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A new species of the genus *Hyleoglomeris* Verhoeff 1910 from Central Japan (Diplopoda: Glomerida: Glomeridae)

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Abstract — A large-sized species of *Hyleoglomeris* collected from Shiga Prefecture, Central Japan, was discriminated from the described species known from Japan and surrounding areas by our careful examination of external body structure as well as male telopods. The new species is similar to *H. stuxbergi* from Japan, but can be distinguished from the latter by the following combination of characters: syncoxital lobe widely bifid forming two sublobes which are extended ventrolaterad (vs. narrowly bifid forming a pair of sublobes extended ventrad in *H. stuxbergi*); syncoxital horns slightly converging to each other (vs. almost parallel in *H. stuxbergi*); femoral trichostele slightly curved mesad (vs. strongly bent laterad in *H. stuxbergi*). On the base of these differences, the species is herein described as *Hyleoglomeris awaumi* Kuroda, Susukida & Eguchi, **sp. nov.** Our *COI*-based phylogenetic tree involving *H. awaumi* and other five congeneric Japanese species also shows the genetic distinctiveness of the new species. In addition, our analysis further suggests that Japanese *Hyleoglomeris* is non-monophyletic.

Key words — *COI,* male telopods, phylogeny, pill millipede, Shiga Prefecture, taxonomy

Introduction

The genus *Hyleoglomeris* Verhoeff 1910, which belongs to the family Glomeridae Leach 1815, is one of the most speciose genera of the class Diplopoda, consisting of 101 valid species distributed in the Palaearctic and Oriental regions (Sierwald & Spelda 2022). Recently Golovatch et al. (2006) reviewed this genus and listed 11 valid species in Japan: *H. insularum* Verhoeff 1936, *H. japonica* Verhoeff 1936, *H. lucida* Haga 1956, *H. magy* Nakama, Nakamura, Tatsuta & Korsós 2022, *H. nigra* Verhoeff 1942, *H. sakamotoensis* Takano 1981, *H. stuxbergi* (Attems 1909), *H. sulcata* Verhoeff 1942, *H. triangularis* Haga 1968, *H. uenoi* Miyosi 1955, and *H. yamashinai* Verhoeff 1937. All the 11 species are endemic to Japan. Among them, so far, four species have been known only from the type locality: *H. sakamotoensis* from "Sakamoto-mura," Shinyatsushiro-shi, Kumamoto Pref.; *H. nigra* from Kochi Pref.; *H. triangularis* from Goya Limestone Cave, Tagawa-shi, Fukuoka Pref.; *H. sulcata* from Jinmuji, Zushi-shi, and Takashima, Yokohama-shi, Kanagawa Pref. (Attems 1909, Verhoeff 1936, 1937, 1942, Miyosi 1955, Takashima & Haga 1956, Haga 1968, Takano 1981, Golovatch et al. 2006, Nakama et al. 2022). The remaining seven species are more widely distributed. Nevertheless, for each species the known localities are scattered, and there are several areas that have not been properly surveyed (Miyosi 1959, Sugiyama & Haga 1989, Nakamura & Korsós 2010). An exception is *H. magy* of which the geo-

graphic distribution is well documented, ranging from Central to Southern Ryukyus (Nakama et al. 2022).

In the conventional discrimination of *Hyleoglomeris* species, morphology of telopods of the male has been considered an essential diagnostic character. Body color, pattern and morphology of thoracic shield in both male and female have been additionally or complementarily used for species identification. However, some species (e.g., the Japanese species *H. insularum* and *H. sulcata*), have been described based on females only. DNA barcoding, a method particularly useful for species descrimination and for revealing conspecific male-female combinations, have not yet been conducted for Japanese species. Consequently, the classification of Japanese *Hyleoglomeris* species still involves many potential problems and obscurities. For this reason, A. D. Nguyen and K. Eguchi jointly initiated to examine the Japanese *Hyleoglomeris* species as part of their long-term project "Taxonomic Revision of Asian Glomeridae." The latter is also leading a nationwide sampling in Japan.

In this paper, an undetermined morphospecies, "*Hyleoglomeris* sp. A", that was first discovered by Katsushi Sakamoto (one of the present authors) from Omihachiman-shi (Shiga Pref., Central Japan), is taxonomically examined using a combination of conventional morphological characters and DNA barcoding. Based on the results of this study the putative species is herein described as new to science.

Material and methods

A total of 26 specimens of *Hyleoglomeris* collected by the present authors from different localities in Japan were examined. Of them, 22 specimens were used for phylogenetic analyses (Table 1). The concept of the genus as revised by Golovatch et al. (2006 and 2012) was followed in the present study. Species-level identification was carried-out by referring to the original descriptions of all Japanese species (Attems 1909, Verhoeff 1936, 1937, 1942, Miyosi 1955, Takashima & Haga 1956, Haga 1968, Takano 1981, Nakama et al. 2022), and other taxonomic articles (Miyosi 1959, Golovatch 1978, Golovatch et al. 2006, 2010, 2012, Mikhaljova & Lim 2006, 2018).

The voucher specimens used in this study will be housed in the following institutions: Museum of Nature and Human Activities, Hyogo (MNHAH); National Museum of Nature and Science, Tokyo, Japan (NSMT); private collection of the corresponding author (EG-coll). In addition, four specimens of four glomerid species collected from Vietnam were used as outgroups in molecular phylogenetic analyses (Table 1).

Specimens, which had been preserved in ethanol at concentrations greater than 70% after collection, were observed or photographed under a Nikon SMZ1270 and AZ100 streomicroscopes. Therefore, it should be noted that ethanol may have altered the coloration. Telopods were dissected from the body, and observed or photographed directly or after removing tissues using the Chelex-TE-ProK method (Satria et al. 2015). Focus stacking was performed using Helicon Focus Pro 7.5.3 software (Helicon Soft Ltd., Ukraine) based on a series of source images taken with a Canon EOS Kiss X9 digital camera attached to a Nikon AZ100 stereomicroscope. Artifacts were erased using the retouch function of the software.

