

First Record of *Leipopus linnei* Wallin, Nylander & Kvamme, 2009 (Coleoptera: Cerambycidae) from Kosovo: Morphological and Molecular Evidence

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ABSTRACT

This study documents the first record of *Leipopus linnei* in Kosovo based on an integrative taxonomic approach combining morphological evidence and DNA barcoding. The specimen was collected in June 2024 in the Bjeshkët e Nemuna National Park, located in the Deçan region of western Kosovo characterized by coniferous forest habitats. Both morphology and *COI* barcode sequences confirmed the identity of the specimen as *L. linnei*. This finding expands the known distribution of the species into the western Balkans and represents a notable eastward extension of its range. The results highlight the value of integrating molecular and morphological data when dealing with morphologically similar taxa and emphasize the importance of continued faunistic research in Kosovo, where many beetle groups remain insufficiently explored.

Keywords: Longhorn beetles, Western Balkans, DNA barcoding, Morphology, Faunistics, Integrative taxonomy.

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INTRODUCTION

The genus *Leiopus* Audinet-Serville, 1835 comprises approximately 20 species, distributed across the Northern Hemisphere (Lobl & Smetana, 2010; Monné, Bezark, & Hovore, 2007). All Nearctic species were transferred into separate genera (Linsley & Chemsak, 1995). This reclassification has contributed to a clearer understanding of the genus' biogeography and phylogenetic relationships, highlighting the concentration of diversity in the Palearctic.

In Europe, excluding Cyprus, six species of *Leiopus* have been recorded (Lobl & Smetana, 2010). Two of these are considered local endemics: *Leiopus insulanus* Slama, 1985, occurring in Crete; and *L. settei* Sama, 1983, confined to the Apennine Peninsula. The status of both species remains unclear: *Leiopus insulanus* was proposed as a synonym of *L. nebulosus* (Lobl & Smetana, 2010), and *L. settei* is likely a synonym of *L. femoratus* Fairmaire, 1859 (Zamoroka, 2025). The remaining four species are more widely distributed: *L. nebulosus* (Linnaeus, 1758) and *L. linnei* are present throughout Europe, including the Ural and Caucasus Mountains. *Leiopus femoratus* once occurred only in the northern Mediterranean and Black Sea regions but now spans all of Europe (Zamoroka, 2025). Finally, *L. punctulatus* (Paykull, 1800) inhabits Northern and Eastern Europe. This distribution pattern reflects historical biogeographic processes and habitat specialization, with some species demonstrating strong regional affinity while others occupy a broader ecological range.

Leiopus linnei and *L. nebulosus* were separated based on detailed morphological and genetic analyses (Wallin et al, 2009), although the two species exhibit high morphological similarity. Accurate differentiation between these species relies primarily on examination of male genitalia and the sclerotized part of the female spermatheca. Additional morphological traits, such as the shape of the head and pygidium, can serve as supporting characters, though they exhibit considerable individual variability (Wallin et al., 2009).

Integrative approaches combining morphological and molecular data are essential for correctly identifying species within the *nebulosus* group (Zamoroka, 2025). Morphologically similar taxa often present challenges for traditional taxonomy, as external characters may overlap or vary within populations. Molecular tools, particularly DNA barcoding (Hebert et al, 2003), have proven effective in confirming species boundaries and resolving cryptic diversity in a wide range of taxa (e.g., Zangl et al, 2021; Yin et al, 2022; Kärnäs, Hansson, & Wahlberg, 2025). The application of such methods is particularly important in understudied regions like Kosovo, where faunal inventories are incomplete and the presence of previously unrecorded species remains likely.

The present study reports one of the southernmost records of *L. linnei*, and the first for Kosovo, contributing to the understanding of its geographic range and providing baseline data for future biodiversity and conservation research in the western Balkans. This record underscores the importance of integrative taxonomy in documenting insect diversity and highlights the potential for further discoveries in regions that have received limited entomological attention (Bilalli, Ibrahim, Musliu, Geci, & Grapci-Kotori, 2024;

Ibrahimi, Bilalli, Musliu, Geci, & Grapci-Kotori 2025; Ibrahimi, Bilalli, Geci, & Musliu, 2024; Ibrahimi, Bilalli, Geci, & Grapci-Kotori 2024; Ibrahimi et al, 2023, 2021a, 2021b, 2019).

