A novel free-living marine nematode species Pseudochromadora thinaiica sp. n. (Nematoda: Desmodoridae) from the seagrass bed of Vietnam

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A novel free-living marine nematode species *Pseudochromadora thinaiica* sp. n. (Nematoda: Desmodoridae) from the seagrass bed of Vietnam

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Summary. *Pseudochromadora thinaiica* sp. n. is described from intertidal sediment in Thi Nai Lagoon (Vietnam). *Pseudochromadora thinaiica* sp. n. is characterised by the combination of the following characters: a cephalic capsule subdivided into two parts (main head region and helmet-shaped labial region); six longitudinal rows of somatic setae; no precloacal supplements; boat-shaped gubernaculum with proximal end curved dorsally, buccal cavity with a large dorsal tooth and two ventrosublateral teeth. *Pseudochromadora thinaiica* sp. n. is most similar to *P. parva* Gagarin & Thanh, 2008 in the shape of gubernaculum, but differs from it by longer body, stoma armature, bigger spicules and gubernaculum, the number of postcloacal thorns, absence of sexual dimorphism in the shape of the *fovea amphidialis*, absence of ventral hillock with thorns. Phylogenetic relationships using 18S and 28S rDNA confirm monophyly of *Pseudochromadora*.

Key words: Desmodoridae, free-living nematodes, molecular taxonomy, morphology, seagrass community.

Vietnam has diverse wetland ecosystems (*e.g.*, lagoon, fluvial bog, mangrove forest and lakes), spreading throughout the country (Mai *et al.*, 2008). Communities of seagrass meadows are of great importance for the functioning of such ecosystems. The total area of seagrass beds in Vietnam is estimated to be approximately 17,000 ha (Van Luong *et al.*, 2012). Despite intensive studies in recent decades, the compositional features of seagrass communities in Vietnam remain poorly understood (Pavlyuk *et al.*, 2020).

In the south-central coastal region of Vietnam, one of the largest wetland areas is the Thi Nai Lagoon covering an area of 5,060 ha. *Zostera japonica* Ascherson & Graebner, 1907 is one of the dominant seagrass species here. In 2021, during the study of the nematofauna of the *Zostera japonica* communities in the Thi Nai Lagoon, several new nematode taxa were identified. In particular, representatives of the genus *Pseudochromadora* were found morphologically different from the known species, including the *P. parva* described earlier from the brackish water area of Vietnam.

Representatives of this genus have been recorded in coastal communities of all continents, except for Antarctica. However, recent research suggests that conclusions about cosmopolitanism may be incorrect and sometimes based on insufficient knowledge of individual populations (Datta *et al.*, 2018).

Small individual sizes do not always enable differences to be distinguished based only on optical microscopy. In such situations, an integrative approach is required, including the involvement of molecular data. The aim of this study is to give an integrative description of a new species of *Pseudochromadora*.

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MATERIAL AND METHODS

Sediment samples (upper 10 cm layer) containing nematodes were taken during a low tide using hand cores (10 cm diam.) from seagrass *Zostera japonica* bed from Thi Nai Lagoon (Vietnam) in April 2021. Sediments were stirred thoroughly and the supernatant poured through a 40 μm mesh sieve and washed with filtered sea water. The operation was repeated 5 times. One half of the sample was fixed with 4% buffered formaldehyde, the other half was fixed with 96% ethanol and then stored in the laboratory at –20°C. In the laboratory, the meiofauna samples were washed with tap water, passed through a 32 mm sieve and then centrifuged three times (3214 g, 6 min) with colloidal silica (Ludox HS40; Sigma-Aldrich). Nematodes were picked out from the samples under a stereoscopic microscope, transferred to glycerin using Seinhorst's (1959) rapid method as modified by De Grisse (1969), and mounted on permanent slides. Drawings were made on an optical microscope Olympus CX41 with the aid of a drawing tube. DIC (differential interference contrast) photographs were taken with Olympus BX 53 and Leica DM 2500 light microscopes furnished with a digital camera.

For the scanning electron microscopy, specimens were gradually dehydrated in a series of baths of increasing ethanol content, dried in a critical-point dryer, sputter-coated with gold and observed and imaged with a Ziess Sigma 300 VP scanning electron microscope (SEM).

For re-examination of *Pseudochromadora parva* Gagarin & Nguyen Vu Thanh, 2008 slide no. 12/III with holotype and paratypes was found in the Museum of Helminthological Collections at the Center of Parasitology, A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia. Unfortunately, all specimens were mounted in one slide so it is not possible to identify holotype among them. Specimens of *P. parva* were also found in the seagrass *Zostera japonica* bed from Thi Nai Lagoon (Vietnam) in April 2021. For light and scanning electron microscopy specimens from Thi Nai Lagoon were processed as described above.

For molecular analyses, four specimens of *Pseudochromadora thinaiica* sp. n. were picked out from the ethanol samples under a stereoscopic microscope, mounted on temporary slides with sterile distilled water and observed at different magnifications using a light microscope (Olympus BX 53) with differential interference contrast, and equipped with a digital camera. After the vouchering, total DNA was extracted from the whole body of adult nematodes using the Invitrogen Qiagen DNeasy extraction kit according to the manufacurer's instructions. PCR mixture contained 5 μl Go Taq Green Master Mix (Promega) 0.5 μM of each primer, 3 μl of nuclease free water (Ambion) and 1 μl of genomic DNA. Two gene loci commonly used for marine nematodes were sequenced: 18S small subunit ribosomal rDNA and 28S large subunit ribosomal rDNA (D2-D3 region). For 18S rDNA, we used the primer set SSU_F_03 and SSU_R_81 (Blaxter *et al.*, 1998), which amplifies a fragment of *ca* 1800 bp, whereas the D2-D3 region of the 28S ribosomal DNA region was amplified using the primers D2A and D3B (Nunn, 1992). The length of the obtained amplicon was 700 bp. PCR products were visualised on a 1.5% agarose gel with ethidium bromide after electrophoresis. Single bands were purified with Exonuclease I and Thermosensitive Alkaline Phosphatase (Thermo Fisher Scientific). Purified PCR products were sequenced directly in both directions using an automated sequencer (ABI 3130xl Genetic Analyzer Sequencer, Applied Biosystems, USA) at department of Cell Biology and Genetics of Far Eastern Federal University. We use additional primers to sequence 18S rDNA amplicons: SSU_F_24_1 (Meldal *et al.*, 2007) and SSU_R_13 (Blaxter *et al.*, 1998). Forward and reverse sequences were manually assembled and edited using Finch TV (Geospiza Inc., Seattle, WA) and MEGA 7 (Kumar *et al.*, 2016). Alignment of the DNA sequences was performed using the T-Coffee algorithm (Notredame *et al.*, 2000). Base frequencies and molecular character statistics were calculated in MEGA 7. Phylogenetic trees were constructed using Maximum Likelihood (ML) and Bayesian inference (BI) approaches. The optimal nucleotide substitution model for BI was selected using PartitionFinder 2.1.1 (Lanfear *et al.*, 2012) while for the ML analysis was used GTR (Tavare, 1986) + G (Gamma distribution). The best models of nucleotide substitution for large and small subunit rDNA were GTR + I (a proportion of invariable sites) + G. ML analysis was performed in RAxML v. 8.2.4 using bootstrapping with 1000 replications (Stamatakis, 2006). BI was carried out using Markov Chain Monte Carlo (MCMC) randomisation in MrBayes v3.2.7 (Ronquist *et al.*, 2003). Four Markov chains (three heated chains, one cold) were run for 5 million generations, with the first 25% of sampled trees discarded as burn-in. Moreover, trace files were visually inspected in Tracer 1.7 (Rambaut *et al.*, 2018) and then the consensus tree was visualised in FigTree v. 1.4.4. Bayesian posterior probabilities and ML bootstrap

values were used to evaluate branch support. Sequences of *Pseudochromadora thinaiica* sp. n. obtained in this study have been deposited in GenBank (accession numbers, MZ958843-MZ958846 for 18S rDNA and MZ958836-MZ958839 for 28S rDNA).

