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Article

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Revision of DNA barcode records of selected torrenticolid mites (Acari, Hydrachnidia, Torrenticolidae) from the Balkan Peninsula, with the description of a new species from Montenegro

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Abstract

The applicability of public barcode reference library for assessing the faunistic and genetic documentation of water mite diversity depends on the accuracy of the species identification. In this paper, we revise and comment on DNA barcode records of several tagged torrenticolid species from the Balkans, for which we found discrepancies resulting from either incorrect species identification or taxonomic challenges, such as the annotation of a potentially undescribed species. *Torrenticola graecula* Di Sabatino & Gerecke, 2003, previously known only from Greece, is newly reported for the water mite fauna of Serbia, and one species from Montenegro (*Torrenticola vladika* n. sp.) is described as new to science.

Key words Water mites, DNA barcoding, cytochrome c oxidase subunit I (COI), integrative taxonomy, systematics.

Introduction

With nearly 400 known species (Zhang *et al.* 2011), water mites of the family Torrenticolidae Piersig, 1902 are one of the most diverse groups of water mites. They are found on all continents except Antarctica (Smit 2020). However, the knowledge of torrenticolid mites in many parts of Europe, including the Balkan Peninsula remains insufficient. The recent checklist of water mites in the Balkans

published by Pešić *et al.* (2025c) list 28 torrenticolid species, including 20 species of *Torrenticola*, one *Pseudotorrenticola* and seven *Monatractides* species.

Over the past 15 years, the number of DNA sequences of torrenticolid mites included in major public libraries such as Barcode of Life Data Systems (BOLD) and GenBank has greatly increased (Pešić *et al.* 2012, 2021a, 2023, 2024, 2025a, b, c; Pešić & Smit 2022; Pešić & Goldschmidt 2023). The study of Pešić *et al.* (2025c) revealed that 18 out of 28 torrenticolid species are represented in the BOLD database with sequences from material collected in the Balkans. The applicability of these data, as emphasized by numerous authors (e.g., Peláez *et al.* 2022; Pešić *et al.* 2025a, b), depends on the accuracy of species identification, particularly the morphological identification of vouchers, which should provide records with a reliable taxonomy. Taxonomic misidentifications are considered the primary cause of the most frequent data discrepancies in barcode reference libraries. The study conducted by Peláez *et al.* (2022) highlighted the relatively small proportion of errors (almost 5% of analyzed species) in the genetic data of water mites available in the main public databases, with the largest number of errors due to misidentifications. Nevertheless, the latter authors, as well as other studies (e.g. Pešić *et al.* 2025a, b), emphasize the dangers associated with using inaccurate or inconsistent DNA sequence data from public databases, especially when comparing data of morphological and molecular origin. This is recognized as the "Achilles heel" of using existing and future DNA data in species identification (Pešić *et al.* 2025b).

In this paper, we revise and comment on DNA barcode records of several tagged torrenticolid species for which we found discrepancies, resulting from either incorrect species identification, sequence mislabeling or taxonomic difficulties such as annotation of a potentially undescribed species as another species from the same complex to which it belongs.

Material and Methods

Water mites were collected with kick nets and immediately preserved in 96% ethanol for the purpose of molecular analyses. Water mite specimens used for the molecular study are listed in Table 1. After non-destructive, whole-body DNA extraction, the specimen vouchers were stored in 96% ethanol and morphologically examined. Some of these vouchers were dissected and slide mounted in Faure's medium, while the rest was transferred to Koenike's fluid.

Morphological nomenclature follows Gerecke *et al.* (2016). The dorsal platelets of *Torrenticola* spp. were measured on both sides, therefore their dimensions are given as a range of values, rather than a single number. The holotype and paratypes of the new species are deposited in Naturalis Biodiversity Center in Leiden (RMNH).

All measurements are given in μm . The photographs of selected structures were made using a camera on a Samsung Galaxy smartphone. The following abbreviations are used: asl = above sea level; cb = gnathosomal bay, Cx-I = first coxae, Cxgl-4 = coxoglandularia of first coxae, dL = dorsal length, dp = dorsal plate, ds = dorsal shield, expo = excretory pore, f pl = frontal dorsal platelets, gf = genital field, H = height, ec = ejaculatory complex, I-L-4 = first leg, fourth segment, L = length, mL = medial length, P-1 = palp, first segment, sh pl = shoulder dorsal platelets, RMNH = Naturalis Biodiversity Center in Leiden, Vgl = ventroglandularia, vL = ventral length, W = width.

Molecular and DNA barcode analyses

The molecular analysis was conducted at the Institute of Biology, University of Szczecin (IoB-UoS), and at the University of Lodz (UniLodz), Lodz, Poland. DNA was extracted using a non-destructive protocol as described in Pešić *et al.* (2025b). At UniLodz amplification DNA sequencing using Oxford Nanopore Technology was done according to the protocol in Pešić *et al.* (2025b). Raw reads were demultiplexed using the Pacific Biosciences SMRT Link software. Consensus sequences were generated with the PacBio Amplicon Analysis (pbaa) tool. Primer trimming, translation and stop codon checking were performed using Geneious Prime 2024.0.1. Consensus sequences were made available in the BOLD database (Ratnasingham & Hebert 2007). Relevant voucher information, photos, and newly generated DNA barcodes are publicly accessible through the Dataset "DS-BALHYD DNA barcode reference library of Balkan water mites" (<https://portal.boldsystems.org/recordset/DS-BALHYD>; doi.org/10.5883/DS-BALHYD).

Sequence alignments were performed using MUSCLE (Edgar 2004). Intra- and interspecific genetic distances were calculated based on the *p*-distance using MEGA11 (Tamura *et al.* 2021). The latter software was used to calculate Neighbor-Joining (NJ) trees based on K2P distances (standard for barcoding studies) using pairwise deletion for missing data. Branch support was calculated using nonparametric bootstrap (Felsenstein 1985) with 1000 replicates and shown next to the branches.

