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Morphology and molecular phylogeny of controversial tintinnids *Tintinnopsis fimbriata* and *T. uruguayensis* (Protozoa: Ciliophora) collected from coastal waters of South Korea

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Two tintinnid species with stout campanulate loricae were collected from coastal waters of the Yellow Sea, South Korea. These species were identified as *Tintinnopsis fimbriata* Meunier, 1919 and *T. uruguayensis* Balech, 1948. The loricae morphology of fixed cells from both species was examined under light and scanning electron microscopes. Also, the phylogenetic positions of the two species were inferred using the gene sequences from SSU rDNA, ITS1, 5.8S rDNA, and ITS2. They share very similar loricae that consist of an obconical collar, a globular bowl, and a cylindrical posterior process. However, *T. fimbriata* can be distinguished from *T. uruguayensis* by the lorica size (61−71 × 34−41 μm vs. 52−61 × 23−29 μm) and the ratio of lorica length to collar opening diameter (1.6−1.8 vs. 1.9−2.7). The two species showed high similarity to each other as follows: 99.86% (2 nucleotide differences) in SSU rDNA and 99.76% (1 nucleotide difference) in ITS1−5.8S rDNA−ITS2. Given the morphological and molecular similarities between the Korean *T. fimbriata* and *T. uruguayensis*, as well as the discrepancies between the neotype of *T. fimbriata* and its original description (e.g., posterior process of the lorica), further studies are required to clarify their conspecificity or the potential existence of sibling species.

Keywords: 18S rDNA sequences, biodiversity, ciliate, lorica morphology, marine

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Introduction

Tintinnids are one of the best-studied groups of ciliates and their characterization is mainly based on their lorica morphology (see Moon and Jung, 2024). Among them, the genus *Tintinnopsis* Stein, 1867 exhibits the highest species diversity, with approximately 160 species (see Agatha, 2010), with 25 species recorded in Korea (National Institute of Biological Resources, 2023; Moon and Jung, 2024). Within the genus, three species namely *T. amoyensis* Nie, 1934, *T. fimbriata* Meunier, 1919, and *T. uruguayensis* Balech, 1948, possess very similar, stout campanulate loricae (Meunier, 1919; Nie, 1934; Balech, 1948). In this study, we collected two of these species and conducted comparative analyses. Since its discovery in 1919, *Tintinnopsis fimbriata* has been the subject of taxonomic discussion, including its generic assignment and synonymization (Meunier, 1919; Kofoid and Campbell, 1929; Balech, 1948). However, a neotype was designated by Agatha (2008), providing detailed information on its nomenclature and infraciliature. After the original description by Balech (1948), *Tintinnopsis uruguayensis* was redescribed three times, offering additional information on its infraciliature and genetic data (Strüder-Kypke and Lynn, 2008; Santoferrara *et al*., 2013; Bai *et al*., 2020).

These two species have very similar lorica morphology but the possibility of treating them as synonyms has not been discussed in the study reporting the neotype of *T. fimbriata*. While comparing infraciliature has been proposed as a solution, this approach is challenging because only 3% of all tintinnids have been described to date (see Moon and Jung, 2024). To address this limitation, alternative genetic markers, beyond SSU rDNA, have been proposed (Santoferrara *et al*., 2013; Jung *et al*., 2018), but genetic material from the neotype of *T. fimbriata* is not available for comparison. In the present study, we isolate these species as the first report in South Korea (National Institute of Biological Resources, 2023). To clarify the identification of both species, we provide both morphological and molecular phylogenetic information. The data include images from both light and scanning electron microscopes and phylogenetic analyses based on SSU rDNA sequences; in addition, the sequences of ITS1, 5.8S rDNA, and ITS2 are provided.

Materials and Methods

Samples collection and identification

Two tintinnids species were collected using a 20 μm plankton net from coastal waters in South Korea. *Tintinnopsis fimbriata* was collected at the Gomso Port on 20 May 2021. The water temperature and salinity were 20.0 to 20.3°C and 28.5 to 29.5, respectively. *Tintinnopsis uruguayensis* was collected at the sampling site near the Janghang Port on 17 Aug 2021. The water temperature and salinity were 27.9°C and 28.6, respectively. At each sampling site, these net-tow samples were fixed using two fixatives: one fixed in the Bouin's fluid with a final concentration of 10%, and the other fixed in ethanol (final concentration of 70%) (Coats and Heinbokel, 1982). The sampling site, along with the locality details, are described in the "material examined" section for each species.

Cells were isolated from the Bouin's fluid-fixed samples under a stereo microscope (SZ61; Olympus, Tokyo, Japan). The loricae features were examined at high magnifications using an inverted microscope (12.5−400×, IX73; Olympus) and an upright microscope (1,000×, BX53; Olympus) with brightfield and differential interference contrast optics.

For slide preparation, the isolated cells from the Bouin's fluid-fixed samples were rinsed with distilled water and then were substituted with glycerol overnight at 60°C. The glycerol-substituted cells were mounted on a slide, and a circular coverslip was attached using resin (Sigma, St. Louis, MO, USA). To prevent the lorica from being compressed by the coverslip, beads of ≥100 μm in diameter were placed between the slide and the coverslip.

The concave regions of a lorica were considered the borderline separating the collar, bowl, and posterior process. Box plots of correlation between *T. fimbriata* and *T. uruguayensis* were plotted using the 'ggpubr' package in R (Kassambara and Kassambara, 2020). Terminology and systematics follow Kofoid and Campbell (1929), Alder (1999), Agatha and Riedel-Lorjé (2006), Santoferrara and McManus (2020).

