

First record of the tropical-subtropical coral snail *Coralliophila pulchella* (Muricidae: Coralliophilinae) in South Korea

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ABSTRACT

The genus *Coralliophila* H. Adams and A. Adams, 1853, is one of the most diverse groups within the subfamily Coralliophilinae. This group comprises approximately 110 species worldwide and is found in warm temperate to tropical marine environments. To date, only six species have been sparsely recorded in Korean waters, suggesting that further taxonomic studies are necessary to explore the species diversity of this group. In this study, we discovered *Coralliophila pulchella* (A. Adams, 1854) species for the first time in Korea and provided a detailed description of its morphological characteristics. In addition, morphology-based species identification was confirmed using a partial sequence of the mtDNA *cox1* gene, as DNA barcode reference sequence. The morphological information and molecular data presented in this study will help species identification of *C. pulchella*. Given the global changes in distribution pattern of coral reef due to climate change, which essentially impact the primary habitats of *Coralliophila* species, it is necessary to pay attention to the changes in species diversity and distributional patterns of *Coralliophila* species from Korean waters.

Keywords: Muricidae, Coralliophilinae, *Coralliophila pulchella*, mtDNA *cox1*, Korea

INTRODUCTION

The genus *Coralliophila* H. Adams and A. Adams, 1853, commonly known as "coral snails", is one of the most diverse groups in the subfamily Coralliophilinae (family Muricidae). Approximately 110 species have been recorded mostly from subtropical and tropical marine environments worldwide (Oliverio, 2009; Nocella *et al.*, 2024; MolluscaBase eds, 2024). Members of this genus are typically found from subtidal zone to deeper coral reefs, reaching depths of up to 150 meters, where they feed on a wide range of coral species (Nocella *et al.*, 2024). Members of the

genus *Coralliophila* are morphologically characterized by ovate to fusiform shells with rough spiral cords and a widely open aperture that is typically violet, purple, or whitish in color. Interestingly, unlike many other gastropod species, they lack a radula, instead employing a parasitic feeding strategy that use a proboscis-like organ to extract coral tissues and mucus (Ott and Lewis, 1972). Despite their ecological impact on coral reef ecosystems, the fauna of this group in Korean waters remain largely unknown.

In Korean waters, only six species of *Coralliophila* have been recorded to date (National Marine Biodiversity Institute of Korea, 2024): *C. abnormis* (E. A. Smith, 1878), *C. bulbiformis* (Conrad, 1837), *C. erosa* (Röding, 1798), *C. jeffreysi* E. A. Smith, 1879, *C. morishima* Kuroda and Shikama, 1966, and *C. rubrococcinea* Melvill & Standen, 1901. These relatively few species reported so far suggest that further studies are needed to explore the species diversity from the Korean coast. Moreover, species of this genus exhibit a broad range of shell morphological variation including host-dependent

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size variation (Potkamp *et al.*, 2017), often leading to taxonomic confusions including misidentification of species. In this study, we discovered *C. pulchella* (A. Adams, 1854) from Korean waters for the first time. We provide a detailed morphological description of the shell characters and nucleotide sequence of the mtDNA *cox1* gene, as DNA barcode reference sequence.

MATERIALS AND METHODS

A specimen was collected from the subtidal zone at Seopseom, Jeju-do, Korea by SCUBA diving and preserved in 95% ethanol. For species identification, the shell morphology was examined using a high-precision microscope (Leica MDG41, Germany).

