

Descriptions of Two New Species of Valenciniidae (Nemertea) from Japanese Waters

Natsumi Hookabe^{1,2}

¹ Research Institute for Global Change (RIGC), Japan Agency for Marine–Earth Science and Technology (JAMSTEC),
Yokosuka, Kanagawa 237-0061, Japan

² Institute for Extra-cutting-edge Science and Technology Abant-garde Research of Life (X-Star), JAMSTEC,
Yokosuka, Kanagawa 237-0061, Japan

E-mail: hookaben@jamstec.go.jp; sofeechn312@gmail.com

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I describe two new species of the nemertean family Valenciniidae from Japanese waters: *Baseodiscus jimii* sp. nov. from subtidal habitats and *Cephalomastax fujiwarai* sp. nov. from a piece of deep-sea sunken wood. The new species in *Baseodiscus* Diesing, 1850 is clearly distinguishable from its congeners by unique external coloration patterns and head morphology, whereas *C. fujiwarai* sp. nov. is readily separated from the only previously known congener, *C. brevis* Iwata, 1957, by its uniform body coloration. In addition, a new record of *B. aff. marmoratus* (Bürger, 1890) from Japanese waters is provided in this study. Phylogenetic analyses based on a concatenated dataset of partial sequences of two mitochondrial and three nuclear genes recovered their phylogenetic positions among Valenciniidae.

Key Words: deep sea, nemertean, SCUBA, *Shinkai 6500*, Marine Protected Area (MPA).

Introduction

The class Pilidiophora represents one of the three major lineages within the phylum Nemertea and comprises heteronemerteans together with hubrechtellids and allied taxa (Thollessen and Norenburg 2003). Most pilidiophoran species belong to the family Lineidae, which is characterized by horizontally oriented lateral cephalic slits, whereas several non-lineid heteronemertean genera lack such lateral cephalic slits. Molecular phylogenetic studies have shown that some non-lineid heteronemerteans, including *Baseodiscus* Diesing, 1850, *Oxypolella* Bergendal, 1902, and *Sonnenemertes* Chernyshev, Abukawa, and Kajihara, 2015, form a clade sister to Lineidae (Chernyshev et al. 2015; Chernyshev and Polyakova 2018).

The genus *Baseodiscus* is the most species-rich genus within Valenciniidae, currently comprising 52 described species worldwide (Norenburg et al. 2025). Although most species occur in tropical and subtropical regions, members of the genus are also known from temperate, polar, and deep-sea environments. In contrast, *Cephalomastax* Iwata, 1957 is a poorly known monospecific genus, established for *C. brevis* Iwata, 1957 from Sagami Bay (Iwata 1957).

Japanese waters encompass a wide range of marine environments, from shallow subtropical reefs to the deep sea. However, the species diversity of Valenciniidae in this region remains incompletely understood. In this study, I describe two new species of Valenciniidae from Japanese waters: *Baseodiscus jimii* sp. nov. from subtidal habitats and

Cephalomastax fujiwarai sp. nov. from a piece of sunken wood collected in Hōei Seamount, Nishi-Shichito Ridge. The present study also documents a new record of *B. aff. marmoratus* (Bürger, 1890) in Japanese waters. These species are diagnosed based on external morphological characters, and their phylogenetic positions are inferred using a concatenated dataset of partial sequences of mitochondrial genes [16S rRNA (16S) and cytochrome *c* oxidase subunit I (COI)] and nuclear genes [18S rRNA (18S), 28S rRNA (28S), and histone H3 (H3)].

Materials and Methods

Specimens of Valenciniidae were collected from shallow subtidal to intertidal habitats and from bathyal sediments in Japanese waters between 2018 and 2026. Shallow-water specimens were collected by hand during SCUBA diving or from the intertidal zone, whereas a deep-sea specimen was obtained during the R/V *Yokosuka* (JAMSTEC) cruise YK22-17C in Hōei Seamount, Nishi-Shichito Ridge. Details of collection localities, depths, and voucher information are provided in the systematic accounts.

Living specimens were photographed immediately after collection using a digital camera (Olympus Tough TG-5 or NIKON D5600). Voucher specimens were fixed and preserved either in 99% ethanol or in Bouin's fluid. Tissue subsamples from the posterior end of the body were fixed/preserved in 99% ethanol and used for DNA extraction.

