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A new species of *Torrenticola ungeri* complex (Acari, Hydrachnidia, Torrenticolidae), and new water mite records for Portugal

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Abstract

A new species belonging to the *Torrenticola ungeri* complex, *T. galaica* **sp. nov.**, is described from northwestern Portugal. It differs from other closely related congeners by its roundish idiosoma, distinctive dorsal shield shape and color pattern, and divergent DNA barcode sequences. Additionally, *Torrenticola ungeri disparilis* Walter, 1947, previously synonymized with *T. ungeri ungeri* (Szalay, 1927), is resurrected as a valid subspecies. New faunistic data from Portugal based on DNA barcoding are presented, with six species recorded for the first time for Portugal.

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

Introduction

The water mite genus *Torrenticola* Piersig, 1896 comprises of two subgenera in the Palaearctic region: *Torrenticola* s. str. and *Megapalpis* Halbert, 1944. Most species within the genus inhabit lotic habitats, although some have been reported from interstitial waters (Di Sabatino *et al*. 2010) and, more rarely, from lentic habitats such as lakes (Pešić *et al*. 2021). The nominal subgenus, *Torrenticola* s. str., is particularly species-rich and represents the most diverse group among torrenticolids, with approximately 30 species described to date from continental Europe (i.e., Lundblad 1956; Cicolani & Di Sabatino 1990; Di Sabatino & Cicolani 1990; Di Sabatino *et al*. 2003, 2010; Pešić *et al*. 2012, 2024a, 2025c). Recent DNA barcoding studies have revealed a high degree of cryptic and pseudo-cryptic diversity within European torrenticolids (e.g. Pešić *et al*. 2021, 2024, 2025a,b), with many Linnean species found to represent species complexes composed of genetically distinct lineages, often with restricted distributions (Pešić & Smit 2022; Pešić *et al*. 2021, 2023b, 2024a, 2025c).

According to Wiles (1997) and subsequently followed by Pešić & Smit (2009) and Pešić *et al*. (2013b, 2019), the *Torrenticola ungeri* species complex is characterized by the shoulder platelets being fused or partially fused with the dorsal plate, and by the glandularia Cxgl-4 being located posterior to Cxgl-2. In the Western Palaearctic region, this species complex includes two species: *Torrenticola ungeri* (Szalay, 1927), a species reported from Europe, Türkiye, and Russia (Di Sabatino *et al*. 2010; Erman *et al*. 2010; Tuzovskij 2015); and *T. neoungeri* Pešić, Asadi, Etemadi & Smit, 2019, a species known only from males, collected in Khuzestan, southern Iran (Pešić *et al*. 2019). In addition, six Asian species have been assigned to the *T. ungeri* complex: *T. occulta* Lundblad, 1971

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(Java; Lundblad 1971); *T. ussuriensis* (Sokolow, 1940) (Russian Far East, Korea, Japan; Pešić *et al*. 2011, 2013a); *T. microdentifera* Cook, 1967 (India: Maharashtra; Cook 1967); *T. taiwanicus* Pešić, Semenchenko, Chatterjee, Yam & Chan, 2011 (Taiwan; Pešić *et al*. 2011); *T. episce* Pešić, Chatterjee, Das & Bordoloi, 2013 (India: Assam, Uttarakhand; Pešić *et al*. 2013b, 2022b; Bhutan: Pešić *et al*. 2022a); and *Torrenticola* sp. sensu Pešić & Smit, 2009 (Thailand; Pešić & Smit 2009a).

This study is based on specimens collected in continental Portugal in 2023/2024 and represents a continuation of recent research on Portuguese water mites (e.g., Pešić *et al*. 2023a, 2024a,b, 2025a,b), four of them conducted within the framework of the Biodiversity Genomics Europe (BGE) project (https://biodiversitygenomics.eu/). As a result of this investigation, we describe one species new to science and report six water mite species from Portugal for the first time.

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 molecular studies 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.

TABLE 1. Details on DNA barcoded specimens from Portugal, including coordinates of sampling sites, the barcode index number and associated data obtained from BOLD. BOLD data presented here was last accessed on 25th August 2024.

Locality	Coordinates	Voucher Code	BOLD Acc Nos	BIN BOLD
***Pseudohydryphantes parvulus* K. Viets, 1907**				
Viana do Castelo, Ponte da Barca river beach	41.8101°N, 8.4144°W	BGE_00580_E06	BBIOP3474-24	BOLD:AGP6238
		BGE_00712_F08	BBIOP4248-25	
***Torrenticola galaica* sp. nov.**				
Viana do Castelo, Monção, Podame near bridge	42.0351°N, 8.3840°W	BGE_00580_F08	BBIOP3488-24	BOLD:AGP6165
Viana do Castelo, Arcos de Valdevez, Breia, Sieiros picnic park	41.8967°N, 8.4388°W	BGE_00580_H05	BBIOP3509-24	
		BGE_00580_H06	BBIOP3510-24	
***Torrenticola thori* (Halbert, 1944)**				
Viana do Castelo, Monção, Podame near bridge	42.0351°N, 8.3839°W	BGE_00580_F07	BBIOP3487-24	BOLD:AFI1872
***Sperchon denticulatus* Koenike, 1895**				
Viana do Castelo, Melgaço, Porto Ribeiro, watermill and medieval bridge of Lamas de Mouro	42.0446°N, 8.2030°W	BGE_00580_D03	BBIOP3459-24	BOLD:AFW4926
Viana do Castelo, Melgaço, Aldeia de Pontes, stream between the houses	41.9887°N, 8.1634°W	BGE_00580_E03	BBIOP3471-24	
Guarda, Seia, Casa do Loureiro	40.4334°N, 7.7005°W	BGE_00109_E01	BBIOP049-24	
***Limnolegeria longiseta* Motaş, 1928**				
Viana do Castelo, Arcos de Valdevez, Breia, Sieiros picnic park	41.8967°N, 8.4388°W	BGE_00580_H01	BBIOP3505-24	BOLD:AGP6653
Viana do Castelo, Melgaço, Mareco, bridge over Castro Laboreiro river	41.9854°N, 8.1633°W	BGE_00580_F02	BBIOP3482-24	
Vila Real, Cabril, Fafião river	41.7097°N, 8.0933°W	BGE_00580_H08	BBIOP3512-24	

.....continued on the next page

TABLE 1. (Continued)

Locality	Coordinates	Voucher Code	BOLD Acc Nos	BIN BOLD
***Aturus intermedius* Protz, 1900**				
Braga, Vilar da Veiga, Cascata do Arado	41.7226°N, 8.1297°W	BGE_00580_H11	BBIOP3515-24	BOLD:AGP8568
***Arrenurus robustus* Koenike, 1894**				
Viana do Castelo, Arcos de Valdevez, Breia, Sieiros picnic park	41.8967°N, 8.4388°W	BGE_00580_H03	BBIOP3507-24	BOLD:ACS0773

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: Cx-I = first coxae, Cxgl-4 = coxoglandularia of first coxae, dL = dorsal length, H = height, I-L-4 = first leg, fourth segment, L = length, mL = medial length, P-1 = palp, first segment, 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 University of Florence (Florence, Italy). DNA was extracted using a non-destructive protocol as described 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-BGEPL04 BGE Biodiversity Genomics Europe: Portuguese water mites IV—A new species of *Torrenticola ungeri* complex from Portugal" in BOLD (dx.doi.org/10.5883/DS-BGEPL04).