Total genomic DNA was extracted from each individual by Chelex-TE-ProK method. Mitochondrial *COI* gene fragment was amplified by polymerase chain reaction (PCR) using a thermal cycler (MiniAmp Thermal Cycler, Applied Biosystems). The following PCR primers were used: LCO1490 and HCO2198 (Folmer et al. 1994). The *COI* fragment was amplified with KOD FX Neo (TOYOBO) using 10 µl reaction volume in the thermal cycler under the following parameters: 94°C for 2 min followed by 45 cycles of 98°C for 10 s, 48.5°C for 30 s, 68°C for 45 s, and finally 68°C for 7 min. After confirming the PCR amplification on a 1.0% agarose gel, the amplified products were incubated at 37°C for 4 min. and 80°C for 1 min with ExoSAP-IT Express (Applied Biosystems) to remove any excess of primers and nucleotides. The cycle sequencing reactions were carried out using a SupreDye v3.1 Cycle Sequencing Kit (M & S TechnoSystems, Japan) according to the user manual. The sequencing reaction products were purified, and their nucleotide sequences were determined using an automated sequencers (ABI PRISM 3130xl, Applied Biosystems). The sequences obtained were submitted to the GenBank (accession numbers are shown in Table 1).

The *COI* sequences were then aligned together with the sequences of four different glomerid species obtained from GenBank (Table 1), using the program MUSCLE (Edgar 2004). The aligned 658-bp sequence dataset contained no indels or gaps. After pruning identical sequences, a total of 12 *Hyleoglomeris* sequences and four outgroup sequences were used for Bayesian inference analysis. The GTR + I + G model was selected as the best-fit substitution model for the dataset by hLRT in MrModeltest 2.2 (Nylander 2004). The Bayesian inference analysis was performed using MrBayes version 3.1.2. (Ronquist & Huelsenbeck 2003), for 1,000,000 generations with four chains, with samples taken every 100 generations.

Pairwise p-distances and Kimura-two-parameter (K2P) distances were calculated using MEGA7 (Kumar et al. 2016) for the 658-bp *COI* dataset (Table 2).

Results and discussions

A total of 17 undetermined *Hyleoglomeris* specimens (9 adult males, 8 adult females), collected in the Hachiman-koen park of Omihachiman-shi (Shiga Pref.), were considered to be morphologically a single morphospecies: "*Hyleoglomeris* sp. A". *Hyleoglomeris* sp. A was clearly morphologically discriminated from all the other valid named congeners known from Japan (including *H. stuxbergi* that is the most similar species for morphology of telopods), Taiwan and Korean Peninsula, using the series of characters mentioned in the Remarks of the Taxonomic Accounts.

The remaining nine specimens newly collected from Japan were morphologically assigned to five species already

Table 1. List of specimens examined in this study with locality, voucher information, and accession number of *COI*.

Taxa	Locality	Voucher ID	Sex	OTU ID	Accession No.
H. awaumi Kuroda, Susukida & Eguchi, **sp. nov.**	Japan: Shiga Pref., Omihachiman-shi, Miyauchi-cho, Hachiman-koen	EG20210711-227-01	F	1	LC713407
		EG20210711-227-02	F	2	LC713408
		EG20210711-227-03	M	3	LC713409
		EG20210711-227-04	F	4	LC713410
		EG20210711-227-05	M	5	LC713411
		EG20210711-227-06	F	6	LC713412
	Japan: Shiga Pref., Omihachi-man-shi, Miyauchi-cho	KS20210513-01	M	7	LC713413
		KS20210513-02	M	8	LC713414
		KS20210513-03	M	9	LC713415
		KS20210513-04	M	10	LC713416
		KS20210513-05	F	11	LC713417
		KS20210513-06	F	12	LC713418
		KS20210513-07	F	13	LC713419
		KS20210513-08	F	14	LC713420
H. insularum Verhoeff 1936	Japan: Kanagawa Pref., Odawara-shi, Nebukawa	EG20201213-09	F		LC713421
H. japonica Verhoeff 1936	Japan: Kanagawa Pref., Fujisa-wa-shi, Enoshima Island	MS20210617-01	M	1	LC713422
		MS20210617-02	M	2	LC713423
		MS20210617-03	M	3	LC713424
H. lucida Haga 1956	Japan: Saitama Pref., Chichi-bu-shi, Kamikagemori	EG20210718-240-01	M	1	LC713425
	Japan: Saitama Pref., Chichi-bu-shi, Arakawakuna	MS20210426-11	M	2	LC713426
		MS20210426-15	M	3	LC713427
H. sulcata Verhoeff 1942	Japan: Kanagawa Pref., Zushi-shi, Numata, Jimmuji	MS20210521B-05	F		LC713428
H. uenoi Miyoshi 1955	Japan: Yamaguchi Pref., Ube-shi, Higashikibe	ST20211028	M		LC713429
Hyperglomeris simplex Nguyen & Sier-wald & Marek 2019	Viet Nam	IEBR-605	—		MT749403*
Peplomeris magna Golovatch 1983	Viet Nam	IEBR-677	—		MT749405*
Rhopalomeris sauda Nguyen & Sier-wald & Marek 2019	Viet Nam	IEBR-801	—		MT749398*
Tonkinomeris napoensis Nguyen & Sierwald & Marek 2019	Viet Nam	IEBR-804b	—		MT749396*

Note. Sex: male, M; female, F. *: Nguyen et al. (2021)

described and known from Japan: *H.* cf. *insularum*, *H. japonica*, *H. lucida*, *H. sulcata* and *H. uenoi*. The "cf." (confer) means a tentative identification made without the topotype being unavailable in the present study. The following species were not involved in our collection: *H. magy*, *H. nigra*, *H. sakamotoensis*, *H. stuxbergi*, *H. triangularis* and *H. yamashinai*. Therefore, the present *COI*-based phylogenetic tree (Fig. 1) is provisional.