Genomic DNA was extracted from ethanol-preserved

tissue using standard protocols. Partial sequences of mitochondrial genes (16S and COI) and nuclear genes (18S, 28S, and H3) were amplified by PCR amplification using primers and thermal cycling conditions described in Hookabe et al. (2019). PCR products were purified and sequenced by Sanger sequencing performed in FASMAC (Kanagawa, Japan).

Sequence chromatograms were checked and assembled using Geneious Prime v11.0.24+8. Newly obtained sequences were aligned using MAFFT v7.490 (Kato and Standley 2013) or Clustal Omega v1.2.3 (Sievers et al. 2011), together with the datasets used in Kajihara et al. (2022) and Abato et al. (2025). Ambiguously aligned regions were removed prior to phylogenetic analyses using Gblocks v0.91b (Castresana 2000). Maximum-likelihood phylogenetic analyses were conducted using IQ-TREE v3 (T. K. F. Wong et al., unpublished preprint; available at <https://doi.org/10.32942/X2P62N>) under the MFP + MERGE scheme. The best-fit substitution models selected by ModelFinder (Chernomor et al. 2016; Kalyaanamoorthy et al. 2017) were GTR + MERGE for 16S, 18S, and 28S partitions, and the GY + MERGE codon model for COI and H3. Branch support was assessed using 1000 ultrafast bootstrap replicates (UFboot; Minh et al. 2013). Uncorrected pairwise genetic distances were calculated based on 16S in Geneious Prime. Newly obtained sequences were deposited in GenBank, with accession numbers provided in the species descriptions.

Type specimens have been deposited in National Museum of Nature and Science, Tsukuba (NSMT), Japan.

Results

Systematics

Baseodiscus jimii sp. nov.

[New Japanese name: Chirimen-himomushi]

(Fig. 1)

Material examined. Three specimens examined. Holotype: NSMT-Ne 25, unsectioned complete specimen, fixed in Bouin's fluid, collected on 16 January 2026 by Shouzo Ogiso and Mori Jinza at depths of 15–20 m off Okinoshima, Sukumo, Kochi, Japan; a posterior tip used for DNA extraction. Paratypes: NSMT-Ne 26, unsectioned complete specimen, fixed in Bouin's fluid, collected on 16 January 2026 by Shouzo Ogiso and Mori Jinza at depths of 15–20 m off Okinoshima, Sukumo, Kochi, Japan; a posterior tip used for DNA extraction; NSMT-Ne 27, unsectioned complete specimen, fixed in Bouin's fluid, collected on 13 May 2019 by Naoto Jimi at depths of 15–20 m off Ie Island, Okinawa, Japan; a posterior tip used for DNA extraction.

Description. Anaesthetized body 32–80 cm in length, 7–15 mm in width, background color pale yellowish cream,

