

A New Euryhaline Species of the Genus *Ficopomatus* Southern 1921 (Polychaeta: Serpulidae) from China

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Shi-Chang Li, An-Tai Wang, and Li Deng (2012) A new euryhaline species of the genus *Ficopomatus* Southern 1921 (Polychaeta: Serpulidae) from China. *Zoological Studies* 51(7): 1165-1174. A new species of serpulid, *Ficopomatus shenzhensis* sp. nov., from brackish-water and freshwater habitats of the Zhujiang River estuary shore in Shenzhen City, Guangdong Province, China, is described. Morphological differences between brackish-water and freshwater specimens were noted. However, nuclear ribosomal RNA (18S rDNA) sequences of specimens from brackish-water and freshwater habitats were identical. Morphological characters in combination with molecular evidence confirm that the present material is a new species belonging to the genus *Ficopomatus* Southern, 1921. <http://zoolstud.sinica.edu.tw/Journals/51.7/1165.pdf>

Key words: Serpulidae, Taxonomy, *Ficopomatus shenzhensis* sp. nov., China.

The family Serpulidae is a discrete group of sedentary calcareous tubeworms within the large clade Sabellida, which shares the presence of a radiolar crown and separation of the body into thoracic and abdominal regions (ten Hove and Kupriyanova 2009). Pillai (1971) proposed that the genera *Ficopomatus* Southern 1921, *Sphaeropomatus* Treadwell 1934, *Mercierella* Fauvel 1923, and *Neopomatus* Pillai 1960 be grouped in a separate subfamily, the Ficopomatinae. ten Hove and Weerdenburg (1978), in their revision of brackish-water serpulids, synonymized the genera *Mercierella*, *Sphaeropomatus*, *Mercierellopsis* Rioja 1945, and *Neopomatus*, with *Ficopomatus*. More recently, Pillai (2008) reinstated the genus *Neopomatus* and suggested that the genera *Ficopomatus*, *Neopomatus*, and *Marifugia* together formed the subfamily Ficopomatinae.

Four species of *Ficopomatus* have hitherto been described, namely, *F. macrodon* Southern

1921, *F. enigmaticus* Fauvel 1923, *F. miamiensis* Treadwell 1934, and *F. talehsapensis* Pillai 2008. They are extremely euryhaline, and are found in freshwater, brackish-water, marine, and hypersaline environments (Southern 1921, Fauvel 1923, Treadwell 1934, Pillai 2008). A new species that lives in both brackish-water and freshwater habitats, *F. shenzhensis* sp. nov. is described in the present paper.

MATERIALS AND METHODS

Collection of samples

Tubes and worms were carefully scraped off rocks with a scalpel. Worms for type specimens were kept in a 4% (v/v) formaldehyde solution. Worms for DNA extraction were anesthetized with ethyl carbamate and kept in 70% (v/v) ethanol at -20°C.

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Morphological examination

The morphological characteristics of the serpulids were examined after 24 h of starvation. Cross-sections of tubes were prepared by whetting the tube on a whetstone and polishing it on frosted glass. Chaetae and uncini were separated in a lactate-phenol solution, which was composed of lactic acid, phenol, poly (vinyl alcohol), and fuchsin acid. Images of live individuals were captured using a Leica DC 300 camera (Leica MZ16, Leica Microsystems, Glattbrugg, Switzerland) and measured with the camera's software. The uncini and chaetae were observed with an Olympus BX51 microscope (Olympus, Tokyo, Japan) and their images captured with an Olympus DP72 digital camera.

DNA extraction, amplification, and sequencing, and the phylogenetic analysis

Genomic DNA of 10 starved individuals, 5 from brackish-water habitats and 5 from fresh water, was extracted with the E.Z.N.A™ Mollusk DNA Isolation Kit (Omega, Norcross, GA, USA). The target 18S ribosomal (r)DNA

sequence at approximately 1770 bp was amplified by a polymerase chain reaction (PCR) with Premix Ex Taq™ Hot Start Version (TaKaRa, Otsu, Japan) using the primer pairs (ggc18f: taagccatgcacgtgtaagt and ggc18r: cagtctagttcgaacttctt), which were designed according to the homology of reported 18S rDNA sequences of *F. enigmaticus* (GenBank accession no. AY577889), *F. macrodon* (EU167532), and *F. miamiensis* (EU167531). Resulting PCR fragments were cloned into a pGEM-T vector (Promega, Madison, WI, USA) and sequenced by the Beijing Genomics Institute (BGI; Shenzhen, China). The sequence was deposited in GenBank with the accession no. HQ433336 (Table 1). We also included previously obtained sequences of the Serpulidae in this study to confirm the taxonomic status of this proposed new species. GenBank accession numbers for those additional species are listed in table 1.

A similarity search of the obtained nucleotide sequence was performed with the blastn tool available at the NCBI website (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Maximum-parsimony (MP) and maximum-likelihood (ML) methods were used to infer phylogenetic relationships. To root a tree,