Genomic DNA was extracted from the foot tissue using the QIAamp DNA Micro Kit (QIAGEN, Germany), according to the manufacturer's protocol. Polymerase chain reaction (PCR) amplification of the mtDNA *cox1* gene fragment was conducted using the LCO1490 and HCO2198 primer set (Folmer *et al.*, 1994). PCR reactions were carried out in a total volume of 25 μ L, containing 17.375 μ L of distilled water, 2.5 μ L of 10 \times Ex Taq buffer, 2 μ L of dNTP mixture, 1 μ L of each primer, 0.125 μ L of TaKaRa Ex Taq polymerase (TaKaRa Bio, Japan), and 1 μ L of genomic DNA. The PCR conditions included an initial denaturation at 94°C for 30 seconds, followed by 40 cycles of denaturation at 94°C for 30 seconds, annealing at 48°C for 1 minute, and extension at 72°C for 1 minute, with a final extension at 72°C for 10 minutes. The purified PCR products were sequenced on an ABI PRISM 3700 DNA analyzer (Applied Biosystems, USA), and the sequence data were processed and analyzed using Geneious Prime v.2023.0.4 (Biomatters, New Zealand). The partial mtDNA *cox1* sequences were aligned with available sequences from *Coralliophila* species obtained from the NCBI database using MAFFT (Katoh and Standley, 2013) in Geneious software. Genetic distances were calculated using uncorrected *p*-distances with MEGA X (Stecher *et al.*, 2020). Phylogenetic relationships were inferred using the maximum likelihood method

implemented in RAxML v.8.2.12 (Stamatakis, 2014), with two *Coralliophilinae* species *Leptoconchus vangoethemi* and *Leptoconchus ingrandifungi* as outgroups. Branch supports for each node were estimated from bootstrap analysis with 1,000 iterations. Branch supports for each node were estimated from bootstrap analysis using 1,000 bootstrap replicates.

SYSTEMATIC ACCOUNTS

Phylum Mollusca Linnaeus, 1758

Class Gastropoda Cuvier, 1795

Order Neogastropoda

Family Muricidae Rafinesque, 1815

Subfamily Coralliophilinae Chenu, 1859

Genus *Coralliophila* H. Adams and A. Adams, 1853

Type species. *Coralliophila violacea* (Kiener, 1836)

Diagnosis. Shells ovate to fusiform, purple in color; spire short; sutures deep, whorls not inflated; axial ribs present or absent; spiral cords rough; aperture wide, generally violet or purple, sometimes whitish; columella flattened or hollowed, with tooth-like projection at basal region; siphonal canal short, nearly closed; operculum small with lateral nucleus or absent.

***Coralliophila pulchella* (A. Adams, 1854) (Fig. 1)**

Rapana (Rhizochilus) pulchella A. Adams, 1854: 98.

Coralliophila pulchella: Kosuge S, Suzuki M, 1985: 39, Pl. 40, figs. 4, 5; Okutani T, 2000: 414–415, Pl. 206, fig. 272; Oliverio M, 2008: 513–515, figs. 41, 42, 161; Poppe GT, 2008: 242–243, Pl. 416, figs. 9, 10; Okutani T, 2017: 264, 969, Pl. 264, fig. 1; Nocella E *et al.*, 2024: 7–8.

Material examined. 1 individual (MOXXXXX); Seopseom, Bomok-dong, Seogwipo-si, Jeju-do (33°13'54.31"N, 126°35'51.65"E), collected by SCUBA diving, 03 December 2022.

Measurement. Shell height [SH] 13.5 mm; Shell width [SH] 10.3 mm.