Five of the six Japanese species, namely *H.* sp. A, *H.* cf. *insularum*, *H. japonica*, *H. lucida*, and *H. sulcata,* grouped in the same clade with a 0.95 of posterior probability value (pp). However, *H. uenoi* was not included. Consequently, it is possible that the Japanese *Hyleoglomeris* species may not be monophyletic. This preliminary result agrees with Nguyen et al. (2021) in which Vietnamese *Hyleoglomeris* species were also recovered as non-monophyletic. The boundaries among *Hyleoglomeris* and its surrounding minor genera (e.g., *Tonkinomeris*, *Peplomeris*, *Rhopalomeris,* and *Hyperglomeris*) will be revised more in detail in the near future, using phylogenetic analyses based on a much wider and compre-

Table 2. Pairwise *p*-distances (%; upper right) and K2P distances (lower left) based on 658-bp *COI* sequence dataset.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. *H. awaumi* 1, 2, 4~9, 11, 12		0.2	0.2	0.3	12.0	12.2	12.0	12.6	11.1	13.5	13.2	13.2	14.0	12.9	14.9	13.5
2. *H. awaumi* 3	0.002		0.3	0.5	11.9	12.0	11.9	12.5	10.9	13.4	13.1	13.1	14.1	12.8	14.7	13.5
3. *H. awaumi* 10	0.002	0.003		0.2	11.9	12.0	11.9	12.6	11.2	13.4	13.1	13.1	14.1	12.8	15.0	13.7
4. *H. awaumi* 13, 14	0.003	0.005	0.002		12.0	12.2	12.0	12.8	11.4	13.5	13.2	13.2	14.3	12.9	15.2	13.8
5. *H. japonica* 1	0.134	0.132	0.132	0.134		0.2	0.0*	12.7	13.1	14.5	14.8	13.7	14.0	13.4	13.9	14.0
6. *H. japonica* 2	0.136	0.134	0.134	0.136	0.002		0.0*	12.8	13.2	14.6	14.9	13.9	14.2	13.5	14.0	14.2
7. *H. japonica* 3	0.134	0.133	0.133	0.134	0.000*	0.000*		12.7	13.1	14.5	14.8	13.7	14.0	13.4	13.9	14.0
8 *H. insularum*	0.141	0.139	0.139	0.143	0.141	0.142	0.141		9.7	13.1	12.8	13.5	13.2	14.2	14.6	14.8
9. *H. sulcata*	0.121	0.119	0.119	0.125	0.146	0.148	0.146	0.106		12.3	12.3	13.4	12.2	12.3	12.6	12.0
10. *H. lucida* 1, 3	0.151	0.149	0.149	0.151	0.163	0.165	0.163	0.146	0.136		0.3	11.9	15.2	12.9	14.9	14.1
11. *H. lucida* 2	0.147	0.145	0.145	0.147	0.167	0.169	0.167	0.142	0.136	0.003		12.2	15.2	12.9	15.2	14.1
12. *H. uenoi*	0.148	0.146	0.146	0.148	0.153	0.155	0.153	0.152	0.149	0.130	0.134		12.9	12.3	12.6	13.5
13. *Tonkinomeris napoensis*	0.158	0.160	0.160	0.162	0.157	0.159	0.157	0.149	0.135	0.172	0.172	0.143		12.3	12.3	13.8
14. *Peplomeris magna*	0.143	0.141	0.141	0.143	0.149	0.151	0.149	0.159	0.136	0.144	0.144	0.136	0.136		12.9	12.6
15. *Rhopalomeris sauda*	0.169	0.167	0.167	0.173	0.155	0.157	0.155	0.166	0.140	0.168	0.172	0.140	0.136	0.143		13.4
16. *Hyperglomeris simplex*	0.151	0.151	0.151	0.155	0.157	0.158	0.157	0.168	0.132	0.158	0.158	0.151	0.155	0.139	0.149	

*Among *H. japonica* samples, *H. japonica* 1 and *H. japonica* 2 showed a 1-bp sequence difference (131 position: #1 = A, #2 = G), but *H. japonica* 3 showed R (A or G) in position 131.

