

Fecampiid flatworms parasitic in a tanaidacean crustacean

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Short Communication

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Abstract

We report the first record of fecampiidan platyhelminths parasitic in tanaidacean crustaceans. Two fecampiidans (0.75 mm and 1.10 mm in length) were found in a female of *Pseudotanaais* sp. (Pseudotanaidae; 1.75 mm in length) collected at 794 m depth off the southern coast of Japan, northwestern Pacific. Fresh individuals were yellow or light yellow, but completely faded in ethanol. In a maximum likelihood tree based on 28S rRNA sequences, the parasite was placed in a moderately-supported Fecampiidae clade, suggesting it is a member of Fecampiidae. The 28S sequence from the parasite was 25.0%, 32.6%, and 35.5% divergent in Kimura 2-parameter (K2P) distance from *Fecampia* cf. *abyssicola*, *Kronborgia* cf. *amphipodicola*, and *Kronborgia isopodicola* sequences, respectively.

Introduction

Fecampiida, a group of parasitic platyhelminths, comprises four families (Laumer and Giribet 2017; Tyler *et al.* 2006–2024). Notenteridae contains two species, the polychaete-parasitic *Notentera ivanovi* and the octopus-parasitic *Octopoxenus antarcticus* (Gordeev *et al.* 2022; Joffe *et al.* 1997; Raikova *et al.* 2017). Piscinquilinidae contains one fish-parasitic species, *Ichthyophaga subcutanea* (Syromjatnikova 1949). Urastomidae contains *Urastoma cyprinae*, parasitic on various bivalve species (Robledo *et al.* 1994). Fecampiidae is the most species-rich fecampiidan family, with four *Fecampia*, one *Glanduloderma*, and five *Kronborgia* species. Previously reported hosts for the family include myzostomids (Annelida), amphipods, barnacles, decapods, and isopods (Crustacea, Arthropoda); Sudo *et al.* (2021) suggested that helminth parasites found from sea slugs (Mollusca) may belong to this family (Supplementary Table S1; Kakui 2024b). In addition to the 14 named species, there are possibly more than 10 undescribed species in Fecampiida (e.g., Christensen 1981a, b, 1988; Fiege *et al.* 2007; Handl and Bouchet 2007; Sudo *et al.* 2011).

Tanaidacea is a group of small aquatic crustaceans, with about 1500 species (Anderson 2023). Most species are free living and inhabit benthic marine habitats. Tanaidaceans are widely distributed geographically (all oceans) and vertically (intertidally to about 9000 m deep), and occasionally occur at very high densities (e.g., 140,000 individuals/m² in *Allotanaais hirsutus*; Delille *et al.* 1985). Given their broad distribution and high abundance, tanaidaceans might serve as hosts for many parasitic organisms in aquatic ecosystems, though they have received little attention in this context, with only a few works on tanaidacean parasites published in the past decade (Błażewicz *et al.* 2020; Boyko *et al.* 2021; Chatterjee *et al.* 2022; Chim and Bird 2021; Cortés *et al.* 2021; Jakiel *et al.* 2019; Kakui 2014, 2016; Kakui and Fujita 2024; Kakui and Shimada 2022).

In 2024, a tanaidacean containing vermiform organisms inside was collected around Japan. A 28S ribosomal RNA (28S) sequence determined from the parasite revealed that it is a fecampiidan flatworm, a group not previously been reported from tanaidaceans. Here, we describe the gross morphology of the fecampiidan and infer its phylogenetic position in Fecampiida based on 28S data.

