

A new species of *Phalacrostemma* (Annelida, Sabellariidae) from the West Mariana Ridge, northwestern Pacific

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Abstract

A new species of *Phalacrostemma* (Annelida, Sabellariidae) is described based on the specimens collected at a depth of 675 m on the Ritto Seamount of the West Mariana Ridge, northwestern Pacific. This record represents both the deepest occurrence of Sabellariidae in Japan and the first record of the genus *Phalacrostemma* from the region. *Phalacrostemma ritto* **sp. nov.** dwells in a tube made of small sand particles and foraminiferans, which is attached to the spines of a cidarid sea urchin. The new species is characterized by having 22–30 pairs of outer paleae arranged in a spiral, outer paleae with acute tips and compact thecae, one or two inner paleae in each row, 8–13 opercular papillae on each side, five pairs of nuchal hooks with curved tips, a pair of slender ventral lobes on the first chaetiger, a single pair of conical papillae on the second chaetiger, bilobed notopodia in the middle to posterior abdomen, and abdominal uncini bearing three rows of teeth. A phylogenetic analysis, which included the new species and the newly sequenced *Idanthysus okudai* and *Sabellaria isumiensis* and was based on sequences of four gene fragments (COI, 16S, 18S, and 28S), was conducted. The new species was nested within the fully supported *Phalacrostemma* clade and recovered as the sister taxon to *Gesaia csiro*, whereas support values for phylogenetic relationships among sabellariid species were generally low.

Key words: Deep sea, Offshore Seabed Natural Environment Conservation Area, polychaete, Ritto Seamount, taxonomy

Introduction

The family Sabellariidae Johnston, 1865 comprises 150 species in 12 genera (Read and Fauchald 2025a). Most sabellariids inhabit intertidal to sublittoral zones, although the genera *Mariansabellaria*, *Phalacrostemma*, *Gesaia*, *Bathysabellaria*, and *Tetreres* are known exclusively from the deep-sea environments

(Capa and Hutchings 2014). The deep-sea genus *Phalacrostemma* Marenzeller, 1895 currently includes 15 valid species (Read and Fauchald 2025b). The shallowest record is for *P. gloriae* Kirtley, 1994, which was reported from the Gulf of Mexico at a depth of 228 m (Zhang et al. 2020), whereas the deepest records are for *P. perkinsi* Kirtley, 1994 from the Bahamas at 3000 m, and an unidentified *Phalacrostemma* species from the North Atlantic at the same depth (Chávez-López 2022).

A notable morphological feature of *Phalacrostemma* is its tube, which is composed of sand granules and dead foraminiferans (Kirtley 1994; Lechapt and Kirtley 1998; Chávez-López 2022). Some species attach their tubes to hard substrates, such as molluscan shells and sea urchin spines. For example, *P. maloga* Hutchings, Capa & Peart, 2012 was reported from a molluscan shell (Hutchings et al. 2012), *P. timoharai* Zhang, Hutchings, Burghardt & Kupriyanova, 2020 was living on a molluscan shell as a solitary individual (Zhang et al. 2020), *P. cidariophilum* Marenzeller, 1895 was reported from sea urchin spines, and *P. dorotheae* Kirtley, 1994 was found attached to both a gastropod shell and sea urchin spines (Chávez-López 2022).

In Japanese waters, five genera and 14 species of Sabellariidae have been recorded (Nishi and Kato 2002; Nishi et al. 2010; Jimi 2024; Nishi et al. 2025), and there are currently no confirmed records of *Phalacrostemma*. *Phalacrostemma elegans* Fauvel, 1911, reported by Imajima (2006) from 78–79 m off the Miura Peninsula in Sagami Bay without a description of its morphological characters, was subsequently transferred to the genus *Gesaia* by Kirtley (1994). Furthermore, records of deep-sea sabellariids other than *Phalacrostemma* from waters around Japan remain scarce; only *Lygdamis giardi* (McIntosh, 1885) has been reported from depths of 40–250 m in Tosa Bay (Imajima 2001) and 422–425 m off the Pacific coast of northern Honshu (Imajima 2009).

Offshore Seabed Nature Conservation Areas are deep-sea marine protected zones (MPA) designated in December 2020 under Japan's Nature Conservation Act (Ministry of the Environment 2020a, 2020b). These areas include four regions: the southernmost part of the Japan Trench and areas around the Izu-Ogasawara Trench; areas including the Naka-Mariana Ridge and West Mariana Ridge; areas including the Nishi-Shichito Ridge; and the northern part of the Mariana Trench. Five research voyages onboard the research vessel (RV) *Kaimei* in 2020–2022 and the deep-sea submersible support vessel *Yokosuka* in 2022–2024 documented unique deep-sea faunae, including new and rarely recorded species. Ritto Seamount, located in the southern part of the Offshore Seabed Natural Environment Conservation Area (Fig. 1), has yielded three new species of decapod crustaceans (Komai et al. 2023a, 2023b), as well as rare decapods and newly recorded fishes (Komai et al. 2022; Koeda et al. 2024). However, no annelids have yet been recorded from the southern part of the area.

In the present study, we describe a new species of *Phalacrostemma* collected from the bathyal zone of Ritto Seamount. This finding represents the deepest record of Sabellariidae in Japanese waters and the first confirmed record of *Phalacrostemma* from Japan. The individuals inhabit tubes composed of small sand particles and foraminiferans attached to sea urchin spines.

Materials and methods

Benthic samples were collected during a dive of the deep-sea submergence vehicle (DSV) *Shinkai 6500* operated from RV *Yokosuka*, during research cruise YK24-15C at Ritto Seamount, West Mariana Ridge, in October 2024 (Fig. 1). An unidentified cidarid sea urchin collected during this cruise bore short polychaete tubes composed of sand grains and dead foraminiferans attached to its spines (Fig. 2A–C). Two worms were extracted from the tubes, and photographs of the living individuals were taken on board (Fig. 2D, E). The worms and their tubes were fixed and preserved in 70% ethanol.