Abbreviations of the measured variables in the description are: a – body length divided by maximum body diameter; a.b.d. – anal body diam. (μm); amph.dist. – distance from anterior end to amphid (μm); amph.w. – width of the amphidial fovea (μm); b – body length divided by pharyngeal length; c' – tail length divided by body diameter at cloacal level; c – body length divided by tail length; diam.c.s. – body diameter at the level of cephalic setae (μm); gub.l. – length of gubernaculum (μm); h.c. – length of head capsule (μm); L – body length (μm); l.tail – tail length (μm); M – maximum body diameter (μm); ph.l. – pharyngeal length (μm); ph.b.d. – pharyngeal bulb diam. (μm); S' – length of spicules divided by a.b.d.; spic.arch – length of spicule along the arch (μm); tmr – length of non-annulated tail end; V – distance of the vulva from the anterior end (μm); V (%) – distance of the vulva from the anterior end as percentage of body length (%).

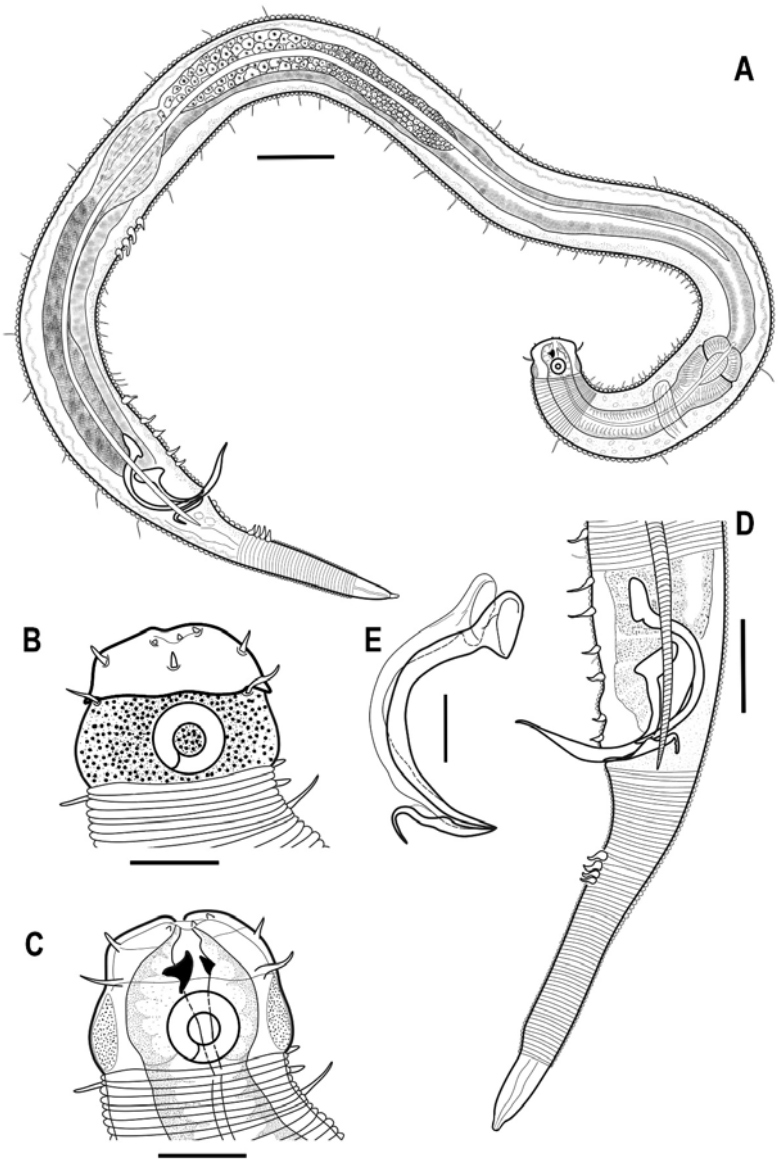

Fig. 1. *Pseudochromadora thinaiica* sp. n. A. Male holotype, entire body, lateral view; B. Male head, surface view; C. Male head, internal view; D. Male tail, lateral view; E Copulatory apparatus. Scale bars: A = 30 μm; B, C, E = 10 μm; D = 20 μm.