Table 1. List of species used in this study, along with localities, GenBank accession numbers, and references cited

| Family | Species | Collecting locality | Accession no. | Reference |
|-----------------------------|---|--------------------------|-------------------------|----------------------------|
| Sabellidae | <i>Sabella spallanzanii</i> | Australia | HM800962 | Capa et al. 2011 |
| Serpulidae | <i>Crucigera tricornis</i> | Australia | EU184056 | Kupriyanova et al. 2008 |
| | <i>Ditrupa arietina</i> | Banyuls, France | DQ317114 | Kupriyanova et al. 2006 |
| | <i>Ficopomatus enigmaticus</i> | Australia | AY577889 | Rouse et al. 2004 |
| | <i>Ficopomatus macrodon</i> | Australia | EU167532 | Kupriyanova et al. 2009 |
| | <i>Ficopomatus miamiensis</i> | USA | EU167531 | Kupriyanova et al. 2009 |
| | <i>Ficopomatus shenzhensis</i> sp. nov. | Shenzhen, China | HQ433336 | This study |
| | <i>Filograna implexa</i> | Banyuls, France | DQ317116 | Kupriyanova et al. 2006 |
| | <i>Galeolaria caespitosa</i> | Bondi Beach, Australia | AB106257 | Hall et al. 2004 |
| | <i>Hyalopomatus biformis</i> | Patton-Murray Seamounts | GU441858 | Kupriyanova and Nishi 2010 |
| | <i>Hydroides brachyacanthus</i> | South Australia | DQ317117 | Kupriyanova et al. 2006 |
| | <i>Laminatubus alvini</i> | East Pacific Rise | DQ317118 | Kupriyanova et al. 2006 |
| | <i>Marifugia cavatica</i> | Bosnia Herzegovina | EU167530 | Kupriyanova et al. 2009 |
| | <i>Metavermilia acanthophora</i> | South Australia | DQ317119 | Kupriyanova et al. 2006 |
| | <i>Protis hydrothermica</i> | East Pacific Rise | DQ317122 | Kupriyanova et al. 2006 |
| | <i>Protula tubularia</i> | Spain | DQ317123 | Kupriyanova et al. 2006 |
| | <i>Pseudochitinopoma occidentalis</i> | British Columbia, Canada | DQ242542 | Kupriyanova et al. 2006 |
| | <i>Salmacina</i> sp. 1 | SA, Australia | DQ317126 | Kupriyanova et al. 2006 |
| | <i>Serpula uschakovi</i> | Russia | EU184065 | Kupriyanova et al. 2008 |
| | <i>Serpula vermicularis</i> | Banyuls, France | DQ317128 | Kupriyanova et al. 2006 |
| <i>Spirobranchus lima</i> | Banyuls, France | DQ317130 | Kupriyanova et al. 2006 | |
| <i>Vermiliopsis labiata</i> | Banyuls, France | DQ317131 | Kupriyanova et al. 2006 | |

the 18S rDNA sequence of *Sabella spallanzanii* (Sabellida, Sabellidae) was chosen as the outgroup (HM800962) (Table 1). All sequences were trimmed to the length of the shortest sequence obtained, resulting in 1680-bp-long aligned sequences. ClustalW multiple alignment and phylogenetic analyses were carried out with BioEdit 7.0.1 (<http://www.mbio.ncsu.edu/bioedit/bioedit.html>) and Mega 5.0 (Tamura et al. 2011) respectively.

RESULTS

Taxonomic description

***Ficopomatus shenzhensis* sp. nov.**
(Figs. 1, 2)

Type material: Holotype: SAB 1, 1 ♂. Paratypes: SAB 2-11, 10 ♂♂, SAB 12-21, 10 ♀♀. Type specimens deposited in National Zoological Museum, Institute of Zoology, Chinese Academy of Sciences, Beijing, China.

Etymology: The species is named after the seashore city, Shenzhen City, Guangdong Province, China, from where it was collected.

Additional material: Type specimens collected from rocks in brackish-water (with salinity of 6.0‰) of Zhujiang River estuary shore, Bao-an District, west Shenzhen City, Guangdong Province, China (22°43'16"N, 133°46'2"E) on 25 Nov. 2009. Freshwater samples collected from a man-made seaside freshwater (with salinity of 0.2‰) wetland park, Shenzhen Waterland Resort, which was built in the tidal-flat area in 1998. Ponds in the park are supplied with fresh water from a neighborhood reservoir. Brackish-water specimens were collected in the estuary, about 1 km away from the locality where the freshwater specimens were collected (Fig. 3).

Morphological description

In brackish-water specimens, tubes 8.25 ± 0.08 mm long ($n = 5$), white or gray, circular in cross-section, and lacking longitudinal ridge (Fig. 1A-C); worms, including branchial crown, thorax,