Scanning electron microscopy

Cells of each species were isolated from the Bouin's fluid-fixed samples and then rinsed thoroughly with distilled water at least three times. The rinsed cells were attached onto a poly-L-lysine coated coverslip. The coverslip was dehydrated using an ethanol series (30 to 100%), dried in a critical point dryer (EMCPD300; Leica, Wetzlar, Germany), and then coated with platinum. The samples were observed in JSM-IT500 (Jeol, Tokyo, Japan) in the Center for Research Facilities at Gangneung-Wonju National University.

DNA extraction, PCR amplification, and sequencing

Cells were isolated from the ethanol-fixed samples and thoroughly rinsed with distilled water. Each cell was then photographed under an inverted microscope (400×, IX73; Olympus) equipped with a digital camera (DP74, Olympus) before being transferred to a separate 1.5 mL tube with a minimum amount of distilled water. The tubes were dried at 60°C for 30 minutes in the centrifugal evaporator (CVE-2200; Eyela, Tokyo, Japan) with the lids open while rotating.

The dried cells in each tube were used to extract genomic DNA using a RED Extract-N-Amp Tissue PCR Kit (Sigma) following 1/10 of manufacturer's recommended volume. The SSU rDNA sequence of *Tintinnopsis fimbriata* was amplified with the primers 18S-Tin3F and 28S-TinR1 (Bachy *et al*., 2012). The PCR conditions were as follows: denaturation at 94°C for 3 min, followed by 35 cycles of denaturation at 94°C for 15 s, annealing at 52°C for 30 s, and extension at 72°C for 2 min, and a final extension step at 72°C for 15 min. The SSU rDNA sequence of *T. uruguayensis* was amplified with the primers New Euk A (Jung and Min, 2009) and 28S-TinR1 (Bachy *et al*., 2012); it should be noted that the aforementioned primer pair for *T. fimbriata* did not successfully amplify its gene fragment. The PCR conditions were as follows: denaturation at 94°C for 1 min 30 s, followed by 40 cycles of denaturation at 98°C for 10 s, annealing at 54°C for 30 s, and extension at 72°C for 3 min, and a final extension step at 72°C for 7 min.

The PCR products were confirmed through electrophoresis, and then purified using the MEGA quick-spin Total Fragment DNA Purification Kit (iNtRON, Seongnam, Korea). The sequence fragments were initially obtained using the forward primer for each species. For cells with high-quality of the DNA fragment, the remaining regions were sequenced. Sequencing was performed using an ABI PRISM 3730XL Analyzer (Applied Biosystems, Foster City, CA, USA) with the following internal primers: 18SR300, 18SF790v2 (Park *et al*., 2017; Jung *et al*., 2018).

Phylogenetic analyses

The sequence fragments of each species were assembled using Geneious Prime 2024.0.3 (Kearse *et al*., 2012). The SSU rDNA sequences of the two species were analyzed together with 58 tintinnids and three outgroup species obtained from the NCBI database. A total of 63 sequences were aligned and they were trimmed at both ends to a final length of 1,474 base pairs using Geneious Prime 2024.0.3. Using jModelTest 2.1.10 (Darriba *et al*., 2012), the TIM2+I+Γ model was selected based on the Akaike information criterion and applied to construct trees using Bayesian inference (BI) and maximum likelihood (ML) methods. For BI, MrBayes 3.2.7 (Ron-

quist *et al*., 2012) was conducted under the following conditions: Markov chain Monte Carlo simulations for 1,000,000 generations, with a sampling frequency of every 100 generations, and a burn-in of 3,000 trees. The ML tree was inferred using IQ-tree 1.6.12 (Nguyen *et al*., 2015) using 100,000 ultrafast bootstrap replicates (Minh *et al*., 2013). Sequence identities and differences between the sequences were computed in Geneious Prime 2024.0.3. Phylogenetic trees were visualized using the free software package FigTree v1.4.4 by A. Rambaut at http://tree.bio.ed.ac.uk/software/figtree/.

Results and Discussion

Phylum Ciliophora Doflein, 1901
Class Spirotrichea Bütschli, 1889
Order Tintinnida Kofoid and Campbell, 1929
Genus *Tintinnopsis* Stein, 1867 incertae sedis in order Tintinnida

Tintinnopsis fimbriata **Meunier, 1919**
(Table 1, Figs. 1, 2, 5) 넓은종꼴소모충 (신칭)

Tintinnopsis fimbriata Meunier, 1919: 31, pl. 22, figs. 38, 39; Hofker, 1931: 321, fig. 5; Agatha, 2008: 261–272, figs. 1–3.
Tintinnopsis sp. Brandt, 1906: 16, pl. 17, figs. 5, 7, pl. 18, fig. 10; Brandt, 1907: 180.
Tintinnopsis meunieri Kofoid and Campbell, 1929: 40, fig. 59.
Codonaria fimbriata Balech, 1948: 15, pl. 6, figs. 69–86.