Digital photographs of the preserved specimens and tubes were taken using a Sony α77D camera equipped with a Minolta Macro-Zoom 1–3× lens. Photographs of chaetae were taken with an iPhone 7 (Apple Inc.) connected to a Leica CM-E compound microscope. The iPhone 7 camera was inserted into the eyepiece tube of the compound microscope through the microscope adapter i-NTer LENS, and optimal images were captured using Micronet i-NTer SHOT software. The microscope adapter and associated application software were manufactured by MeCan Imaging Co. Ltd, Saitama, Japan. Digital images were edited using ©Adobe Photoshop Elements version 10 (Adobe Systems Inc.).

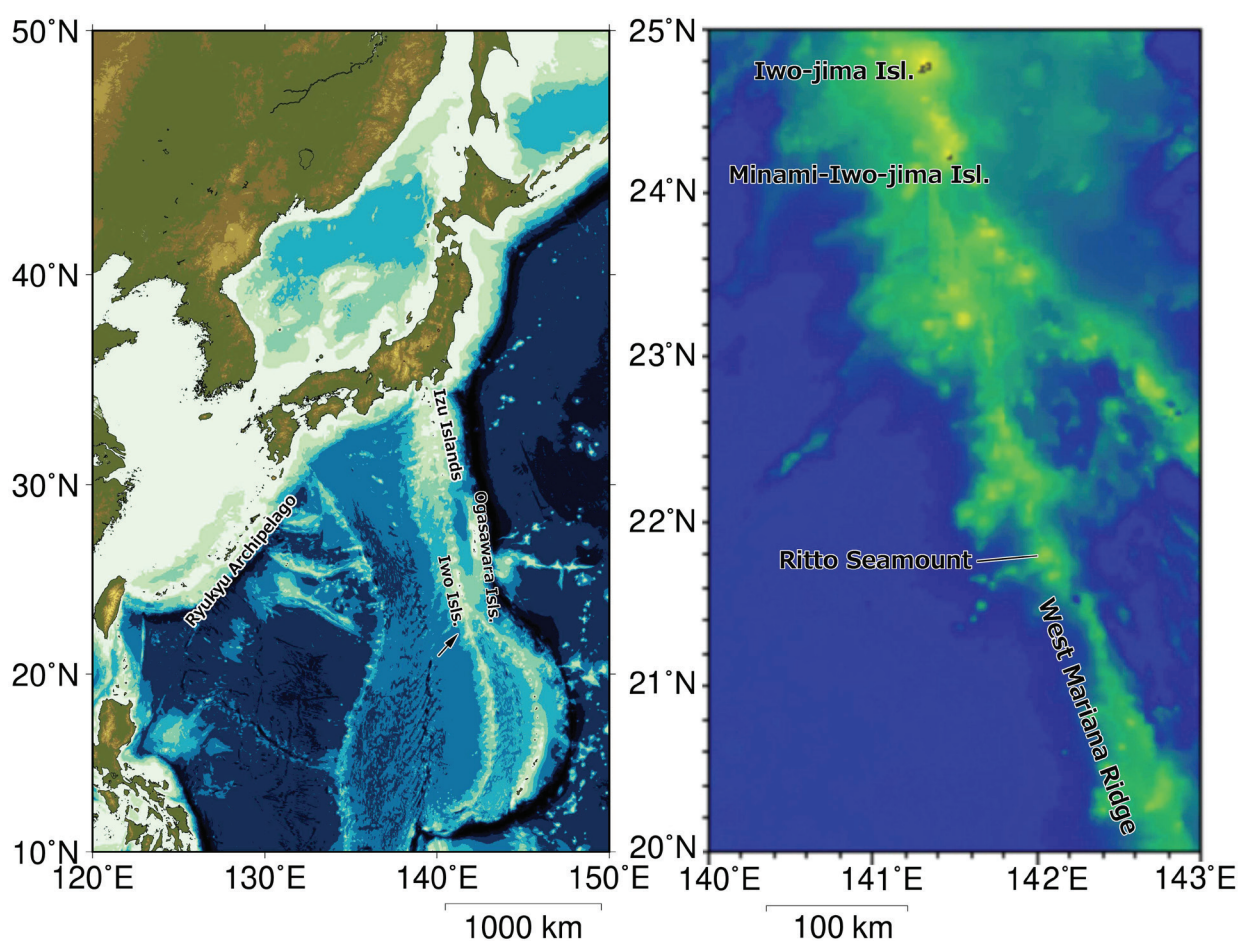


Figure 1. Map of the collection site in Japanese waters (left) and the Western Mariana Ridge, Ritto Seamount, Japan (right). The arrow on the left indicates the location of Ritto Seamount and the adjacent area. The base map on the right has been modified from the U.S. NOAA SRTM15_PLUS dataset.

For scanning electron microscopy (SEM), the parapodia with chaetal tufts were dehydrated through a gradual series of ethanol for 10 min each and finally washed with 100% ethanol for 10 min. The samples were then washed with a 1:1 and 1.5:0.5 mixture of 100% ethanol and hexamethyldisilazane (HMDS) for 10 min each, followed by 100% HMDS for 10 min as per Nation (1983) and Nishi et al. (2022a). Specimens were left overnight to ensure HMDS evaporation, then sputter-coated with platinum and examined using a Hitachi FE SU8010 at the Instrumental Analysis Center of Yokohama National University.

Terminology for morphological description follows Capa and Hutchings (2014) and Capa et al. (2012, 2015). The holotype and paratype specimens were deposited in the Japan Agency for Marine-Earth Science and Technology (JAMSTEC), Yokosuka, Kanagawa, Japan, and the comparative material was deposited in the Coastal Branch of the Natural History Museum and Institute, Chiba (CMNH), Katsuura, Japan.