Material and methods

The host tanaidacean was found in a mud sample collected with a suction sampler (slurp gun) from the deep submergence research vehicle *Shinkai 6500* (Japan Agency for Marine-Earth Science and Technology; JAMSTEC) at Station 1 (Shima Spur, 33°57.0212'N, 136°53.8682'E, 794 m depth), Dive 6K#1782, on 12 June 2024 during cruise YK24-09S of RV *Yokosuka* (JAMSTEC). The fresh tanaidacean was photographed and then fixed and preserved in 99% ethanol. Measurements were made from digital images of the fresh individual. Body length (BL) of the host was measured from the base of the antennules to the tip of the pleotelson, and body width (BW) at the widest portion of the cephalothorax. The BL of the parasites was measured from the anterior to posterior ends, and BW at the widest part. Part of one parasite

was removed from the host with sharpened needles for DNA extraction. The remaining part was deposited as a voucher specimen in the Invertebrate Collection of the Hokkaido University Museum (ICHUM), Sapporo, Japan, under catalog number ICHUM8960. DNA sequences (28S) were also determined for two cocoons of *Fecampia* cf. *abyssicola*, collected in the Kumano Sea (Stn D4: 33° 59.7'N 136°56.9'E to 33°59.9'N 136°57.2'E; 802–812 m depth) on 27 June 2023 during cruise 2312 of the TRV *Seisui-maru* (Mie University).

DNA was extracted from one tanaidacean parasite and the two cocoons of *F. cf. abyssicola* by using a NucleoSpin Tissue XS Kit (Macherey–Nagel, Germany; tanaidacean parasite) or DNeasy Blood & Tissue Kits (Qiagen, Germany; cocoons). Primers 28S_1F (Álvarez-Presas *et al.* 2008) and Fe28R (newly designed; GTTTGGTTTCATCC-CACAGC) were used for PCR amplification (the portion containing expansion segments D1–D5 was amplified; cf. Gillespie *et al.* 2006), and 28S_1F, Fe28R, 300F, 300R (Lockyer *et al.* 2003), and 28S_b5F (Kakui and Tsuyuki 2024) for cycle sequencing (primer 300R was not

used in sequencing the cocoons). PCR amplification conditions with KOD FX Neo (Toyobo, Japan) were 94°C for 2 min; 45 cycles of 98°C for 10 s, 60°C for 30 s, and 68°C for 1 min; and 68°C for 2 min (tanaidacean parasite); and with KOD One PCR Master Mix (Toyobo) were 94°C for 2 min; 35 cycles of 94°C for 40 s, 52°C for 75 s, and 72°C for 1 min; and 72°C for 7 min (cocoons). PCR products from the tanaidacean parasite were separated on a 2% agarose gel, excised with a micro spatula, and purified with a MagExtractor PCR & Gel Clean Up Kit (Toyobo) before cycle sequencing. All nucleotide sequences were determined with a BigDye Terminator Kit ver. 3.1 and a SeqStudio Genetic Analyzer (Thermo Fisher Scientific, USA; tanaidacean parasite) by KK or at FASMAC (Kanagawa, Japan; cocoons). Fragments were concatenated by using MEGA7 (Kumar *et al.* 2016). The sequences we determined were deposited in the International Nucleotide Sequence Database Collaboration (INSDC) participating databases through the DNA Data Bank of Japan (DDBJ), under accession numbers LC844707 (tanaidacean parasite), and LC847139 and LC847140 (cocoons).