Material examined. Marine water, collected from Gomso Port, Jinseo-myeon, Buan-gun, Jeonbuk-do, Republic of Korea (35°35′08″N, 126°36′20″E) on 20 May 2021.
Description (n = 7). Lorica 61–71 × 34–41 μm (on average 64.4 × 38.1 μm) in size, agglutinated, composed of obconical collar and globular to ellipsoidal bowl with cylindrical posterior process (Figs. 1A–E, 2A–F). Collar 7.0–10.5 μm (on average 8.6 μm) high, crown-shaped, with irregular rim; inner constriction 28–32 μm (on average 30.4 μm) in diameter. Ratio of lorica length to opening of collar diameter 1.6–1.8 : 1 (on average 1.7 : 1). Bowl occupies about 66% of lorica length, 33–37 μm (on average 34.4 μm) in diameter; end of bowl 61–86° (on average 72.3°) angle (Figs. 1A, 2A–C). Posterior process 11–15 ×

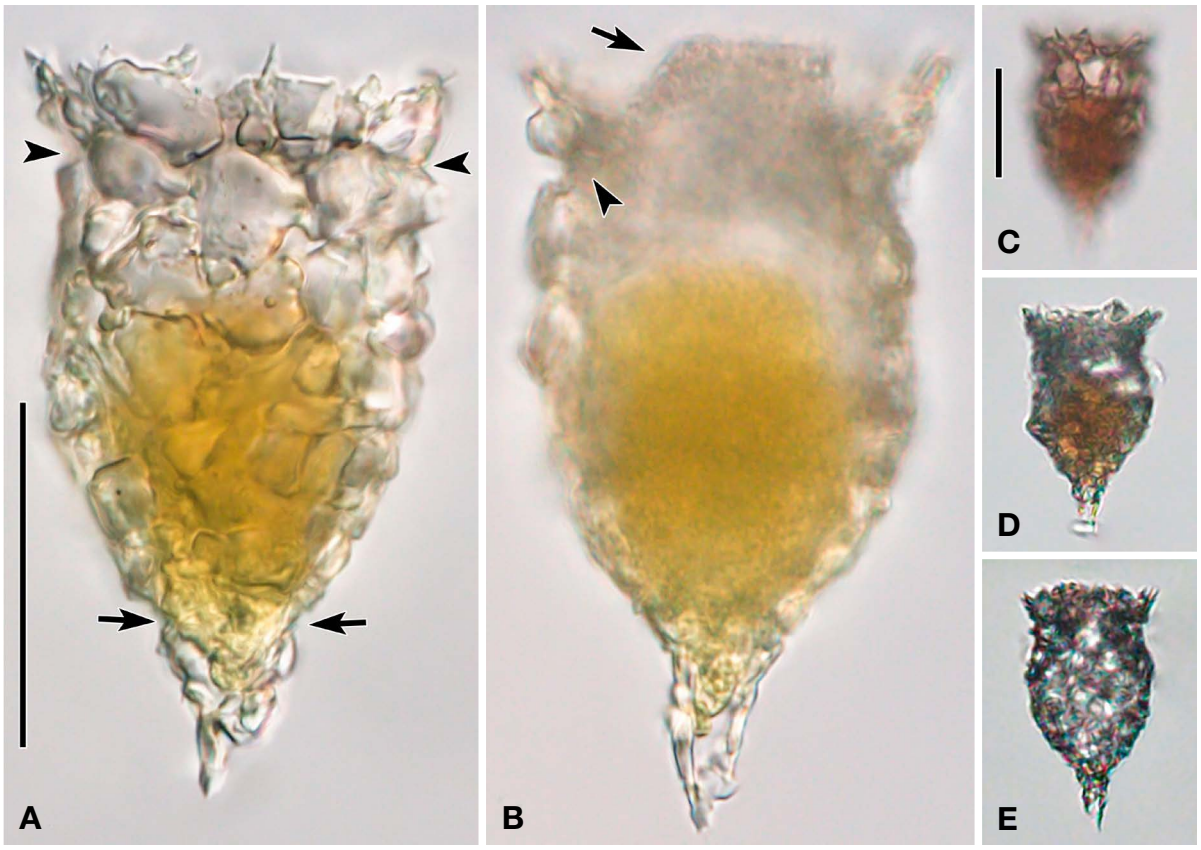

Fig. 1. *Tintinnopsis fimbriata* from a Bouin's fluid-fixed sample. A, C–E, Lateral views of the loricae, arrowheads marking boundary between the collar and the bowl, arrows indicating the borderline between the bowl and the posterior process; B, Optical section of the middle of the cell inside the lorica, arrow showing the closing apparatus and arrowhead indicating the estimated attachment point on the inner surface of lorica. The same scale is applied for comparison of size variation (A, B; C–E). Scale bars: A, C = 30 μm.