A piece of the abdomen was removed using a scalpel and placed in 1.5 ml vials containing the mixture of 9 µL of proteinase K solution (Nacalai Tesque, Kyoto, Japan) and 100 µL of 10% solution of Chelex 100 Resin (Bio-Rad, Hercules, CA). The vial was incubated at 56 °C for 30 min, followed by 100 °C for 20 min, and the resulting supernatant was used as template DNA. In addition, DNA templates were prepared for one specimen each of two sabellariid species, *Idanthyrus okudai* Kirtley, 1994 (31 August 2015, from Tateyama, Chiba, Japan; CMNH-ZW 2341; identified according to Nishi and Kirtley 1999) and *Sabellaria isumiensis* Nishi, Bailey-Brock, Santos, Tachikawa & Kupriyanova, 2010 (16 July 2022, from Kunisaki, Oita, Japan; CMNH-ZW 2342; reported by Nishi et al. 2022b). Partial sequences of mitochondrial [16S rRNA (16S), COI] and nuclear [18S rRNA (18S), 28S rRNA (28S)] genes were obtained from the DNA templates (the holotype, the paratype, and the comparative specimens of *I. okudai* and *S. isumiensis*). The primer sets used are listed in Table 1.

PCR (35–40 cycles) was performed following Kobayashi and Nishi (2026) or Kobayashi et al. (2025), using the following enzymes: MightyAmp DNA Polymerase v. 3 (TaKaRa Bio, Kusatsu, Japan) for 16S; KOD One PCR Master Mix (TOYOBO, Osaka, Japan) for 18S and 28S; GoTaq G2 Hot Start Colorless Master Mix (Promega, WI, USA) for COI and 16S; or TaKaRa Ex Premier DNA Polymerase (TaKaRa Bio, Kusatsu, Japan) for COI, 18S, and 28S. The annealing temperature was 50 °C, except for COI (45–48 °C). PCR products were checked by electrophoresis on a 2% agarose gel, and the PCR products were purified using ExoSAP-IT (Thermo Fisher Scientific, Waltham, MA).

Sequencing was outsourced to Eurofins Genomics (Tokyo, Japan) or performed using an ABI 3500xl automated DNA sequencer (Applied Biosystems (ABI), MA, USA) after cycle sequencing with BigDye Terminator Cycle Sequencing Kit v3.1 (ABI) and subsequent purification by ethanol precipitation. The obtained nucleotide sequences were deposited in the DNA Data Bank of Japan (DDBJ) under DDBJ/EMBL/GenBank accession numbers (Table 2).

A phylogenetic analysis of sabellariids was conducted using concatenated COI, 16S, 18S, and 28S gene sequences. The outgroup, *Marenzelleria viridis* (Verrill, 1873) (Spionidae), was chosen following Nishi et al. (2025). The sequences were aligned using MAFFT v. 7.294b (Katoh and Standley 2013), and ambiguously aligned regions were removed with trimAl v. 1.4.rev22 (Capella-Gutiérrez et al. 2009) using the -gappypout option, resulting in alignments of 634 (COI), 537

Table 1. Primers used in the present study.

Locus	Primer	Sequence (5'–3') ¹	Usage ²	Reference
COI	COI1f	GTATAAGAGACAGGACAG AYTCNACNAAAYCAYAARGAYATYGG	P	Kobayashi and Abe (2024)
	COI1r	GTATAAGAGACAGTTCT CGGNGGRTANACNGTYCANCC	P/S	Kobayashi and Abe (2024)
	COI2f	GTATAAGAGACAGGACAG CCNGAYATRKCNNTTYCCNCG	P/S	Kobayashi and Abe (2024)
	COI2r	GTATAAGAGACAGTTCTCT AAACTTCAGGRTGNCCRAARAAYCA	P	Kobayashi and Abe (2024)
	LCO-annelid	CTCAACWAAYCAYAAAGAYATTGG	P/S	Kobayashi et al. (2022)
	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	P/S	Folmer et al. (1994)
16S	16Sa-ann	TCGMCTGTTTANCAAAAACA	P/S	Kobayashi et al. (2023)
	16Sb-ann	CGGTCTRAACTCARCTCAYG	P/S	Kobayashi et al. (2023)
	16Sann-f2	CCTGACYGTGCWAAGGTAGC	P/S	Kobayashi and Kojima (2021)
	16Sann-r2	CCYTAAGYCAACAYCGAGGT	P/S	Kobayashi and Kojima (2021)
18S	18SA1	CCTACCTGGTTGATCCTGCCAG	P	Steiner and Dreyer (2003)
	NS2	GGCTGCTGGCACCAGACTTGC	S	White et al. (1990)
	NS5	AACTTAAAGGAATTGACGGAAG	S	White et al. (1990)
	189r	TCGGAATTAACCAGACAAATC	S	Nakamura et al. (2007)
	1800r	ATGATCCTTCGCGAGGTTCAAC	P	Steiner and Dreyer (2003)
	18S1f	GTATAAGAGACAGGACAG TGCGCTTGTCTCAAAGATTAAGCC	P	Kobayashi and Abe (2024)
	18S1r	GTATAAGAGACAGTTCTC GCCTGCTGCCTTCCTTRGAWGTGG	P/S	Kobayashi and Abe (2024)
	18S_2f	GTATAAGAGACAGGACAG ACGGGTRRCGGRGAATYAGGGTTC	P/S	Kobayashi and Abe (2024)
	18S_2r	GTATAAGAGACAGTTCTC GARCACTCTAATTTTTTCAAAG	P	Kobayashi and Abe (2024)
28S	D1	ACCCSCTGAAYTTAAGCAT	P/S	Brown et al. (1999)
	D3	GACGATCGATTTCACGTCA	P/S	Vonnemann et al. (2005)
	28S_1f	GTATAAGAGACAGGACAG CGACCTGAGATCAGRCGRGRYTACC	P	Kobayashi and Abe (2024)
	28S_1r	GTATAAGAGACAGTTCTC TRCGGTMCYAYYMGTTTRMCT	P/S	Kobayashi and Abe (2024)
	28S_2f	GTATAAGAGACAGGACAG GAAAAGRACTTTGAAGAGAGAGT	P/S	Kobayashi and Abe (2024)
	28S_2r	GTATAAGAGACAGTTCTC CCCTTGGTCCGTGTTTCAAGACGGGT	P	Kobayashi and Abe (2024)

¹The regions in bold indicate binding sites used for next-generation sequencing (Kobayashi and Abe 2024), which may not be required for Sanger sequencing.