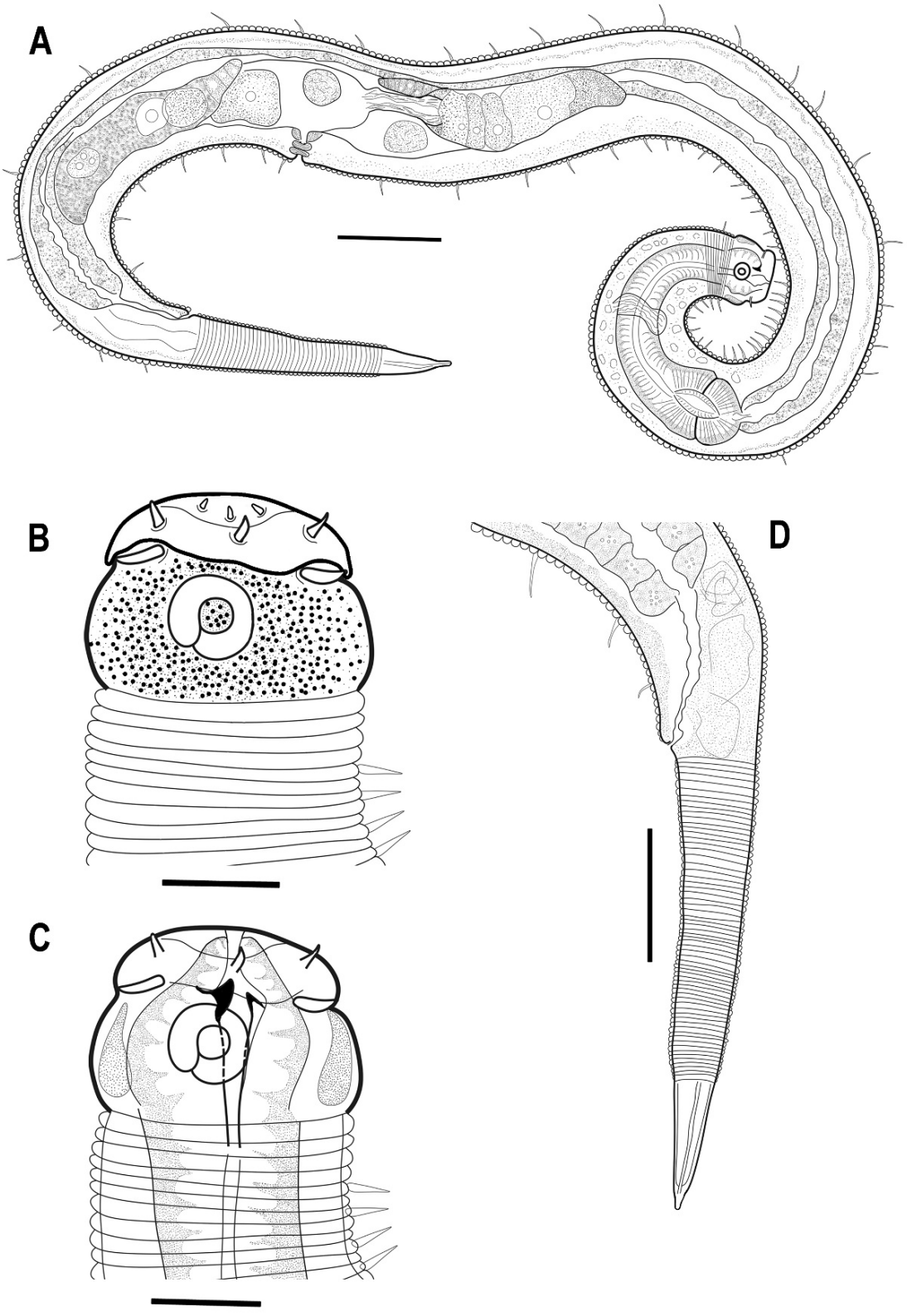

Fig. 2. *Pseudochromadora thinaiica* sp. n. A. Female paratype, entire body, lateral view; B. Female head, surface view; C. Female head, internal view; D. Female tail, lateral view. Scale bars: A = 30 μm; B, C = 10 μm; D = 20 μm.

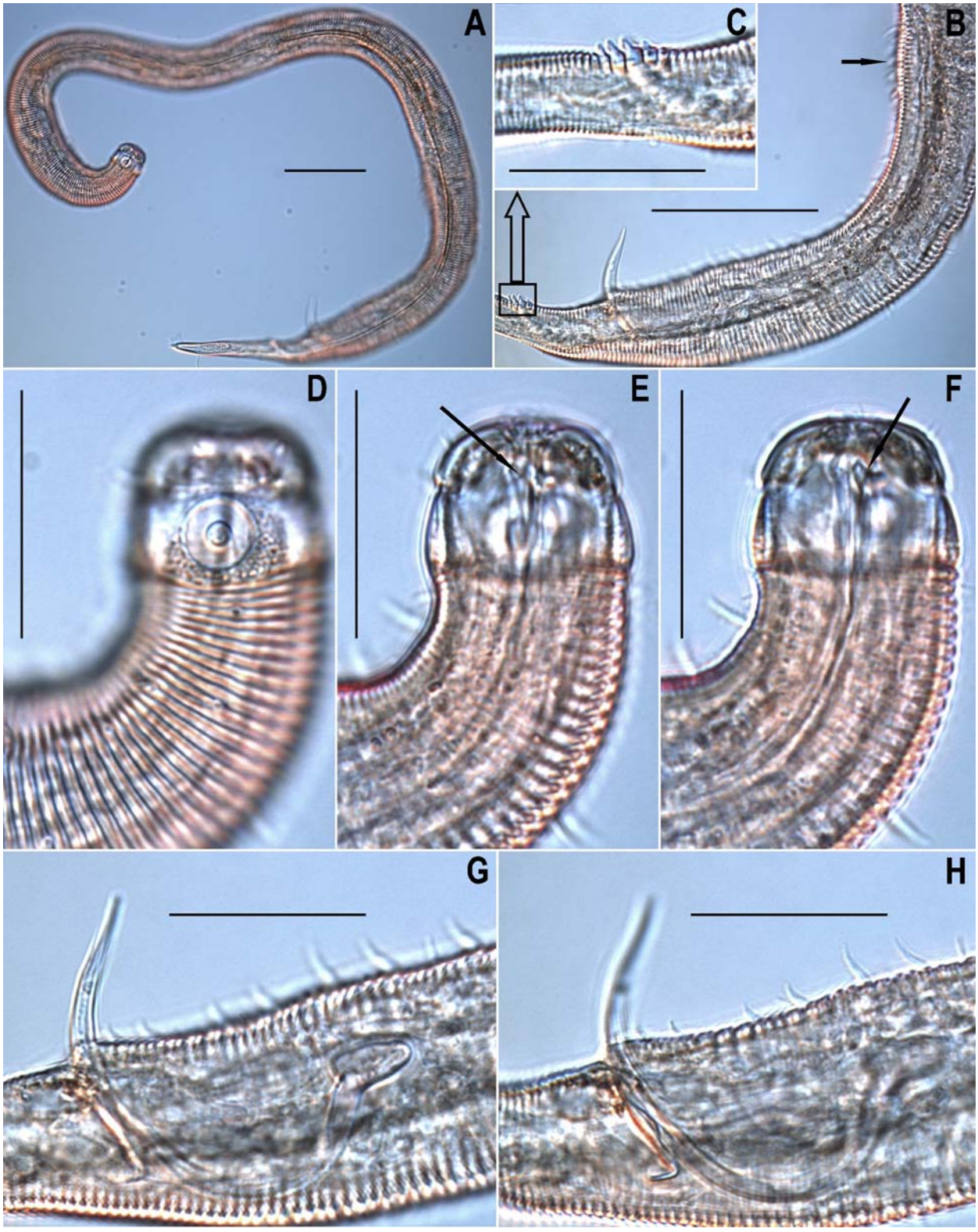

Fig. 3. *Pseudochromadora thinaiica* sp. n. Male, holotype. Light microscopy. DIC. A. General view; B. Posterior part of the body with cloaca region, pre- (arrow) and postcloacal thorn; C. Postcloacal thorns; D-F. Anterior end, arrows indicate left ventrosublateral tooth (E) and dorsal tooth (F); G, H. Cloacal region with spicules and gubernaculum. Scale bars: A, B = 50 μm; C-H = 25 μm.