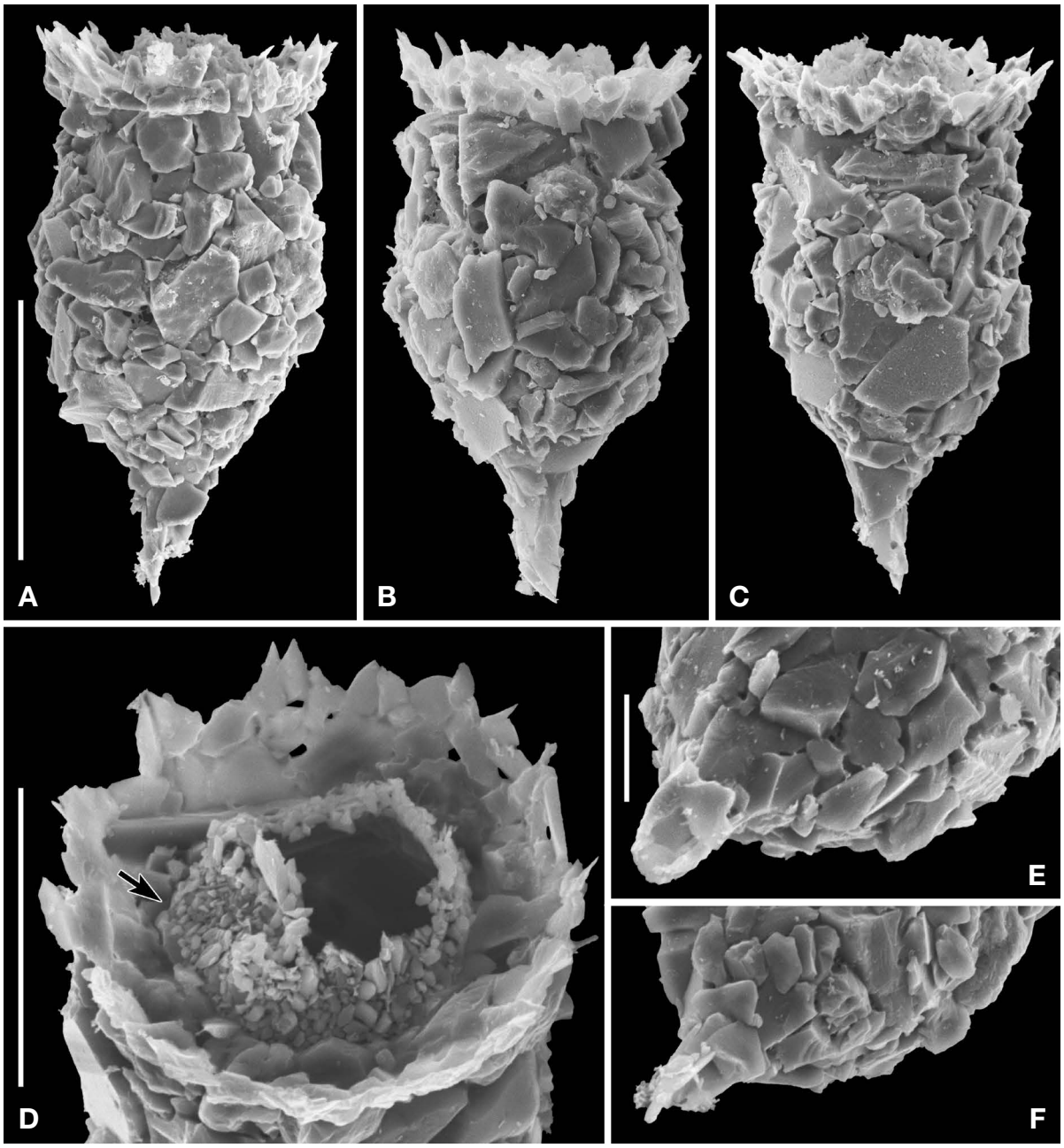

Fig. 2. *Tintinnopsis fimbriata*, isolated from a Bouin's fluid-fixed sample, under a scanning electron microscope. A–C, Lateral views of the loricae; D–F, Anterior and posterior ends of the loricae, arrow indicating the attachment point between the inner surface of the collar and the closing apparatus. The closing apparatus was constructed by finer particles than those on the lorica (D). The same scale is applied for comparison of size variation (A–C; E, F). Scale bars: A = 30 μm, D = 20 μm, E = 10 μm.

6.0–8.5 μm (on average 12.0 × 7.6 μm) in size, with usually obliquely truncate open end (Figs. 1A, B, 2A–C, E, F). Closing apparatus present, agglutinated with small particles (Figs. 1B, 2D).

Habitat. Marine.

Distribution. Nieuwpoort in Belgium (Meunier, 1919), Zuiderzee in the Netherlands (Hofker, 1931), Elbmündung, the Kiel Canal, and coastal waters of Sylt in Germany (Brandt, 1907; Kofoid and Campbell, 1929; Agatha, 2008), Atlántida in Uruguay (Balech, 1948), Fort Pierce in the United States of America (Strüder-Kypke and Lynn, 2003), and near Gomso Port in Korea (present study).

Phylogenetic analyses. The SSU rDNA–ITS1–5.8S rDNA–ITS2–partial LSU rDNA sequence of *Tintinnop-*

sis fimbriata is 2,122 base pairs long with a GC content of 47.5% (GenBank accession no: PQ650933). The SSU rDNA sequence of the Korean population of *T. fimbriata* shows an identity of 96.25% (54 nucleotide differences) to the American population (AY143560), which is the only available sequence and does not cluster together in the phylogenetic tree (Fig. 5). The gene sequence rather clusters together with *Stenosemella steini*.

Additionally, the Korean SSU rDNA sequence of *Tintinnopsis fimbriata* is identical to those of the two American (EU399542, JN831838) and Chinese (MT435075) populations of *T. uruguayensis* (Fig. 5), but there are two nucleotide differences between the Korean populations of *T. fimbriata* and *T. uruguayensis* (GenBank accession No. PQ650934, this study). Furthermore, the ITS1, 5.8S rDNA, and ITS2 sequence of *T. fimbriata* shows identities of 99.76% (one nucleotide difference) to the Korean population and 99.53% (two nucleotide differences) to the Chinese population (MT435062) of *T. uruguayensis*.

Remarks. Among the three congeners sharing similar lorica morphology, *Tintinnopsis amoyensis* is easily distinguished from the Korean *T. fimbriata* by its smaller size (45−50 × 25−27 μm vs. 61−71 × 34−41 μm) (Nie, 1934). *Tintinnopsis uruguayensis* differs from *T. fimbriata* by the slender lorica (ratio of lorica length to opening of collar diameter: 1.6−2.7 vs. 1.3−1.8) (Meunier, 1919; Balech, 1948; Agatha, 2008; Bai *et al*., 2020; this study).

The Korean specimens of *T. fimbriata* match the dimensions estimated from the original illustrations in terms of the lorica shape and size (61−71 × 34−41 μm vs. 68−75 × 52−54 μm) (Meunier, 1919) (Table 1). However, in terms of the collar width, the Korean population does not match closely with the original population (34−41 μm vs. 52−54 μm) but corresponds more closely to the neotype (38−56 μm vs. 34−41 μm) (Agatha, 2008).