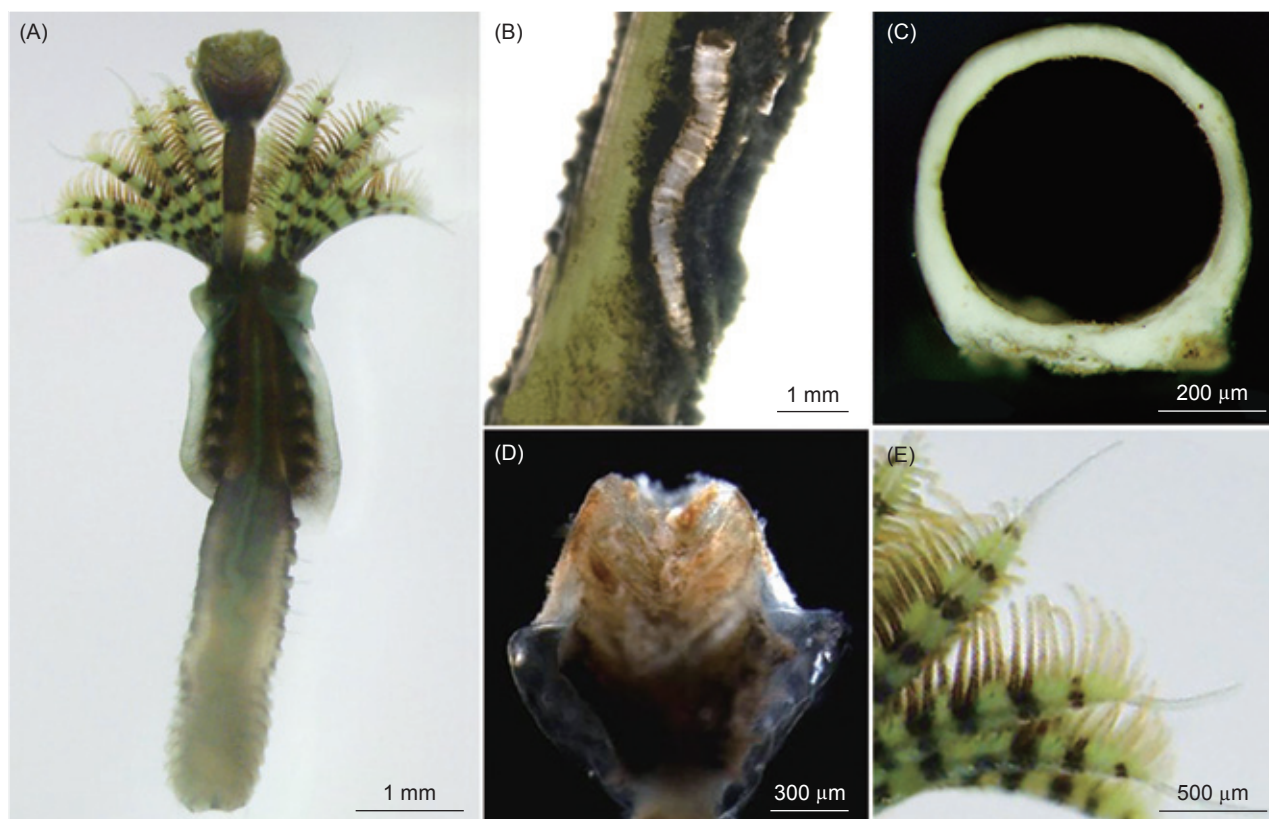


Fig. 1. Photographs of *F. shenzhensis* sp. nov., paratype, SAB 2. (A) Dorsal view of a worm removed from its tube; (B) tube; (C) cross-section of tube; (D) dorsal view of operculum; (E) branchial radioles.