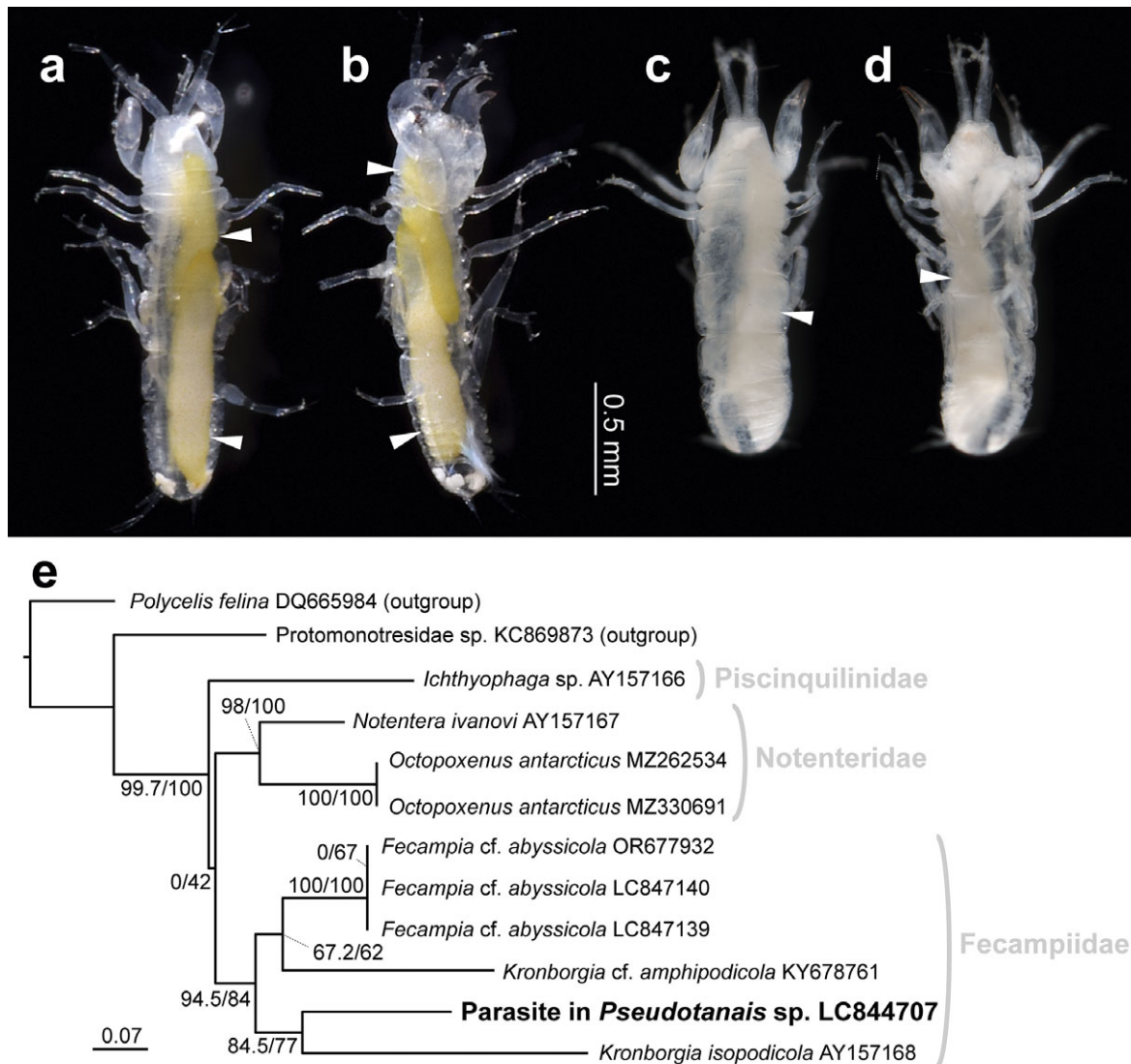


Figure 1. Fecampiida flatworms parasitic in a female of the tanaidacean *Pseudotanaeis* sp. (a–d) Parasites (arrowheads) in the host, fresh (a, b) and ethanol-fixed (c, d) specimens, dorsal (a, c) and ventrolateral (b, d) views; the border between two parasites was not distinguishable after ethanol fixation. (e) Maximum-likelihood tree for Fecampiida reconstructed from 28S sequences (868 positions); numbers near nodes are Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) / ultrafast bootstrap (UFBoot) values as percentages; the scale at the bottom indicates branch length in substitutions per site.