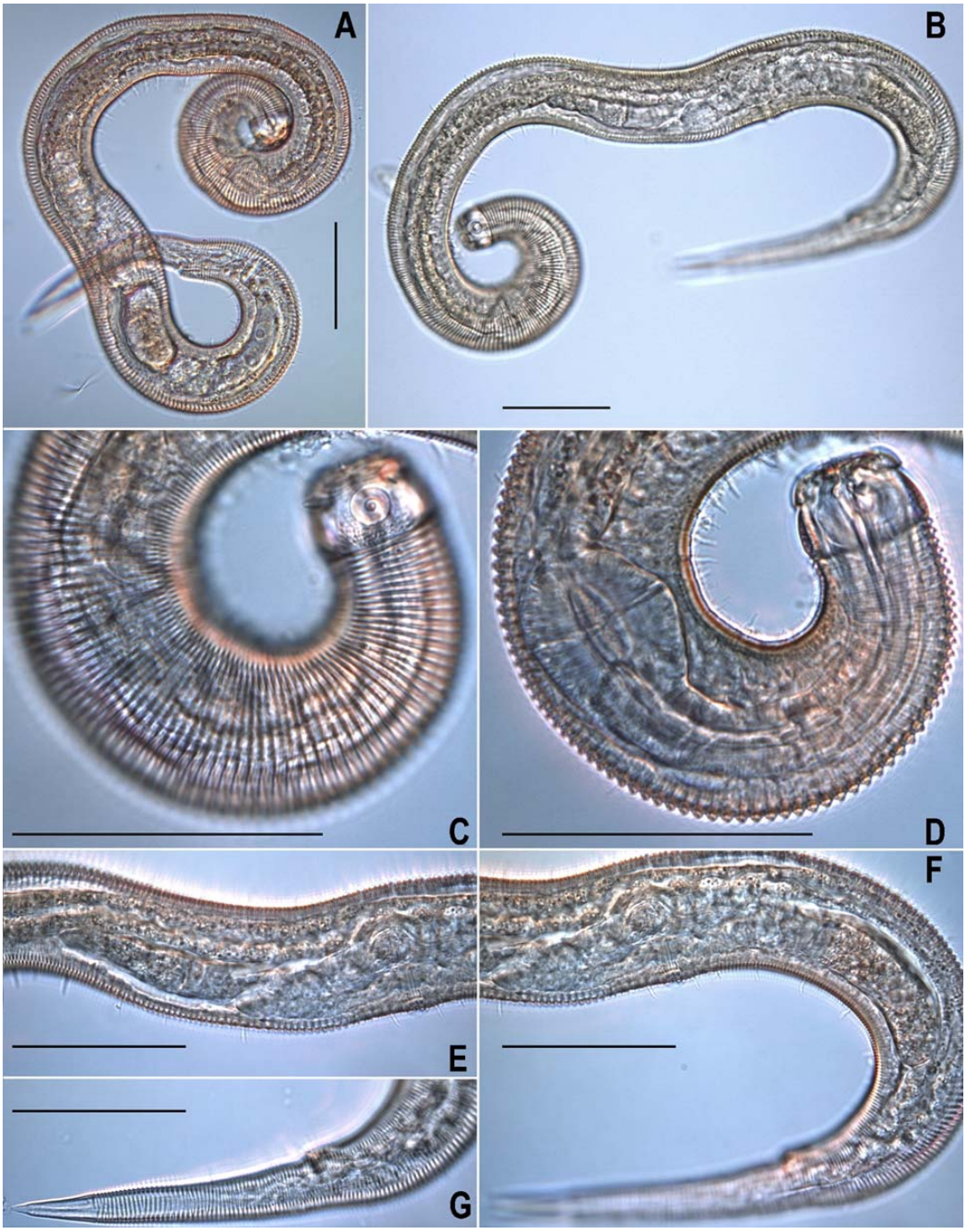

Fig. 4. *Pseudochromadora thinaiica* sp. n. Female paratypes. Light microscopy. DIC. A, B. General view; C, D. Anterior end; E. Vulva region and anterior gonad; F. Vulva region and posterior gonad; G. Tail. Scale bars = 50 µm.

SYSTEMATICS

Family Desmodoridae Filipjev, 1922
Subfamily Desmodorinae Micoletzky, 1924
Genus *Pseudochromadora* Daday, 1899

Desmodorinae (diagnosis after Mordukhovich *et al.*, 2015). Short cylindrical body with short head capsule and short conical tail. Body annuli with distinct spaces in between. Lateral alae extending from posterior to the pharynx as far as the beginning of the tail. Short somatic setae arranged in six or eight longitudinal rows. Two (or three) part head capsule: slender labial region, followed by main part of the head capsule, which has an extra-thick inner layer of the cuticle; a sutura can be present between

the two (or three) regions of the head capsule. Four cephalic setae located either on the labial region or on the anterior rim of the main part of the head capsule. Unispiral amphids (at least in females in case of sexual dimorphism) located on main region of the head capsule. Short cylindrical pharynx with bipartite terminal bulb. Males of most species have copulatory thorns and postcloacal thorns. Arched spicules; gubernaculum with capitulum.

Type species:

Pseudochromadora quadripapillata Daday, 1899 (Syn. *Micromicron cephalatum* Cobb, 1920 and *Micromicron luticola* Timm, 1952)

Other species:

Pseudochromadora benepapillata (Timm, 1961) Datta, Gangulu & Chakraborty, 2018

Pseudochromadora buccobulbosa Verschelde & Vincx, 1995

Pseudochromadora cazca (Gerlach, 1956) Gerlach, 1963 (Syn. *Desmodora cazca* Gerlach, 1956)

Pseudochromadora coomansi Verschelde & Vincx, 1995

Pseudochromadora galeata Verschelde, Nicholas & Vincx, 2006

Pseudochromadora incubans Gourbault & Vincx, 1990

Pseudochromadora interdigitatum Muthumbi, Verschelde & Vincx, 1995

Pseudochromadora parva Gagarin & Nguyen Vu Thanh, 2008

Pseudochromadora reathae Leduc & Wharton, 2010

Pseudochromadora rossica Mordukhovich, Fadeeva, Semenchenko & Zograf, 2015

Pseudochromadora securis Verschelde, Nicholas & Vincx, 2006

DESCRIPTION
Pseudochromadora thinaiica sp. n.
Figs 1-5

Type specimens. Five males (holotype and four paratypes) and five females (paratypes). The holotype is deposited in the Zoological Museum of A.V. Zhirmunsky National Scientific Center of Marine Biology, Vladivostok, Russia (MIMB 42293). Paratypes are deposited in the Zoological Museum of A.V. Zhirmunsky National Scientific Center of Marine Biology, Vladivostok, Russia (MIMB42294-MIMB42996).

Locality. Vietnam, Thi Nai Lagoon, 13.811° N, 109.228° E, *Zostera japonica* community, intertidal flat, muddy sediment, salinity 19 ‰.

Etymology. The species name is an adjective derived from the name of type locality, Thi Nai Lagoon.

Measurements. See Table 1.

Males. Short cylindrical body with blunt head and slender conical tail (Figs 1 & 5A). Cuticle annulated posterior to cephalic capsule. Lateral alae 1.6-2.8 µm wide (Figs 1 & 5E), start from posterior to pharyngeal bulb extending to the level of cloaca. Distance from anterior end to the beginning of lateral alae 116-160 µm; from anus to the end of lateral alae 97-139 µm. Annuli with spines on the dorsal side (Fig. 5E). Six longitudinal rows (one dorsal, one ventral, two subventral and two subdorsal) of somatic setae running from head capsule to tail.

Table 1. Morphometrics of *Pseudochromadora thinaica* sp. n. (all measurements are given in µm unless dimensionless).

Character	Holotype male	Paratype males (n = 4)		Paratype females (n = 5)	
		min	max	min	max
L	697	412	605	514	647
V				288	385
M	31	30	37	38	41
ph. l.	98	88	92	84	97
a.b.d.	22	18	25	13	17
diam. c.s.	20	18	21	17	21
l. tail	92	61	85	73	95
tmr	17	14	21	17	24
l.c.s.	2	2	2.5	2	2.5
h.c.	3	3	3.5	3	3.5
amph. dist.	8	5	7	4	8
amph. w.	6,5	6.5	7	5	7
ph.b.d.	23	21	24	22	26
spic. arch.	46	39	48		
gub. l.	15.5	16	19		
a	22.5	11	19	13.3	16.5
b	7.1	4.9	6.6	5.8	7.2
c	7.6	6.7	7.1	6.6	7.5
c'	4.2	2.4	4.7	4.6	5.9
S'	2.1	1.6	2.6		
V%				56	59.8

Well developed head capsule, consisting of two regions: a shorter anterior lip region and a larger posterior main region with extra layer of thick cuticle. Lip region helmet-shaped (Fig. 5C). Main head region wider than lip region and ornamented with numerous tiny vacuoles in the inner layer. Six setiform inner labial sensilla, six setiform outer labial sensilla (2-2.5 µm long), and four cephalic setae (3-3.5 µm long) in three separate circles (Fig. 5C). Amphids situated laterally on the main head