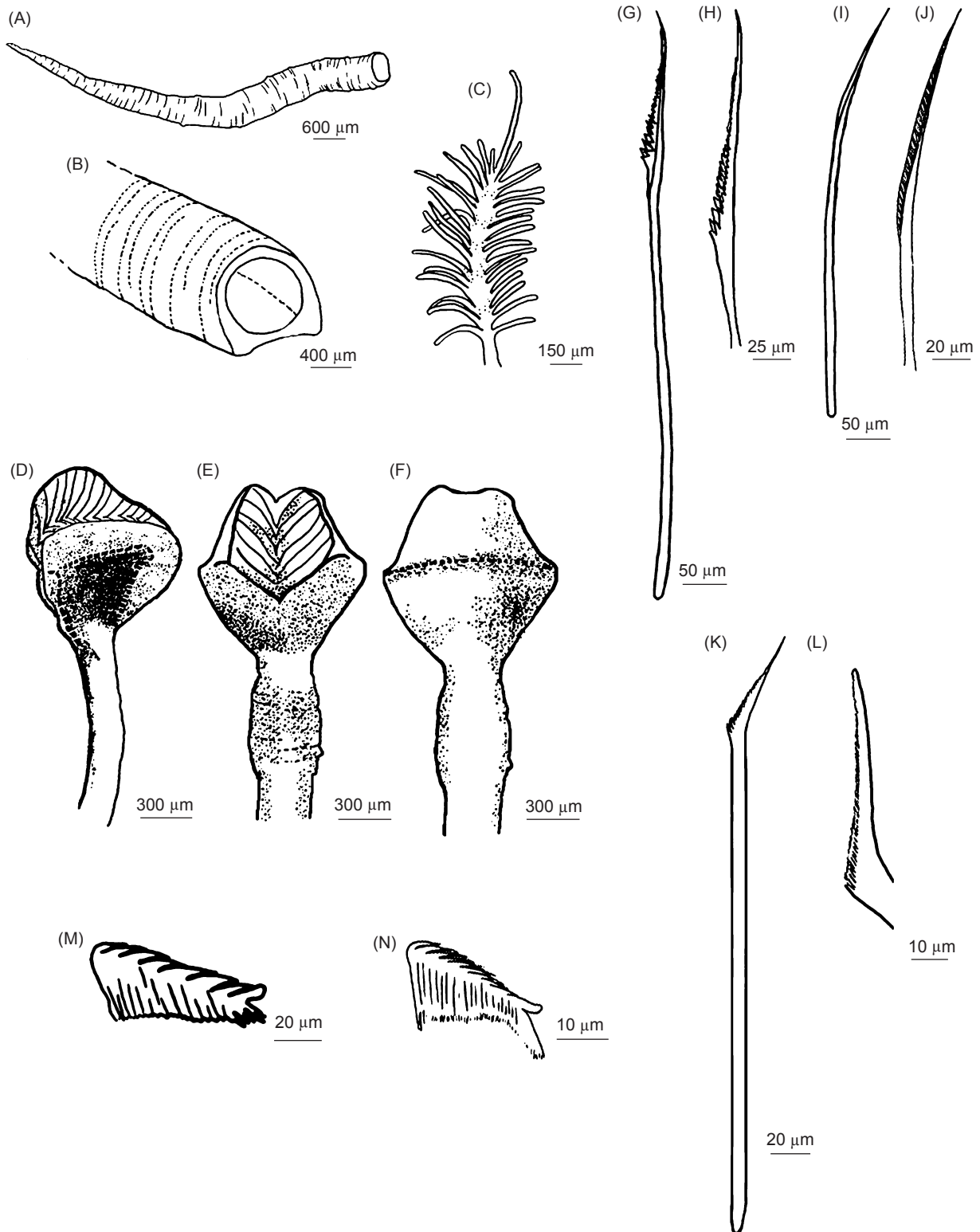


Fig. 2. Structure of the tube, operculum, chaetae and uncini of *F. shenzhensis* sp. nov. (A) Tube; (B) cross-section of tube; (C) branchial radiole; (D-F) operculum, lateral, dorsal, and ventral views; (G, H) collar chaetae; (I, J) thoracic chaetae; (K, L) abdominal chaetae; (M) thoracic uncini; (N) abdominal uncini.

and abdomen, 6.47 ± 1.00 mm long ($n = 8$).

Branchial crown composed of operculum and branchial radioles. Operculum and its peduncle occurring in position of 1st branchial radiole on left side (Fig. 1A). Operculum 0.81 ± 0.15 mm long ($n = 8$), 0.73 ± 0.17 mm wide ($n = 8$), pear-shaped, spines absent, consisting of dark brown hemispherical proximal part with circular black spot, and yellow convex distal horny plate with light brown spot. Dorsally, horny plate with V-shaped furrow (Figs. 1D, 2E) and 7 or 8 fine microscopic parallel ridges occurring along each side of furrow (Fig. 2C). Similar microscopic parallel ridges also occurring laterally along horny plate (Fig. 2D). Opercular peduncle smooth, 1.08 ± 0.21 mm long ($n = 8$). It decreases in diameter from distal part to proximal attachment to branchial lobe. Brown distally, yellow towards middle, and brown proximally. Branchial radioles arising from pair of lobes, 9 filaments on each side, 1.85 ± 0.19 mm long ($n = 8$) (Fig. 1E). Branchial radioles yellow, with 6-12 transverse brown spots. They bear row of ciliated filamentous pinnules, 0.30 ± 0.08 mm long ($n = 8$).

Thorax cylindrical, 1.17 ± 0.16 mm long ($n = 6$). Thorax composed of 7 chaetigers, and fleshy thoracic membranes which are white and not joined over thorax. Collar chaetal fascicle on each side consisting of 7-10 chaetae of 2 types, those that end distally in simple blades (Fig. 2G), and those that are toothed (Fig. 2H). They are long,

slender, needle-like, 0.62 ± 0.05 mm long ($n = 6$). Toothed chaetae bearing 2 or 3 comparatively large teeth proximally, and 1 or 2 rows of sharp thin teeth distally. Remaining thoracic segments bearing fascicles of chaetae with simple blades dorsally (Fig. 2I, J), 0.47 ± 0.02 mm long ($n = 6$), and uncinal tori ventrally. Thoracic uncini saw-shaped, with 9 teeth, 26 ± 12 μ m long ($n = 6$) (Fig. 2M).

Abdomen light greenish-yellow, 3.25 ± 0.24 mm long ($n = 8$). Each segment bearing uncinal torus dorsolaterally on each side, and fascicle of 2-4 trumpet-shaped geniculate chaetae ventrolaterally (Fig. 2K, L). Shaft and distal end of the latter 267 ± 24 ($n = 6$) and 49 ± 4 ($n = 6$) μ m long, respectively. Abdominal uncini (Fig. 2N) rasp-shaped, bearing 2 rows of 10-12 teeth each.

Analysis of 18S rDNA sequences

The alignment analysis revealed that 18S rDNA sequences of individuals from 5 brackish-water and 5 freshwater habitats were completely identical. The sequence was submitted to GenBank with accession no. HQ433336. By a blastn search, the sequence showed maximum identities of 94%, 93%, and 92% with the 18S rDNA sequences of *F. enigmaticus* (AY577889), *F. miamiensis* (EU167531), and *F. macrodon* (EU167532), respectively (Table 2).