MATERIAL AND METHODS

Fieldwork and laboratory processing

A single female specimen was collected in June 2024 in the Deçan Mountains - Zalli i Rupës (42.58106, 20.15062 1247 m a.s.l.). The material was collected using entomological net and then preserved in 75% alcohol and one leg of the specimen was preserved 90% alcohol for molecular analysis. Pictures of the new species were taken with an Olympus SC50 camera attached to the Olympus SZX16 Stereomicroscope and were subsequently processed using Adobe Photoshop CC software. The material is deposited in the collection of the Faculty of Mathematics and Natural Science, Department of Biology, Prishtinë, Kosovo (UP). The map was produced in R (version 4.5.2) using the packages ggplot2 (Wickham, 2016) for visualization and *naturalearth* (Massicotte & South, 2023) for spatial data. All measurements are in millimetres.

Female genitalia were dissected and compared with published descriptions and illustrations. Identification followed the taxonomic frameworks and keys provided by Wallin et al, (2009), Rossa, Goczał, & Tofilski (2017), and the updated identification keys of Zamoroka (2025).

Materials examined: 1 ♀, Bjeshkët e Nemuna National Park - Deçan Mountains (42.58106, 20.15062. 1247 m a.s.l.), 14.VI.2024, Kosovo.

DNA-Barcoding analyses

Whole genomic DNA was extracted from the foreleg of the ethanol-fixed specimen using a modified Chelex protocol (Pfungstl et al, 2019). DNA barcodes (*sensu* Hebert, Cywinska, Ball, & deWaard, 2003) were generated by means of nanopore sequencing, which allows the rapid and cost-efficient generation of DNA barcodes (Cuber et al, 2023; Ibrahimi et al, 2022, 2021a, 2021b, 2016; Koblmüller et al, 2024; Geci et al, 2025a, 2025b). PCR amplification of a 658 bp fragment of the mitochondrial cytochrome c oxidase subunit I gene (COI) – using the primer pair LCO1490_JJ2 and HCO2198_JJ2 (Astrin et al, 2016), tagged with individual index oligos (Srivathsan et al, 2019), with an annealing temperature of 48°C –, purification of PCR-product, library preparation and sequencing on a Flongle flow cell (version R10.4.; FLO-FLG114), were conducted as part of a pool of samples from various projects following Koblmüller et al, (2024). Real-time data acquisition was carried out using MinKNOW software (Oxford Nanopore Technologies). Raw signal data (FAST5 files) were basecalled and converted to FASTQ format using the Dorado basecaller (Oxford Nanopore Technologies) with a minimum Q score threshold of 5. Consensus DNA barcodes were generated using ONT-barcoder 2.3.0 (Srivathsan et al, 2024) with default settings. The DNA barcode of the studied specimen is available in the Barcode of Life Data System (BOLD) under the processing ID COLXK001-26. We blasted our newly generated DNA barcode sequence against available sequences on NCBI and BOLD.

In addition, to visualize phylogenetic relationships among our samples and previously published sequences of *Leiopus* species, we downloaded all available COI sequences from GenBank and BOLD (Table 1). Sequences were aligned in MEGA v. 11.0 (Tamura et al, 2021) using the integrated MUSCLE algorithm (Edgar 2004). The final alignment included 72 sequences with 658 nucleotide sites. Additionally, in MEGA, we calculated pairwise genetic distances (p-distances) for a subset of closely related species. MEGA was also used to infer a Neighbour-Joining (NJ) tree based on K2P distances (Kimura 1980), the standard model typically employed in DNA barcoding studies.

In the NJ tree, several specimens were reassigned to a different species following the guidelines of Zamoroka (2025) due to previous misidentifications.

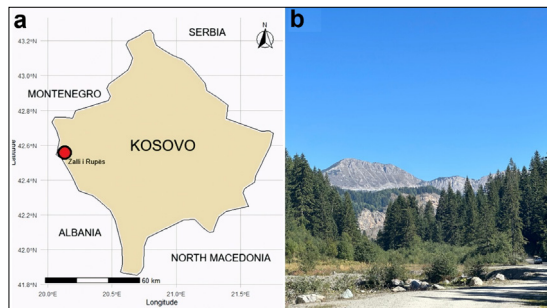


Figure 1. Map showing the distribution of *Leiopus linnei* in Kosovo (A) and photo of the sampling locality in the Deçan Mountains (B).

RESULTS

During field surveys conducted on June 2024, a single female specimen of *Leiopus linnei* was recorded in the Deçan Mountains, western Kosovo (Fig. 1). The species was observed at the edge of a montane beech forest with developed shrub and herbaceous vegetation.