Systematics

Family Torrenticolidae Piersig, 1902

Genus *Torrenticola* Piersig, 1896

Torrenticola (Torrenticola) graecula Di Sabatino & Gerecke, 2003

Material examined: 2♂ (barcoded; DCCDB084-21, DCCDB085-21), Serbia, Stara Planina Mt., Crnovrška rijeka stream, 43.4045° N, 22.5131° E, 28 Jul. 2019, leg. Pešić, 1♂ (voucher Id: CCDB38233 H01) dissected and slide mounted (RMNH).

Remarks: Re-examination of the male specimens from Serbia belonging to BOLD:AEI3403 showed that these specimens morphologically match description of *T. graecula* Di Sabatino & Gerecke, 2003, a species previously known only from the type localities in northern Peloponnesus, Greece (Di Sabatino *et al.* 2003). With its roundish idiosoma and short postgenital area, *T. graecula* is similar to *T. barsica* (Szalay, 1933). According to the original description, *T. graecula* differs from *T. barsica* by a relatively larger extension of the genital field (L ratio genital field/idiosoma 0.24-0.26%, 0.19-0.23% in *T. barsica*), a shortened postgenital area (10-12% of the total idiosoma L, 19-23% in *T. barsica*) and a relatively longer ejaculatory complex (240-280 µm in *T. graecula*, 180-210 µm in *T. barsica*). Nevertheless, the taxonomic status of populations from Serbia requires confirmation by collecting and barcoding of *T. graecula* specimens from its type locality in Greece. Measurements of the examined male are provided in Table 1.

Note: The examined specimens from Serbia were mistakenly reported by Pešić *et al.* (2021b) as belonging to *T. anomala* (Koch, 1837).

Torrenticola (Torrenticola) similis (K. Viets, 1939) - complex

Fig. 1; Table 1

Torrenticola meridionalis [in part] Pešić *et al.* 2021b, 2025c; Szezejko *et al.* 2023.

Material examined: Montenegro: “*T. meridionalis*“ 2♂ (barcoded; DCDDJ020-21, DCDDJ037-21), Crkvine, Bistrica stream, 42.8054° N, 19.4456° E, 11 Jun. 2021, leg. Pešić, Jovanović & Manović, 1♂ (voucher Id: CCDB 38361 B08) dissected and slide mounted (RMNH); “*T. meridionalis*“ 1♂ (barcoded; DCCDB022-21), Kolašinska rijeka stream, 42.8391° N, 19.5749° E, 30 Jul. 2020, leg. Pešić; “*T. meridionalis*“ 1♂ (barcoded; HYDBH002-22), Kutska river, 42.6561° N, 19.7875° E, 23 Mar. 2021, leg. Pešić; “*T. meridionalis*“ 1♀ (barcoded; DCCDB048-21), Tara River canyon, Bistrica stream, 42.9871° N, 19.4338° E, 29 Jul. 2020, leg. Pešić.

“*T. similis*“ 1♀ (barcoded; DCDDJ021-21), Crkvine, Bistrica stream, 42.8054° N, 19.4456° E, 11 Jun. 2021, leg. Pešić, Jovanović & Manović; “*T. similis*“ 1♂ (barcoded; HYDMN564-24), Crkvine, Bistrica stream, 42.80528° N, 19.446667° E, 23 May 2028, leg. Zawal & Pešić, dissected and slide mounted (voucher Id: K76_37; RMNH).

Remarks: Pešić *et al.* (2021b) showed that the Balkan populations assigned to *T. meridionalis* Sabatino & Cicolani, 1990, a species originally described from south Italy (Calabria, Sicily) and later on reported from different part of the Balkans (Di Sabatino *et al.* 2010), belong to two widely distributed haplogroups, BOLD:AED7519 and BOLD:AEI3402, respectively. Re-examination of the specimens assigned to BOLD:AEI3402 and published by Pešić *et al.* (2021b) under the name *T. meridionalis* Clade

3 (=TorrM-III Clade) revealed that this identification was erroneous; these specimens actually belong to *T. similis*.

Moreover, the record by Szenejko *et al.* (2023) of a male specimen (BGS1 B14a) collected from a limnocrenic spring in Babia Góra Mountain, Poland, which molecularly falls into *T. meridionalis* Clade 3 sensu Pešić *et al.* 2021b (=BOLD:AEI3402), should also be assigned to *T. similis*. The Polish specimen, as clearly shown in the photographs provided by Szenejko *et al.* (2023), is characterized by an elongated idiosoma and an excretory pore distinctly embedded in the area of primary sclerotization.

Table 1. Measurements of selected *Torrenticola* species from the Balkan Peninsula.