²P, PCR; S, sequencing.

(16S), 1696 (18S), and 912 (28S) characters, respectively. Maximum likelihood (ML) analysis was performed in IQ-TREE v. 2.2.0.3 (Minh et al. 2020) with 1000 ultrafast bootstrap (ufBS) replicates and SH-aLRT tests (Anisimova et al. 2011). The best-fit substitution models for each locus were selected using ModelFinder (Kalyaanamoorthy et al. 2017) for the datasets as follows: GTR+F+I+G4 for COI, GTR+F+G4 for 16S, TNe+G4 for 18S, and TIM3+F+G4 for 28S. The resulting tree was edited using FigTree v. 1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Nucleotide sequences of 18S, 28S, and both mitochondrial genes of *Phragmatopoma caudata* (Krøyer in Mörch, 1863) included in the phylogenetic analysis were obtained from contigs assembled from NGS reads deposited in the NCBI Sequence Read Archive (SRR5818305). Assembly followed Kobayashi (2023) using SPAdes v. 4.2.0 (Bankevich et al. 2012), and gene searches were conducted with nhmmer implemented in HMMER v. 3.4 (Wheeler and Eddy 2013) and MitoS2 (Bernt et al. 2013). The assembled gene sequences were deposited as Third Party Data (TPA) in the DNA Data Bank of Japan (DDBJ) (Table 2).

Table 2. Species used for phylogenetic analysis with GenBank accession numbers. Bold indicates sequences obtained or assembled in the present study. As only the longest sequence of each gene per species was used, sequences not used for the phylogenetic analysis are shown in parentheses.

Family	Species	COI	16S	18S	28S
Sabellariidae	<i>Phalacrostemma ritto</i> sp. nov., holotype	(LC931932)	(LC931933)	(LC931930)	(LC931931)
	<i>Phalacrostemma ritto</i> sp. nov., paratype	LC931928	LC931929	LC931926	LC931927
	<i>Gunnarea gaymardi</i>	MN045177	—	DQ317111	EU256544
	<i>Gesaia csiro</i>	MN852335	MN850402	MT524308	MT524314
	<i>Idanthyrus australiensis</i>	KX342947	HM800975	HM800960	HM800996
	<i>Idanthyrus okudai</i>	LC788092	LC931936	LC788094, (LC931934)	(LC788095, LC788096), LC931935
	<i>Neosabellaria cementarium</i>	MH242863	—	AY732223	AY732226
	<i>Neosabellaria upopoy</i>	LC855022	LC855041	LC854982	LC855002
	<i>Phragmatopoma caudata</i>	YABB01000007	YABB01000001	YABB01000002	YABB01000003
	<i>Phalacrostemma timoharai</i>	MN852334	MN850398	MT524312	MT524317
	<i>Phalacrostemma</i> sp. AM W.50676	MN852332	MN850399	MT524313	MT524318
	<i>Sabellaria alveolata</i>	KR002647	AY340479	AY340442	AY340416
Spionidae	<i>Sabellaria isumiensis</i>	LC931940, (LC931943)	LC931937, (LC931941)	LC931938, (LC931942)	LC931939
	<i>Marenzelleria viridis</i>	HQ024089	EF431973	EU418860	EU418868

Results

Taxonomy

Family Sabellariidae Johnston, 1865

Genus *Phalacrostemma* Marenzeller, 1895

New Japanese name. Shinkai-Kanmurigokai.

Phalacrostemma ritto sp. nov.

<https://zoobank.org/B7D78E72-6451-4CC5-A38E-CD48516CB9A4>

Figs 2–4

New Japanese name. Ritto-Shinkai-Kanmurigokai.

Material examined. Holotype: JAPAN • Western Mariana Ridge, Ritto Sea-mount, 21°47.830'N, 142°2.382'E (Fig. 1), depth 675 m; 10 October 2024, DSV *Shinkai 6500* operated from RV *Yokosuka*, Cruise YK24-15C; leg. Jimi Naoto; on a spine of a cidarid sea urchin (Fig. 2A–C); with tube; GenBank accession numbers: **LC931930–LC931933** (Table 2); JAMSTEC #11820 An93-1. **Paratype:** 1 specimen with tube broken into two pieces between the anterior region and mid-abdomen; sampling data as for the holotype; GenBank accession numbers: **LC931926–LC931929** (Table 2); JAMSTEC #11820 An93-2.

Description. Based on the holotype and the paratype (paratype data in parentheses).



Figure 2. *Phalacrostemma ritto* sp. nov. **A.** Habitat of the sea urchin of the family Cidaridae; **B.** Tubes attached to sea urchin spines; **C.** Close-up view of the tube; **D, E.** Live animal (holotype); **F.** Dorso-lateral view of preserved specimen (holotype); **G.** Ventral view of head and operculum; **H.** Dorsal view of head and operculum; **I.** Anterior view of operculum; **J.** Middle to posterior abdomen, arrows indicate lobes of notopodia. Abbreviations: bf: buccal flap; ca: cauda; ip: inner palea; mo: median organ; nc: neuropodial cirri; nh: nuchal hook; op: outer palea; p: palp. Scale bars: 0.5 mm.