The 28S dataset for phylogenetic analysis included the three sequences we determined, and seven fecampiidan sequences and two outgroup sequences from the INSD (Álvarez-Presas *et al.* 2008; Gordeev *et al.* 2022; Hookabe *et al.* 2023; Laumer and Giribet 2014, 2017; Lockyer *et al.* 2003). The 28S sequences from *Urustoma cyprinae* (AJ313230, AY157165; Lockyer *et al.* 2003; Noren and Jondelius 2002) were excluded because they could be aligned with the other sequences only in a short region. The method for alignment was as described in Kakui (2024a); the aligned dataset contained 868 positions (Supplementary Files S1 and S2). Methods for selecting the optimal substitution model (GTR+F+I+R2), the maximum likelihood (ML) analysis, estimation of clade support (analyses of 1000 pseudoreplicates for both Shimodaira–Hasegawa-like approximate likelihood ratio tests [SH-aLRT] and ultrafast bootstraps [UFBoot]), and drawing the tree were as described by Shimada *et al.* (2023). Kimura (1980) 2-parameter (K2P) distances among the aligned sequences were calculated with MEGA7.

Results and discussion

Two fecampiidans were found in the body cavity of a single host tanaidacean (BL 1.75 mm, BW 0.35 mm) (Figure 1a–d). The host was identified as a preparatory female of *Pseudotanaïs* sp. in Pseudotanaidae (cf. Jakiel *et al.* 2019; Kakui *et al.* 2017). Both parasites were cylindrical. The larger one (BL 1.10 mm, BW 0.20 mm) was light yellow, with both ends slightly deeper in color. The smaller one (BL 0.75 mm, BW 0.15 mm) was yellow. Both were completely faded in ethanol and strongly shrunken, forming a single white mass. Since the part of the mass we used for DNA extraction was from the host pleon, the 28S sequence we determined was likely from the larger individual.

In the 28S-based ML tree (Figure 1e), the parasite lay in a moderately well supported (SH-aLRT/UFBoot = 94.5%/84%) Fecampiidae clade. Relationships among the taxa within the clade were unclear due to lack of high nodal support. The parasite was the sister taxon to *Kronborgia isopodicola*, though with low support (84.5%/77%). The parasite 28S sequence was 25.0%, 32.6%, and 35.5% divergent (K2P distance) from *Fecampia* cf. *abyssicola*, *Kronborgia* cf. *amphipodicola*, and *K. isopodicola* sequences, respectively. Although our analysis lacked urastomid sequences, and the anatomy and cocoon shape of our parasites were unknown, based on gross morphology (i.e., the cylindrical body typical of fecampiids) and the phylogenetic position in our tree, we concluded that the parasites belong in Fecampiidae.

With 73 valid species (WoRMS 2024), *Pseudotanaïs* tanaidaceans are highly diverse and abundant in the macrobenthos, have been reported from all oceans, and show a broad depth range from several meters to 6050 m (Błażewicz *et al.* 2021; Hansen 1913). They are probably epifaunal or burrowers in shallow sediment (Błażewicz *et al.* 2021) or inhabit a self-woven tube in sediment (cf. Bird and Holdich 1989). Their high abundance and broad distribution suggest *Pseudotanaïs* as a likely candidate host group for parasites, but only nematodes had been reported to date as parasites in this genus (Błażewicz *et al.* 2020). The fecampiids in the host tanaidacean were strongly deformed and had completely lost their color in ethanol (Figure 1c, d); the lack of previous records of fecampiids from Tanaidacea may likely have been due to simple oversight. Parasites in or on small, inconspicuous, burrowing or tube-dwelling crustaceans have been poorly investigated. As a case in point, despite their high prevalence in hosts commonly found in such an easily accessible environment as a river estuary, trematodes were first reported in a

burrowing isopod (*Cyathura muromiensis*) only in 2024 (Shiraki and Kakui 2024). Targeted examination of such understudied groups will likely detect additional unexpected host species for fecampiids.

Supplementary material. The supplementary material for this article can be found at <http://doi.org/10.1017/S0022149X25000057>.

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Competing interest. The authors declare none.

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