In this study DNA was extracted from 14 specimens from Portugal listed in Table 1. For all other species, COI sequence data were taken from the respective sequence data archives (Table 2). Sequence alignments were performed using MUSCLE (Edgar 2004). Intra- and interspecific genetic distances were calculated based on the Kimura 2-parameter (K2P) model (Kimura 1980), using MEGA11 (Tamura *et al.* 2021). The latter software was used to calculate Neighbour-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. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option).

TABLE 2. List of *Torrenticola* specimens used for building the Neighbour-Joining (NJ) tree (Fig. 4). Sequences marked with an asterisk were derived from the GenBank database, otherwise, sequences are downloaded from the BOLD database. BINs are based on the barcode analysis from 25 August 2025.

Process ID	Sample ID	BIN	Country
Torrenticola amplexa			
MARBN1283-23	MARB UIB 891	BOLD:ACR0665	Norway
MARBN1282-23	MARB UIB 890		Norway
MARBN1281-23	MARB UIB 889		Norway
MARBN1242-23	MARB UIB 850		Norway
MARBN1241-23	MARB UIB 849		Norway

.....continued on the next page

TABLE 2. (Continued)

Process ID	Sample ID	BIN	Country
MARBN1138-23	MARB UIB 651		Norway
MARBN1015-23	MARB UIB 1003		Norway
MARBN807-23	MARB UIB 1080		Norway
MARBN647-23	MARB UIB 730		Norway
MARBN812-23	MARB UIB 1085		Norway
MARBN1187-23	MARB UIB 795		Norway
MARBN646-23	MARB UIB 729		Norway
MARBN1243-23	MARB UIB 851		Norway
MARBN1016-23	MARB UIB 1004		Norway
MARBN844-23	MARB UIB 1117		Norway
MARBN713-23	MARB UIB 1176		Norway
MARBN640-23	MARB UIB 723		Norway
MARBN626-23	MARB UIB 709		Norway
MARBN710-23	MARB UIB 1173		Norway
MARBN809-23	MARB UIB 1082		Norway
MARBN878-23	MARB UIB 1246		Norway
MARBN1188-23	MARB UIB 796		Norway
MARBN1278-23	MARB UIB 886		Norway
MARBN631-23	MARB UIB 714		Norway
MARBN1018-23	MARB UIB 1006		Norway
MARBN1022-23	MARB UIB 1010		Norway
MARBN876-23	MARB UIB 1244		Norway
MARBN715-23	MARB UIB 1178		Norway
MARBN648-23	MARB UIB 731		Norway
MARBN615-23	MARB UIB 698		Norway
MARBN1017-23	MARB UIB 1005		Norway
MARBN1190-23	MARB UIB 798		Norway
MARBN845-23	MARB UIB 1118		Norway
MARBN714-23	MARB UIB 1177		Norway
MARBN641-23	MARB UIB 724		Norway
MARBN616-23	MARB UIB 699		Norway
MARBN707-23	MARB UIB 1170		Norway
MARBN716-23	MARB UIB 1179		Norway
MARBN877-23	MARB UIB 1245		Norway
MARBN1134-23	MARB UIB 647		Norway
MARBN1195-23	MARB UIB 803		Norway
MARBN627-23	MARB UIB 710		Norway
MARBN712-23	MARB UIB 1175		Norway
MARBN810-23	MARB UIB 1083		Norway
MARBN979-23	MARB UIB 967		Norway
MARBN1189-23	MARB UIB 797		Norway
MARBN1274-23	MARB UIB 882		Norway
MARBN811-23	MARB UIB 1084		Norway

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TABLE 2. (Continued)

Process ID	Sample ID	BIN	Country
MARBN1014-23	MARB UIB 1002		Norway
MARBN630-23	MARB UIB 713		Norway
MARBN1019-23	MARB UIB 1007		Norway
MARBN1194-23	MARB UIB 802		Norway
MARBN709-23	MARB UIB 1172		Norway
MARBN711-23	MARB UIB 1174		Norway
MARBN808-23	MARB UIB 1081		Norway
MARBN708-23	MARB UIB 1171		Norway
MARBN1021-23	MARB UIB 1009		Norway
MARBN611-23	MARB UIB 694		Norway
MARBN1275-23	MARB UIB 883		Norway
HYDCA109-18	HYDCA109		Norway
DCBDJ064-21	CCDB 38392 F04		Germany
HYDOC079-22	CCDB 44300 G07		Croatia
HYDOC083-22	CCDB 44300 G11		Croatia
HYDOC081-22	CCDB 44300 G09		Croatia
DCCDB076-21	CCDB38233 G04		Montenegro
DNCBD069-20	CCDB-3867-F09		Montenegro
DNCBD068-20	CCDB-3867-F08		Montenegro
HYDMN162-24	K68 18		Montenegro
BSNTN1909-24	BGE 00247 A09		Greece
HYDAL028-23	CCDB-44301-C04		Portugal
NLACA453-15	RMNH.ACA.881	BOLD:ACS0261	Netherlands
NLACA080-15	RMNH.ACA.1112		Netherlands
NLACA081-15	|RMNH.ACA.1113		Netherlands
NLACA082-15	RMNH.ACA.1114		Netherlands
NLACA454-15	RMNH.ACA.883		Netherlands
SEPTB081-21	CCDB 38362 G09		Croatia
Torrenticola elisabethae			
BSNTN984-23	BGE 00227 C10	BOLD:AFW5336	Portugal
BSNTN1040-23	BGE 00227 H06		Portugal
BBIOP135-24	BGE 00108 D04		Portugal
Torrenticola episce			
HYDME092-22	CCDB 41823 H08	BOLD:AER7328	India
HYDME093-22	CCDB 41823 H09		India
HYDME091-22	CCDB 41823 H07		India
HYDME090-22	CCDB 41823 H06		India
Torrenticola ischnophallus			
DCBDJ061-21	CCDB 38392 F01	BOLD:ACI0619	Germany
HYDBH089-22	CCDB 41824 H05		Germany
Torrenticola lukai			