The topological structures of the MP and ML

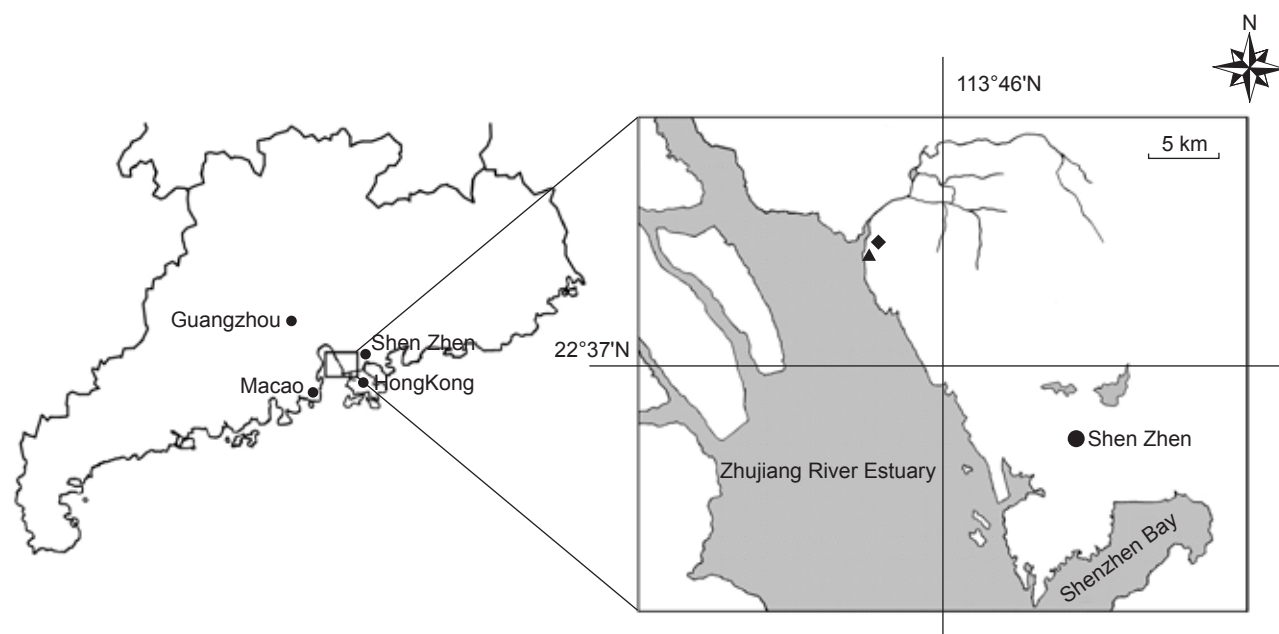


Fig. 3. Map showing localities from which *F. shenzhensis* sp. nov. was collected. ▲, Brackish-water samples; ◆, freshwater samples.

trees based on the partial 18S rDNA sequence were similar. The MP and ML analyses inferred 2 major clades within the Serpulidae (Figs. 4, 5). Species *F. shenzhensis* sp. nov., *F. enigmaticus*, *F. macrodon*, and *F. miamiensis* formed a well-supported clade (with 100% bootstrap probabilities in both the MP and ML trees). *Marifugia cavatica* Absolon and Hrabě, 1930 was included in the *Ficopomatus* clade. In addition, *M. cavatica* and *F. shenzhensis* sp. nov. formed a clade, a sister taxon to *F. enigmaticus*, *F. macrodon*, and *F. miamiensis*, with 89% bootstrap probability support.

DISCUSSION

Comparison between *Ficopomatus shenzhensis* sp. nov. and other species of *Ficopomatus*

A species belonging to the genus *F.* occurring in fresh water in China was originally reported and identified as *F. cf. macrodon* Southern 1921 by Lin et al. (2009). However, subsequent morphological and 18S rDNA sequence studies suggested that the species reported by Lin et al. (2009) is the same as that described in the present study.

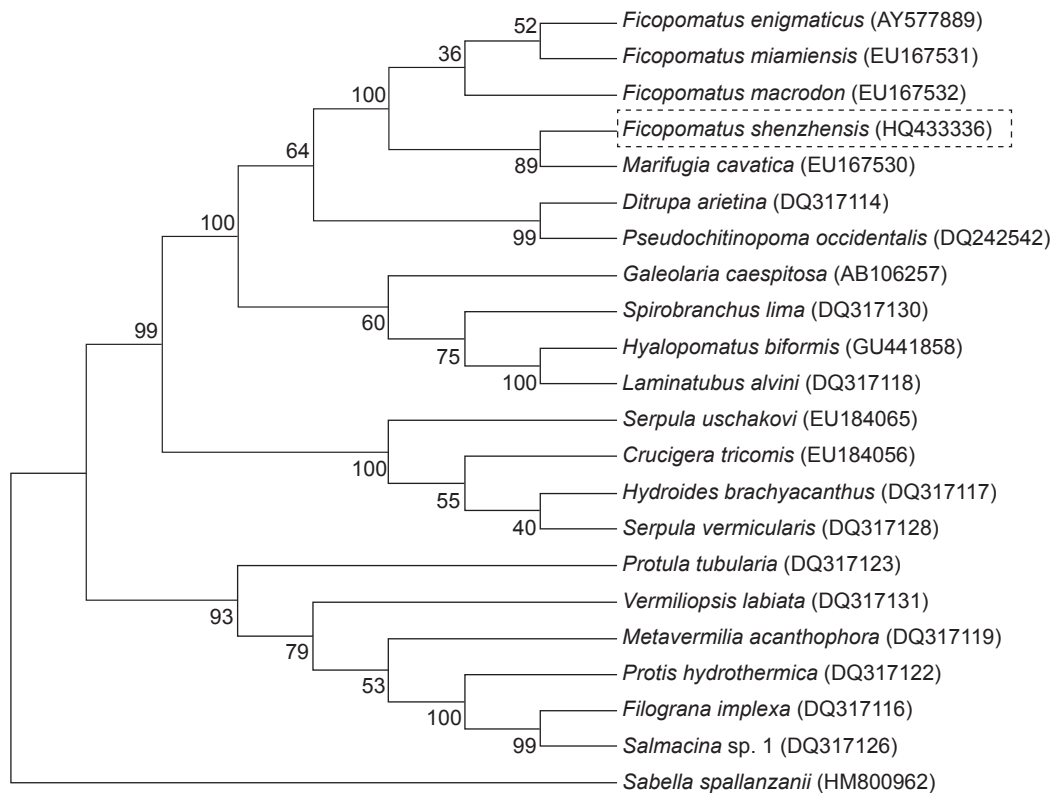


Fig. 4. Phylogenetic tree based on a maximum-parsimony (MP) phylogenetic analysis of the 18S rDNA gene (partial sequence) of species in the genus *Ficopomatus* and 3 species in other genera within the family Serpulidae (Kimura-2 parameter model, outgroup: *Sabella spallanzanii*). Numerals near the nodes indicate bootstrap values (%) based on 1000 replicates. The scale indicates the number of substitutional steps.