As noted above, the Korean population of *T. fimbriata* is morphologically consistent with the neotype (Table 1). However, the sequence of the neotype is unavailable, and sequence AY143560 (assigned to *T. fimbriata*) is presumed to have been derived from a misidentified specimen due to the unclear posterior process of the lorica (Strüder-Kypke and Lynn, 2003; Agatha, 2008). Even though the Chinese population of *T. uruguayensis* differs from the neotype of *T. fimbriata* in the infraciliature pattern (left ciliary field: 4−6 vs. 6−8; lateral ciliary field: 11−14 vs. 9−16) (Agatha, 2008; Bai *et al*., 2020), it is challenging to definitively reject their conspecificity due to the unavailability of the SSU rDNA sequence for the neotype.

The identical SSU rDNA sequences between congeners are well-documented in some ciliates (e.g., *Tetrahymena*, *Parafavella*) and this may be one such case (Lynn and Strüder-Kypke, 2006; Jung *et al*., 2018). Therefore, there

Table 1. Comparison of main features of *Tintinnopsis fimbriata*, *T. uruguayensis*, and *T. amoyensis*.

Characteristics	Lorica, total length	Lorica, collar opening diameter	Lorica, inner constriction diameter	Lorica, bowl width	Lorica length: collar opening diameter, ratio	GenBank acc. no. (SSU)	Reference
T. fimbriata (type pop.)	68−75[a]	52−54[a]	38−42[a]	50−52[a]	1.3[a]	NA	Meunier (1919)
T. fimbriata	79[a]	60[a]	51[a]	58[a]	1.3[a]	AY143560	Strüder-Kypke and Lynn (2003)
T. fimbriata (neotype pop.)	48−74	38−56	15−31	36−50	1.5−1.8	NA	Agatha (2008)
T. fimbriata	61−71	34−41	28−32	33−37	1.6−1.8	PQ650933	Present study
T. uruguayensis (type pop.)	54−63	22−27	19−21	23−26	1.8−2.1[a]	NA	Balech (1948)
T. uruguayensis	70−80	40−50	NA	40	1.6[a]	EU399542	Strüder-Kypke and Lynn (2008)
T. uruguayensis	64	34	27[a]	35	1.9[a]	JN831838	Santoferrara *et al*. (2013)
T. uruguayensis	50−73	24−42	17−29	25−41	1.6−2.3	MT435075	Bai *et al*. (2020)
T. uruguayensis	52−61	23−29	18−21	23−25	1.9−2.7	PQ650934	Present study
T. amoyensis (type pop.)	45−50	25−27	NA	NA	1.7−1.9	NA	Nie (1934)

[a]Estimated from the illustrations.

is no doubt that an in-depth taxonomic discussion between *T. fimbriata* and *T. uruguayensis* is necessary. When focusing on the key character of collar opening diameter, *T. fimbriata* and *T. uruguayensis* observed in this study are clearly distinguishable (Fig. 6). However, when including the original, neotype, and Chinese populations of *T. uruguayensis* in the comparison, the measurements overlapped within the range of 23–56 μm, making it difficult to determine their relationships.

When comparing these populations separately based on Table 1, the morphology of *T. fimbriata* and *T. uruguayensis* from Korea does not overlap, and differences in their sequences also suggest they are distinct species. Moreover, the collar opening diameter of *T. uruguayensis* reported by Strüder-Kypke and Lynn (2008) appears to differ significantly from that mentioned in the original description (40–50 μm vs. 22–27 μm) but is more similar to those in the original description of *T. fimbriata* (40–50 μm vs. 52–54 μm), raising the possibility of misidentification.

To address these issues, we performed molecular analyses, but the commonly used genetic markers did not provide clear differentiation, and the analysis of markers with higher discriminatory power was unsuccessful (e.g., CO1). Based on the observed differences between the two Korean species, we identified them as more similar species compared to the original or neotype descriptions. Therefore, it is important to recognize the challenges, posed by lorica variation and genetic conservation, in future studies. Additionally, further research utilizing genetic markers capable of precisely identifying *T. fimbriata* and *T. uruguayensis* is needed.

Voucher specimens. The three slides were deposited at the National Marine Biodiversity Institute of Korea (MABIK PR00045100–MABIK PR00045102).

***Tintinnopsis uruguayensis* Balech, 1948**
(Table 1, Figs. 3–5) 좁은종꼴소모충 (신칭)
Tintinnopsis uruguayensis Balech, 1948: 14, pl. 5, figs. 64–68; Bai *et al*., 2020: 10–12, figs. 5, 6.

Material examined. Marine water, collected from near Janghang Port, Janghang-eup, Seocheon-gun, Chungcheongnam-do, Republic of Korea (36°0′26.6″N, 126°41′51.9″E) on 17 Aug 2021.