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TABLE 2. (Continued)

Process ID	Sample ID	BIN	Country
HYDMN011-24	K65 11	BOLD:ACH9685	Montenegro
HYDMN012-24	K65 12		Montenegro
HYDMN173-24	K68 29		Montenegro
HYDMN409-24	K73 26		Montenegro
HYDMN064-24	K66 16		Montenegro
HYDMN065-24	K66 17		Montenegro
HYDMN066-24	K66 18		Montenegro
HYDMN163-24	K68 19		Montenegro
HYDMN399-24	K73 16		Montenegro
HYDMN400-24	K73 17		Montenegro
HYDMN401-24	K73 18		Montenegro
HYDMN612-24	K77 40		Montenegro
HYDMN665-24	K78 45		Montenegro
HYDMN563-24	K76 36		Montenegro
HYDMN225-24	K69 33		Montenegro
HYDMN336-24	K72 1		Montenegro
HYDMN369-24	K72 34		Montenegro
HYDMN534-24	K76 7		Montenegro
HYDMN542-24	K76 15		Montenegro
HYDMN560-24	K76 33		Montenegro
DCDDJ036-21	CCDB 38361 C12		Montenegro
HYDBH030-22	CCDB 41824 C06		Bosnia and Herzegovina
HYDBH022-22	CCDB 41824 B10		Bosnia and Herzegovina
HYDBH023-22	CCDB 41824 B11		Bosnia and Herzegovina
HYDBH029-22	CCDB 41824 C05		Bosnia and Herzegovina
HYDBH031-22	CCDB 41824 C07		Bosnia and Herzegovina
HYDBH036-22	CCDB 41824 C12		Bosnia and Herzegovina
HYDBH025-22	CCDB 41824 C01		Bosnia and Herzegovina
Torrenticola lundbladi			
JX629052.1*			Spain
JX629050.1*			Spain
JX629051.1*			Spain
Torrenticola ramini			
HYDIR058-23	CCDB 39399 E10	BOLD:AFF4076	Iran
Torrenticola tenuipalpis			
BSNTN1013-23	BGE 00227 F03	BOLD:AFV2021	Portugal
Torrenticola ungeri disparilis			
HYDMN410-24	K73 27	BOLD:AFD1056	Montenegro
Torrenticola ungeri ungeri			

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TABLE 2. (Continued)

Process ID	Sample ID	BIN	Country
SEPTA051-21	CCDB 38363 E03	BOLD:AED2307	Serbia
DNCBD079-20	CCDB-3867-G07		Montenegro
DNCBD044-20	CCDB-3867-D08		Montenegro
DNAEC057-20	19. M19 24 6 E10		Montenegro
DNAEC058-20	20. M19 24 6 E11		Montenegro
HYDMN320-24	K71 33		Montenegro
HYDMN321-24	K71 34		Montenegro
HYDMN213-24	K69 21		Montenegro

Systematics

Family Torrenticolidae Piersig, 1902

Genus *Torrenticola* Piersig, 1896

Torrenticola (*Torrenticola*) *ungeri* (Szalay, 1927)

Material examined: "*T. ungeri ungeri*" Serbia, Zlatibor, Crni Rzav stream near Vodice, 43.6559°N, 19.704°E, 22 Jul. 2021, leg. Pešić 1♂ (DNA barcoded; SEPTA051-21), dissected and slide mounted (voucher Id: CCDB 38363 E03; RMNH). "*T. ungeri ungeri*" Montenegro, Bar, Vruća rijeka stream, 42.0852°N, 19.1382°E, 26 Jul. 2015, leg. Pešić, 1♀ (DNA barcoded; HYDMN213-24) dissected and slide mounted (voucher Id: K69_21; RMNH). "*T. ungeri disparilis*" Montenegro, Tuzi, Cijevna river, 42.4067°N, 19.4364°E, 26 Jun. 2023, leg. Zawal & Pešić, 1♀ (juven.) (DNA barcoded; HYDMN410-24) dissected and slide mounted (voucher Id: K73_27; RMNH).

Remarks: The water mite *Torrenticola ungeri* (Szalay, 1927) includes two subspecies: *T. ungeri ungeri* (Szalay, 1927), originally described from Hungary, and *T. ungeri disparilis* (Walter, 1947), a subspecies described based on a single male collected from interstitial waters of a stream in Romania (Walter 1947). Later on, K.O. Viets (1958) placed the latter subspecies into synonymy with the nominal subspecies. According to Lundblad (1956), and followed by Szalay (1964), P-3 of the nominal subspecies lacks fine serration on the ventral margin, while the ventral margin of P-4 bears fine serration in addition with 2–4 ventral tubercles. In contrast, in *T. ungeri disparilis*, the ventral margin of P-3 shows fine serrations similar to those of P-4, although these are less conspicuous (see Walter 1947).

In our molecular study, two well-supported clades were recovered among specimens identified as *T. ungeri*, corresponding to Barcode Index Numbers (BINs) BOLD:AED2307 and BOLD:AFD1056. Re-examination of specimens assigned to BOLD:AED2307 showed that their palp morphology (ventral margin of P-3 lacking fine serrations; ventral margin of P-4 in addition to fine serration with 2–4 ventral tubercles; Fig. 1A) matches the description of *T. ungeri ungeri*. In contrast, a single juvenile female from BOLD:AFD1056 exhibited palp characteristics consistent with *T. ungeri disparilis*, with both P-3 and P-4 bearing fine serrations, and P-4 additionally bearing 6–7 small ventral tubercles (Fig. 1B). The COI genetic divergence between these clades was estimated at 6.14% (K2P), indicating clear genetic separation. Therefore, we propose the resurrection of *Torrenticola ungeri disparilis* as a valid subspecies, distinct from the nominal *T. ungeri ungeri*.

Note: Based on palp morphology—with both P-3 and P-4 bearing fine serrations, and P-4 additionally bearing 6–7 small ventral tubercles—the male specimen from the Mrtvica stream in Montenegro, illustrated by Pešić *et al*. (2019; figs. 3A–B), should be assigned to *T. ungeri disparilis*.