Description. Shell (Fig. 1A) small to medium (in

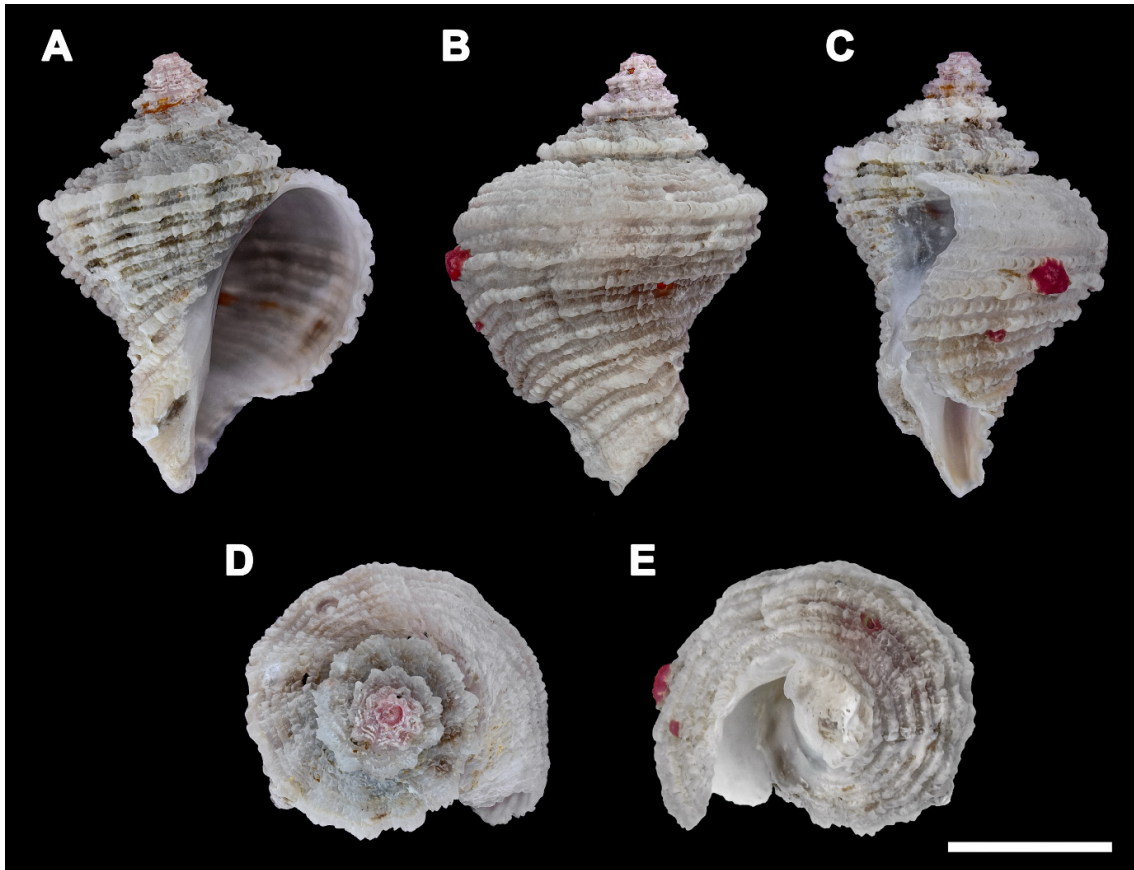


Fig. 1. *Coralliophila pulchella* (A. Adams, 1854). **A.** a ventral view; **B.** a dorsal view; **C.** a lateral view; **D.** an apical view; **E.** a basal view. Scale bar: 5 mm.

examined specimen SH 13.5 mm in height), rounded-fusiform. Shell thin and solid with 7 whorls. Surface non-glossy, whitish or pinkish in color, with apex tinted pink. Spire low, approximately 3/10 of total shell height. Spire whorls with deep sutures, not inflated, widening toward the base. Protoconch (Fig. 1D) approximately 0.5 mm in diameter, flattened with two distinct, reddish pink spiral keels. Body whorl around 4/5 of total shell height. Axial ribs weak and regular, approximately 10 per whorl, intersected by rough spiral cords, forming a wavy pattern sculpture (Fig. 1B, 1D). Single prominent spiral cord at lower part of each whorl, forming distinct shoulder. Aperture broad, oval. Inner surface white, non-glossy. Outer lip serrated due to the presence of spiral cords. Inner lip narrow, with white callus. Columella straight, elongated. Siphonal canal short, open, curved toward posterior. Operculum absent (Fig. 1E).

GenBank accession number. PQ416114

Distribution. Indo-West Pacific Ocean (Japan, Philippines, and Korea).

Habit. On corals in the subtidal zone at depths of 20 to 150 m.