Description (n = 15). Lorica 52–61 × 23–29 μm (on average 56.4 × 26.5 μm) in size, agglutinated, composed of obconical collar and ellipsoidal bowl with cylindrical posterior process (Figs. 3A–G, 4A–G). Collar 8.5–12.0 μm (on average 10.0 μm) high, crown-shaped, with irregular rim; inner constriction diameter 18–21 μm (on average 19.4 μm). Ratio of lorica length to opening of collar diameter 1.9–2.7 : 1 (on average 2.2 : 1). Bowl occupies about 62.3% of lorica length, 23–25 μm (on average 23.8 μm) in diameter; end of bowl 47–86° (on average 69.7°) angle (Figs. 3A, 4A–C). Posterior process 9–15 × 5.5–8.5 μm (on average 11.5 × 6.7 μm) in size, with usually obliquely truncate open end (Figs. 3A, B, 4A–C, F). Closing apparatus present, agglutinated with small particles (Figs. 3B,

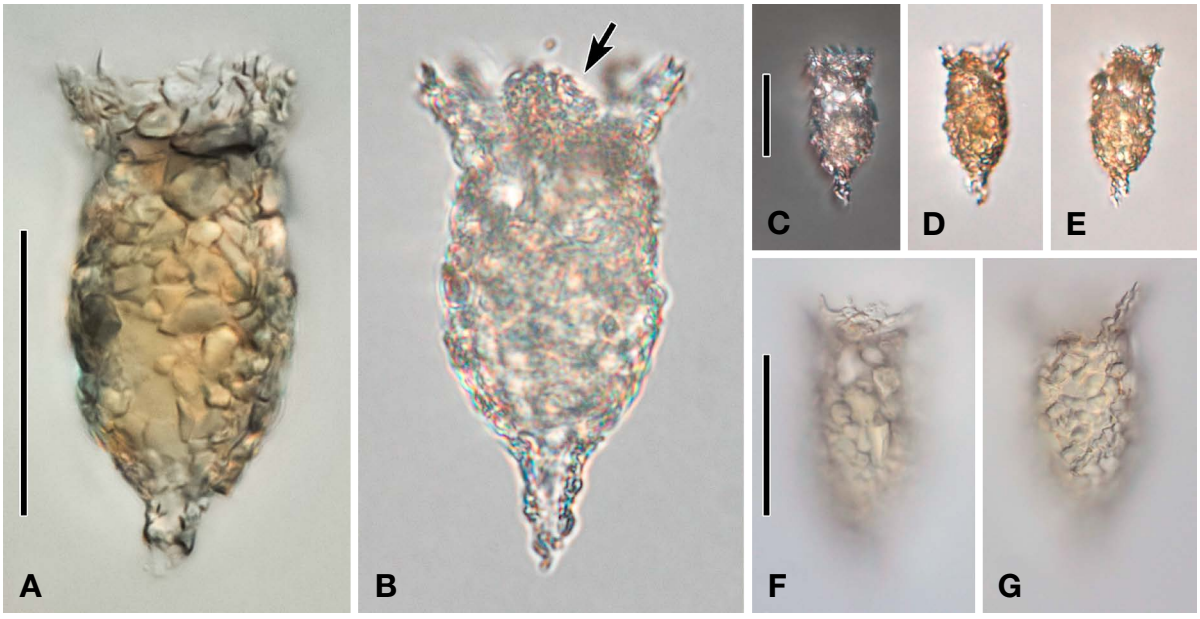

Fig. 3. *Tintinnopsis uruguayensis* from a Bouin's fluid-fixed sample. A, C–G, Lateral views of the loricae; B, Optical section of the middle of the cell inside the lorica, arrow showing the closure of the closing apparatus. The same scale is applied for comparison of size variation (A, B; C–E; F, G). Scale bars: A, C, F = 30 μm.