The recorded locality belongs to beech forest ecosystems occurring at mid-to-high elevations and characterized by old-growth stands and mixed canopy structure. These habitats are considered relict and regionally rare.

Our finding represents the first confirmed record of *L. linnei* for Kosovo and one of the southernmost occurrences currently known from the Balkan Peninsula. The species has previously been documented from Albania, North Macedonia, and southwestern Bulgaria, while its presence in Greece remains unconfirmed but plausible. Overall, the record confirms the presence of the species in southern Europe and extends its known distribution range in the Balkan Peninsula.

Morphological identification

The collected specimen was assigned to *L. linnei* based on concordant morphological evidence following the original description and subsequent diagnostic revisions. Diagnostic characters include a wide and protruding frons, a transverse pronotum, a broad prosternal process, smoothly thickened femora, and a dense plume

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of long hairs on the ovipositor (Figs. 2-4). The dissected spermatheca is short with an elongated head, fully corresponding to published descriptions of *L. linnei*.

Hind wing morphometry also supported the identification (Fig. 3). Measured distances were $d1-14 = 4.08$ mm and $d10-15 = 0.69$ mm, resulting in an index value of $i = 5.91$, which falls within the diagnostic range for *L. linnei*.

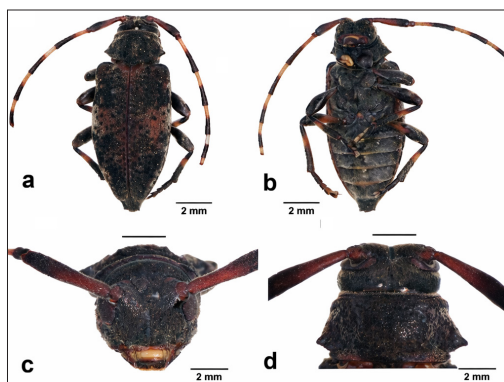


Figure 2. *Leiopus linnei*. a) Habitus view dorsal, b) habitus view ventral, c) the frontal shape of head, d) the pronotum.

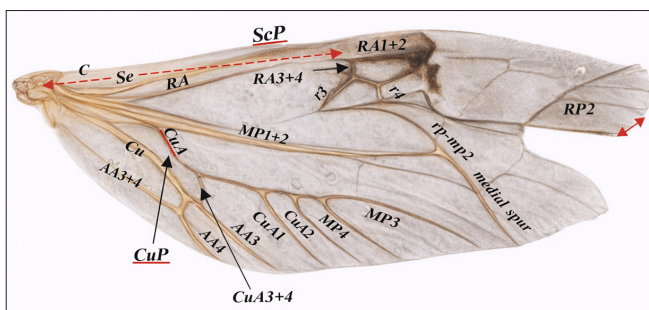


Figure 3. The hind wings of *Leiopus linnei*, showing the main longitudinal and cross veins (ScP, RA, RA1+2, RA3+4, RP2, r3, r4, MP1+2, MP3, MP4, CuA1, CuA2, CuA3+4, Cu, CuP, AA3+4, AA4) and the medial spur. Venation nomenclature accepted after Kukalová-Peck & Lawrence (2004)

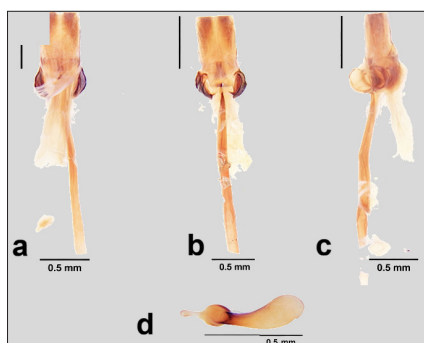


Figure 4. *Leiopus linnei*. a) Female genital dorsal view, b) ventral view, c) lateral view, d) Spermat.

Molecular confirmation

DNA barcoding of the mitochondrial COI gene further confirmed the taxonomic identity. The obtained sequence showed very low genetic divergence from reference *L. linnei* barcodes deposited in GenBank, ranging between 0.43% and 0.68%. The lowest divergence (0.43%) was observed relative to specimen KM445160.1, while sequences EU436851.1 and EU436852.1 - established reference barcodes - differed by 0.68% and 0.51%, respectively (Fig. 5).