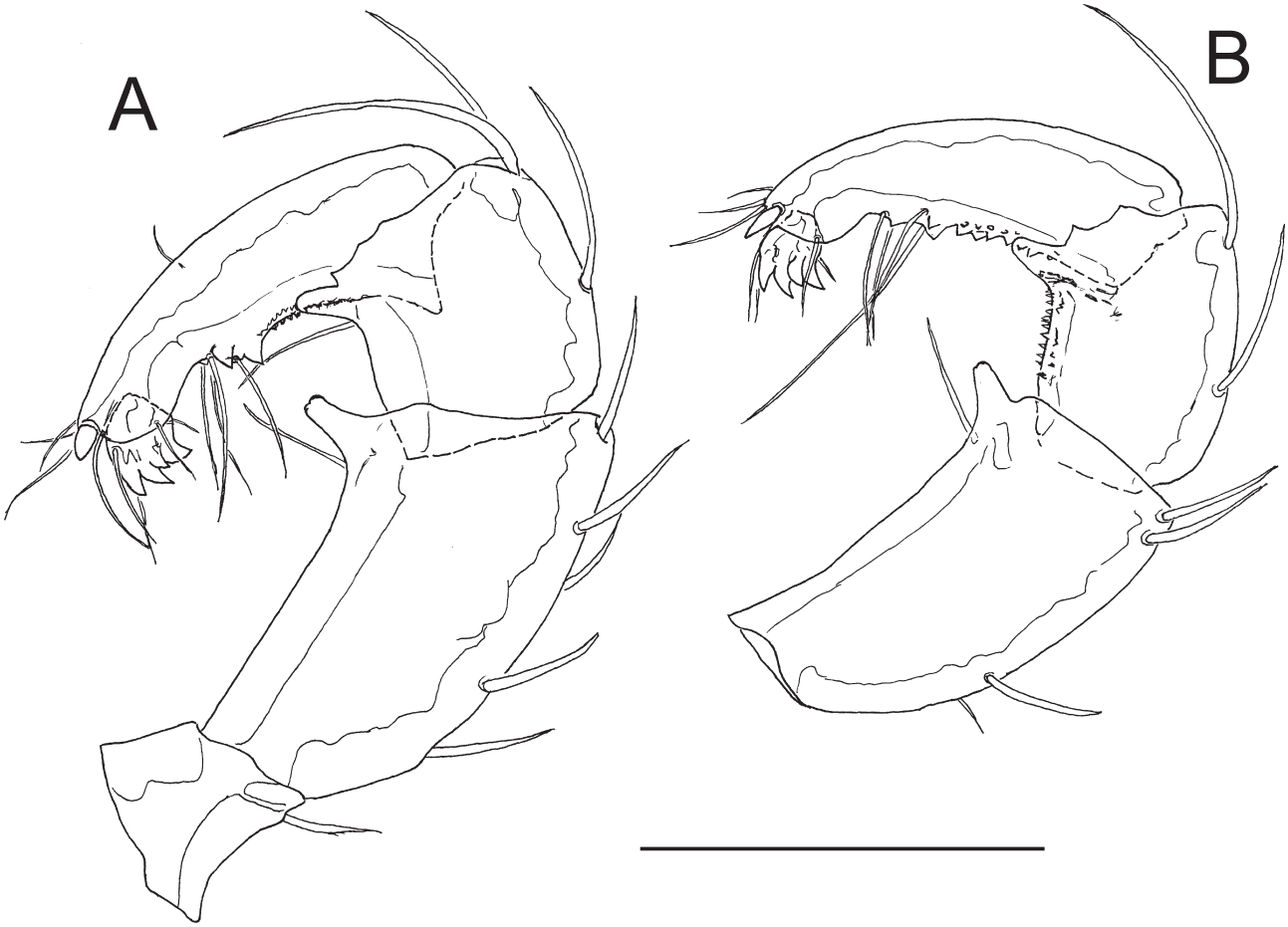

FIGURE 1. **A**—*Torrenticola ungeri ungeri* (Szalay, 1927), ♂ [CCDB 38363 E03], Crni Rzav, Serbia; **B**—*T. ungeri disparilis* Walter, 1947, ♀ (juven.) [K73_27], Cijevna river, Montenegro: palp, medial view (P-1 lacking). Scale bars = 100 μm.

***Torrenticola* (*Torrenticola*) *galaica* Pešić sp. nov.**

https://zoobank.org/urn:lsid:zoobank.org:act:DD73BF59-BB83-4EEB-8F9F-A66BC80245C9

Figs. 2, 3A–B

Material examined: Holotype ♀, Portugal, Viana do Castelo, Monção, Podame, near bridge, 42.0351°N, 8.3839°W, 40 m asl, 19 Aug. 2024, leg. Ferreira, Girão & da Silva, dissected and slide mounted (DNA barcoded; voucher Id: BGE_00580_F08; RMNH). Paratypes: 2♀ (DNA barcoded; BGE_00580_H05, BGE_00580_H06), Viana do Castelo, Arcos de Valdevez, Breia, Sieiros picnic park, 41.8967°N, 8.4388°W, 53 m asl., 19 Aug. 2024, leg. Ferreira, Girão & da Silva.

Diagnosis (Males unknown): *Morphological:* Characters of the *Torrenticola ungeri* species group (shoulder platelets fused or partially fused with dorsal plate, Cxgl-4 posterior to Cxgl-2); dorsal shield with colour pattern as illustrated in Fig. 3A–B; the angle of the dorsal plate between the frontal plates slightly pointed, with the anterior part of the dorsal plate lying relatively wide between the traces of the shoulder plate delimitation; tip of Cx-I with several long setae; excretory pore slightly posterior to Vgl-2; ventral margin of P-3 without serration, ventral margin of P-4 with fine serration. *Molecular*: This lineage corresponds to a unique Barcode Index Number (BIN) BOLD: AGP6165, which differs from the *T. ungeri ungeri* clade (BOLD:AED2307) by 8.60% K2P divergence in the COI gene.