	<i>T. graecula</i> ♂, [CCDB38233 H01] BOLD:AEI3403	<i>T. similis</i> ♂, [K76_37] BOLD:AEK9661	<i>T. similis</i> ♂, [CCDB 38361 B08] BOLD:AEI3402
Idiosoma L	734	903	994
Idiosoma W	583	619	650
Ds L	625	763	863
Ds W	463	459	513
Ds L/W ratio	1.35	1.66	1.68
Dp L	575	718	806
Sh plate L	206	206-216	234-241
Sh plate W	75	75-81	86-90
Sh plate L/W	2.75	2.67-2.75	2.6-2.8
F plate L	128-131	142-147	147-153
F plate W	66	66	79-83
F plate L/W ratio	1.94-1.99	2.15-2.23	1.84-1.86
Sh pl L/f pl L ratio	1.57-1.61	1.4-1.52	1.53-1.64
Gnathosomal bay L	153	154	170
Cx-I L	316	322	359
Cx-I mL	163	168	189
Cx-II+III mL	109	102	122
Cx-1 L/Cx-II+III mL	2.9	3.2	2.9
Cx-I mL/Cx-II+III mL ratio	1.5	1.65	1.55
Genital field L	178	188	203
Genital field W	153	142	150
Gf L/W ratio	1.17	1.32	1.35
Distance gf—expo	88	166	191
Distance gf—cauda	125	269	278
Gf L/Idiosoma L ratio (%)	24	20.8	20.4
Postgenital L/idiosoma L ratio (%)	17	29.8	28
Ec L	259	278	300
Gnathosoma vL	309	303	319
Chelicera L	350	336	359
Palp, total L	328	310	346
P-1 dL/H	38/36	34/34	41/34
P-2 dL/H	106/58	100/55	106/59
P-3 dL/H	63/52	59/49	66/53
P-4 dL/H	100/30	98/29	111/33
P-5 dL/H	21/13	19/11	22/14
dL P-2/P-4 ratio	1.06	1.02	0.95

An examination of the male specimen from Montenegro assigned to BOLD:AEK9661 and published by Pešić *et al.* (2021b, 2025c) as *T. similis*, revealed that it morphologically matches the description of the aforementioned BOLD:AEI3402 specimens. Both BINs share the following diagnostic features: the excretory pore is located in a mediposterior indentation of primary sclerotization; Vgl-2 is shifted posterior to the excretory pore and the postgenital area is elongated (28-30% of the total idiosoma L). Differences include the P-2 shorter than P-4 in the BOLD:AEI3402 specimen and the excretory pore being incorporated into the area of primary sclerotization (though traces of fusion are still visible) in the same specimen (compare Figs. 1B and 1D, and measurements in Table 1). The *p*-distance between these two BINs was estimated 11.4%, indicating a long history of genetic isolation. To clarify the taxonomic status of the above-described lineages, more specimens need to be molecularly analysed, including specimens from the type locality of *T. similis* in the French Pyrenees.

Measurements of the examined males are provided in Table 1.

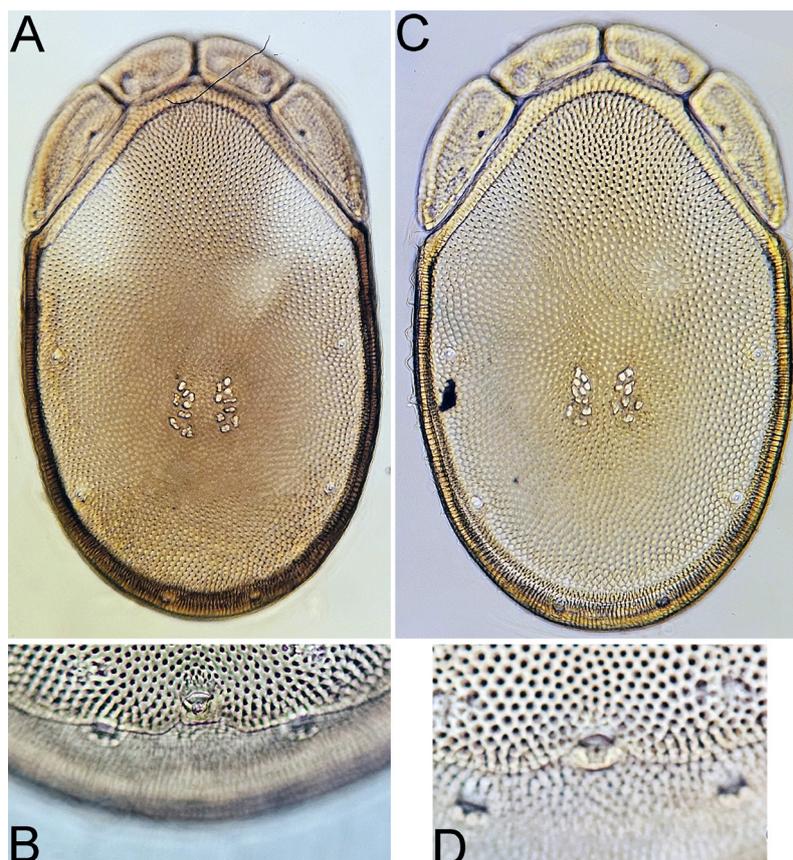


Figure 1. Photographs of selected parts. A-B *Torrenticola similis* ♂ [CCDB 38361 B08], Crkvine, Bistrica stream; C-D *T. similis* ♂ [K76_37], Crkvine, Bistrica stream: A, C – dorsal shield; B, D – excretory pore and accompanying glandularia.

***Torrenticola (Torrenticola) vladika* Pešić, Zawal & Smit n. sp.**

<https://zoobank.org/urn:lsid:zoobank.org:act:27FD377E-5BF7-4241-A197-29B38B9FEEDD>

Figs. 2-3

Material examined: Holotype ♂ (barcoded; HYDMN637-24), Montenegro, Žabljak, Durmitor Mt., Mlinski potok stream near Cno Lake, 43.14983° N, 19.09009° E, 1466 m asl., 22 Jun. 2018, leg. Zawal & Pešić, dissected and slide mounted (voucher Id: K78_17; RMNH). Paratypes: 1 ♂ (sequenced; HYDMN635-24), same data as the holotype, dissected and slide mounted (voucher Id: K78_15; RMNH); 1 ♀ (barcoded; HYDMN018-24), Montenegro, Crkvine, inflow of the Bistrica stream, 42.80528° N, 19.446667° E, 14 Jun. 2024 leg. Zawal & Pešić, dissected and slide mounted (voucher Id: K65_18; RMNH).