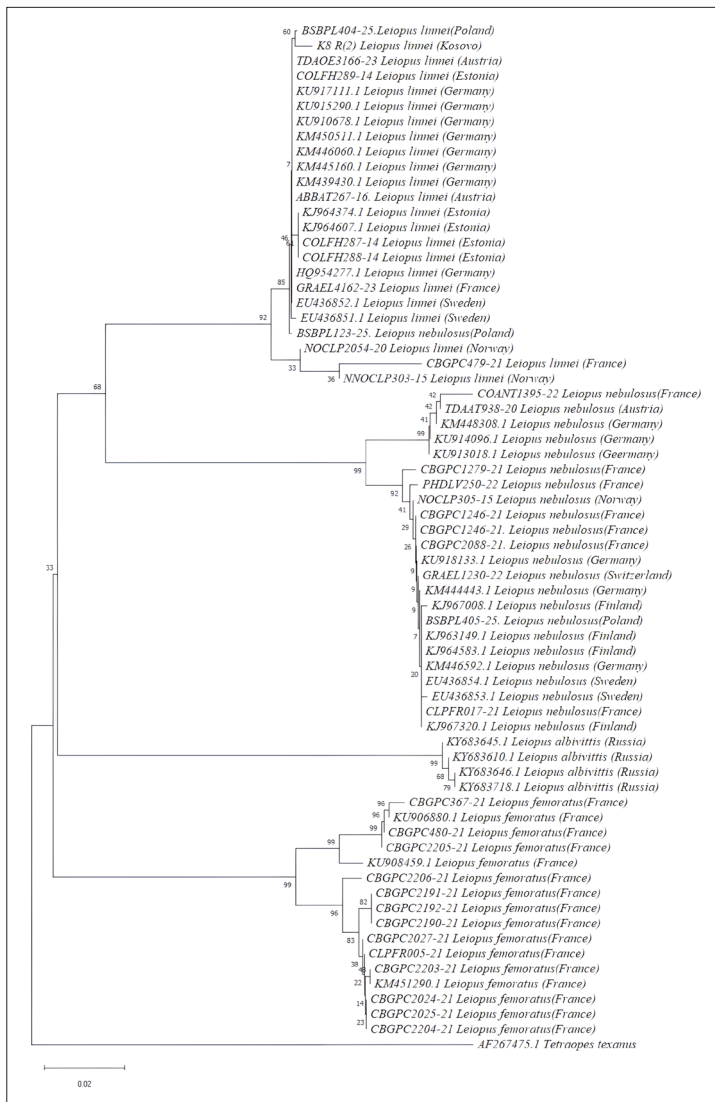


Figure 5. Neighbour-Joining tree of *Leiotopus* sequences on GenBank for this study, showing relative position of *Leiotopus linnei* from Kosovo (K8 R(2)).

Taken together, both morphological and molecular evidence provide confirmation of the presence of *Leiopus linnei* in Kosovo.

DISCUSSION

Leiopus linnei was the first longhorn beetle species originally described using an integrative taxonomic framework (Wallin et al., 2009), combining detailed morphology with DNA barcoding. This approach provides a robust toolkit for distinguishing closely related and morphologically similar taxa. In the present study, the combined application of morphological and molecular methods yielded fully concordant results and allowed confirmation of the species' identity. Morphological characters enabled the initial assignment, while DNA barcoding provided an independent and objective line of evidence, excluding potential confusion with *L. nebulosus*.

The Neighbour-Joining tree obtained in this study (Fig. 5), constructed using the newly generated COI sequence together with reference sequences from Wallin et al, (2009) and additional GenBank data, shows strong statistical support for all major branches. The analyzed specimen is robustly placed within the same clade as the reference sequences EU436851.1 and EU436852.1 reported by Wallin et al, (2009). Moreover, the overall topology of our phylogenetic reconstruction closely resembles that presented by Zamoroka (2025), further supporting the reliability of our identification. Importantly, the slight discrepancies observed may be attributed to the current underrepresentation of Balkan beetle taxa in DNA barcode databases. The lack of comprehensive barcoding data from this region can impact subtle population-level genetic patterns and may lead to underestimation of local diversity. Incorporating more specimens from the Balkans in future barcoding efforts will help refine species boundaries, improve the resolution of taxonomic identifications, and contribute to a more complete understanding of regional biodiversity.

Our analyses also corroborate the taxonomic issues highlighted by Zamoroka (2025) concerning persistent misidentifications of *Leiopus* specimens in public genetic databases. In several cases, sequences attributed to *L. nebulosus* clearly correspond to *L. linnei*, while some specimens labeled as *L. linnei* possess sequences attributable to *L. nebulosus*. Such inconsistencies likely contributed to earlier interpretations treating both taxa as a species complex (Soydabaş-Ayoub, 2021). In contrast, our results, together with those of Wallin et al, (2009) and Zamoroka (2025), clearly demonstrate the distinct species status of *L. linnei* and *L. nebulosus*. Molecular confirmation in this context is therefore essential for resolving long-standing taxonomic ambiguity.

