yunnan (Coleoptera: Staphylinidae: Paederinae). *Beiträge zur Entomologie*, 63 (1), 53–128.
<https://doi.org/10.21248/contrib.entomol.63.1.53-128>
- Assing, V. (2015) New species and additional records of *Lathrobium* and *Elytrobium* from the Palaearctic region, with special reference to the fauna of East Yunnan (Coleoptera: Staphylinidae: Paederinae). *Beiträge zur Entomologie*, 65 (1), 41–74.
<https://doi.org/10.21248/contrib.entomol.65.1.41-74>
- Assing, V. (2019) New species and records of *Lathrobium*, with the first and southernmost record of the genus from Vietnam (Coleoptera: Staphylinidae: Paederinae). *Acta Musei Moraviae, scientiae biologicae*, 104 (2), 87–107.
- Faircloth, B.C. (2016) PHYLUCE is a software package for the analysis of conserved genomic loci. *Bioinformatics*, 32, 786–788.
<https://doi.org/10.1093/bioinformatics/btv646>
- Haberski, A. & Caterino, M.S. (2025) Endogean habits drove cryptic diversification in Appalachian *Lathrobium* Gravenhorst (Coleoptera, Staphylinidae). *Molecular Phylogenetics and Evolution*, 204, 108252.
<https://doi.org/10.1016/j.ympev.2024.108252>
- Kumar, S., Stecher, G., Suleski, M., Sanderford, M., Sharma, S. & Tamura, K. (2024) Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. *Molecular Biology and Evolution*, 41, 1–9.
<https://doi.org/10.1093/molbev/msae263>
- Newton, A. (2025) StaphBase. Version August 2022. In: Bánki, O., Roskov, Y., Döring, M., Ower, G., Hernández Robles, D.R., Plata Corredor, C.A., Stjernegaard Jeppese, T., Örm, A., Vandepitte, L., Hobern, D., Schalk, P., DeWalt, R.E., Ma, K., Miller, J., Orrell, T., Aalbu, R., Abbott, J., Adlard, R., & Aedo, C.A. (Eds.), *Catalogue of Life. Annual Checklist 2024*. Catalogue of Life, Amsterdam. Available from: <https://www.catalogueoflife.org/data/dataset/1204> (accessed 21 October 2025)
<https://doi.org/10.48580/dg9ld-3gk>

Tokareva, A. & Żyła, D. (2025) Insights for the subtribal-level phylogenetic reconstructions in Paederinae (Coleoptera: Staphylinidae): a study on mesoventral plate with elements of comparative morphology. *Arthropod Structure & Development*, 88, 101473.
<https://doi.org/10.1016/j.asd.2025.101473>

Supplementary Material. The following supporting information can be downloaded at the DOI landing page of this paper:

Supplement File 1. COI alignment.