Diagnosis: *Morphological:* Male medial suture of Cx-II+III short (L 55-70 μm); genital field large, posterior margins of genital flaps with a few short setae only in both sexes; male ejaculatory complex with short proximal and distal arms, proximal chamber large, proximal horns reduced; gnathosoma ventral margin curved, rostrum longer; P-2 and P-3 with well-developed, finger-like, apically serrated, ventrodistal projections. *Molecular:* this lineage is represented by a unique BIN (BOLD:AGG3818) which differs from *T. anomala* clade by 16.11% *p*-distance for COI.

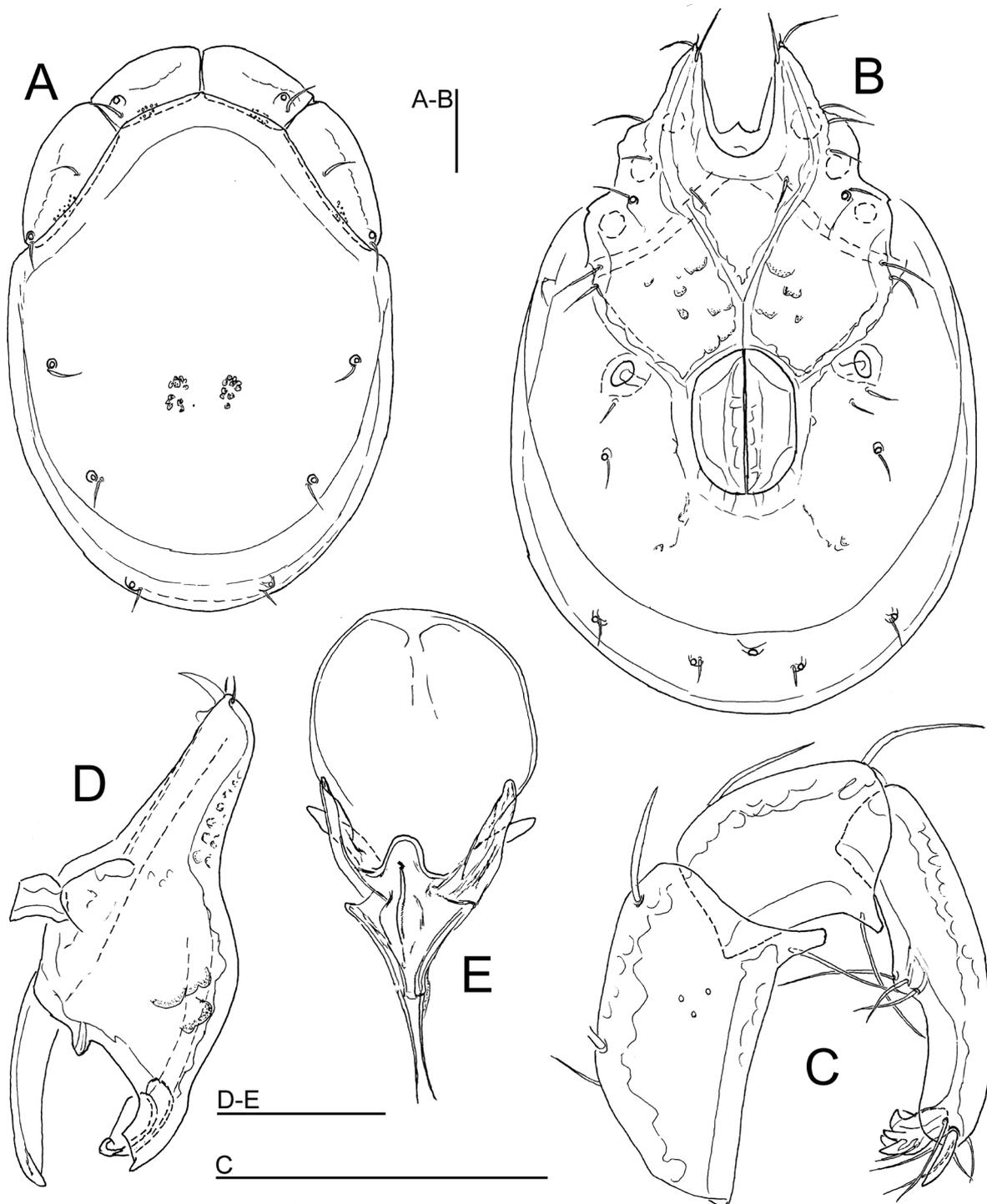


Figure 2. *Torrenticola vladika* n. sp., ♂ (A-D holotype; E paratype), Mlinski potok stream, Montenegro: A – dorsal shield; B – ventral shield; C – palp, medial view (P-1 lacking); D – gnathosoma and chelicera; E – ejaculatory complex. Scale bars = 100 μm .