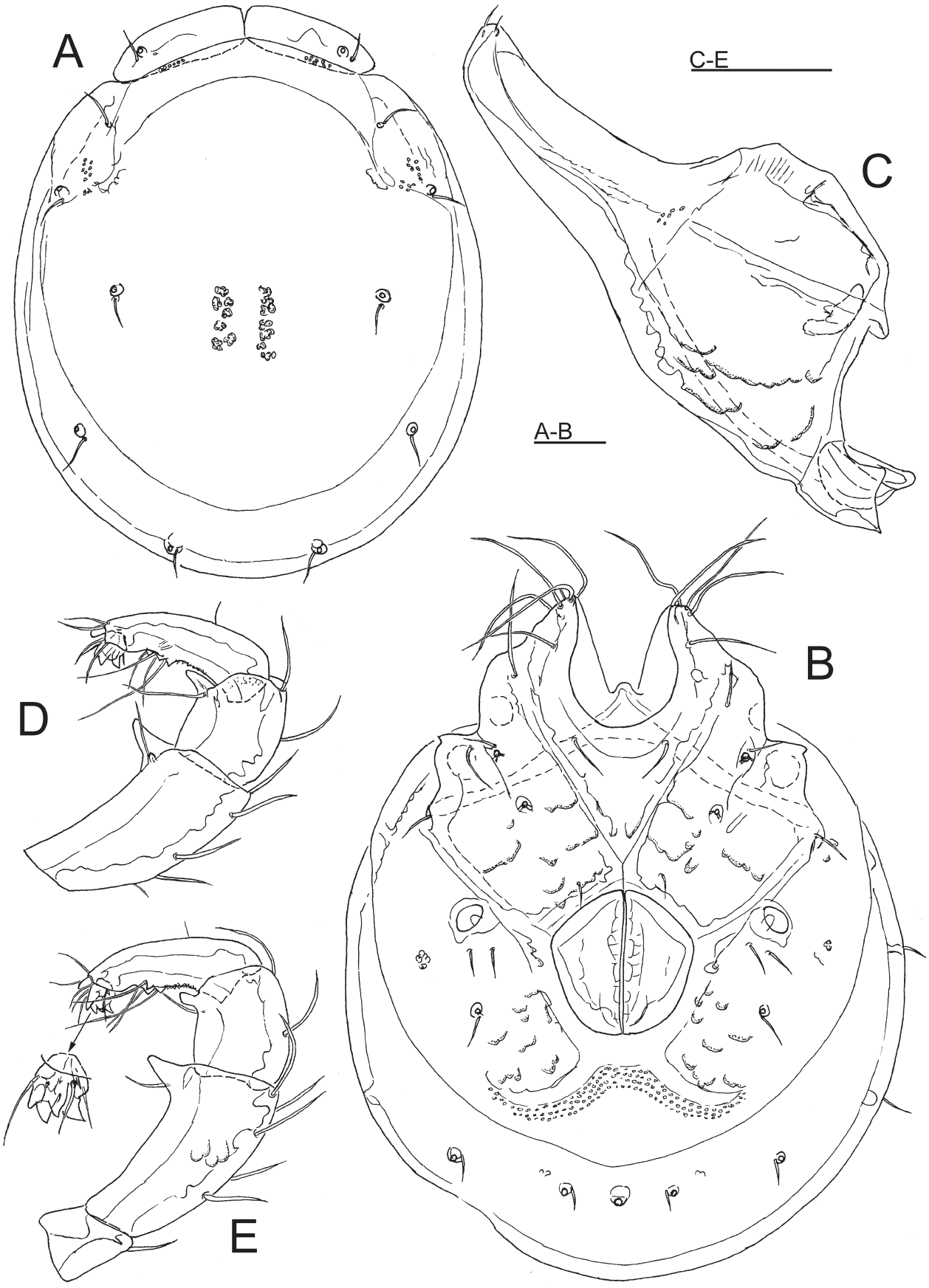

FIGURE 2. *Torrenticola galaica* **sp. nov.**, ♀ holotype [BGE_00580_F08], Podame, Portugal: A—dorsal shield; B—ventral shield; C—gnathosoma; D—palp, lateral view (P-1 lacking); E—palp, medial view (inset: P-5, enlarged 2x). Scale bars = 100 μm.