Although our record is regional in scope, it contributes to clarifying the southern distribution boundary of *L. linnei* in Europe. The species is generally regarded as predominantly northern, being common in the Circum-Baltic region and within the Alpine-Carpathian mountain system (Gutowski et al, 2010; Hegyessy & Kutasi, 2010; Bukejs & Balalaikins, 2011; Zamoroka & Kapelyukh, 2012; Klausnitzer, Klausnitzer, Wachmann, & Hromadko, 2016; Vitali, 2018), and extending eastward to western Siberia (Zamoroka, 2025). Toward the southern margin of its range, however, the

distribution becomes fragmented and largely restricted to montane environments. Isolated occurrences from the Pyrenees (Touroult et al, 2019; Micas & Van Meer, 2020), the Maritime Alps (Touroult et al, 2019), the Dinaric Alps (Siering, 2014; Siering & Shumka, 2015; Plewa et al, 2018), the Rhodope Mountains (Plewa et al, 2015; Georgiev, Gradinarov, Gjonov, & Sakalian, 2018; Georgiev et al, 2019), and the North Caucasus (Zamoroka, 2025) collectively suggest a pattern of southern relict populations associated with high-elevation forest ecosystems. The bioclimatic distribution model proposed by Zamoroka (2025) further supports a predominantly montane distribution in southern Europe.

The habitat in which *L. linnei* was recorded in Kosovo corresponds to beech and mixed beech-fir forests of the eastern Dinarides and the Rhodopes. These forests extend across northern Albania (e.g., Lumi i Gashit), the Dinaric highlands of Serbia, the Sharr and Pelister mountain ranges of North Macedonia, and the Bulgarian Rhodopes. They typically occur on steep limestone slopes at elevations between approximately 800 and 1,800 m a.s.l. and are characterized by *Asperulo-Fagetum* and *Cephalanthero-Fagion* associations, often accompanied by *Pinus peuce*. The forests exhibit mixed canopies with beech dominance frequently exceeding 80%, and the presence of exceptional old-growth trees reaching several centuries in age. These ecosystems reflect historical biogeographic processes characteristic of the Balkan Peninsula, which functioned as a major glacial refugium, and represent transitional zones between Mediterranean and continental climatic influences. The occurrence of *L. linnei* within such habitats supports the view that southern populations of the species are closely linked to long-term ecological stability and relict forest structures.

Records of *L. linnei* on the Balkan Peninsula remain scarce. Only some reliably documented specimens are known from Albania (Siering, 2014; Siering & Shumka, 2015; Plewa et al, 2018), North Macedonia (Plewa et al., 2015), and Bulgaria (Doychev et al, 2018; Georgiev et al, 2018, 2019), indicating that the species is genuinely rare in the region rather than merely underreported. The Kosovo record therefore represents not only the first confirmed occurrence for the country but also one of the southernmost verified localities in southeastern Europe. At the same time, the absence of confirmed records from Greece, including the Pindus Mountains, is noteworthy, although ecological conditions and the bioclimatic model of Zamoroka (2025) suggest that its presence there is plausible.

The situation in Turkey and the Caucasus remains insufficiently resolved. Soydaş-Ayoub (2021) reported the first record of *L. linnei* from north-western Turkey, relatively close to Bulgarian localities (Doychev et al, 2018), but treated the taxon as part of a species complex due to intermixed barcodes. This interpretation contrasts with the clearer separation demonstrated by Wallin et al, (2009) and Zamoroka (2025). A likely explanation lies in persistent morphological misidentifications that have propagated into molecular datasets. Zamoroka (2025) addressed this issue by correcting molecular identifications using validated reference sequences, yet further targeted sampling is required. The distribution of the species in the Caucasus is even more poorly studied, with only two reliable records from the North Caucasus currently known (Zamoroka, 2025), underscoring the need for additional research along the south-eastern margin of its range.

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In summary, the southern distribution limit of *Leipopus linnei* in Europe remains only partially resolved due to historical identification difficulties and the scarcity of reliable material. By applying an integrative taxonomic approach and documenting the species within a well-defined refugial forest ecosystem, our study provides robust evidence of its presence in the south-western Balkans and contributes to a more precise understanding of its continental biogeography.