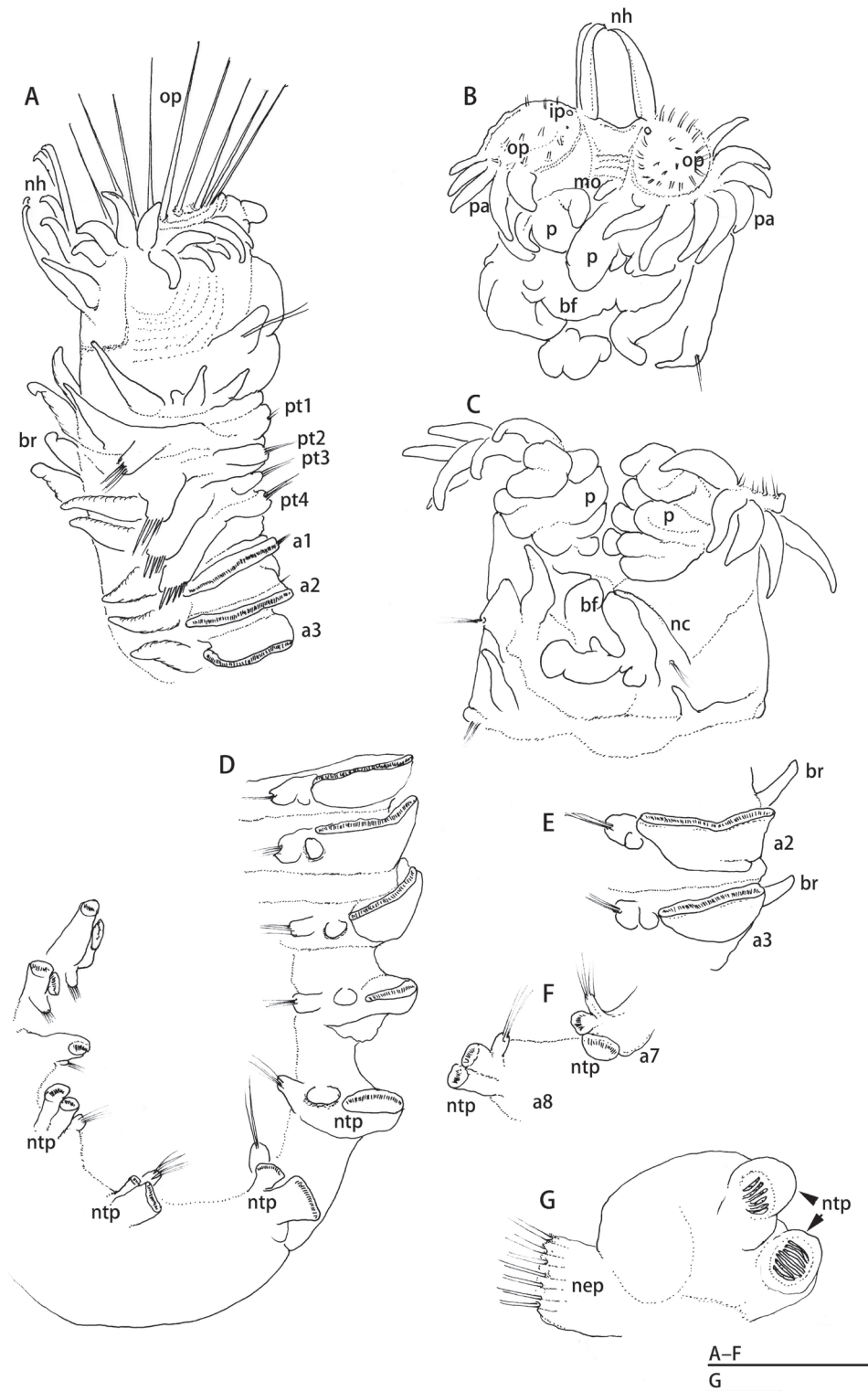


Figure 3. *Phalacrostemma ritto* sp. nov. **A, B, G.** Paratype; **C–F.** Holotype. **A.** Lateral view from head to parathoracic region, half of operculum omitted; **B.** Antero-ventral view of operculum, paleae omitted; **C.** Ventral view of head and operculum, paleae omitted; **D.** Ventral view of abdomen (right side), showing notopodia and neuropodia, left side omitted; **E.** Close-up view of second and third abdominal parapodia; **F.** Close-up view of 7th and 8th parapodia; 9th parapodium also shown. pt1–4 in A indicate first to 4th parathoracic chaetiger, a1–a3 in A, a2 and a3 in E, a7 and a8 in F indicate abdominal chaetiger number. Abbreviations: bf: buccal flap; br: branchia; ip: inner paleae; mo: median organ; nc: neuropodial cirri; nep: neuropodium; nh: nuchal hook; ntp: notopodium; op: opercular palea; p: palp; pa: opercular papillae; pt: parathoracx. Scale bars: 1 mm (**A–F**); 0.1 mm (**G**).

Holotype 10.0 mm in length without paleae and cauda (7.5 mm without paleae and cauda), 2.0 mm in width at parathoracic region. Operculum divided into two short, free lobes with distal ends positioned perpendicular to the longitudinal axis (Figs 2G–I, 3A–C). Opercular paleae longer than the operculum (Figs 2I, 3A); outer row with 25 paleae on the right, 28 on the left (22 on the left, 30 on the right), arranged spirally (Figs 2F–I, 3B).

Paleae simple, straight, with acute tips (Fig. 4B, H); distal portions of some paleae black (Figs 2I, 4E, F). Paleal thecae compact, with straight margins (Fig. 4B–F, H–K). Paleae arranged in two rows; inner row with one palea on the left and two on the right (two on the left and one on the right), simple and straight with tapering tips, shorter than those of the outer row (Fig. 4G, L, M). Eight conical opercular papillae on the right side and 11 on the left (13 on the right, 11 on the left), arranged peripherally to the outer paleae (Figs 2F–I, 3A–C); papillae with blunt tips (Fig. 3A–C), approximately $\frac{1}{2}$ length of the outer paleae, with a basal width/length ratio of 0.6–0.8.