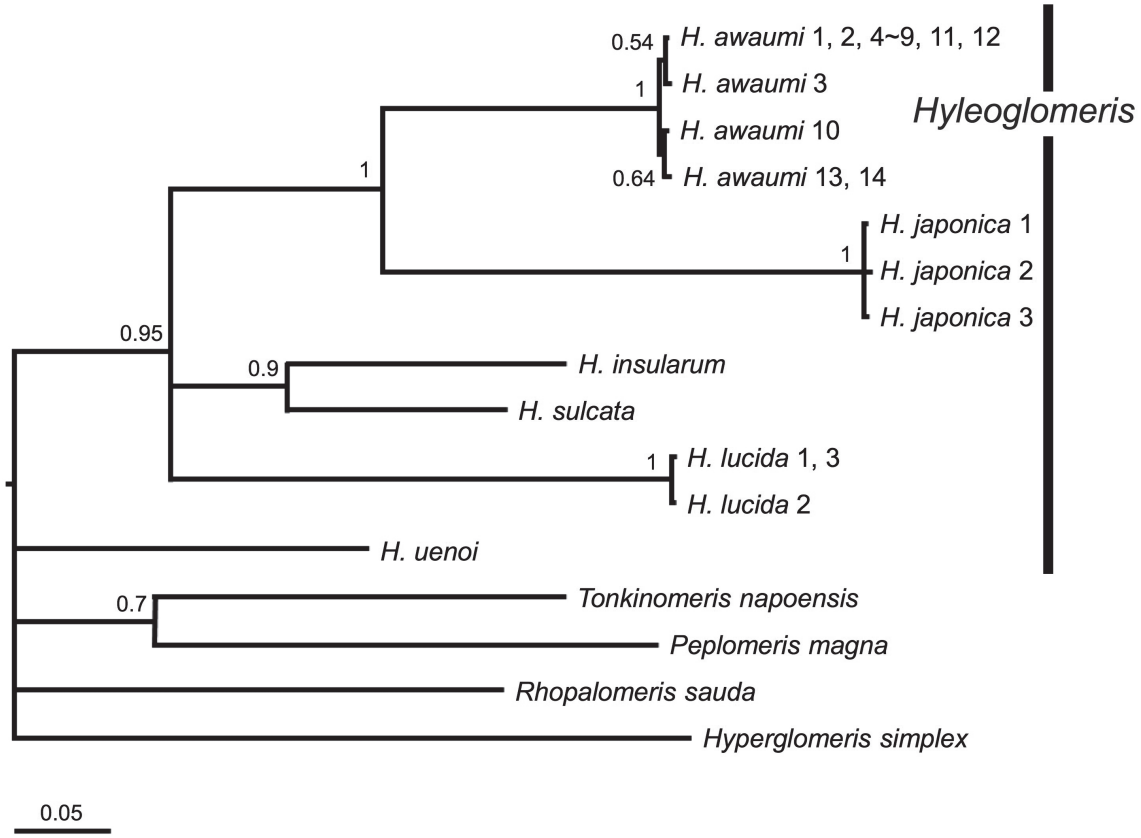

Fig. 1. Bayesian phylogenetic tree inferred based on the 658-bp *COI* sequence dataset involving *H. awaumi* Kuroda, Susukida & Eguchi, **sp. nov.** and five Japanese congeners. Bayesian posterior probabilities are indicated at the corresponding nodes. The scale bar indicates a branch length corresponding to 0.05 substitutions per site. The present *COI*-based phylogenetic tree is still provisional because the sequences of the following six Japanese congeners were not available: *H. magy*, *H. nigra*, *H. sakamotoensis*, *H. stuxbergi*, *H. triangularis* and *H. yamashinai*.

hensive dataset that is currently under construction by us for Japanese and Eastern and Southeast Asian species and lineages.

All of the 14 individuals of *H.* sp. A were grouped within a single clade with high support (pp = 1), and the maximum intraspecific diversity was 0.5% in p-distance and 0.005 in K2P (Table 2). On the other hand, the minimal interspecific divergence between *H.* sp. A and the five Japanese congeners examined ranged 10.9–13.5% in p-distance and 0.119–0.151 in K2P. Wesener & Conrad (2016) examined the local genetic diversity of Northern Italian *Glomeris* spp. of the family Glomeridae, and showed that the maximum intraspecific diversity and minimal interspecies divergence are 5.0 % and 6.7% (p-distance) in *COI,* respectively. If this barcode gap can be applied to the present study, *H.* sp. A appears to differ at the species level from the five Japanese congeners examined.

Based on the present morphological evidence and phylogenetic support, *H.* sp. A is reasonably concluded to be a new species, and is herein described.

Taxonomic accounts

Family Glomeridae Leach 1815
Subfamily Doderiinae Silvestri 1904
Genus *Hyleoglomeris* Verhoeff 1910

***Hyleoglomeris awaumi* Kuroda, Susukida & Eguchi, sp. nov.**
[Japanese name: Awaumi-tamayasude, アワウミタマヤスデ]
(Figs. 2A–J, 3A–F, 4A–D)

Holotype. Male adult (specimen ID: EG20210711-227-03); JAPAN, Shiga Pref., Omihachiman-shi, Miyauchi-cho, Hachiman-koen (park), 35.142235˚N, 136.085019˚E, 152 m alt.; 11 July 2021; K. Eguchi leg.; depository: MNHAH (A2014139).

Paratypes. 4 male adults (specimen ID: EG20210711-227-05, 07–09), 4 female adults (specimen ID: EG20210711-227-01, 02, 04, 06); same locality as the holotype; depository: MNHAH (EG20210711-227-01, A2014140; 02, A2014141; 05, A2014142), NSMT (EG20210711-227-04, 06–08), EG-coll (EG20210711-227-09).

Non-type materials examined. 4 male adults (KS20210513-01–04), 4 female adults (KS20210513-05–08);