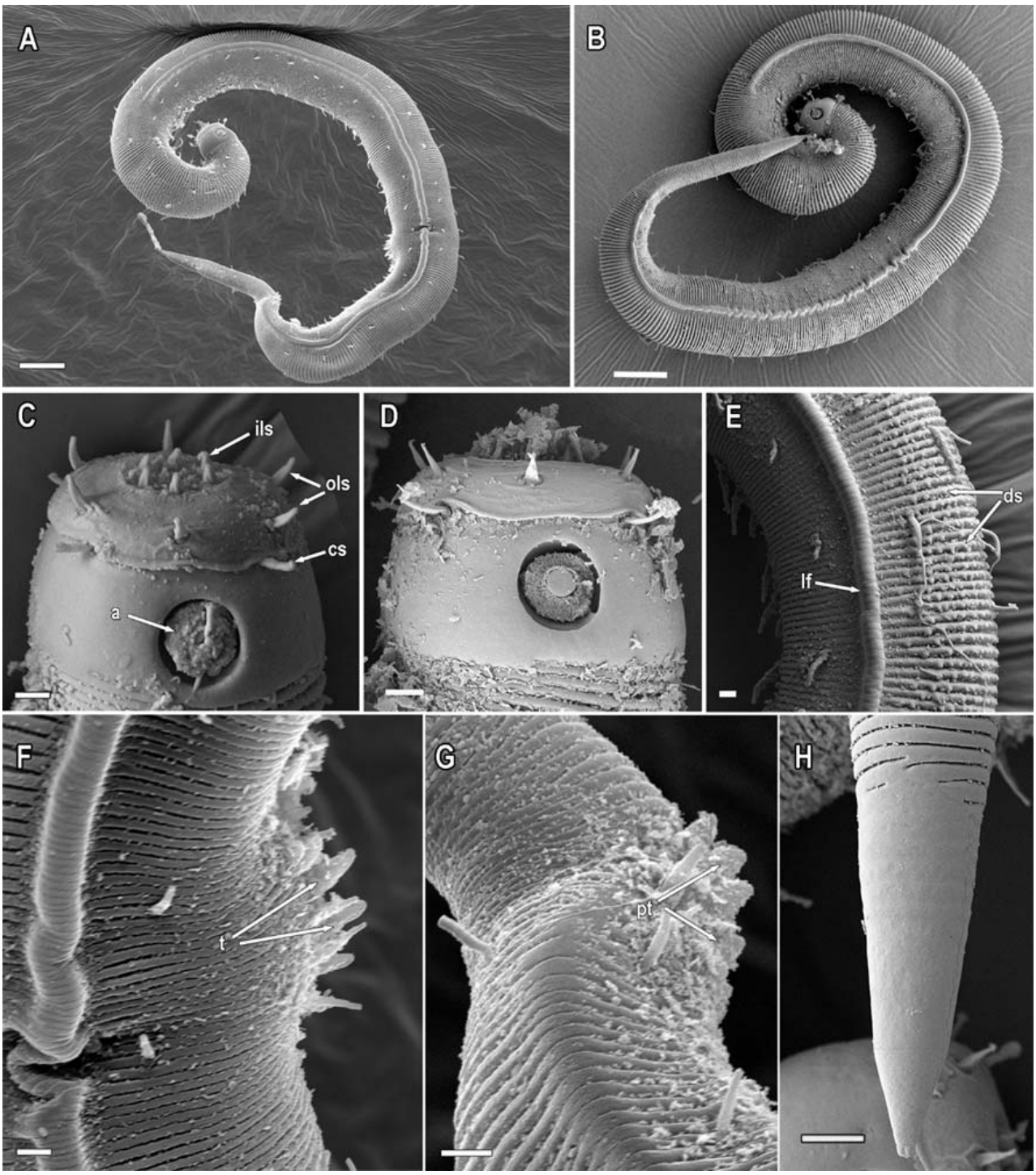

Fig. 5. *Pseudochromadora thinaiica* sp. n. SEM microphotographs. A. Entire male, subdorsal view; B. Entire female, lateral view; C. Head of male with cryptospiral *fovea amphidialis*; D. Head of female with cryptospiral *fovea ampidialis*; E. Cuticular spines (ds) on the dorsal side of male; F. copulatory thorns (t); G. Postcloacal copulatory thorns (pt); H. Non-annulated tail tip. Abbreviations: a – amphid; cs – cephalic setae; ds – cuticular spines; ils – inner labial setae; lf – lateral alae; ols – outer labial setae; pt – postcloacal copulatory thorns; t – mid-body copulatory thorns. Scale bars: A, B = 20 µm; C, H = 3 µm; D-G = 2 µm.

region, 5-8 µm from anterior end, characterised by the slightly cryptospiral *fovea amphidialis* (Figs 1, 3D & 5C), 17-24% of corresponding body diameter.

Buccal cavity with one large dorsal tooth and two slightly smaller ventrosublateral teeth (Figs 3E & F). Muscular pharynx with large oval bipartite terminal bulb. Internal cuticular lining of the pharynx is thickened within terminal bulb. Nerve ring situated at *ca* 64-70% of pharyngeal length.

Reproductive system monorchic with one outstretched testis, situated to the right of intestine. Spicules arcuate with large capitula, 1.6-2.6 a.b.d. (Figs 1, 3G & H). Gubernaculum boat-shaped with proximal end curved caudally, three times shorter than spicules (Figs 1 & 3H). A group of ventral and subventral thorns is found at 97-139 µm anterior to cloaca (Figs 1 & 5F). A ventral row of broad somatic setae located between precloacal group of copulatory thorns and cloaca (Fig. 3H). On the tail, 22-28 µm posterior to cloaca a group of medioventrally located postcloacal thorns (4) (Figs 1, 3C & 5G). Tail is conical with a non-annulated tip and slender spineret.

Females. Similar to males, with slightly cryptospiral *fovea amphidialis* (Figs 2, 4C & 5D) situated 4-8 µm from anterior end, 17-21% of corresponding body diameter. Reproductive system is didelfic, amphidelphic with reflexed ovaries (Figs 1 & 4E-F). Cuticular *vagina vera* and *vagina uterina* surrounded by constrictor muscles. Thorns and spines absent. Some specimens are covered with ecto-symbiotic organisms.