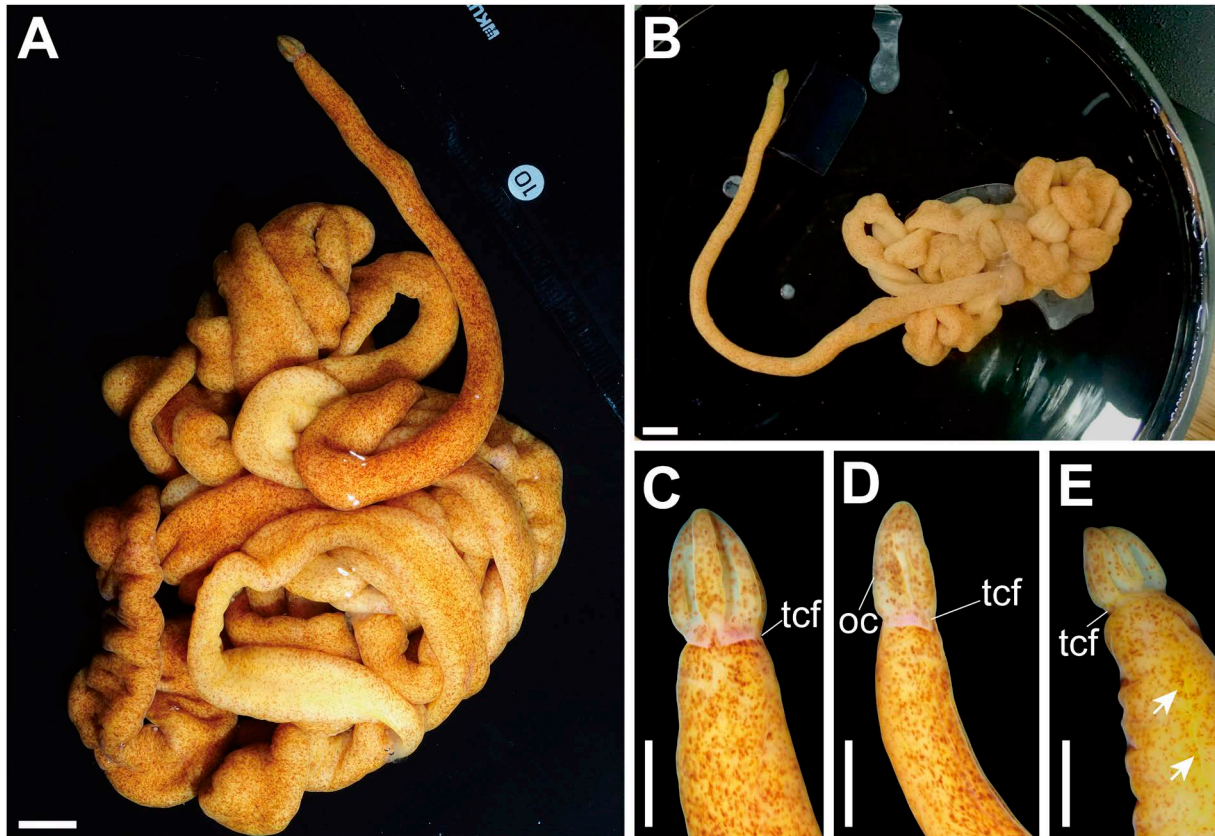


Fig. 1. Living specimens of *Baseodiscus jimii* sp. nov., holotype, NSMT-Ne 25 (A, C–E), and paratype, NSMT-Ne 27 (B). A, B, Whole body; C, magnification of head, dorsal side; D, lateral side; E, ventral side, white arrows pointing to mouth slit. Abbreviations: oc, ocelli; tcf, transverse cephalic furrows. Scales: A, B, 1 cm; C–E, 5 mm.

densely mottled with fine yellow-brown speckles (Fig. 1A, B). Pigmentation is less dense ventrally than dorsally (Fig. 1A). Head demarcated from body with transverse cephalic furrow; secondary furrows present (Fig. 1C–E). More than 17 ocelli arranged along head margin (Fig. 1D). Cerebral ganglia marked as a red spot. Mouth 6–7 mm long, slit-like (Fig. 1E).

DNA sequences. NSMT-Ne 25: GenBank accession nos PX971395 (16S), PX970517 (COI); NSMT-Ne 27: PX971393 (16S), PX970515 (COI), PX971398 (18S), PX971401 (28S), PZ000045 (H3).

Etymology. The specific name is a noun in the genitive case, after Dr. Naoto Jimi (Nagoya University), a Japanese polychaete researcher, who first discovered this species.

Distribution and habitat. The species is currently known off Okinoshima, Kochi and off Ie Island, Okinawa Japan; among rocks and rubble at depths of 15–20 m.

Remarks. The external coloration of *B. jimii* sp. nov. is characterized by a pale yellowish-cream background densely mottled with fine yellow-brown speckles, a pattern that most closely resembles those of *B. komatsui* Kajihara, Abukawa, and Chernyshev, 2022 and *B. takakurai* Gibson, 1995. However, *B. jimii* sp. nov. is readily distinguishable from both species by the color and contrast of the mottling and background pigmentation. In *B. jimii* sp. nov., the mottles are fine and yellow-brown, whereas in *B. komatsui* they consist of brown to dark-olive dots and in *B. takakurai* they are dark brown to nearly black.

Baseodiscus* aff. *marmoratus (Bürger, 1890)
[New Japanese name: Shibo-himomushi]
(Fig. 2A–C)

?*Eupolia marmorata* Bürger, 1890: 24, pl. I, fig. 11, pl. II, fig. 26, pl. V, fig. 73.

?*Baseodiscus delineatus* (Delle Chiaje, 1822): Gibson 1979: 139 (in part).