Five pairs of flattened nuchal hooks; concave side limbate, with tips curved at approximately 45° , wider than limbation (Figs 2H, I, 4A). Median organ present at the dorsal junction of opercular lobes (Figs 2H, 3B); median organ slender, about $\frac{1}{2}$ length of the conical opercular papillae (Fig. 3B). Eyes not observed. Tentacular filaments absent. Buccal flaps present below a pair of palps (Figs 2G, I, 3B, C).

Chaetiger 1 (= segment 1) with neuropodial lobes and capillary neurochaetae (Fig. 3A). Chaetiger 2 with a pair of triangular lateral lobes, a pair of neuropodial lobes, and branchiae (Figs 2F, G, 3A). Dorsal tapering branchiae present from chaetiger 2 onwards (Figs 2H, 3A). Chaetigers 3–6 (parathorax) with two types of notochaetae—lanceolate ones interspersed with fine capillaries (Figs 3A, 4N)—and neurochaetae comprising slender lanceolate chaetae and fine capillaries.

Eleven abdominal chaetigers in the holotype and 13 in the paratype (Fig. 3D). Eight pairs of dorsal branchiae, continuing from the second thoracic chaetiger to the third abdominal chaetiger (Fig. 3A, E). Abdominal notopodia of chaetigers 1–5 unilobed, each with a single horizontal row of uncini (Fig. 3D, E); notopodia of chaetigers 6 to last bilobed, forming erect, expanded tori bearing uncini (Figs 2J, 4O). Each uncinus with three vertical rows of teeth and 8–10 columns (Fig. 4P, Q). Neuropodia with fine capillaries (Figs 2J, 3E, F).

Cauda long, approximately 4.0 mm in length, equal to the combined length of the abdomen and thorax in live specimens (Fig. 2D, E), smooth; about $\frac{1}{4}$ length of the abdomen in preserved specimens (Fig. 2F).

Tubes attached to sea urchin spines and composed of small sand particles (Fig. 2B, C); tubes with dark-brown inner lining; inner diameter of tubes 1.2–1.3 mm, outer diameter 2.5–3.5 mm.

Type locality. Ritto Seamount, West Mariana Ridge, Japan (Fig. 1).

Etymology. The specific name *ritto*, a noun in apposition, refers to the type locality, Ritto Seamount.

Taxonomic remarks

Phalacrostemma ritto sp. nov. is characterized by a unique combination of morphological features: outer paleae with straight edges and without expanded thecae; five pairs of nuchal spines; absence of tentacular filaments; presence of buccal flaps; and bilobed notopodia in the middle to posterior abdomen, with each lobe bearing a row of abdominal uncini with three vertical rows of teeth.