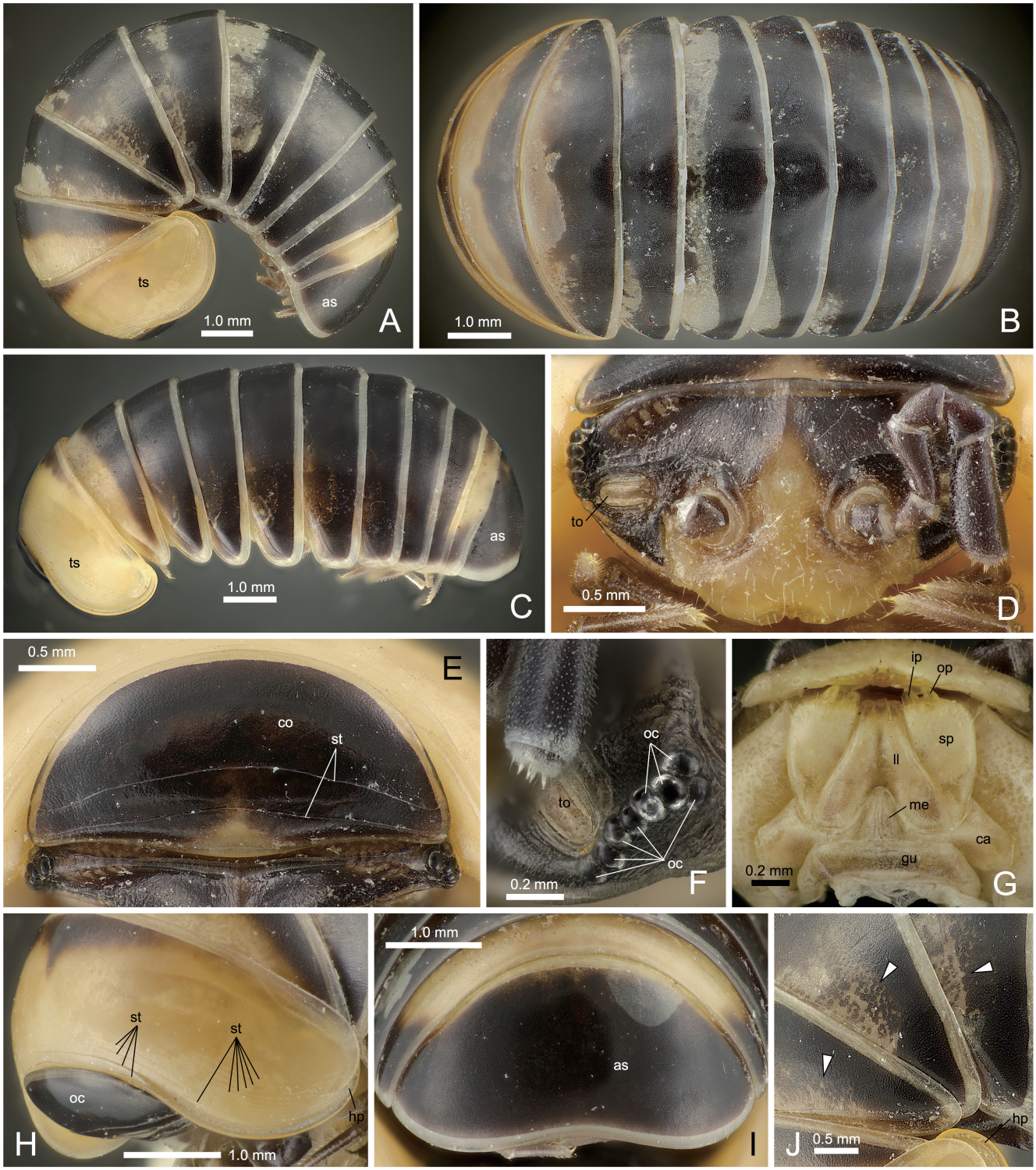

Fig. 2. *Hyleoglomeris awaumi* Kuroda, Susukida & Eguchi, **sp. nov.** A, B, D–J, holotype (male, specimen ID: EG20210711-227-03); C, paratype (male, EG20210711-227-07); A, C, body in lateral view; B, body in dorsal view; D, head in full-face view; E, vertex and column, in anterior view; F, ocelot in lateral view; G, mouthpart in ventral view; H, thoracic shield in anterodorsolateral view; I, anal shield in posterior view; J, lateral part of terga 2–7. Abbreviations: as = annal shield; ca = cardines; co = collum; gu = gula; hp = hyposchism; ip = inner palp of stipite; ll = lamellae lingualis; me = mentum; oc = ocelli; op = outer palp of stipite; sp = stipites; st = transverse striae; to = Tömösváry organ; ts = thoracic shield.