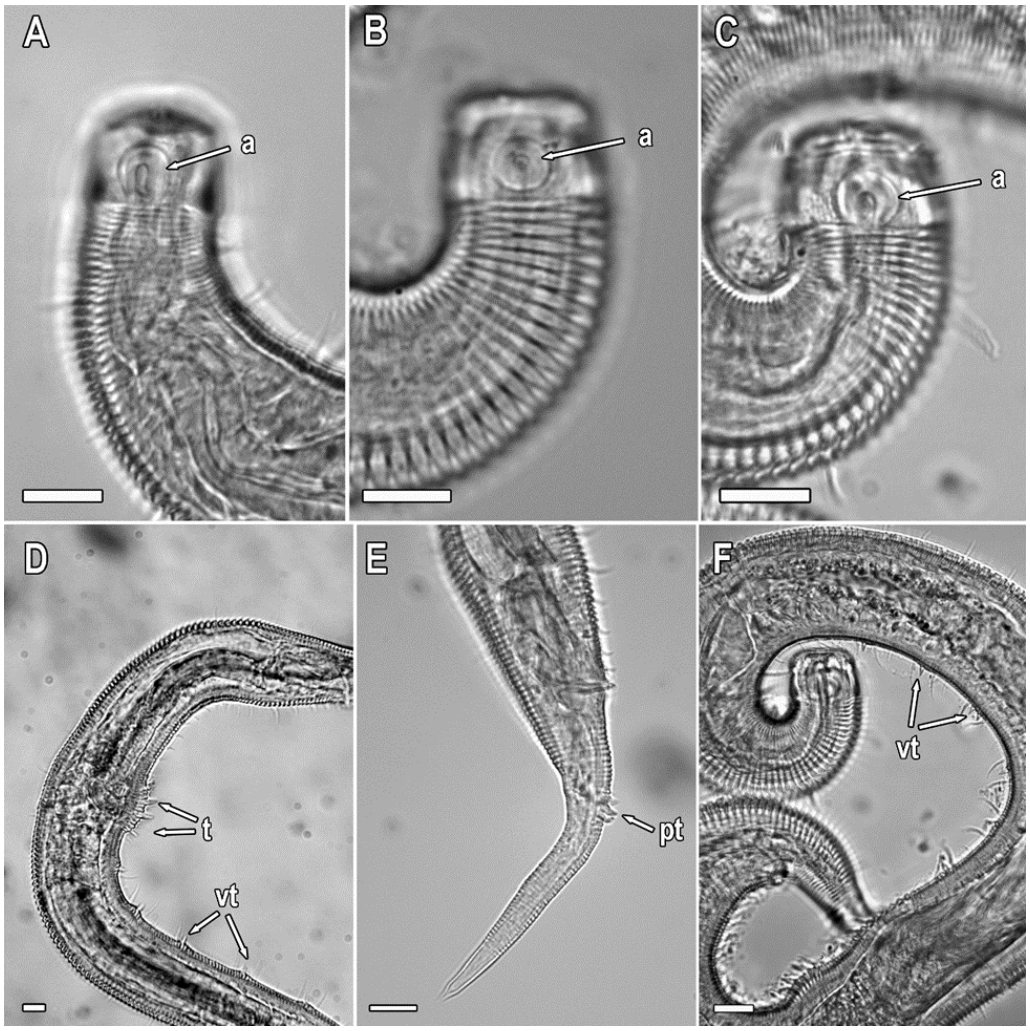

Fig. 6. *Pseudochromadora parva*. A. Head end of male from Red River, lateral view; B. Head end of female from Red River; C. Anterior end of male from Thi Nai Lagoon showing amphid (a); D. Precoacal thorns (t) and hillocks with thorns (vt) on the ventral side of male from Red River; E. Posterior end of male from Red River showing postcloacal thorns (pt); F. Hillocks with thorns (vt) on the ventral side of male from Thi Nai Lagoon. Scale bars: A, D = 50 µm; B, C & F = 10 µm; E = 25 µm.

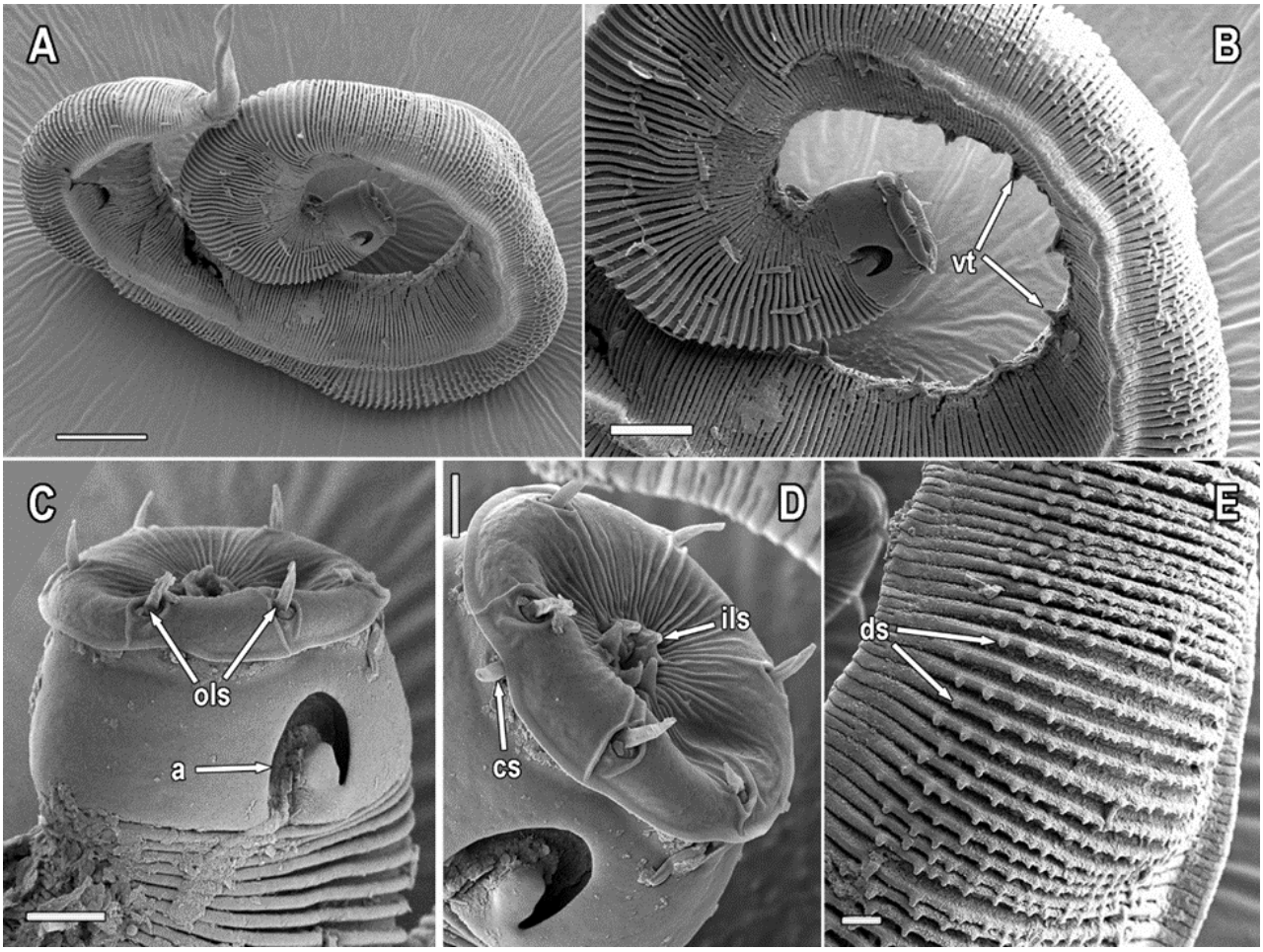

Fig. 7. *Pseudochromadora parva*. SEM microphotographs. A. Entire male, dorso-lateral view; B. Ventral side of male with ventral thorns (vt); C. Anterior end of male showing *fovea amphidialis* (a); D. Anterior end of male; E. Dorsal cuticular spines of male. Abbreviations: a – amphid; cs – cephalic setae; ds – dorsal cuticular spines; ils – inner labial setae; ols – outer labial setae; vt – ventral thorns. Scale bars: A = 20 µm; B = 10 µm; C = 3 µm; D, E = 2 µm.

Diagnosis. *Pseudochromadora thinaiica* sp. n. is characterised by the combination of the following characters: a cephalic capsule subdivided into two parts (main head region and helmet-shaped labial region); six longitudinal rows of somatic setae; buccal cavity with a large dorsal tooth and two ventrosublateral teeth; presence of spines on the cuticle of males; absence of precloacal supplements; boat-shaped gubernaculum with proximal end curved caudally, absence of sexual dimorphism in the shape of the *fovea amphidialis*. The slightly cryptospiral *fovea amphidialis* is unique within the genus.