Table 2. Alignment analysis of the *F. shenzhensis* sp. nov. 18S rDNA sequence (HQ433336) as the query sequence

| Subject sequence | Query coverage (%) | Maximum identity (%) |
|---|--------------------|----------------------|
| <i>F. enigmaticus</i> 18S rDNA (AY577889) | 100 | 94 |
| <i>F. miamiensis</i> 18S rDNA (EU167531) | 100 | 93 |
| <i>F. macrodon</i> 18S rDNA (EU167532) | 99 | 92 |

As shown in table 3, several aspects of *F. shenzhensis* sp. nov. are distinguishable from those of the 4 known species of *Ficopomatus*. Cross-sections of tubes of *F. enigmaticus*, *F. macrodon*, *F. talehsapensis*, and *F. miamiensis* are semicircular, but it is circular in *F. shenzhensis* sp. nov. Spines are present on the operculum in *F. enigmaticus* (Fauvel 1923), but absent in *F. shenzhensis* sp. nov. In addition, a V-shaped furrow is present on the horny plate on the dorsal side of the operculum of *F. shenzhensis* sp. nov., but it is absent from the operculum of *F. enigmaticus*, *F. macrodon*, *F. talehsapensis*, and *F. miamiensis*.

The MP and ML trees based on partial 18S rDNA sequences showed that *F. shenzhensis* sp. nov., *F. enigmaticus*, *F. macrodon*, and *F. miamiensis* formed a clade with 100% bootstrap probabilities. The partial sequence of the 18S rDNA gene in *F. shenzhensis* sp. nov. showed a maximum identity of < 95% with those of *F. enigmaticus*, *F. miamiensis*, and *F. macrodon*. Unfortunately, no 18S rDNA gene sequence is available for *F. talehsapensis*. The molecular data suggested that the present described material

belongs to the genus *Ficopomatus*, while not being identical to *F. enigmaticus*, *F. macrodon*, or *F. miamiensis*. The data on morphology, ecology, and distribution of *M. cavatica*, the world's only freshwater serpulid, show its close relationship with *Ficopomatus* (Kupriyanova et al. 2009). A phylogenetic analysis of nuclear rDNA 18S and 28S sequences using MP, ML, and Bayesian analyses placed *M. cavatica* as a sister group to a clade of *Ficopomatus* species, *F. enigmaticus*, *F. macrodon*, and *F. miamiensis* (Kupriyanova et al. 2009). In accordance with those findings, *M. cavatica* was included in the *Ficopomatus* clade in the present molecular phylogenetic analysis. *Marifugia cavatica* and *F. shenzhensis* sp. nov. formed a clade, a sister taxon to *F. enigmaticus*, *F. macrodon*, and *F. miamiensis*, with 89% bootstrap probability support. As *F. shenzhensis* sp. nov. inhabits both brackish and fresh waters, the present phylogenetic analysis supports the suggestion by Kupriyanova et al. (2009) that *Ficopomatus* and *Marifugia* likely share a common brackish-water ancestor.

Accordingly, morphological characters in combination with molecular evidence confirmed

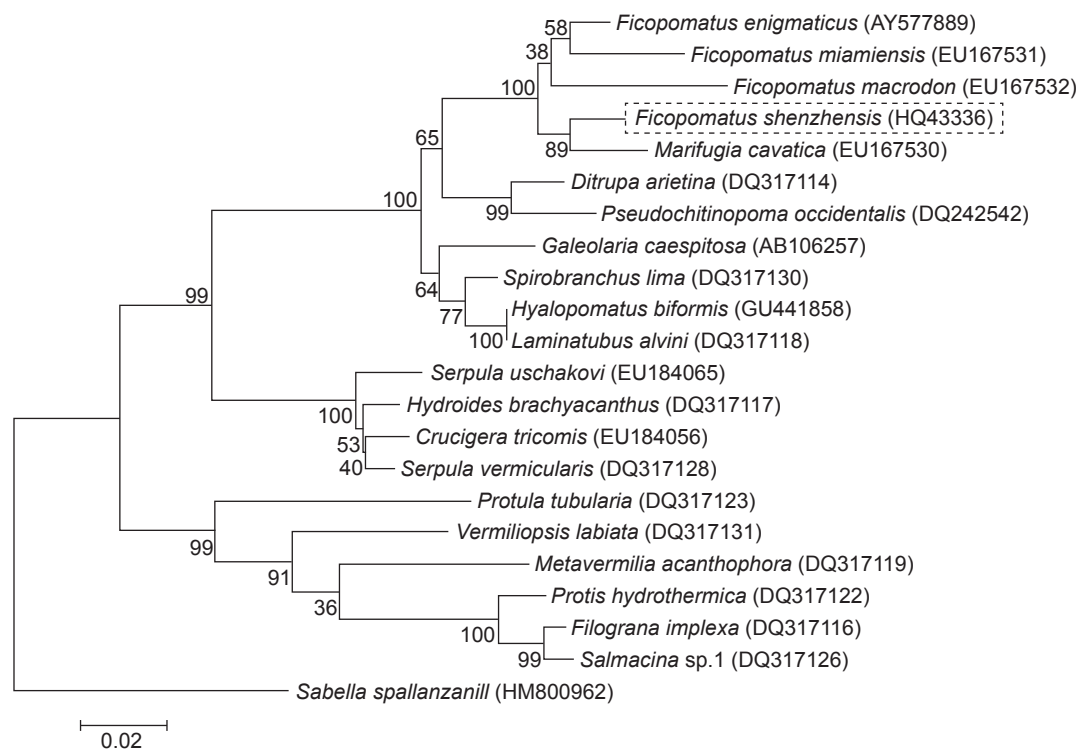


Fig. 5. Phylogenetic tree based on a maximum-likelihood (ML) phylogenetic analysis of the 18S rDNA gene (partial sequence) of species in the genus *Ficopomatus* and 3 species in other genera within the Serpulidae (Tamura-Nei model, outgroup: *Sabella spallanzanii*). Numerals near the nodes indicate bootstrap values (%) based on 1000 replicates. The branch length indicator displays 0.02 substitutions per site.

that the serpulid described here is a new species.