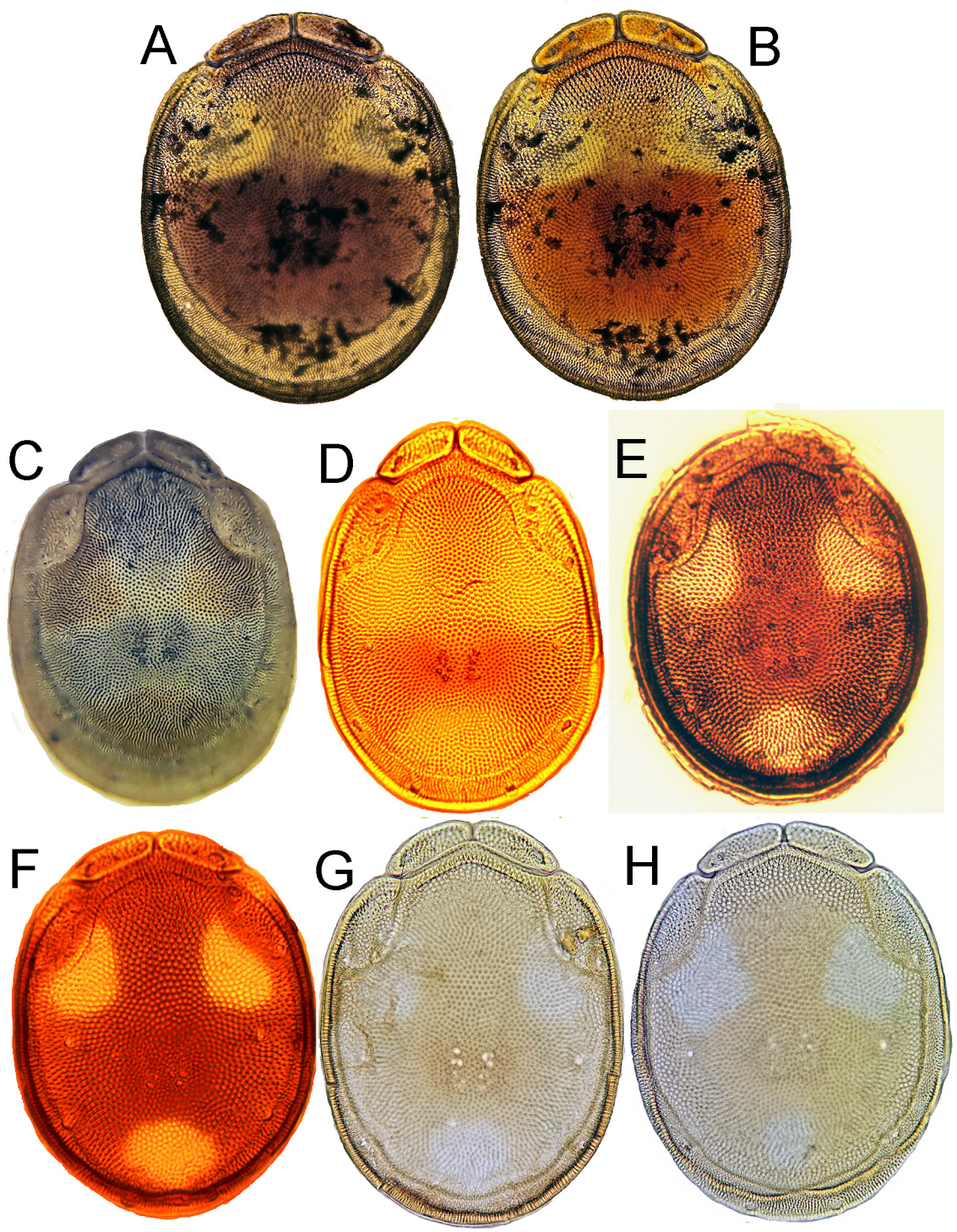

FIGURE 3. Photographs of dorsal shield. **A–B** *Torrenticola galaica* **sp. nov.**, ♀ holotype [BGE_00580_F08]: A—voucher photographed immediately after dissection; B—voucher photographed in Faure's medium. **C & D**—*T. neoungeri* Pešić, Asadi, Etemadi & Smit, 2019, ♂ Andika-Taluk, Iran (photographs taken from Pešić *et al*. 2019): C—conserved paratype, photographed immediately after dissection, D—holotype photographed in Faure's medium; **E & F**—*T. ungeri disparilis* Walter, 1947, ♂, Mrtvica River, Montenegro (photographs taken from Pešić *et al*. 2019): E—conserved specimen, photographed immediately after dissection; F—conserved specimen, photographed in Faure's medium. **G & H**—*T. ungeri ungeri* (Szalay, 1927): G—♂ [CCDB 38363 E03], Crni Rzav, Serbia, voucher photographed in Faure's medium; H—♀ [K69_21], Vruća rijeka, Montenego, voucher photographed in Faure's medium.

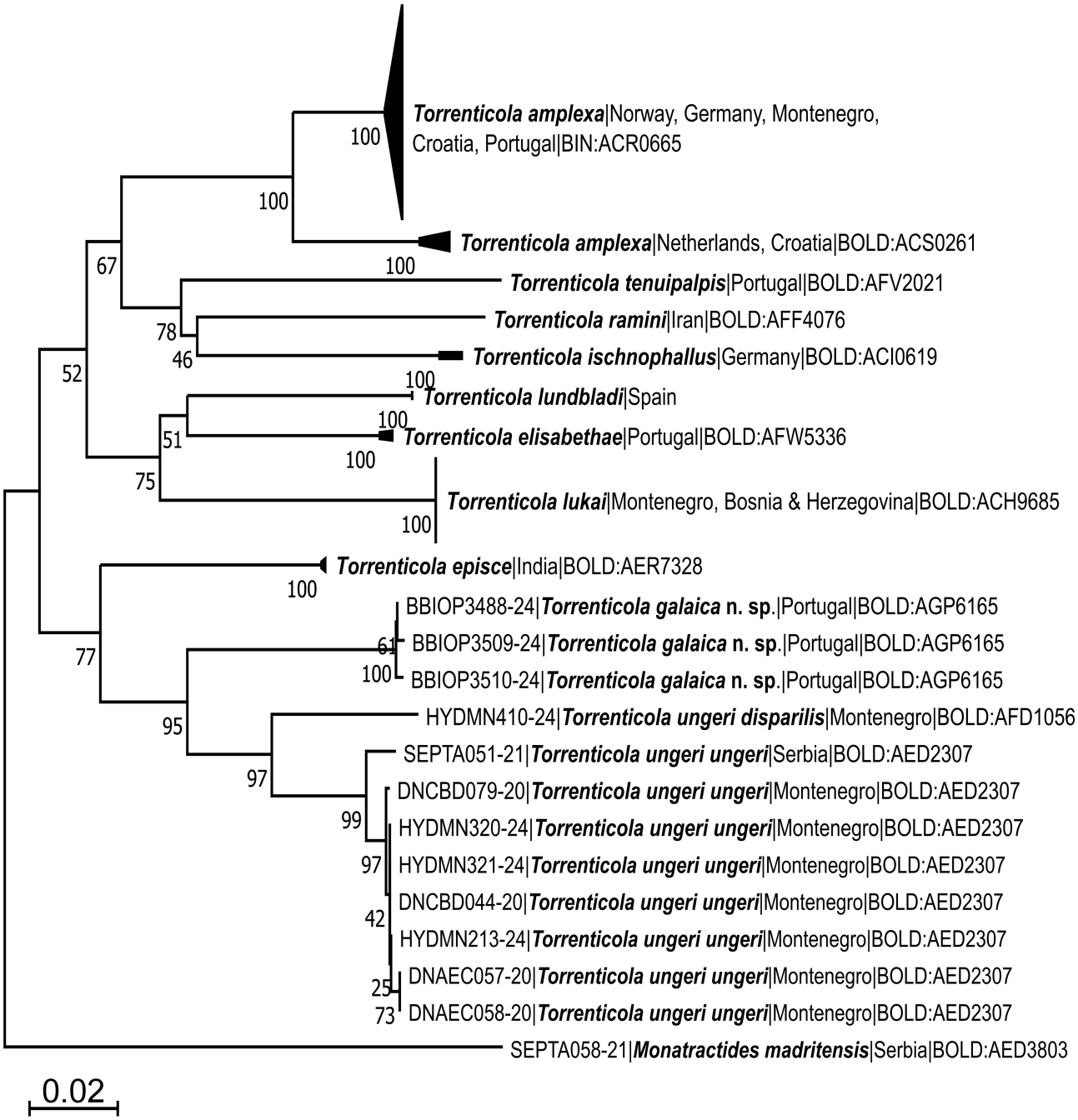

FIGURE 4. Neighbour-Joining tree of the genus *Torrenticola*, obtained from 130 nucleotide COI sequences listed in Table 2. Bootstrap values >50% from 1000 bootstrap replicates on branches.

Description. Female. Idiosoma oval (dorsal shield L/W ratio 1.2); shoulder platelets fused with dorsal plate (Fig. 2A); dorsal shield with colour pattern as illustrated in Figs. 3A–B; gnathosomal bay U-shaped, proximally rounded; tip of Cx-I with long setae; Cxgl-4 posterior to Cxgl-2; medial suture line of Cx-II+III relatively short; posterior suture lines of Cx-IV extending posteriorly beyond posterior margin of genital field, laterally curved; genital field pentagonal in shape; excretory pore and Vgl-2 away from the line of primary sclerotization, excretory pore slightly posterior to Vgl-2; gnathosoma ventral margin curved, rostrum well developed; P-2 ventral margin slightly curved, ventrodistal protrusion slender; ventral margin of P-4 with fine serration and 3–4 ventral tubercles, bearing one longer, and three shorter setae (Figs. D–E).