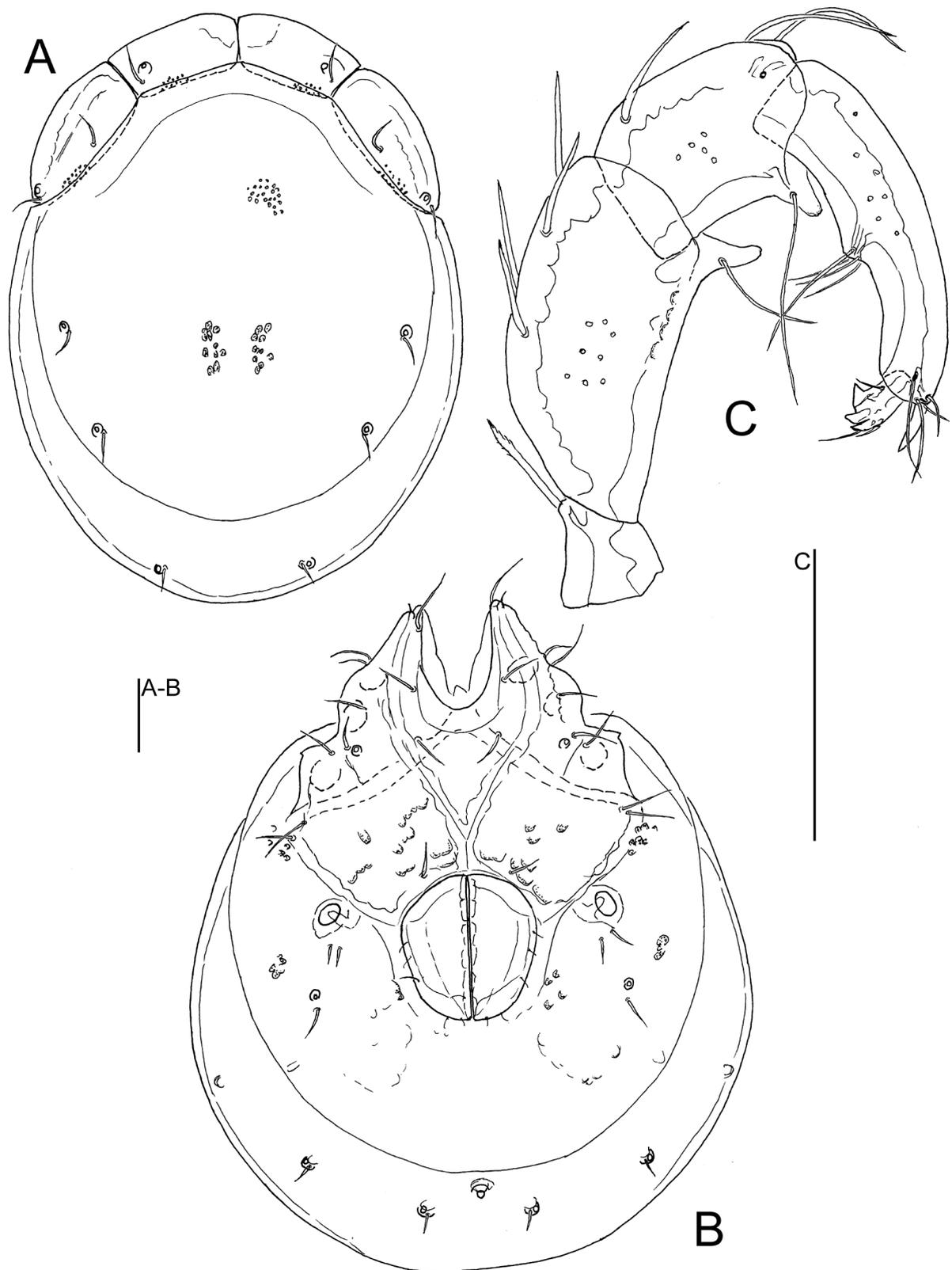


Figure 3. *Torrenticola vladika* n. sp., ♀ paratype, Bistrica Stream, Crkvine, Montenegro: A – dorsal shield; B – ventral shield; D – palp, lateral view. Scale bars = 100 µm.