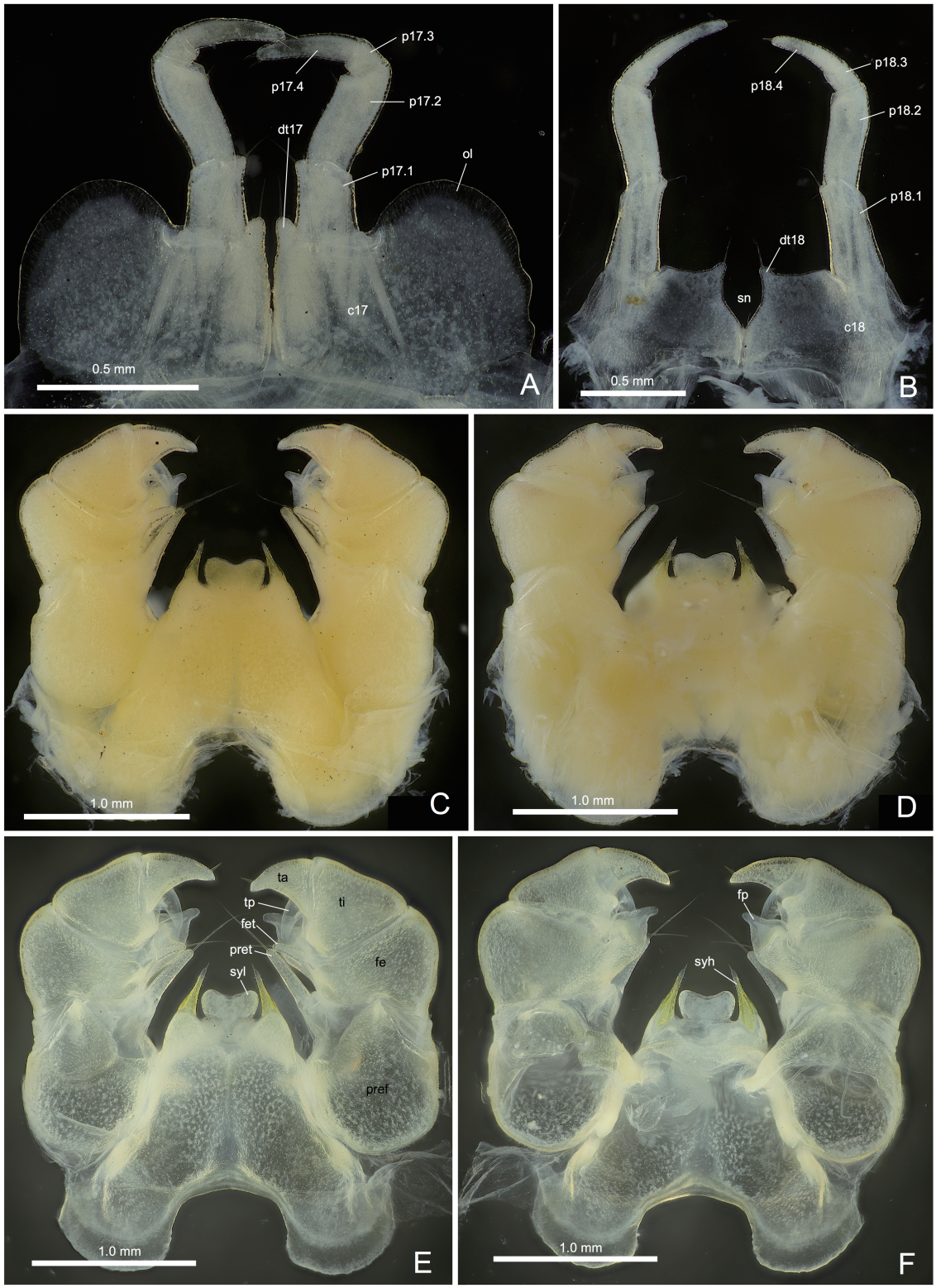

Fig. 3. *Hyleoglomeris awaumi* Kuroda, Susukida & Eguchi, **sp. nov.** A–D, holotype (male, specimen ID: EG20210711-227-03); E, F, paratype (male, EG20210711-227-07); A, leg 17 in anterior view; B, leg 18 in anterior view; C, E, telopods in anterior view; D, F, telopods in posterior view. Abbreviations: c17 = coxite of leg 17; c18 = coxite of leg 18; dt17 = distomesal tubercle of c17; dt18 = distomesal tubercle of c18; fe = femur; fet = femoral trichostele; fp = femoral process; ol = outer lobe of c17; p17.1–17.4 = podomere 1–4 of leg 17; p18.1–18.4 = podomere 1–4 of leg 18; pref = prefemur; pret = prefemoral trichostele; sn = syncoxital notch between c18; syh = syncoxital horns; syl = syncoxital lobe; ta = tarsus; ti = tibia; tp = tibial process.

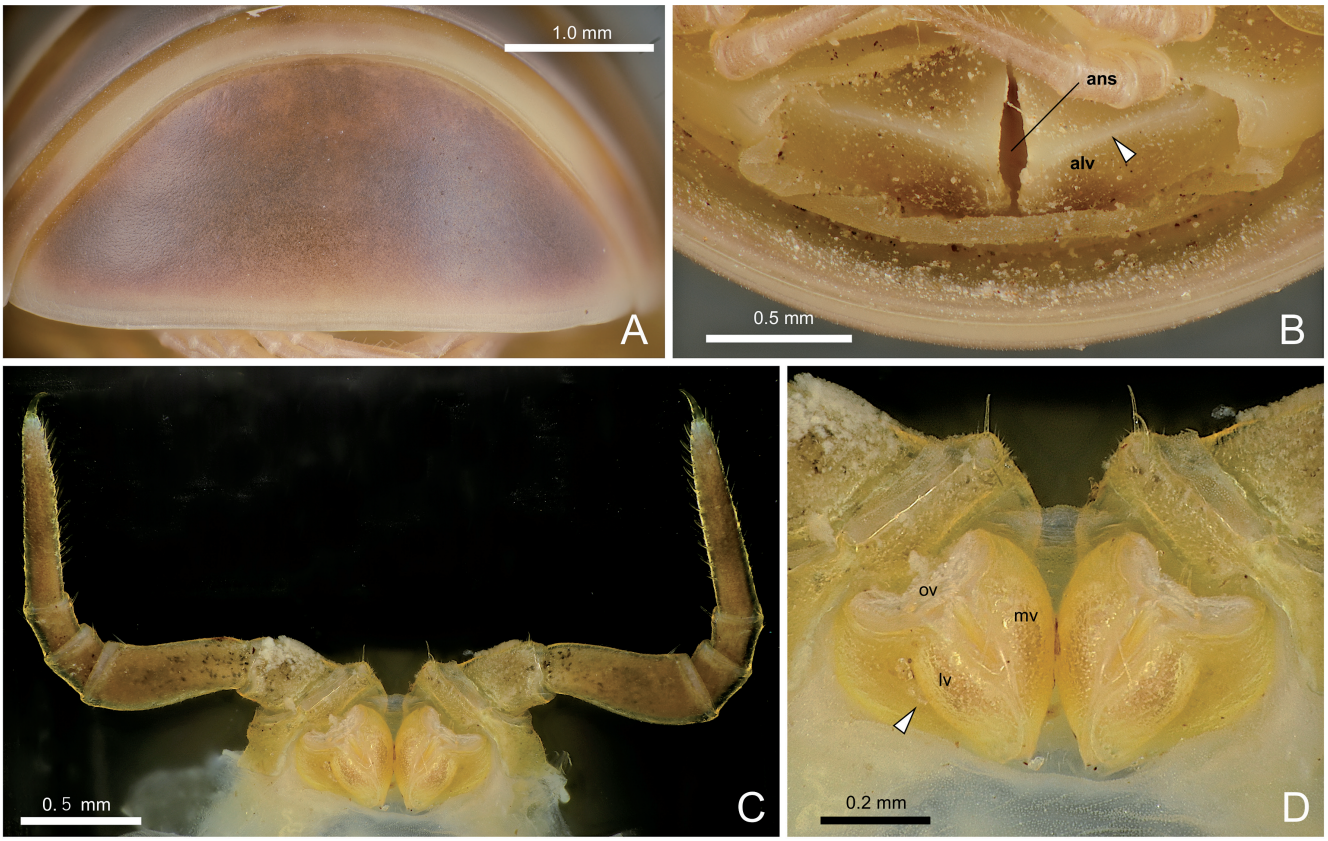

Fig. 4. *Hyleoglomeris awaumi* Kuroda, Susukida & Eguchi, **sp. nov.** A–D, paratype (female, specimen ID: EG20210711-227-01); A, anal shield in posterior view; B, anal part in ventral view; C, leg 2 in posterior view; D, vulva in posterior view. Abbreviations: ans = anal slit; alv, lateral valve of anus; lv, lateral valve of vulva; mv, meal valve of vulva; ov, operculum of valva.