Baseodiscus aff. *marmoratus*: Kajihara et al. 2022: 531–532, fig. 7c.

Material examined. One complete specimen, unsectioned, fixed in 99% ethanol, collected on 16 May 2018 by Hiroshi Kajihara, Naoto Jimi, and Natsumi Hookabe from the rocky intertidal zone of Bisezaki, Motobu, Okinawa, Japan; a posterior tip was used for DNA extraction; currently deposited in the author's personal collection (JAMSTEC) prior to formal description.

Description. Body large, soft, measuring 47 cm in length and 20 mm in width when relaxed (Fig. 2A). Background color uniformly pale beige to creamy white, with a faint pinkish hue; dorsal surface exhibiting a fine brown bark-like pattern (Fig. 2A–C), whereas the ventral surface is uniformly creamy white. Head rounded and distinctly demarcated from the body by a transverse cephalic furrow (Fig. 2B, C). A total of 20–22 ocelli arranged along the head margin (Fig. 2C). Proboscis pore terminal. Mouth slit approximately 3 mm in length (Fig. 2C).

DNA sequences. 16S: GenBank accession no. PX971394;

COI: PX970514; 18S: PX971399; H3: PZ000044.

Distribution and habitat. The species is currently known from Bisezaki, Motobu, Okinawa, Japan (present study), Cù Lao Thu Island, Cù Lao Chàm Island, Vietnam (Kajihara et al. 2022); among rocks and dead corals, intertidal to subtidal at depths of 5–10 m.

Remarks. The Okinawan specimen shares a general body-coloration pattern with several western Pacific congeners, including *B. amboinensis* (Staub, 1900), *B. cf. amboinensis*, *B. curtus* (Hubrecht, 1879), *B. cf. curtus*, *B. delineatus*, *B. striatus* (Quoy and Gaimard, 1833), *B. marmoratus*, and *B. mindanaoensis* Abato and Kajihara in Abato, Abatay, Along, Aspe, Awa, Burias, L. Calagui, S. I. Calagui, Caneos, Dahilog-Caralde, Demetillo, Jovita, Leones, Niez, Seronay, and Kajihara, 2025, characterized by a pale background with brown longitudinal dorsal stripes and a uniformly pale ventral surface. However, the Okinawan specimen differs from *B. curtus* and *B. cf. curtus* in lacking sharply demarcated whitish head margins, and from *B. mindanaoensis* in lacking transverse dark pigmentation on the anterior neck region.

Based on its phylogenetic placement and overall agreement with Bürger's (1890) description of *E. marmorata*, particularly in terms of body coloration and dorsal striping pattern, the Okinawan specimen is provisionally identified as *B. aff. marmoratus* (Fig. 3). The uncorrected *p*-distance between the Okinawan (GenBank accession no. PX971394; present study) and Vietnamese specimens (DDBJ accession no. LC178656; Kajihara et al. 2022) is approximately 0.2% based on 495 bp of 16S. Species-level identification awaits barcode data, particularly COI, from topotypic material of *B. marmoratus* from Ambon, Indonesia.

Cephalomastax fujiwarai sp. nov.

[New Japanese name: Shinkai-maru-himomushi]
(Fig. 2D–F)

Material examined. A single specimen examined. Holotype: NSMT-Ne 28, unsectioned specimen, fixed in Bouin's fluid, collected on 25 September 2022 by Natsumi Hookabe and Hiroyuki Yokooka from a piece of sunken wood collected during the submersible dive 6K#1650 in Hōei Seamount, Nishi-Shichito Ridge (30°46.067'N, 138°45.3851'E).

Description. Body soft and cylindrical, measuring 2.8 cm in length and 4.5 mm in width (Fig. 2D). Body uniformly pale pink to light salmon, slightly darker anteriorly and gradually fading toward the posterior end, without any distinct body coloration pattern. Head rounded and clearly demarcated from the adjacent body region by transverse cephalic furrows (Fig. 2E). Secondary cephalic furrows absent. Ocelli not observed. Proboscis pore terminal. Mouth pit-like (Fig. 2F), situated posterior to the transverse cephalic furrow. Posterior portion of body broken during sampling.

DNA sequences. 16S: GenBank accession no. PX971392; COI: PX970516; 18S: PX971397; 28S: PX971400; H3: PZ000046.