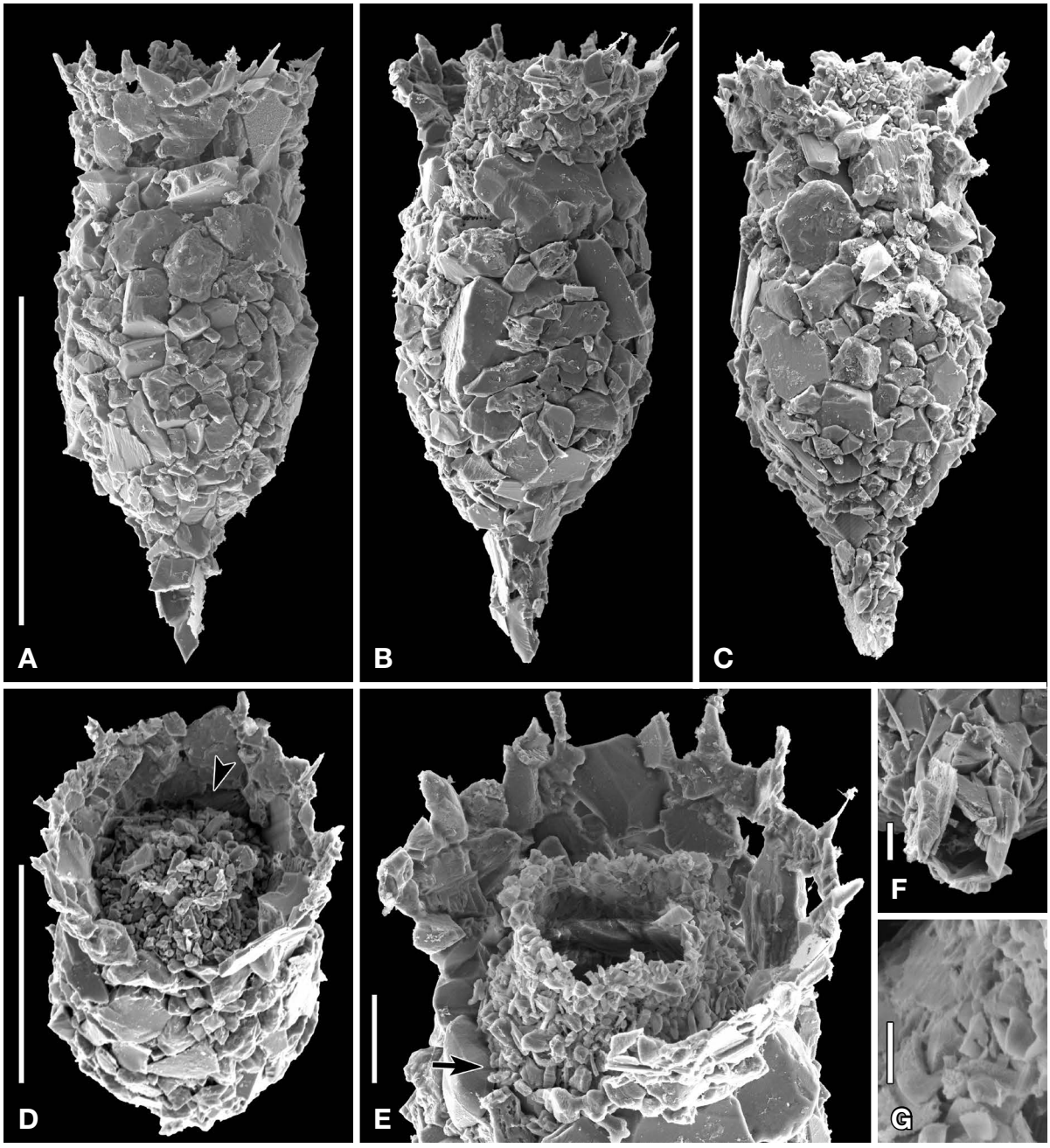

Fig. 4. *Tintinnopsis uruguayensis*, isolated from a Bouin's fluid-fixed sample, under a scanning electron microscope. A–C, Lateral views of the loricae; D, E, Anterior ends of the loricae, arrowhead indicating the closure of the closing apparatus, arrow showing the possibility of the presence of an agglutinated lorica sac; F, Posterior end of the posterior process; G, Smooth inner surface of the closing appartus. The same scale is applied for comparison of size variation (A–C). Scale bars: A = 30 μm, D = 20 μm, E = 5 μm, F = 2 μm, G = 1 μm.

4B–D, E, G).

Habitat. Marine.

Distribution. Atlántida in Uruguay (Balech, 1948), Fort Pierce and Long Island Sound in the United States of America (Strüder-Kypke and Lynn, 2008; Santoferrara *et al*., 2013), coastal waters of Qingdao in China (Bai *et al*., 2020), and Janghang Port in Korea (present study).

Phylogenetic analyses. The SSU rDNA–ITS1–5.8S rDNA–ITS2–partial LSU rDNA sequence of *Tintinnopsis uruguayensis* is 2,318 base pairs long with a GC content of 46.8% (GenBank accession no: PQ650934). The SSU rDNA sequence of *T. uruguayensis* shows an identity of 99.86% (two nucleotide differences) to the two American populations (EU399542, JN831838) and the Chinese pop-