JAPAN, Shiga Pref., Omihachiman-shi, Miyauchi-cho, 35.142115˚N, 136.085003˚E; 13 May 2021; K. Sakamoto leg; depository: EG-coll.

Diagnosis: male. Total body length ca. 9–11 mm; width of thorasic shield ca. 4–5 mm. Thoracic shield, anterior half of tergum 3, and dorsal part of tergum 11 largely yellow; the rest of the terga largely blackish-brown; terga 1–12 distinctly micro-scabrous and lacking luster. Ocelli 6+1 or 7+1. Thoracic shield with 4, 5 or 6 distinct transverse striae which all fully crossing the dorsum, and with 4 or 5 additional transverse striae in lateral part only; hyposchism reaching posterior margin of thoracic shield. Telopods with syncoxital lobe of telopods in anterior view widely bifid to form two sublobes which extend ventrolaterad; syncoxital horns ca. 1.5 times longer than syncoxital lobe, almost straight, tilting slightly toward syncoxital lobe (slightly converging each other), but not crossing each other, with short simple setae, with a pointed spine at the apex; both prefemoral and femoral trichosteles present, well developed, finger-shaped; femora in anterior view with strongly convex lateral outline; tibial process well developed, claw-shaped, strongly curved dorsomesad.

Description: holotype (male). Body large; total body length ca. 9 mm; maximum width of thoracic shield ca. 4.5 mm.

Vertex blackish-brown, with marbled yellowish lateral part; frons largely blackish-brown, with yellow lower-median area; labrum yellow. Collum (**co**) blackish-brown, with a small yellow anteromedian area. Thoracic shield and terga 3–11 with ivory-yellow lateral and posterior margins. Thoracic shield (**ts**; tergum 2) largely yellow, with black-brown posteromedian part. Tergum 3 yellow in anterior half and blackish-brown in posterior half. Terga 4–8 largely blackish-brown, with marbled yellowish anterolateral area (arrows in Fig. 2J). Terga 9–10 largely blackish-brown. Tergum 11 yellow dorsally and blackish-brown laterally. Annal shield (**as;** tergum 12) largely blackish-brown, with yellow anteromedian margin, with ivory-yellow posterior margin. Thoracic terga 1–12 distinctly micro-scabrous and lacking luster. (The body color of the holotype is partially bleached due to drying during photography.)

Ocelli 7 + 1 (**oc**); lenses convex, black. Tömösváry organ (**to**) transverse oval, ca. 1.5 times wider than long. Antennomere 6 large, clavate, longer than antennomere 4 and 5 combined, ca. 2.5 times longer than wide; antennal tip with four large, apical sensory cones. Gnathochilarium in ventral view basally consisting of wide and short gula (**gu**) and large cardines (**ca**); stipite (**sp**) subtriangular, ca. 2 times longer than wide (when excluding palps), with several seta along anterior margin, with inner palp (**ip**) and outer palp (**op**); both palps short and digitiform, almost same in length; lamellae lingualis (**ll**) fused but with a longitudinal groove

along masal line, with several seta apically; mentum (**me**) subtriangular, with inverted U-shaped apical outline, subdivided longitudinally along masal line.

Collum semicircular, with two transverse striae (**st**). Anterior marginal area of thoracic shield with 4 distinct transverse striae (**st**) fully crossing the dorsum, with 6 additional transverse striae (**st**) in lateral part only; hyposchism (**hp**) narrow, reaching posterior margin of thoracic shield. Other terga with a few short striae running anterodorsad from the posterolateral corner of each tergum (as seen in Fig. 1C). Anal shield in posterodorsal view with broadly and weakly concave posteromedian margin. Ozopores invisible in the mid-dorsum, behind the posterior margin of the tergites 3–10 (Fig. 2B).

Leg 17 strongly reduced, 4-segmented; coxite (**c17**) with a short and stout distomesal tubercle (**dt17**) bearing a long seta, with outer lobe (**ol**) roundly and relatively broadly produced ventrolaterad; podomere 1 (**p17.1**) ca. 1.3 longer than wide, with a small distomesal knob bearing a long seta; podomere 2 **(p17.2**) ca. 2.3 times longer than wide, with a short seta near the distomesal corner; podomere 3 (**p17.3**) ca. 0.9 times longer than wide, without seta; podomere 4 (**p17.4**) ca. 3.7 times longer than wide, with 2 short setae at the tip.

Leg 18 less strongly reduced; syncoxital notch (**sn**) roughly V-shaped; coxite (**c18**) with stout distomesal tubercle (**dt18**) which produces ventromesad and bears a long seta; podomere 4-segmented; podomere 1 (**p18.1**) ca. 1.9 times longer than wide, with a small distomesal knob bearing a seta; podomere 2 (**p18.2**) ca. 2.6 times longer than wide, with a short seta near the distomesal corner; podomere 3 (**p18.3**) almost as long as wide, with a short seta at the mid-length of mesal margin; podomere 4 (**p18.4**) ca. 4.3 times longer than wide, with a short and stout seta at the tip.

Telopods massive incrassate mesad. Syncoxital lobe (**syl**) in anterior view broader than long, widely bifid to form two sublobes which extend ventrolaterad, in ventral view curved and convex posterad. Syncoxital horns **(syh**) ca. 1.5 times longer than syncoxital lobe, almost straight, tilting slightly toward syncoxital lobe (slightly converging each other), but not crossing each other, with short simple setae, with a pointed spine at the apex. Prefemur (**pref**) in anterior view semi-globular; prefemoral trichostele (**pret**) very long and slender, digitiform (= finger-shaped), straight, apically with a long seta (seta on right trichostele missing in Fig. 2C, 2D). Femur (**fe**) in anterior view with strongly round lateral outline; femoral trichostele (**fet**) digitiform, slightly curved mesad, a little slenderer than and ca. 0.55 times longer than **pret**, apically with a long seta. Femoral process (**fp**) broadly based, with a short, digitiform tip directing ventromesad. Tibia (**ti**) in anterior view semi-trapezoidal, with a short seta near the distomesal corner. Tibial process (**tp**) well developed, claw-shaped, strongly curved dorsomesad; tip in posterior view hidden behind femoral process. Tarsus (**ta**) massive, claw-shaped, with a very short conical seta near the tip.