Etymology. The specific name is a noun in the genitive case, honoring Dr. Yoshihiro Fujiwara (JAMSTEC), in rec-

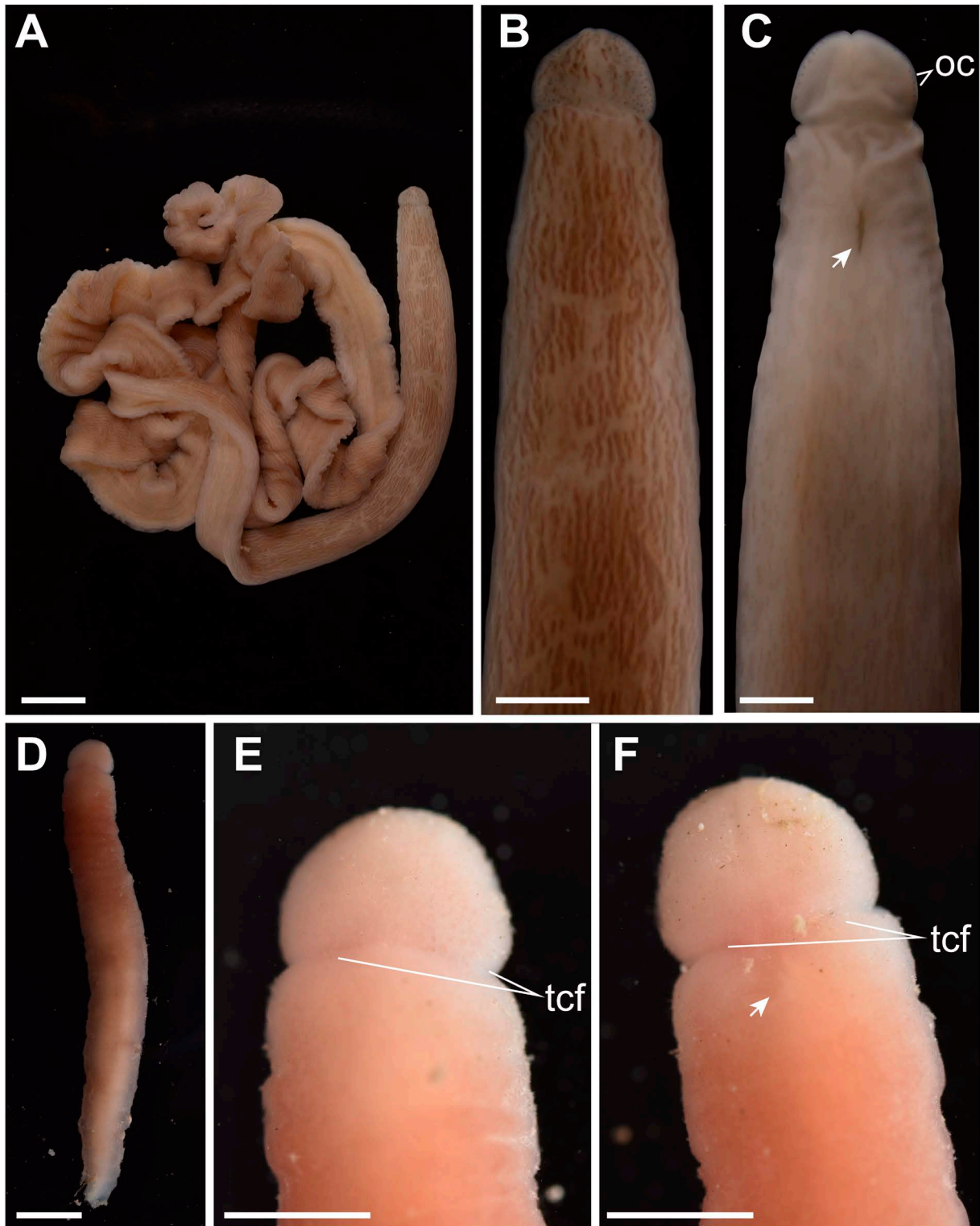


Fig. 2. Living specimens of *Baseodiscus* aff. *marmoratus* (A–C), and *Cephalomastax fujiwarai* sp. nov. (NSMT-Ne 28: D–F). A, D, Whole body; B, E, magnification of head, dorsal side; C, F, ventral side, a white arrow pointing to mouth opening. Abbreviations: oc, ocelli; tcf, transverse cephalic furrows. Scales: A, 1 cm; B–D, 5 mm; E, F, 2.5 mm.

ognition of his significant contributions to deep-sea biology and for leading numerous scientific expeditions including YK22-17C. The holotype was collected during a dive led by Dr. Fujiwara.