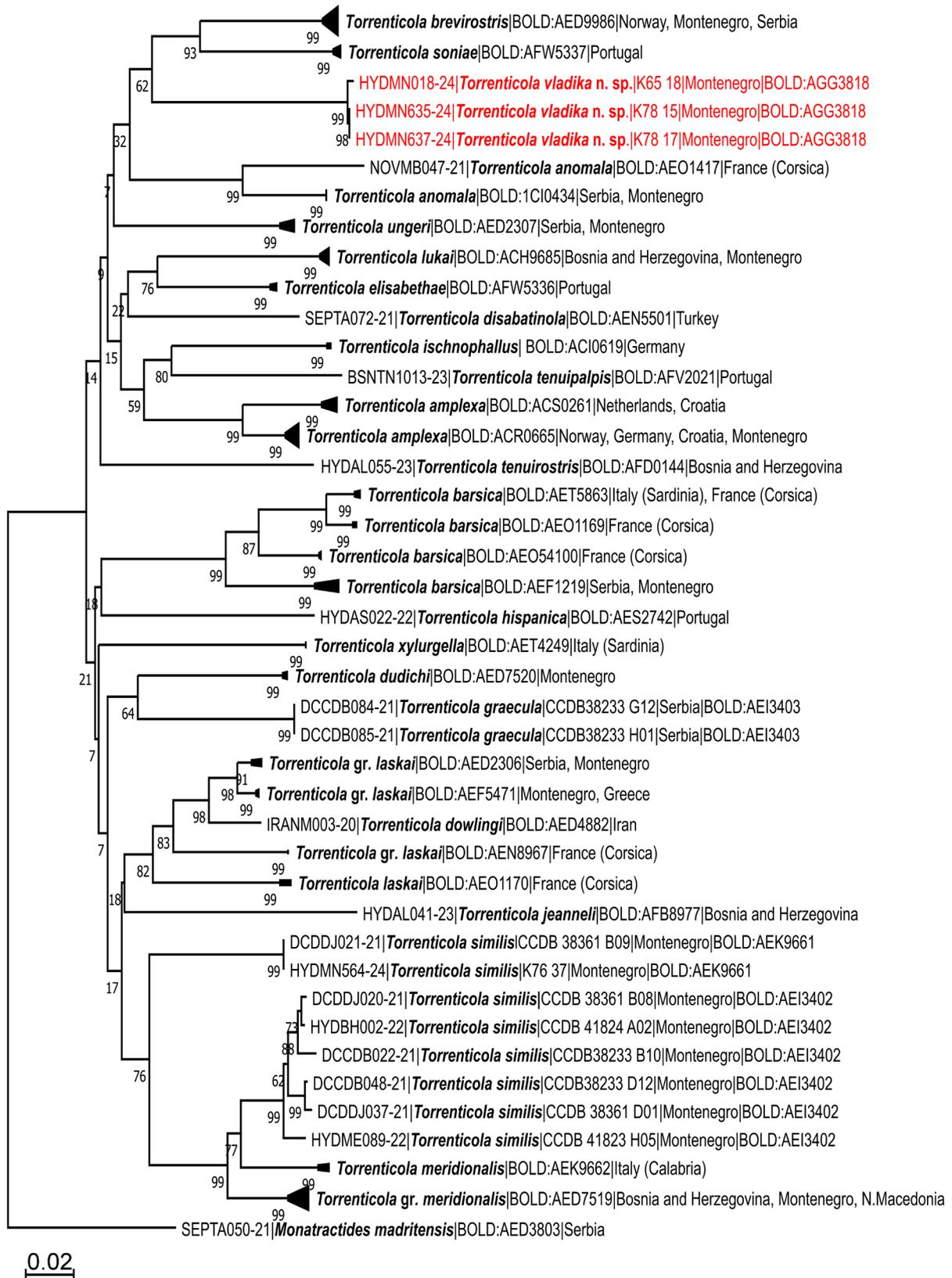


Figure 4. Neighbour-Joining tree of the genus *Torrenticola*, obtained from 118 nucleotide COI sequences listed in Supplementary material. Sequences of *T. vladika n. sp.* are marked in red. Bootstrap values >50% from 1000 bootstrap replicates on branches.

Description. *General features* — Idiosoma roundish; dorsal shield without a colour pattern (possible lost as a result of the molecular analysis process); area of primary sclerotization of the dorsal plate with two pairs of dorsoglandularia (Figure 2A); gnathosomal bay U-shaped, proximally rounded; Cxgl-4 subapical; postgenital area extended; excretory pore and Vgl-2 away from the line of primary sclerotization, Vgl-2 posterior to excretory pore, Gnathosoma ventral margin curved, gnathosomal rostrum well developed (Figure 2D); P-2 ventral margin nearly straight or slightly concave, P-2 ventrodistal protrusion finger-like, bluntly pointed, apically serrated, P-3 with a finger-like, apically serrated ventrodistal projection, P-4 with a ventral tubercle bearing one long and three shorter setae (Figures 2C, 3C). *Male* — Medial suture of Cx-II+III short, suture line of Cx-IV slightly evident; genital field large, subrectangular, with a few short setae on the posterior margins of the genital flaps; ejaculatory complex with short proximal and distal arms, proximal chamber large, proximal horns reduced (Figure 2E). *Female* — Genital field large and pentagonal in shape.

Measurements. *Male* (holotype K78_17; in parentheses measurements of paratype K78_17) — Idiosoma (ventral view: Figure 2B) L 794 (791), W 563 (569); dorsal shield (Figure 2A) L 659 (666), W 459 (444), L/W ratio 1.44 (1.5); dorsal plate L 603 (606); shoulder plate L 186 (181), W 72 (72-75), L/W ratio 2.58 (2.51-2.61); frontal plate L 141-147 (138), W 72 (70-72), L/W ratio 1.96-2.04 (1.92-1.97); shoulder/frontal plate L 1.27-1.32 (1.31). Gnathosomal bay L 141 (147), Cx-I total L 306 (298), Cx-I mL 166 (153), Cx-II+III mL 58 (68); ratio Cx-I L/Cx-II+III mL 5.3 (4.4); Cx-I mL/Cx-II+III mL 2.9 (2.3). Genital field L/W 169 (166)/122 (128), ratio 1.39 (1.30); distance genital field-excretory pore 191 (191), genital field-caudal idiosoma margin 263 (256). Ejaculatory complex L 211 (236).

Gnathosoma vL 296 (292), chelicera L 325 (322); palp total L 330, dL/H: P-1, 34/28 (35/27); P-2, 96/50 (100/56); P-3, 66/45 (69/45); P-4, 112/28 (109/30); P-5, 22/10 (22/11); L ratio P-2/P-4, 0.86 (0.92). dL of I-L-4-6: 98 (105), 118 (121), 120 (107); I-L-6 H 44 (39); dL/H I-L-6 ratio 2.72 (2.74).

Female (paratype K65_18) — Idiosoma (ventral view: Figure 3B) L 911, W 762; dorsal shield (Figure 3A) L 806, W 613, L/W ratio; dorsal plate L 738; shoulder plate L 212-216, W 92-94, L/W ratio 2.3; frontal plate L 170-175, W 86-88, L/W ratio 1.98-2.04; shoulder/frontal plate L 1.23-1.25. Gnathosomal bay L 149, Cx-I total L 313, Cx-I mL 163, Cx-II+III mL 50; ratio Cx-I L/Cx-II+III mL 6.3; Cx-I mL/Cx-II+III mL 3.3. Genital field L/W 193/180, ratio 1.07; distance genital field-excretory pore 234, genital field-caudal idiosoma margin 343.

Gnathosoma vL 338, chelicera L 381; palp total L 379, dL/H: P-1, 38/31; P-2, 117/58; P-3, 75/53; P-4, 123/32; P-5, 26/11; L ratio P-2/P-4, 0.95. dL of I-L-4-6: 105, 122, 105; I-L-6 H 38; dL/H I-L-6 ratio 2.79.

Etymology: The species is named after Vladika Rade – Petar II Petrović Njegoš, who was a Prince-Bishop (*vladika*) of Montenegro, as well as philosopher and poet. The name was chosen because the heavily sclerotized shields of this new torrenticolid species reminded the authors of one of Njegoš' most frequently cited verses: "*A hard nut is a strange fruit, you won't break it, but you'll break your tooth*", a metaphor symbolizing the resilience and struggle of the Montenegrin peoples. The species name is a noun in apposition.