Stability of taxonomic characters in the genus *Ficopomatus*

Characters relating to the operculum and calcareous tube are used to identify species belonging to the genus *Ficopomatus* (ten Hove and Weerdenburg 1978). In addition, those of the special collar chaetae, abdominal chaetae, and uncini are important characters (Pillai 1960 1965 1971 2008, Hartmann-Schröder 1971, ten Hove and Weerdenburg 1978). However, morphological differences were observed in the same species of *Ficopomatus* living in different habitats, such as in the collar-like peristomes on the tube (presence or absence of peristomes) in *F. enigmaticus* (Hartmann-Schröder 1967, p. 454) and the operculum (with or without a horny plate) in *F. miamiensis* (ten Hove and Weerdenburg

1978, Fig. 1f-i). Morphological differences in relation to different habitats were also observed in other species within the family Serpulidae. For example, there are forms in which the marginal radial endings of the operculum of *Hydroides homoceros* differ in relation to salinity variations in habitats along the Suez Canal (Ben-Eliahu and ten Hove 2011). In the present study, the shapes of the operculum and tube of *F. shenzhensis* sp. nov. differed in specimens inhabiting brackish and fresh waters (Fig. 6B, E). In freshwater specimens, there is a longitudinal ridge on the tube, and the operculum is olive-shaped. Chaetal and uncinal characters did not markedly differ between the freshwater and brackish-water specimens (Fig. 7).

In conclusion, a new species of serpulid, *F. shenzhensis* sp. nov., from brackish-water and freshwater habitats of the Zhujiang River estuary shore in Shenzhen City, Guangdong Province, China, is described and illustrated. Morphological

Table 3. Morphological comparisons between *F. shenzhensis* sp. nov. and others species within the genus *Ficopomatus*

| Species | <i>F. macrodon</i> | <i>F. talehsapensis</i> | <i>F. miamiensis</i> |
|-----------------------|---|--|---|
| | Tube | 1-3 longitudinal ridges | 1 longitudinal ridge |
| Cross-section of tube | semicircular | semicircular | semicircular |
| Operculum | pear-shaped, with flat horny plate, spines absent | pear-shaped, with conical horny cap, spines absent | pear-shaped, horny end-plate flat or slightly convex, spines absent |
| Branchial radiole | total 17 | left 5-7, right 6 or 7 | left 6-9, right 6-10 |
| Thoracic uncini | 6-12 teeth | 10-12 teeth | 10-13 teeth |
| Abdominal uncini | 6-14 teeth, 1-4 rows | 13-15 teeth, 3 or 4 rows | 8-12 teeth, 4 or 5 rows |
| Body size (mm) | ~11 | ~7, branchial crown accounts for 1/4 | ~7 (2.5-11), branchial crown accounts for 1/6 |
| Reference | ten Hove and Weerdenburg 1978, Pillai 2008 | ten Hove and Weerdenburg 1978, Pillai 2008 | ten Hove and Weerdenburg 1978 |

| Species | <i>F. enigmaticus</i> | <i>F. shenzhensis</i> sp. nov. | |
|-----------------------|--|--|---|
| | | Brackish-water habitat | Freshwater habitat |
| Tube | 1 longitudinal ridge | no longitudinal ridges | 1 longitudinal ridge |
| Cross-section of tube | semicircular | circular | circular |
| Operculum | pear-shaped, horny end-plate eccentrically concavity, spines curved inward | pear-shaped, horny plate dorsal convex with V-shaped furrow, spines absent | oval, horny plate dorsal convex with V-shaped furrow, spines absent |
| Branchial radiole | left 5-9, right 7-10 | 9 on each side | 9 on each side |
| Thoracic uncini | 6 or 7 teeth | 9 teeth | 9 teeth |
| Abdominal uncini | 6-12 teeth, 2 or 3 rows | 10-12 teeth, 2 rows | 11-13 teeth, 2 rows |
| Body size (mm) | ~20 (7-44), branchial crown accounts for 1/6 | ~6 (5.3-7.1), branchial crown accounts for 1/3 | ~7 (6.3-8.1), branchial crown accounts for 1/5 |
| Reference | ten Hove and Weerdenburg 1978 | this study | this study |