Distribution and habitat. The species is only known from the type locality, Hōei Seamount at a depth of 2180 m,

found among sunken woods.

Remarks. *Cephalomastax fujiwarai* sp. nov. is assigned to the genus *Cephalomastax* based on a combination of external characters used in the generic diagnosis, including a clearly demarcated head lacking lateral (oblique) cephalic furrows and the absence of ocelli (Iwata 1957). However,

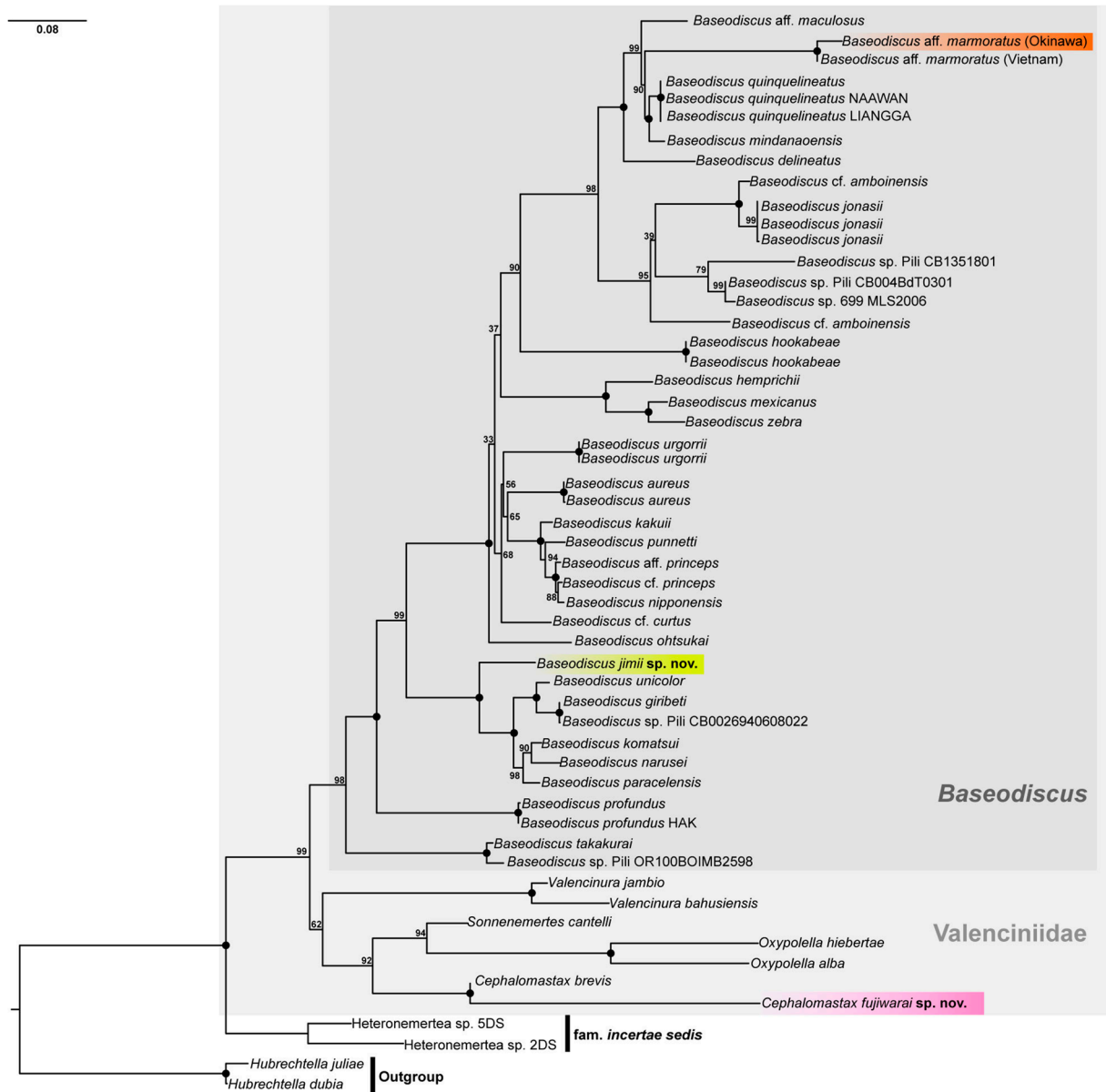


Fig. 3. Maximum-likelihood phylogenetic tree of Valenciniidae based on 16S (467 bp), COI (604 bp), 18S (1,748 bp), 28S (921 bp), and H3 (322 bp). Solid circles indicate full support (100%) of ultrafast bootstrap value calculated with IQ-TREE software (Trifinopoulos et al. 2016).

these characters are not exclusive to *Cephalomastax* and are known to occur in several non-lineid heteronemertean genera. Therefore, the generic placement of the new species is further supported by molecular phylogenetic analyses, which consistently recover *C. fujiwarai* sp. nov. as the sister species to *C. brevis*, the type and only previously described species of the genus. The uncorrected *p*-distance between the two species, calculated from 665 bp of COI is 6.9%, a value comparable to interspecific divergences reported for nemerteans (Sundberg et al. 2016).

Despite their close relationship, *C. fujiwarai* sp. nov. is clearly distinguishable from *C. brevis* by body coloration. The body of *C. fujiwarai* sp. nov. is uniformly pale pink to light salmon without any contrasting color pattern, whereas *C. brevis* exhibits a pale chestnut dorsal coloration with a distinctly whitish neck region and a white ventral surface.

Phylogeny

The maximum-likelihood phylogeny reconstructed from the concatenated dataset (Fig. 3) recovered a well-resolved topology broadly consistent with previous phylogenetic studies of Valenciniidae (Kajihara et al. 2022; Abato et al. 2025). Within Valenciniidae, species of *Baseodiscus* formed a well-supported monophyletic clade. The newly described *Baseodiscus* species were each nested within this clade.

Baseodiscus jimii sp. nov. was recovered as sister to a clade comprising *B. giribeti* Kajihara, Abukawa, and Chernyshev, 2022, *B. komatsui*, *B. paracelensis* Kajihara, Abukawa, and Chernyshev, 2022, *B. unicolor* Stiasny-Wijnhoff, 1925, and an unidentified *Baseodiscus* species; this clade corresponds to “clade A” sensu Kajihara et al. (2022) and “clade I” sensu Abato et al. (2025). The Okinawan specimen of *B. aff. marmoratus* was resolved as sister to the Vietnamese specimen within the clade corresponding to “clade C” sensu Kajihara