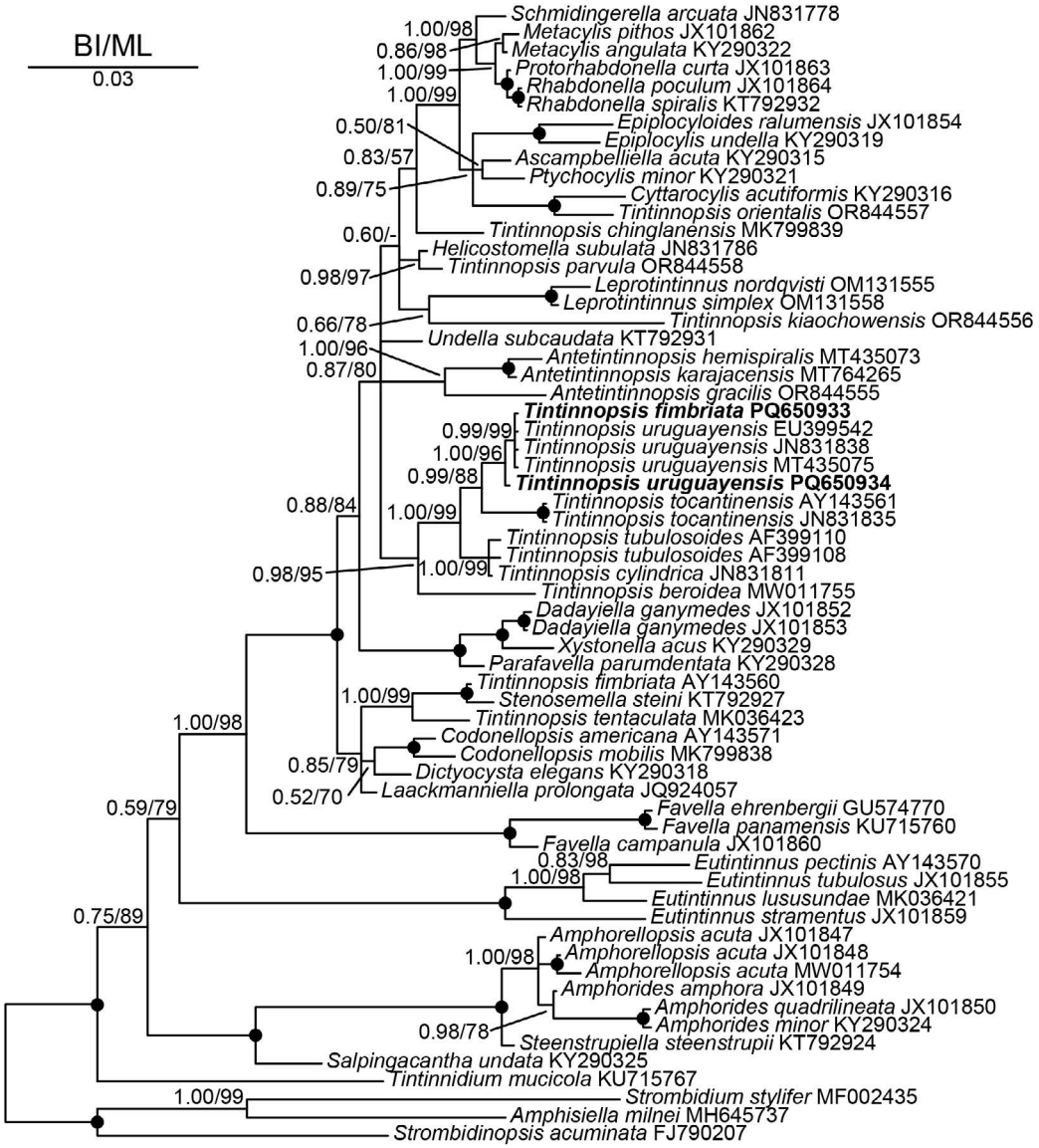

Fig. 5. Bayesian inference (BI) tree based on SSU rDNA sequences, showing the phylogenetic position of *Tintinnopsis fimbriata* and *T. uruguayensis*. Newly obtained sequences are in bold. GenBank accession numbers follow species names. Numbers at the nodes represent the Bayesian inference (BI) posterior probabilities and the maximum likelihood (ML) bootstrap values (solid circles = full supporting values). Dashes indicate posterior probabilities < 0.5, bootstrap values < 50%, or different topologies in BI and ML phylogenies. The scale bar represents three nucleotide substitutions per 100 nucleotides.

ulation (MT435075) of *T. uruguayensis*, and the Korean population of *T. fimbriata* (Fig. 5). Besides, the ITS1–5.8S rDNA–ITS2 sequence of the Korean *T. uruguayensis* shows an identity of 99.29% (three nucleotide differences) to the Chinese population (MT435062).

Remarks. The Korean population of *Tintinnopsis uruguayensis* very closely resembles the type population as for lorica morphology (lorica size: 52–61 × 23–29 μm vs. 54–63 × 22–27 μm; inner constriction diameter: 18–21 μm vs. 19–21 μm; bowl width: 23–25 μm vs. 23–26 μm) (Balech, 1948). In contrast, the Korean population differs from the American and Chinese populations of *T. uruguayensis* in terms of lorica morphology and molecular phylogeny (Table 1; Fig. 5): larger loricae in American populations (70–80 × 40–50 μm and 64 × 34 μm vs. 52–61 × 23–29 μm) (Strüder-Kypke and Lynn, 2008; Santoferrara *et al*., 2013); broader loricae in Chinese population (lorica length:collar opening diameter, 1.6–2.3 vs. 1.9–2.7) (Bai *et al*., 2020). As mentioned above, the American and Chinese populations share the same SSU rDNA sequences and differ by two nucleotides from the Korean population. Considering that the ITS1–5.8S rDNA–ITS2 seq-

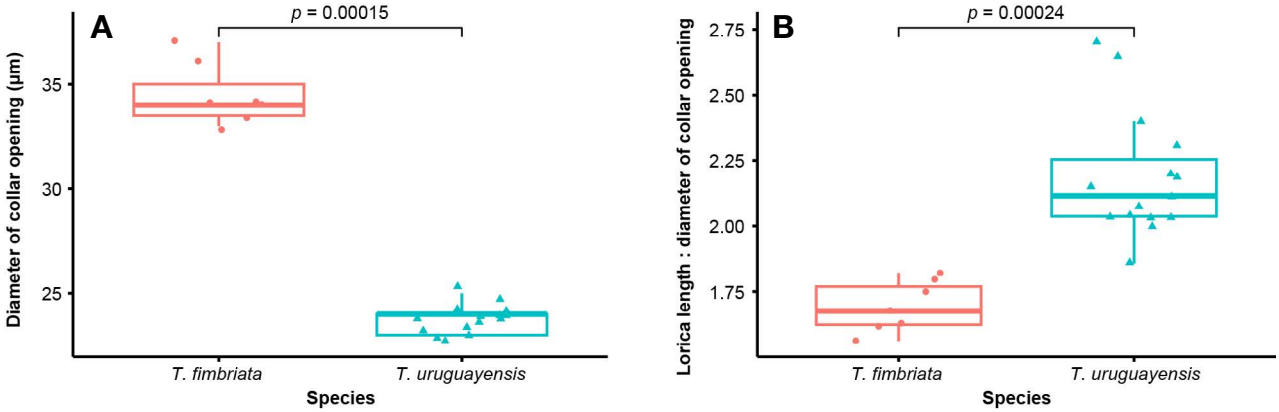

Fig. 6. Morphological differences between *Tintinnopsis fimbriata* and *T. uruguayensis*. A, Box plots showing differences in collar opening diameter; B, Box plots showing differences in the ratio of lorica length to collar opening diameter.

uence of the Chinese population differs by three nucleotides from that of the Korean population, it could represent a distinct species (Jung *et al*., 2018).

Among congeners, *Tintinnopsis amoyensis* exhibits a shape similar to that of *T. uruguayensis* due to an obconical collar and a cylindrical posterior process. However, they differ in lorica length (45−50 μm vs. 52−61 μm) (Nie, 1934). *Tintinnopsis cylindrica* and *T. tocantinensis* have a posterior process, but they lack an obconical collar and their loricae are longer than that of *T. uruguayensis* (Daday, 1887; Kofoid and Campbell, 1929).

Voucher specimens. The three slides were deposited at the National Marine Biodiversity Institute of Korea (MABIK PR00045097−MABIK PR00045099).

Conflicts of Interest

The authors of this paper have no affiliation with any interests and is solely responsible for the paper.

Acknowledgements

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