Relationships. *Pseudochromadora thinaiica* sp. n. is most similar to *Pseudochromadora parva* Gagarin & Thanh, 2008 in the shape of gubernaculum, but differs from it by the longer spicules (39-48 µm *vs* 28-31 µm), bigger gubernaculum (15.5-19 µm *vs* 13-14 µm) the number of precloacal thorns (4 in *P. thinaiica* sp. n. *vs* 3 in *P. parva*), absence of sexual dimorphism in the shape of *fovea amphidialis*, absence of ventral hillock with thorns (beside the pre-cloacal group of thorns). In our samples, individuals of both species were present, which made it possible to compare them with each other and with type specimens of *P. parva* (Figs 6 & 7). Accurate examination of type material revealed the presence of vacuoles in cephalic capsule (Fig. 6C).

All other species of the genus characterised by the gubernaculum without curved proximal end. The new species differs from *P. benepapillata*, *P. buccobulbosa*, *P. galeata*, *P. reathae* and *P. rossica* by the absence of sexual dimorphism in the shape of the *fovea amphidialis*. The new species differs from *P. reathae* and *P. quadripapillata* by the absence of supplements. *P. thinaiica* sp. n. differs from the *P. coomansi* by the shape of spicules (presence of capitulum in *P. thinaiica* sp. n.

vs absence of capitulum in *P. coomansi*) and the number of tail thorns (4 *vs* 6 in *P. coomansi*). From *P. securis* new species differs by the absence of special cuticular plate where dorsal tooth is situated and smaller spicules (59-61 µm in *P. securis vs* 39-48 µm in *P. thinaiica* sp. n.). *P. thinaiica* sp. n. differs from *P. benepapillata* by the bigger subventral teeth (almost equal with dorsal one in *P. thinaiica* sp. n. *vs* much smaller than dorsal one in *P. benepapillata*). New species differs from *P. galeata* by the absence of cuticular spines in female (present in *P. galeata*), and position of the beginning of lateral alae (far behind the cardia in *P. thinaiica* sp. n. *vs* just behind the cardia in *P. galeata*). Described species differs from the *P. buccobulbosa* by the absence of cuticular dorsal plug in the buccal cavity and the absence of cuticular spines in females. *P. thinaiica* sp. n. differs from *P. interdigitatum* by the absence of cuticular spines on females, number of postcloacal copulative thorns (4 in *P. thinaiica* sp. n. *vs* 6 in *P. interdigitatum*). New species differs from *P. incubans* by the position of the amphid (lateral in *P. thinaiica* sp. n. *vs* shifted to dorsal side in *P. incubans*) and the absence of viviparous reproduction. Described species differs from *P. rossica* by the presence of cuticular spines (absent in *P. rossica*). *P. thinaiica* sp. n. differs from *P. cazca* by the absence of cuticular spines in female (present in *P. cazca*).

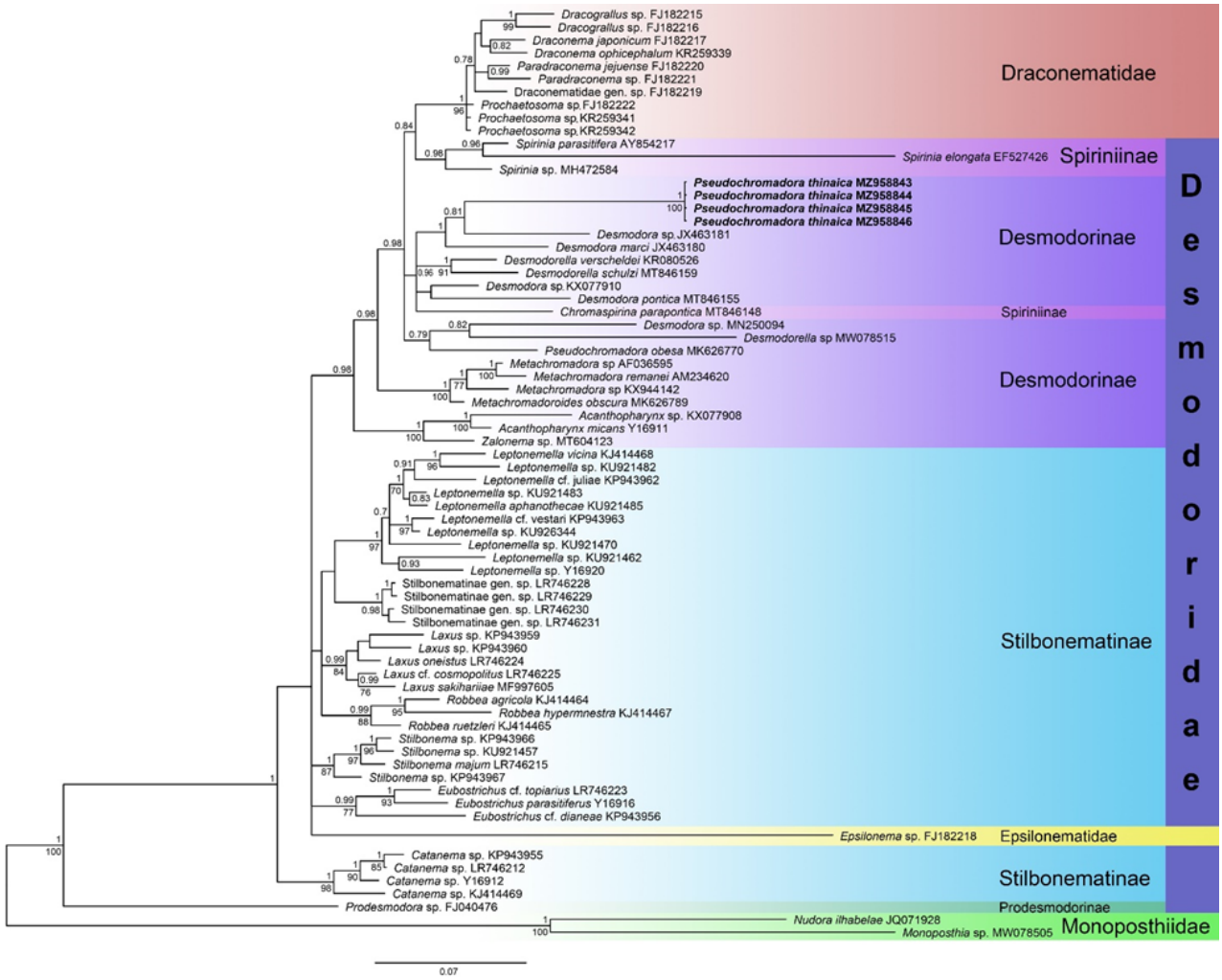

Fig. 8. Bayesian 18S rDNA phylogeny of the Desmodoridae, using the GTR + I + G model of nucleotide substitution. Draconematidae, Epsilonematidae and Monoposthiidae were used as outgroup. Bayesian posterior probabilities (PP) above 0.7 are given above tree nodes and bootstrap support values above 70% found in the ML analysis are shown below nodes.