et al. (2022) and “clade IV” sensu Abato et al. (2025). All clades referred to here (clades A and C sensu Kajihara et al. 2022; clades I and IV sensu Abato et al. 2025) represent well-supported internal lineages of *Baseodiscus* shown in previous multilocus phylogenetic analyses.

Outside the *Baseodiscus* clade, representatives of *Valencinura* Bergendal, 1902, *Sonnenemertes*, *Oxypolella*, and *Cephalomastax* were recovered as distinct lineages within Valenciniidae. *Cephalomastax fujiwarai* sp. nov. was recovered as the sister species to *C. brevis*, the type and only previously known species of the genus. This sister-group relationship provides molecular support for the morphology-based placement of the new species within *Cephalomastax*.

Discussion

The present study provides descriptions of two new valenciniid species and documents a new record of *B. aff. marmoratus* from Japanese waters and inferred their phylogenetic positions within the family. As shown by *B. aff. marmoratus* in this study, several Japanese taxa appear to be closely related to, or possibly conspecific with, species originally described from Southeast Asia; however, molecular data from topotypic material are still lacking for many of these nominal species. In particular, several species described from Ambon, Indonesia, by Bürger (1890) and Staub (1900) remain unsequenced. Future progress in the taxonomy of Valenciniidae, including the discovery and delimitation of new species in Japan, will need the acquisition of molecular data from topotypic materials in Southeast Asia.

Data Availability Statement

The sequences used in this study have been deposited in DDBJ/GenBank/ENA under the accession numbers referred to in the text. All other data supporting the findings of this study are included in the published article.

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Author Contributions

Natsumi Hookabe: Conceptualization; Resources; Investigation, Visualization Writing – original draft.

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Declarations

Competing interests. The author declares no conflicts of interest.

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