Species delimitation using DNA barcodes: The final alignment for species delimitation using COI sequence data comprised 669 nucleotide positions (nps) of the 117 *Torrenticola* specimens listed in Supplementary material and one outgroup, *Monatractides madritensis* (K. Viets, 1930) from Serbia to root the tree. The NJ tree is presented in Figure 4. The COI sequences retrieved from *Torrenticola* specimens from Montenegro, here described as *T. vladika* n. sp., form a strongly supported clade (BOLD:AGG3818). In the phylogenetic tree this clade was nested between the clades of the *T. brevirostris* (*T. brevirostris* (Halbert, 1911) + *T. soniae* Pešić, 2024 from Portugal) and *T. anomala* (*T. anomala* (Koch, 1837) + *T. gr. anomala* from Corsica) complexes, respectively. The *p*-distance between the BIN of the new species and its nearest neighbour, BOLD:AFW5336, (which includes sequences of *T. elisabethae* Pešić, 2024 from Portugal), was estimated at 13.16%, while the *p*-distance to its morphologically most similar congener, *T. anomala* (BOLD:ACI0434), was estimated at 16.11%. The mean intraspecific *p*-distance within the cluster of the new species was 0.2%.

Discussion: With regard to the shape of ejaculatory complex with a large proximal chamber and reduced proximal horns, the new species resembles *T. anomala* (Koch, 1837). However, the latter species differs from the new species in having elongated medial suture Cx-II+III, the genital field is reduced in size and by the presence of long genital setae.

Distribution: Montenegro; known from the two streams (Fig. 5) in northern part of the country.



Figure 5. Photograph of the type locality (Mlinski potok stream near Crno Lake, Durmitor, Montenegro) of *Torrenticola vladika* n. sp. Photo by L. Pešić.

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Supplementary material

List of *Torrenticola* specimens used for building the Neighbour-Joining (NJ) tree (Fig. 4). BINs are based on the barcode analysis from 1 August 2025.

Process ID	Sample ID	BIN	Country
<i>Torrenticola anomala</i>			
NOVMB047-21	CCDB 38559 D11	BOLD:AEO1417	France (Corsica)
SEPTA059-21	CCDB 38363 E11	BOLD:ACI0434	Serbia
HYDMN041-24	K65 41		Montenegro
HYDMN269-24	K70 29		Montenegro
HYDMN270-24	K70 30		Montenegro
HYDMN271-24	K70 31		Montenegro
<i>Torrenticola amplexa</i>			
NLACA081-15	RMNH.ACA.1113	BOLD:ACS0261	Netherlands
NLACA454-15	RMNH.ACA.883		Netherlands
NLACA080-15	RMNH.ACA.1112		Netherlands
NLACA082-15	RMNH.ACA.1114		Netherlands
NLACA453-15	RMNH.ACA.881		Netherlands
SEPTB081-21	CCDB 38362 G09		Croatia
HYDOC081-22	CCDB 44300 G09	BOLD:ACR0665	Croatia
HYDOC079-22	CCDB 44300 G07		Croatia
HYDOC083-22	CCDB 44300 G11		Croatia
MARBN611-23	MARB UIB 694		Norway
MARBN615-23	MARB UIB 698		Norway
MARBN616-23	MARB UIB 699		Norway
DCCDB076-21	CCDB38233 G04		Montenegro
DNCBD068-20	CCDB-3867-F08		Montenegro
DNCBD069-20	CCDB-3867-F09		Montenegro
DCBDJ064-21	CCDB 38392 F04		Germany
<i>Torrenticola barsica</i>			
HYDBH040-22	CCDB 41824 D04	BOLD:AET5863	Italy
HYDCG116-24	CCDB-48501-B09		Italy
HYDBH069-22	CCDB 41824 F09		Italy
NOVMB005-21	CCDB 38559 A05	BOLD:AEO1169	France (Corsica)
NOVMB085-21	CCDB 38559 H01		France (Corsica)
NOVMB028-21	CCDB 38559 C04	BOLD:AEO5410	France (Corsica)
NOVMB037-21	CCDB 38559 D01		France (Corsica)
NOVMB050-21	CCDB 38559 E02		France (Corsica)
HYDOC006-22	CCDB 44300 A06	BOLD:AEF1219	Serbia
SEPTA054-21	CCDB 38363 E06		Serbia
DNCBD057-20	CCDB-3867-E09		Montenegro
DNCBD064-20	CCDB-3867-F04		Montenegro
HYDMN342-24	K72 7		Montenegro
<i>Torrenticola brevisrostris</i>			
MARBN875-23	MARB UIB 1243	BOLD:AED9586	Norway
MARBN1277-23	MARB UIB 885		Norway
MARBN1276-23	MARB UIB 884		Norway
HYDMN408-24	K73 25		Montenegro
HYDMN214-24	K69 22		Montenegro
HYDMN339-24	K72 4		Montenegro
HYDMN359-24	K72 24		Montenegro
HYDMN341-24	K72 6		Montenegro
DNAEC073-20	42. M19 29A 5 G6		Montenegro
SEPTA036-21	CCDB 38363 C12		Montenegro
HYDOC020-22	CCDB 44300 B08		Serbia
HYDOC021-22	CCDB 44300 B09		Serbia