Nucleotide sequences. Based on the SSU molecular phylogenetic tree (Fig. 8), *P. thinaiica* sp. n. was most closely related to *Desmodora* sp. (JX463180), with 81% posterior probability value support. In the D2-D3 of LSU phylogenetic tree (Fig. 9) *P. thinaiica* sp. n. and *P. rossica* sequences formed a clade with posterior probability and bootstrap values of 100%. Comparisons with corresponding regions of 28S rDNA between *P. thinaiica* sp. n and *P. rossica* produced K2P genetic distances of 18.8%, values well associated with interspecific variation.

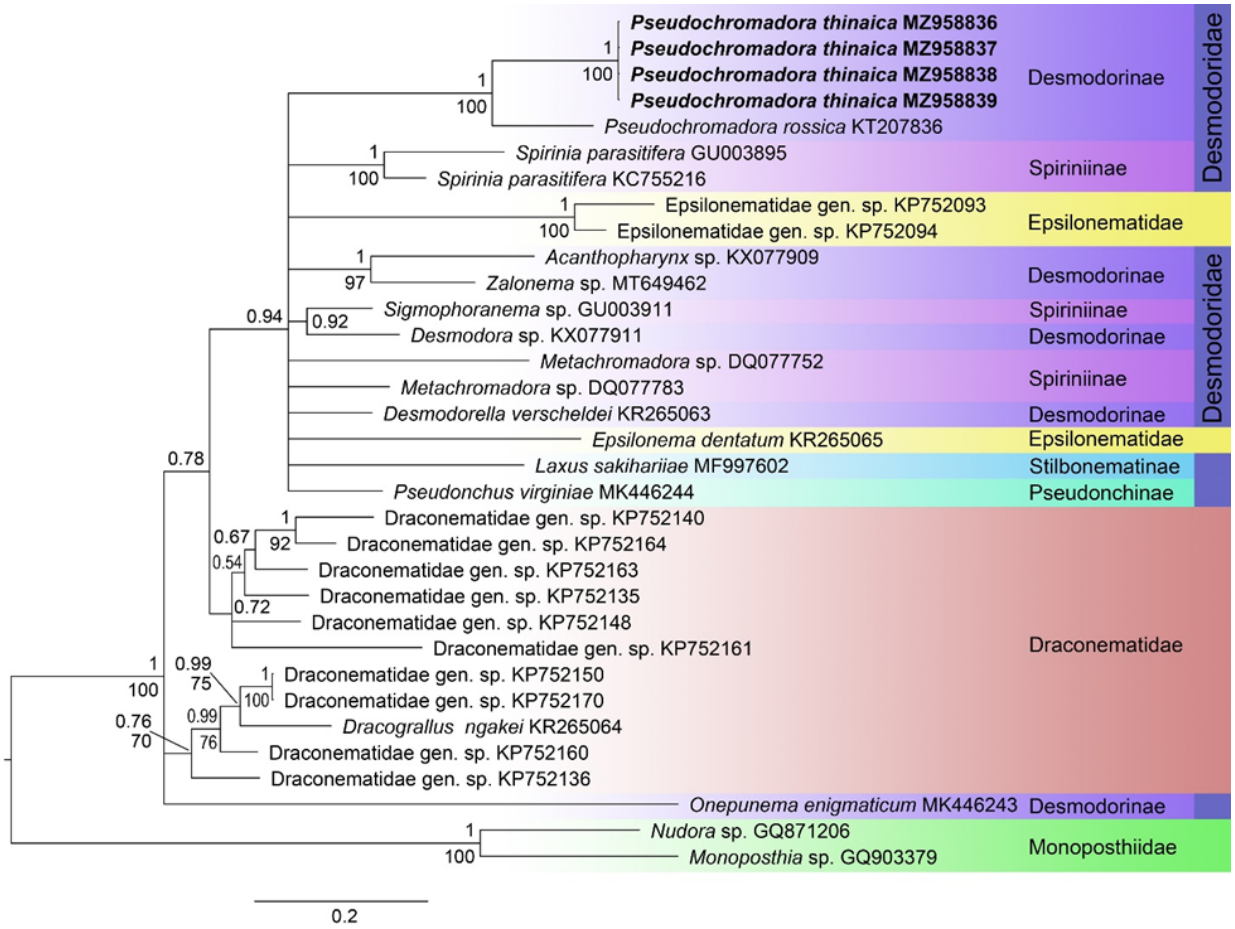

Fig. 9. Bayesian 28S rDNA phylogeny of the Desmodoridae, using the GTR + I + G model of nucleotide substitution. Draconematidae, Epsilonematidae and Monoposthiidae were used as outgroup. Bayesian posterior probabilities (PP) above 0.7 are given above tree nodes and bootstrap support values above 70% found in the ML analysis are shown below nodes.

DISCUSSION

The present study provides the second record of the genus *Pseudochromadora* from Vietnam. *Pseudochromadora parva* was described earlier from mangrove sediment of the Red River estuary (Gagarin & Thanh, 2008). Species of *Pseudochromadora* have been recorded in many oceans in sandy, as well as in muddy sediments in estuarine, mangrove, intertidal and upper subtidal areas from tropical to cold seas (Mordukhovich *et al.*, 2015; Datta, *et al.*, 2018). The present study is one more example of shallow water *Pseudochromadora*. Remarkable that most of the species were found in brackish waters and even in fresh waters, but not far from sea water influx; *e.g.*, *P. parva* and *P. benepapiilata* (Gagarin & Thanh, 2008; Datta *et al.*, 2018) were registered in waters with salinity ranged from 15 to 24 ‰, and *P. quadripapillata* was found in fresh water reservoir (Coomans *et al.*, 1985). Apparently, *Pseudochramodora* can be assigned to the few representatives of brackish-water taxa.

The currently known species of desmodorids are characterised by a very wide distribution. Genetic data indicate that these taxa often hide groups of

species. Misidentification may be responsible for the unrealistic genetic distances observed within some species and genera of the Desmodoridae (Leduc & Zhao, 2016). In particular, the GenBank contains a nucleotide sequence of the *nomen dubium Pseudochromadora obesa*. Such species is not known for *Pseudochromadora* and the authors of sequences available in GenBank made a mistake in the species name when their data were deposited in GenBank. Therefore, researchers must be very careful and bear in mind possible errors in data banks.

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J.K. Zograf, E.R. Skripova, A.A. Semenchenko, Viet DungVu, Thi-Lan Nguyen, Trong Huan Phan and V.V. Mordukhovich. Новый вид свободноживущих морских нематод *Pseudochromadora thinaiica* sp. n. (Nematoda: Desmodoridae) из зарослей морской травы Вьетнама.

Резюме. *Pseudochromadora thinaiica* sp. n. описан из донных осадков литорали лагуны Тхи Най (Вьетнам). *Pseudochromadora thinaiica* sp. n. характеризуется сочетанием следующих признаков: головная капсула разделена на две части (основная часть головной капсулы и шляпообразная губная часть головной капсулы); шесть продольных рядов соматических щетинок; отсутствие преклоакальных супплементов; рулек в форме лодки с проксимальным концом, изогнутым дорсально, стома с большим дорсальным зубом и двумя вентросублатеральными зубами. *P. thinaiica* sp. n. наиболее похожа на *P. parva* Gagarin & Thanh, 2008 по форме рулька, но отличается от нее более длинным телом, вооружением стомы, большими спикулами и рульком, количеством постклоакальных шипов, отсутствием полового диморфизма формы амфида, отсутствием вентральных шипов у самцов (помимо группы преклоакальных шипов). Филогенетические отношения с использованием 18S и 28S рДНК подтверждают монофилию рода *Pseudochromadora*.