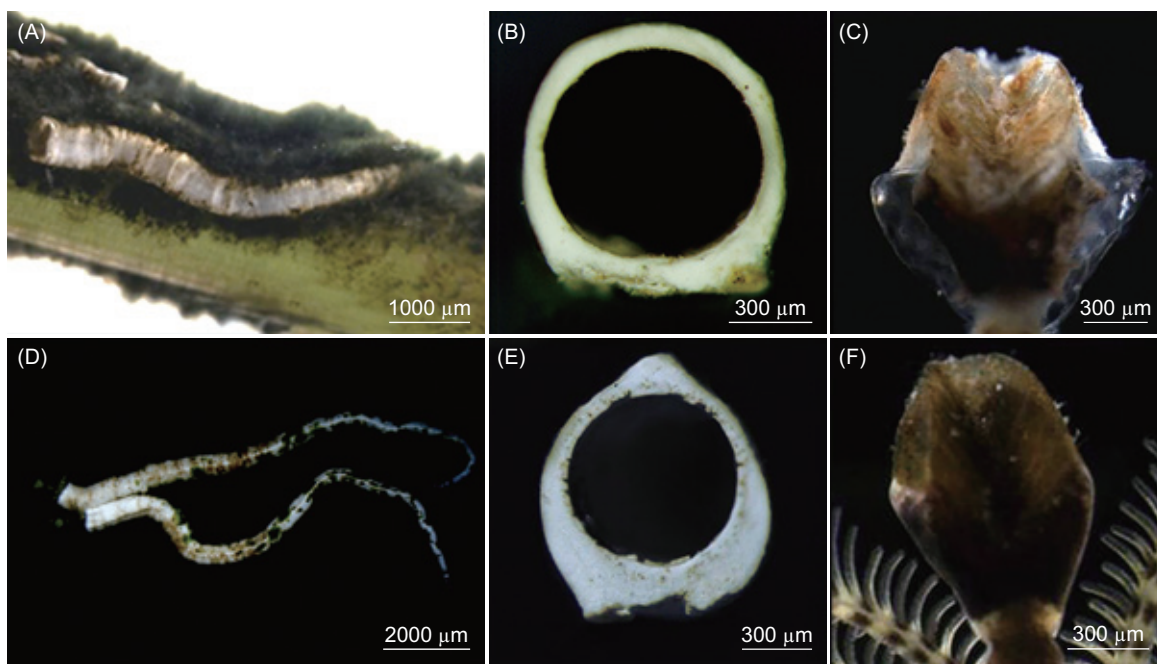


Fig. 6. Photographs of *Ficopomatus shenzhensis* sp. nov., showing individuals from brackish-water and freshwater habitats. (A-C) Brackish-water specimen, paratype, SAB 2; (D-F) freshwater specimen, paratype, SAB 7. (A, D) Tube; (B, E) cross-section of tube; (C, F) operculum.

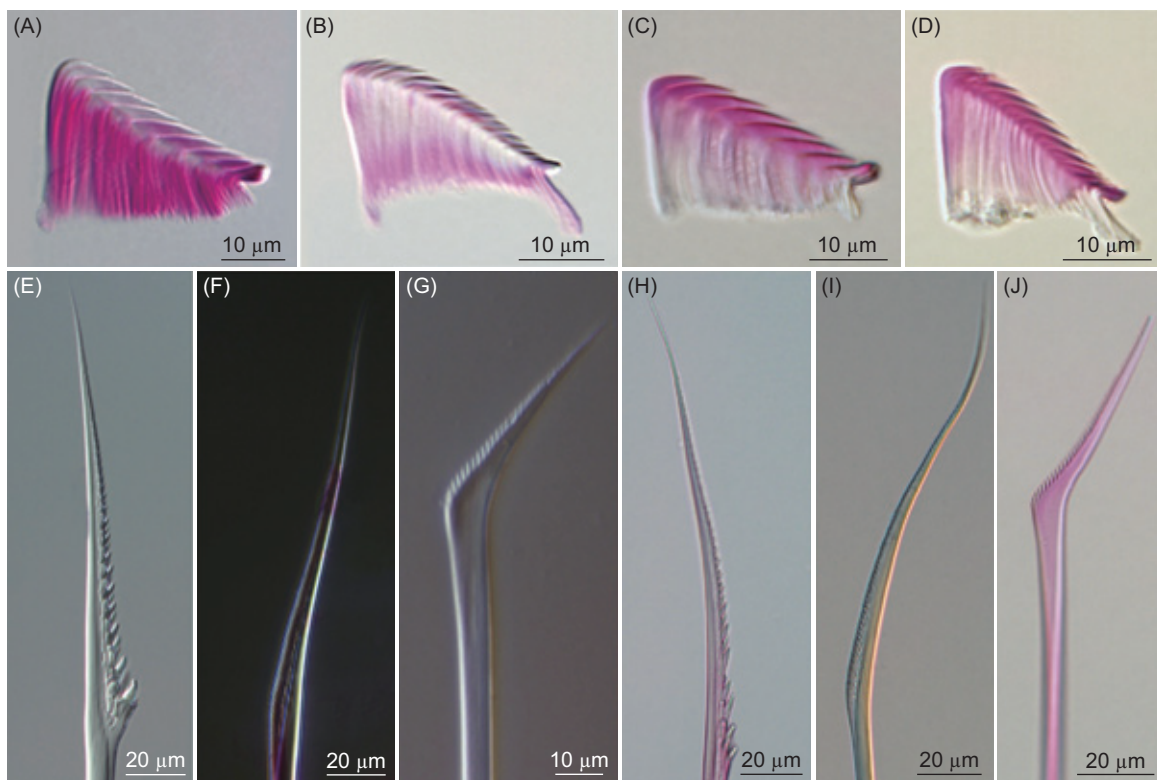


Fig. 7. Photographs of chaetae and uncini of *F. shenzhensis* sp. nov., from brackish-water and freshwater habitats. (A, B, E-G) Thoracic uncini, abdominal uncini, collar chaetae, thoracic chaetae, and abdominal chaetae of *F. shenzhensis* sp. nov. from a brackish-water habitat. (C, D, H-J) Thoracic uncini, abdominal uncini, collar chaetae, thoracic chaetae, and abdominal chaetae of *F. shenzhensis* sp. nov. from a freshwater habitat.

differences in the operculum and tube structures between brackish-water and freshwater specimens were noted.

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