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<i>Torrenticola disabatinola</i>			
SEPTA072-21	CCDB 38363 F12	BOLD:AEN5501	Türkiye
<i>Torrenticola dowlingi</i>			
IRANM003-20	7. IR1 2017 H1	BOLD:AED4882	Iran
<i>Torrenticola dudichi</i>			
DCCDB047-21	CCDB38233 D11	BOLD:AED7520	Montenegro
HYDMN382-24	K72 47		Montenegro
DNAEC074-20	43. M19 16A 4 G7		Montenegro
<i>Torrenticola elisabethae</i>			
BSNTN984-23	BGE 00227 C10	BOLD:AFW5336	Portugal
BSNTN1040-23	BGE 00227 H06		Portugal
BBIOP135-24	BGE 00108 D04		Portugal
<i>Torrenticola graecula</i>			
DCCDB084-21	CCDB38233 G12	BOLD:AEI3403	Serbia
DCCDB085-21	CCDB38233 H01		Serbia
<i>Torrenticola hispanica</i>			
HYDAS022-22	CCDB 39397 B10	BOLD:AES2742	Portugal
<i>Torrenticola ischnophallus</i>			
DCBDJ061-21	CCDB 38392 F01	BOLD:ACI0619	Germany
HYDBH089-22	CCDB 41824 H05		Germany
<i>Torrenticola laskai</i>			
NOVMB067-21	CCDB 38559 F07	BOLD:AEO1170	France (Corsica)
NOVMB083-21	CCDB 38559 G11		France (Corsica)
<i>Torrenticola gr. laskai</i>			
DNAEC036-20	42. SR CRNOVRSKA D3	BOLD:AED2306	Serbia
DNAEC037-20	43. SR CRNOVRSKA D4		Serbia
DNCBD059-20	CCDB-3867-E11		Montenegro
DNCBD022-20	CCDB-3867-B10	BOLD:AEF5471	Montenegro
DNCBD078-20	CCDB-3867-G06		Montenegro
SEPTA094-21	CCDB 38363 H10		Greece
NOVMB061-21	CCDB 38559 F01	BOLD:AEN8967	France (Corsica)
NOVMB072-21	CCDB 38559 F12		France (Corsica)
<i>Torrenticola jeanneli</i>			
HYDAL041-23	CCDB-44301-D05	BOLD:AFB8977	Bosnia and Herzegovina
<i>Torrenticola lukai</i>			
HYDBH029-22	CCDB 41824 C05	BOLD:ACH9685	Bosnia and Herzegovina
HYDBH031-22	CCDB 41824 C07		Bosnia and Herzegovina
HYDBH023-22	CCDB 41824 B11		Bosnia and Herzegovina
HYDBH022-22	CCDB 41824 B10		Bosnia and Herzegovina
HYDBH025-22	CCDB 41824 C01		Bosnia and Herzegovina
HYDBH030-22	CCDB 41824 C06		Bosnia and Herzegovina
DCDDJ036-21	CCDB 38361 C12		Montenegro
<i>Torrenticola meridionalis</i>			
DCBDJ062-21	CCDB 38392 F02	BOLD:AEK9662	Italy (Calabria)
DCBDJ041-21	CCDB 38392 D05		Italy (Calabria)
DCBDJ067-21	CCDB 38392 F07		Italy (Calabria)
<i>Torrenticola gr. meridionalis</i>			
DNAEC023-20	18. CG2019 7 C1	BOLD:AED7519	North Macedonia
DNAEC022-20	15. CG2019 7 B12		North Macedonia
DNCBD049-20	CCDB-3867-E01		Montenegro
DCDDJ038-21	CCDB 38361 D02		Montenegro
DNCBD051-20	CCDB-3867-E03		Montenegro
DNCBD021-20	CCDB-3867-B09		Montenegro
DNCBD073-20	CCDB-3867-G01		Montenegro
DNCBD074-20	CCDB-3867-G02		Montenegro
HYDBH026-22	CCDB 41824 C02		Bosnia and Herzegovina
HYDBH016-22	CCDB 41824 B04		Bosnia and Herzegovina

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<i>Torrenticola similis</i>			
DCDDJ021-21	CCDB 38361 B09	BOLD:AEK9661	Montenegro
HYDMN564-24	K76 37		Montenegro
DCDDJ020-21	CCDB 38361 B08	BOLD:AEI3402	Montenegro
HYDBH002-22	CCDB 41824 A02		Montenegro
DCCDB022-21	CCDB38233 B10		Montenegro
DCCDB048-21	CCDB38233 D12		Montenegro
DCDDJ037-21	CCDB 38361 D01		Montenegro
HYDME089-22	CCDB 41823 H05		Montenegro
<i>Torrenticola soniae</i>			
BBIOP027-24	BGE 00109 C03	BOLD:AFW5337	Portugal
BSNTN961-23	BGE 00227 A11		Portugal
BBIOP140-24	BGE 00108 D09		Portugal
BSNTN1012-23	BGE 00227 F02		Portugal
BBIOP145-24	BGE 00108 E02		Portugal
<i>Torrenticola tenuipalpis</i>			
BSNTN1013-23	BGE 00227 F03	BOLD:AFV2021	Portugal
<i>Torrenticola tenuirostris</i>			
HYDAL055-23	CCDB-44301-E07	BOLD:AFD0144	Bosnia and Herzegovina
<i>Torrenticola ungeri</i>			
SEPTA051-21	CCDB 38363 E03	BOLD:AED2307	Serbia
DNCBD044-20	CCDB-3867-D08		Montenegro
DNCBD079-20	CCDB-3867-G07		Montenegro
DNAEC057-20	19. M19 24 6 E10		Montenegro
DNAEC058-20	20. M19 24 6 E11		Montenegro
<i>Torrenticola vladika n. sp</i>			
HYDMN018-24	K65 18	BOLD:AGG3818	Montenegro
HYDMN635-24	K78 15		Montenegro
HYDMN637-24	K78 17		Montenegro
<i>Torrenticola xylurgella</i>			
HYDBH056-22	CCDB 41824 E08	BOLD:AET4249	Italy (Sardinia)
HYDBH059-22	CCDB 41824 E11		Italy (Sardinia)
HYDBH058-22	CCDB 41824 E10		Italy (Sardinia)