Measurements—Idiosoma (ventral view: Figure 2B) L 956, W 788; dorsal shield (Figure 2A) L 806, W 658,

L/W ratio 1.23; dorsal plate L 763; frontal plate L 193–200, W 64, L/W ratio 3.0–3.1. Gnathosomal bay L 177, Cx-I total L 354, Cx-I mL 178, Cx-II+III mL 38; ratio Cx-I L/Cx-II+III mL 9.3; Cx-I mL/Cx-II+III mL 4.7. Genital field L/W 198/193, ratio 1.03; distance genital field-excretory pore 222, genital field-caudal idiosoma margin 343.

Gnathosoma vL 453; chelicera L 522; palp total L 444, dL/H: P-1, 56/45; P-2, 152/70; P-3, 86/68; P-4, 125/45; P-5, 23/18; L ratio P-2/P-4, 1.22. dL of I-L-4–6: 130, 144, 128; I-L-6 H 40; dL/H I-L-6 ratio 3.2.

Male. Unknown.

Etymology: The species name *galaica* refers to the presence of this species on the northwest Iberian Peninsula from which the new species is currently only known.

Species delimitation using DNA barcodes: The final alignment for species delimitation using COI sequence data comprised 669 nucleotide positions (nps) from 130 *Torrenticola* specimens (representing ten *Torrenticola* spp. characterized by dorsal shield with two free anterior platelets and shoulder platelets partially fused with large dorsal plate) listed in Table 2. *Monatractides madritensis* (K. Viets, 1930) from Serbia was used as outgroup. The Neighbour-Joining (NJ) tree is presented in Figure 4. COI sequences obtained from *Torrenticola* specimens collected in Portugal, here described as *T. galaica* **sp. nov.**, forms a strongly supported clade (BIN BOLD:AGP6165). In the phylogenetic tree, this clade appeared as a sister group to the cluster containing sequences of *Torrenticola ungeri* from the Balkans. The mean K2P genetic distance between the BIN of the new species and its closest neighbour, BOLD:AED2307 (which includes sequences of *T. ungeri ungeri*), was estimated at 8.60%. The mean intraspecific K2P distance within the new species cluster was 0.2%.

Discussion: The new species belongs to the *Torrenticola ungeri* species complex, which currently includes two species known from the Palaearctic region: *T. ungeri* and *T. neoungeri*. The Portuguese species differs from both species in having a more rounded idiosoma (dorsal shield L/W ratio 1.2) and a distinct dorsal shield color pattern (compare Fig. 3A–B with Figs. 3C–E).

Additionally, the new species differs in the shape and configuration of the dorsal plate: the angle between the frontal plates is only slightly pointed, and the anterior part of the dorsal plate lying between the traces of the shoulder plate delimitation is relatively wide. In contrast, both *T. neoungeri* and *T. ungeri* exhibit a more sharply pointed angle between the frontal plates, a narrower anterior section of the dorsal plate between the traces of the shoulder plates, and more strongly pronounced angles of the shoulder plate traces posterior to setae Dgl-3.

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

New faunistic records for Portugal

Family Hydryphantidae Piersig, 1896

Pseudohydryphantes parvulus K. Viets, 1907

Material examined. Portugal, Viana do Castelo, Ponte da Barca, Ponte da Barca river beach, 41.8101°N, 8.4144°W, 17 m asl., 19 Aug. 2024, leg. Ferreira, Girão & da Silva, 2♂ (1♂ DNA barcoded; BBIOP3474-24), 1♂ dissected and slide mounted (voucher Id: BGE_00580_E06; RMNH).

Remarks: The examined specimens in our study match the description of *Pseudohydryphantes parvulus* K. Viets, 1907 following Di Sabatino *et al*. (2010). The sequenced specimens from Portugal form a unique BIN (BOLD: AGP6238), with the nearest neighbouring BIN being BOLD:ACX3676 (*p*-distance 13.71%), which includes three private sequences of one non-identified *Hydryphantes* sp. from Canada, available in BOLD. This is the first DNA barcodes for this genus.

Distribution. Europe. New for Portugal.

FIGURE 5. Photograph of the type locality (Portugal, Viana do Castelo, Monção, Podame) of *Torrenticola galaica* **sp. nov.** Photo by D. Girão.

Family Sperchontidae Thor, 1900

***Sperchon* (*Hispidosperchon*) *denticulatus* Koenike, 1895**
Fig. 6

Material examined. Portugal, Guarda, Seia, Casa do Loureiro, 40.4334°N, 7.7005°W, 415 m a.s.l., 19 july 2023, Ferreira & Cruz-Oliveira, 1 deutonymph (DNA barcoded; Voucher Id: BGE_00109_E01); Viana do Castelo, Melgaço, Aldeia de Pontes, stream between the houses, 41.9887°N, 8.1634°W, 720 m asl., 20 Aug. 2024, leg. Ferreira, Girão & da Silva, 1♂ dissected and slide mounted (DNA barcoded; Voucher Id: BGE_00580_E03; RMNH); Viana do Castelo, Melgaço, Porto Ribeiro, Watermill and medieval bridge of Lamas de Mouro, 42.0446°N, 8.2030°W, 865 m asl., 19 Aug. 2024, leg. Ferreira, Girão & da Silva, 1♂ (DNA barcoded; BGE_00580_D03).

Remarks: Morphological analysis revealed that in regard to the shape of palp (as illustrated in Fig. 6A–B), postgenital plate longitudinally distinctly wider than long (length/width < 1), III–IV-leg-5 with prominent distolateral extension (Fig. 6C) and the tip of anterior ramus of ejaculatory complex indented with laterally rounded, posteriorly slightly pointed extensions, Portuguese males match the description *S. denticulatus*. Genetic data indicate that examined specimens form a unique BIN (BOLD:AFW4926).

Distribution. Western Palaearctic. New for Portugal.