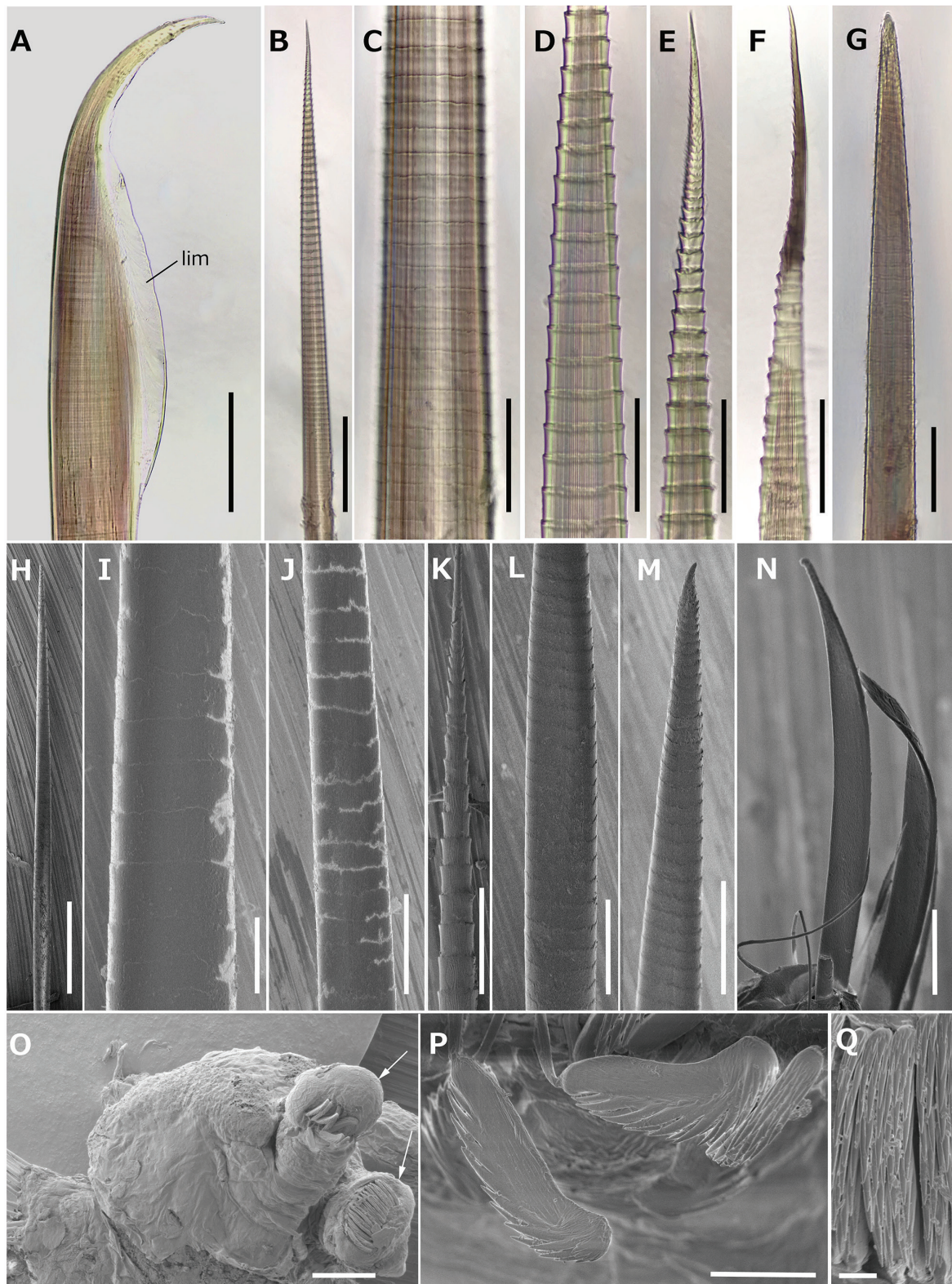


Figure 4. *Phalacrostemma ritto* sp. nov. **A–G.** Light photographs; **H–Q.** SEM micrographs. **A.** Nuchal hook, lim indicates limbation; **B.** Outer palea, whole view; **C.** Outer palea, basal part; **D.** Outer palea, middle part; **E.** Outer palea, tip; **F.** Outer palea, black tip; **G.** Inner palea; **H.** Outer palea, whole view; **I.** Outer palea, basal part; **J.** Outer palea, middle part; **K.** Outer palea, tip; **L.** Inner palea, middle part; **M.** Inner palea, distal tip. **N.** Parathoracic chaetiger showing lanceolate chaetae and fine capillary chaetae; **O.** Middle abdomen; showing bilobed notopodia (right) and neurochaetal tuft (left); arrows indicate lobes of notopodia. **P.** Abdominal uncini, lateral view; **Q.** Abdominal uncini, ventral view. Scale bars: 200 μm (**A**, **B**, **H**); 50 μm (**C–G**, **O**, **J–M**); 20 μm (**I**, **N**); 10 μm (**P**); 5 μm (**Q**).

Moreover, *Phalacrostemma ritto* sp. nov. is the only species in the genus—and, to our knowledge, in the family—with bilobed notopodia in the abdomen; all other species possess unilobed abdominal notopodia.

Regarding the taxonomic value of bilobed (or unilobed) abdominal notopodia, many previous taxonomic studies lack sufficiently detailed descriptions and illustrations of the abdominal parapodia, making direct comparisons difficult. However, some published illustrations clearly show unilobed rather than bilobed parapodia (e.g. Zhang et al. 2020). In addition, the parapodia were likely examined during the extraction of the uncini for microscopic observation. If, as in our new species, the parapodia were divided into two lobes and the row of uncini were correspondingly divided, this feature would likely have been noted in the original descriptions. Thus, although this remains speculative, it is likely that sabellariid species other than the new species described here from the West Mariana Ridge possess unilobed abdominal parapodia and, consequently, a single uninterrupted row of uncini.

Molecular results

The COI gene sequences obtained from the holotype and the paratype (658 bp) were almost identical, differing by 0.46% (*p*-distance). A BLAST search indicated that the COI sequences of the new species were significantly different from those of sabellariids available in GenBank, with the top hit being *Scolecipis mesnili* (Bellan & Lagardère, 1971) (Spionidae) ([MN215916](#); 81% identity).

Although only the posterior part (143 bp) of the target 16S sequence (474 bp) was recovered from the holotype, the overlapping 143-bp region was identical between the holotype and the paratype. A BLAST search of the 16S sequence of the paratype returned *Phalacrostemma* sp. as the top hit ([MN850399](#); 89.3% identity) and *P. timoharai* as the second and third hits ([MN850397](#) and [MN850398](#); 88.8% identity). The 18S and 28S sequences were also nearly identical between the two specimens and showed high similarity to *Phalacrostemma* sp. AM_W50676 (98.3%) and *P. timoharai* (99.3%).

Phylogenetic analysis

Two major clades were recovered: (1) *Gesaia csiro* + *Phalacrostemma* spp. (SH-aLRT = 89.7, ufBS = 92), and (2) a clade comprising other sabellariids (*Idanthyrus*, *Phragmatopoma*, *Neosabellaria*, *Gunnarea*, and *Sabellaria*; SH-aLRT = 100, ufBS = 100) (Fig. 5).

Monophyly of species of *Phalacrostemma* included in the analysis—the new species, *P. timoharai*, and *Phalacrostemma* spp.—was fully supported. Two major clades were recovered: (1) *Gesaia csiro* + *Phalacrostemma* spp. (SH-aLRT = 89.7, ufBS = 92, and (2) a clade comprising other sabellariids (*Idanthyrus*, *Phragmatopoma*, *Neosabellaria*, *Gunnarea*, and *Sabellaria*; SH-aLRT = 100, ufBS = 100) (Fig. 5). Support values for relationships among genera outside these two major clades were generally low. In the *Phalacrostemma* clade, *Phalacrostemma* sp. AM_W50676 was recovered as sister to a poorly supported clade (SH-aLRT = 80.9, ufBS = 85) comprising the new species and *P. timoharai*. All genera represented by multiple species, except for *Idanthyrus*, were recovered as monophyletic. The phylogenetic positions of *I. okudai* and *I. australiensis* remain uncertain due to low support values.