Variation: male paratypes. Body large; total body length ca. 9–11 mm (n = 4); maximum width of thoracic shield ca. 4–5 mm (n = 4). Ocelli 6 + 1; anterior marginal area of thoracic shield with 5 or 6 distinct transverse striae which all fully crossing the dorsum, with 4 or 5 additional transverse striae in lateral part only.

Description: female paratypes. Body large; total body length 10–11.5 mm (n = 5); maximum width of thoracic shield (tergum 2) 4.2–5 mm (n = 5). Vulva in posterior view roughly heart-shaped, large, covering approximately 2/3 of coxa of leg 2 (Fig. 4C); operculum (**ov**) thin dorsoventrally, depressed medially; mesal valve (**mv**) with rounded mesal outline, without a depression on the surface; lateral valve (**lv**) with rounded lateral outline, with a oblique depression (arrow in Fig. 4D); two valves forming a narrow slit between them, and bearing several setae along the slit; **mv** smaller **lv**; coxa forming an distomesal angle (but not a well-produced knob) which bears two setae. Anal shield in posterodorsal view with straight posteromedian margin. Lateral valves of anal part (**alv**) forming a longitudinal anal slit (**ans**); lateral valve with oblique ridge (pink arrow in Fig. 4B).

Remarks. *Hyleoglomeris awaumi* **sp. nov.** can be distinguished from the nine Japanese congeners of which the male is known (Attems 1909, Verhoeff 1936, 1937, 1942, Miyosi 1955, 1959, Takashima & Haga 1956, Haga 1968, Takano 1981, Golovatch et al. 2006, Nakama et al. 2022), by the combination of the following features: body large (total body length ca. 9–11 mm; width of thorasic shield ca. 4–5 mm); thoracic shield, anterior half of tergum 3, and dorsal part of tergum 11 largely yellow, and the rest of the terga largely blackish-brown; syncoxital lobe of telopods in anterior view widely bifid to form two sublobes; syncoxital horns ca. 1.5 times longer than syncoxital lobe, almost straight, tilting slightly toward syncoxital lobe but not crossing each other, with a pointed spine at the apex. *Hyleoglomeris awaumi* **sp. nov.** is morphologically similar to *H. stuxbergi*. Both species are characterized by yellow-colored thoracic shield and a distinctly bifid syncoxital lobe (Attems 1909). However, *H. awaumi* **sp. nov**. is much larger in size than *H. stuxbergi*: total body length 9–11 mm in *H. awaumi* **sp. nov.** vs. 7 mm in *H. stuxbergi*; maximum width of thoracic shield 4–5 mm in *H. awaumi* **sp. nov.** vs. 3 mm in *H. stuxbergi* (Attems 1909). The two species are also distinguished from each other by the shape of male telopods: syncoxital lobe widely bifid forming two sublobes extended ventrolaterad in *H. awaumi* **sp. nov.** vs. narrowly bifid to form a pair of sublobes extended ventrad in *H. stuxbergi*; syncoxital horns slightly converging on each other in *H. awaumi* **sp. nov.,** vs. almost parallel in *H. stuxbergi*; femoral trichostele slightly curved mesad in *H. awaumi* **sp. nov.,** vs. strongly bent laterad in *H. stuxbergi* (interpretation by the present authors based on Fig. 18 of Attems (1909)). According to the illustrations given in Nakama et al. (2022, figs. 3G, H), *H. magy* has its syncoxital lobe with a weakly concave distal margin which is resemble to those of *H. awaumi* **sp. nov.** However, the leg 17 is much reduced in *H. magy* (Nakama et al. 2022, fig. 3E) than in *H.*

awaumi **sp. nov.** (Fig. 3A); syncoxital horns are relatively short in *H. magy* (Nakama et al. 2022, fig. 3G, H) than in *H. awaumi* **sp. nov.** (Fig. 3C–F); body generally light yellow with pairs of blackish spots in *H. magy* (Nakama et al. 2022, fig. 2A–C), and blackish-brown, with largely yellow thoracic shield, anterior half of targum 3 and dorsal part targum 11 in *H. awaumi* **sp. nov.** (Fig. 2A–C, E, H, I).

Hyleoglomeris awaumi **sp. nov.** is morphologically distinguished from the other two Japanese congeners of which the male is unknown, *H. insularum* and *H. sulcata*, by the yellow-colored thoracic shield (black in the latter two species) (Verhoeff 1936, 1942).

Among the three valid named congeners known from Taiwan, *H. sinuata* often has a feebly concave syncoxital lobe (Golovatch et al. 2010), however, the lobe is not "bifid" as seen in *H. awaumi* **sp. nov.**. These two species can also be easily distinguished from each other by their body coloration. In all of the six valid named congeners known from Korea, syncoxital lobe is roundly convex or feebly concave (Golovatch et al. 1978, 2006, Mikhaljova & Lim 2006, 2018), but not bifid as in *H. awaumi* **sp. nov.**

Distribution and Habitat. Known in and around Hachiman-koen park (type locality), Omihachiman-shi (Shiga Pref.). In Hachiman-koen, many individuals (including the holotype and paratypes) were found under fallen leaves that have accumulated along the walking path in a broad-leave forest.

Etymology. Awa-umi (淡海) or Chikatsu-awa-umi (近つ淡海) is an ancient name used for Lake Biwa (琵琶湖) and for Shiga Pref. (= Ōmi no kuni, 近江国). Since the type locality is located in Omihachiman-shi, on the eastern shore of Lake Biwa, the species was named *Hyleoglomeris awaumi*.

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