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Table 1. Available COI sequences of *Leiopus* spp. downloaded from GenBank, BOLD, and newly generated sequence.

GenBankID	Species	Name in Genbank or BOLD	Source	Internal_ID
AF267475.1	<i>Tetraopes texanus</i>	<i>Tetraopes texanus</i>	Farrell, 2001	
EU436851.1	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	Wallin, Nylander, & Kvamme, 2009	
EU436852.1	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	Wallin, Nylander, & Kvamme, 2009	
EU436853.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	Wallin, Nylander, & Kvamme, 2009	
EU436854.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	Wallin, Nylander, & Kvamme, 2009	
HQ954277.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	iBOL	
	<i>Leiopus linnei</i>		This article	K8_R(2)
KM439430.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Hendrich et al, 2015	
KM444443.1	<i>Leiopus nebulosus</i>	<i>Leiopus sp</i>	Hendrich et al, 2015	
KM445160.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Hendrich et al, 2015	
KM446060.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Hendrich et al, 2015	
KM446592.1	<i>Leiopus nebulosus</i>	<i>Leiopus sp.</i>	Hendrich et al, 2015	
KM448308.1	<i>Leiopus nebulosus</i>	<i>Leiopus sp.</i>	Hendrich et al, 2015	
KM450511.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Hendrich et al, 2015	
KM451290.1	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	Hendrich et al, 2015	
KU906880.1	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	Rulik, Eberle, & von der Mark, 2017	
KU908459.1	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	Rulik, Eberle, & von der Mark, 2017	
KU910678.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Rulik, Eberle, & von der Mark, 2017	
KU913018.1	<i>Leiopus nebulosus</i>	<i>Leiopus linnei</i>	Rulik, Eberle, & von der Mark, 2017	
KU914096.1	<i>Leiopus nebulosus</i>	<i>Leiopus linnei</i>	Rulik, Eberle, & von der Mark, 2017	
KU915290.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Rulik, Eberle, & von der Mark, 2017	
KU917111.1	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	Rulik, Eberle, & von der Mark, 2017	
KU918133.1	<i>Leiopus nebulosus</i>	<i>Leiopus linnei</i>	Rulik, Eberle, & von der Mark, 2017	
KY683610.1	<i>Leiopus albivittis</i>	<i>Leiopus albivittis</i>	Grebennikov, Jendek, & Smirnov, 2017	
KY683645.1	<i>Leiopus albivittis</i>	<i>Leiopus albivittis</i>	Grebennikov, Jendek, & Smirnov, 2017	
KY683646.1	<i>Leiopus albivittis</i>	<i>Leiopus albivittis</i>	Grebennikov, Jendek, & Smirnov, 2017	
KY683718.1	<i>Leiopus albivittis</i>	<i>Leiopus albivittis</i>	Grebennikov, Jendek, & Smirnov, 2017	
BSBPL404-25	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	BOLD	
COLFH289-14	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
ABBAT267-16	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	BOLD	
TDAOE3166-23	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
GRAEL4162-23	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
KJ964374.1	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
KJ964607.1	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
COLFH287-14	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
COLFH288-14	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
BSBPL123-25	<i>Leiopus linnei</i>	<i>Leiopus nebulosus</i>	BOLD	
NNOCLP303-15	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
NOCLP2054-20	<i>Leiopus linnei</i>	<i>Leiopus linnei</i>	BOLD	
CBGPC479-21	<i>Leiopus linnei</i>	<i>Leiopus femoratus</i>	BOLD	
TDAAT938-20	<i>Leiopus nebulosus</i>	<i>Leiopus linnei</i>	BOLD	
COANT1395-22	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
CBGPC1279-21	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
PHDLV250-22	<i>Leiopus nebulosus</i>	<i>Leiopus linnei</i>	BOLD	
NOCLP305-15	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
CBGPC1246-21	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	

Table continued

GenBankID	Species	Name in Genbank or BOLD	Source	Internal_ID
CBGPC2088-21	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
GRAEL1230-22	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
BSBPL405-25	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
KJ963149.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
KJ964583.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
KJ967008.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
KJ967320.1	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	
CBGPC367-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC480-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2205-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2206-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2191-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2192-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2190-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2027-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CLPFR005-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2203-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2024-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2025-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CBGPC2204-21	<i>Leiopus femoratus</i>	<i>Leiopus femoratus</i>	BOLD	
CLPFR017-21	<i>Leiopus nebulosus</i>	<i>Leiopus nebulosus</i>	BOLD	