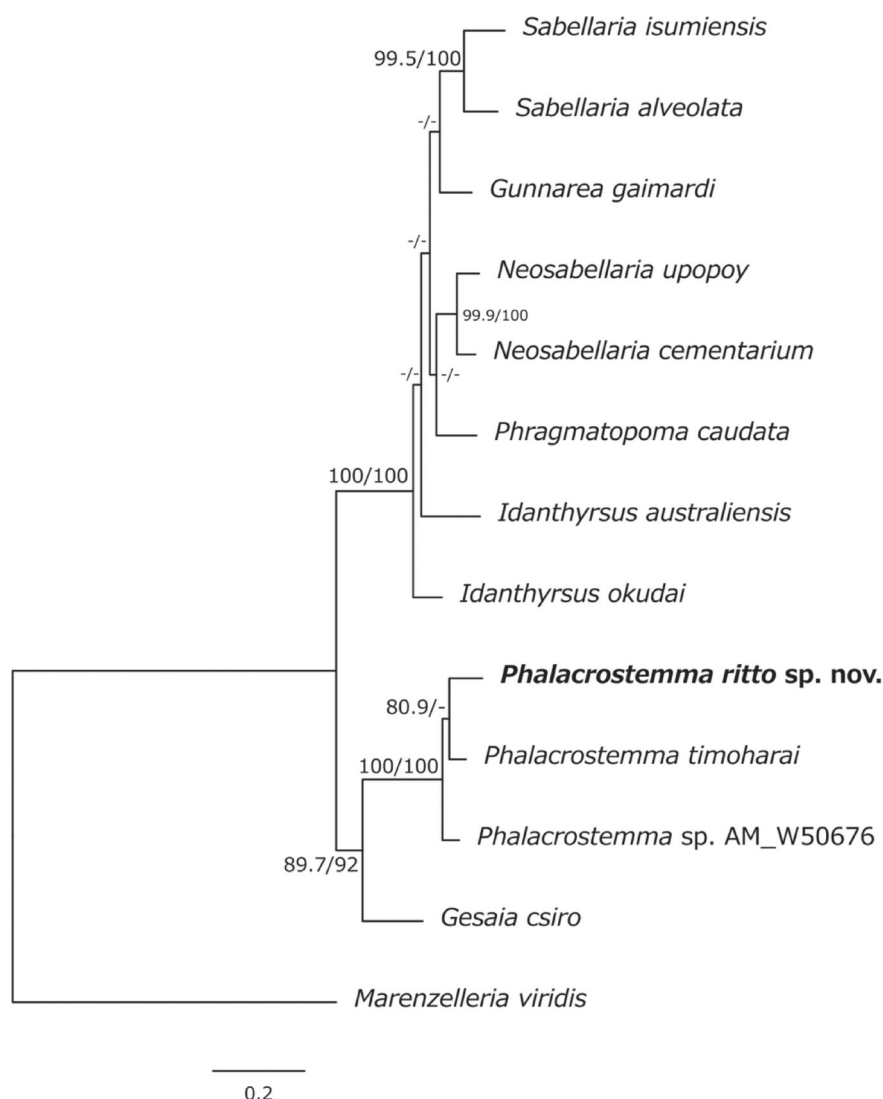


Figure 5. Maximum-likelihood analysis based on COI, 16S, 18S, and 28S gene sequences. Numbers above branches indicate SH-aRLT (≥ 80) and ultrafast bootstrap support values (≥ 90).

Discussion

Phalacrostemma ritto sp. nov. is the 16th species of the genus, and the seventh species recorded from the Pacific following *P. setosa* (Treadwell, 1906) from off Hawaii; *P. tenue* (Augener, 1906) from off New Caledonia; *P. abyssalis* (Caulery, 1944) from off Celebes, Indonesia; *P. profundum* Lechapt & Kirtley, 1998 from off New Caledonia; *P. maloga* Hutchings, Capa & Peart, 2012, from off New South West, Australia; *P. timoharai* Zhang, Hutchings, Burghardt & Kupriyanova, 2020, from the eastern Australian abyssal zone.

Phalacrostemma ritto sp. nov. differs from its congeners in several diagnostic characters. *Phalacrostemma setosa* possesses tentacular filaments and lacks buccal flaps, whereas *P. ritto* sp. nov. has buccal flaps and no tentacular filaments. *Phalacrostemma tenue* has only two pairs of nuchal spines and four pairs of tentacular filaments; in contrast, *P. ritto* has five pairs of nuchal spines and lacks tentacular filaments. *Phalacrostemma abyssalis* bears nuchal spines

with inflated tips, whereas those of *P. ritto* sp. nov. have curved tips. In *P. profundum*, the outer paleae have expanded thecae with irregular margins, whereas in *P. ritto* sp. nov. the thecal margins are not expanded and nearly straight. *Phalacrostemma maloga* has tentacular filaments and nuchal spines with elongate narrow tips, whereas *P. ritto* sp. nov. lacks tentacular filaments and has nuchal spines with curved tips. Finally, *P. timoharai* possesses two pairs of neuropodial cirri on chaetiger 1, whereas *P. ritto* sp. nov. has only a single pair.

Phylogenetic relationships within Sabellariidae remain insufficiently resolved (Capa and Hutchings 2014). The present analysis supports the monophyly of the *Gesaia* + *Phalacrostemma* clade, whereas relationships among the remaining genera remain unresolved. These results are consistent with those of previous molecular phylogenetic analyses (Zhang et al. 2020; Nishi et al. 2025). The closely related genera *Gesaia* and *Phalacrostemma* are morphologically very similar and differ primarily in the limbation on the nuchal hooks: in *Gesaia*, the concave margin lacks limbation, whereas in *Phalacrostemma*, the limbation is present on the concave margin (Capa and Hutchings 2014). A more comprehensive molecular phylogenetic analysis with broader taxon sampling is needed to resolve phylogenetic relationships within Sabellariidae.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI.

No AI tools were used in the preparation of this manuscript.

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Author contributions

Conceptualization: EN. Data curation: GK, YF, NJ, EN, EKK. Formal analysis: EN, NJ, EKK, GK. Funding acquisition: EN, NJ, GK. Investigation: YF, GK, EN. Methodology: NJ, EN, EKK, GK. Project administration: NJ, YF. Resources: GK, YF, NJ. Supervision: EKK. Validation: GK. Writing – original draft: EN, GK. Writing – review and editing: EKK, YF, EN.

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Data availability

All of the data that support the findings of this study are available in the main text.