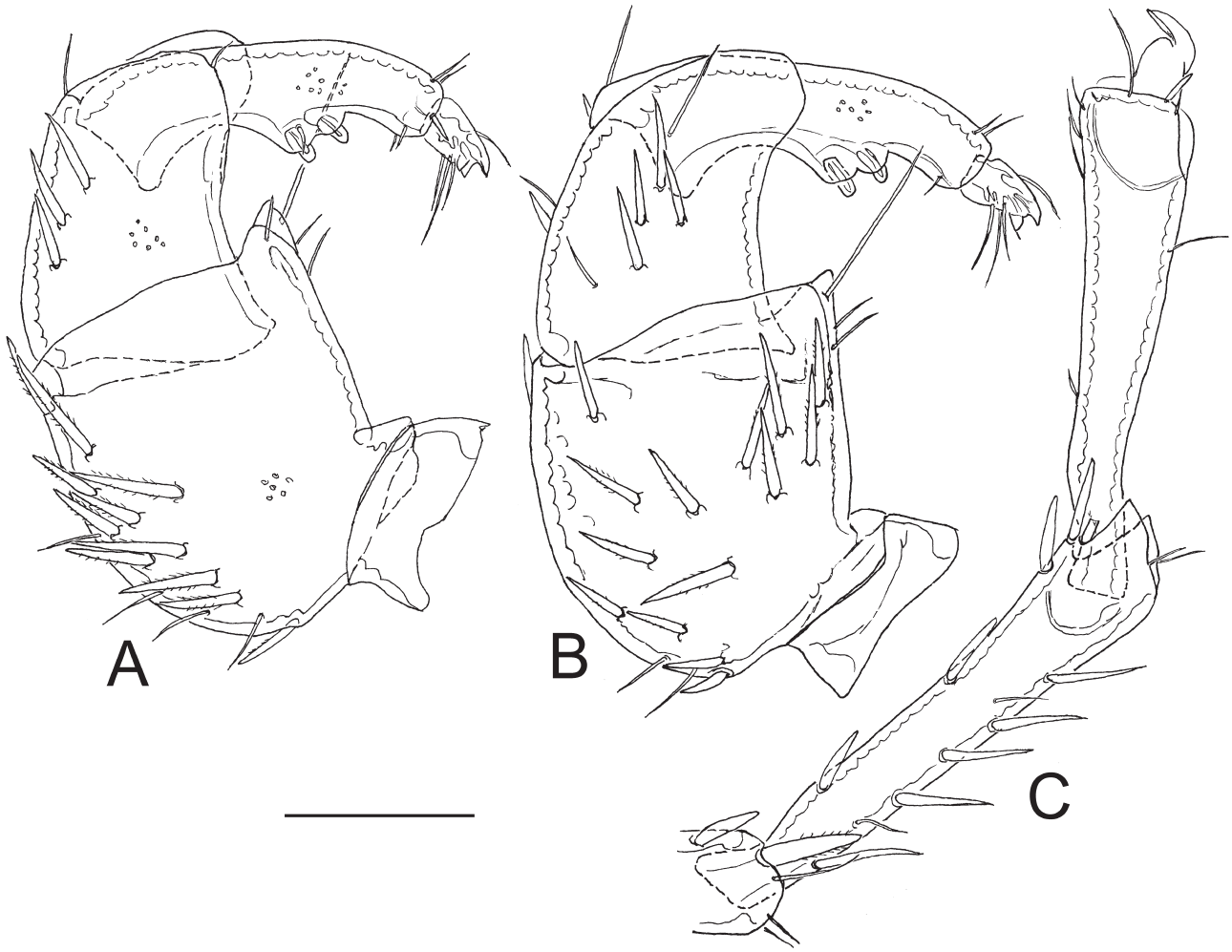

FIGURE 6. *Sperchon denticulatus* Koenike, 1895, ♂ [BGE_00580_E03], Aldeia de Ponte, Portugal; A—palp, medial view; B—palp, lateral view; B—IV-L-5 and -6. Scale bar = 100 µm.

Family Teutoniidae Koenike, 1910

***Limnolegeria longiseta* Motaş, 1928**

Material examined. Portugal, Viana do Castelo, Melgaço, Mareco, Bridge over Castro Laboreiro river, 41.9854°N, 8.1633°W, 715 m asl., 20 Aug. 2020, leg. Ferreira, Girão & da Silva, 1♂ (DNA barcoded; voucher Id: BGE_00580_F02); Vila Real, Cabril, Fafião river, 41.7097°N, 8.0934°W, 352 m asl., 24 May 2024, leg. Cruz-Oliveira, Ferreira & Girão, 1♀ (DNA barcoded; voucher Id: BGE_00580_H08).

Remarks: The examined specimens in our study match the description of *Limnolegeria longiseta* Motaş, 1928, following Di Sabatino *et al*. (2010), and form a unique BIN (BOLD:AGP6653). The only available sequence of *L. longiseta* in the BOLD database (SEPTA083-21) belongs to a specimen from Türkiye, which forms a separate BIN (BOLD:AEM5501). The mean K2P genetic distance between the Portuguese and Turkish BINs of *L. longiseta* was estimated at 20.8%, indicating the need for taxonomic revision of this species.

Distribution. SW France, Italy, Türkiye. New for Portugal.

Family Torrenticolidae Persig, 1902

***Torrenticola* (*Torrenticola*) *thori* (Halbert, 1944)**

Material examined. Portugal, Viana do Castelo, Monção, Podame, near bridge, 42.0351°N, 8.3840°W, 40 m asl, 19 Aug. 2024, leg. Ferreira, Girão & da Silva, 1♀, dissected and slide mounted (DNA barcoded, voucher Id: BGE_00580_F07; RMNH).

Remarks. The Portuguese specimen keyed out to *T. thori* following Di Sabatino *et al*. (2010), form a unique BIN (BOLD:AFI1872).

Distribution. Central, southern and western Europe. New for Portugal.

Family Aturidae Thor, 1900

***Aturus intermedius* Protz, 1900**

Material examined. Portugal, Braga, Vilar da Veiga, Cascata do Arado, 41.7226°N, 8.1297°W, 710 m asl, 24 May 2024, Cruz-Oliveira A, Ferreira & Girão, 1♂, 1♀ (DNA barcoded), 1♂ dissected and slide mounted (voucher Id: BGE_00580_H11; RMNH).

Remarks. The specimens from Portugal match the description of *Aturus intermedius*. Genetic data indicate that all examined specimens form a unique BIN (BOLD:AGP8568), and the closest neighbouring BIN is that of *A. atlantis* (BOLD:AGH8056) from Madeira. The *p*-distance between these two BINs was estimated at 11.075%.

Distribution. SW and W Palaearctic**.** New for Portugal.

Family Arrenuridae Thor, 1900

***Arrenurus* (*Arrenurus*) *robustus* Koenike, 1894**

Material examined. Portugal, Viana do Castelo, Arcos de Valdevez, Breia, Sieiros picnic park, 41.8967°N, 8.4388°W, 53 m asl., 19 Aug. 2024, leg. Ferreira, Girão & da Silva, 1♂ (DNA barcoded, voucher Id: BGE_00580_H03).

Remarks. The sequenced specimen from Portugal clusters within BOLD:ACS0773, which, in addition to the specimens used in this study, includes specimens from the Netherlands and Germany.

Distribution. Western Palaearctic. New for Portugal.

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