Remarks. This species is morphologically similar to *C. caroleae* D'Attilio and B. W. Myers, 1984 in that both show a rounded fusiform shape with a finely sculptured shell surface by numerous scabrous spiral cords. Their distribution ranges overlap in subtropical to tropical regions, including Japan and the Philippines. Nevertheless, these two species differ in external shell morphology: *C. pulchella* has a lower spire, while *C. caroleae* possesses a taller spire. In addition, *C. pulchella* is distinguished by having a single prominent spiral cord at the lower part of each whorl, in contrast to *C. caroleae*, which

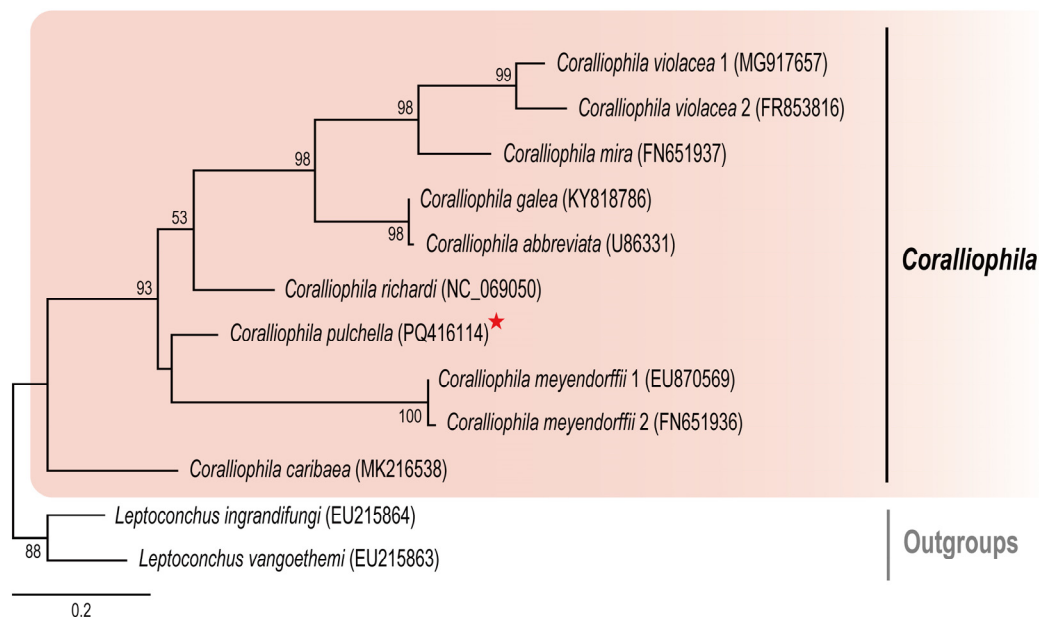


Fig. 2. Phylogenetic relationships among *Coralliophila* species based on the mtDNA *cox1* sequences reconstructed using the maximum likelihood method. Branch supporting values are indicated as bootstrap percentages ($\geq 50\%$). An asterisk indicates the mtDNA *cox1* sequence determined from the newly discovered *C. pulchella* specimen this study.

possesses thin and regularly sculptured spiral ribs, giving its shell surface rather smooth with no spiral shoulder on each whorl. To molecularly confirm the morphology-based species identification of *C. pulchella*, we conducted a phylogenetic analysis using the mtDNA *cox1* sequences of various *Coralliophila* species including *C. pulchella*. The resulting phylogenetic tree indicates that *C. pulchella* is sister

to *C. meyendorffii*, but their sister relationship is weakly supported by bootstrap analysis (bootstrap value of $\leq 50\%$; Fig. 2). The genetic distances of *C. pulchella* from other congeneric species range from 18.7% (*C. caribaea*) to 21.6% (*C. mira* or *C. meyendorffii*) (Table 1).

The distribution patterns of molluscan species are

Table 1. Uncorrected *p*-distances (%) for the mtDNA *cox1* sequences among *Coralliophila* species. The bold type indicates the mtDNA *cox1* sequence determined in this study

	1	2	3	4	5	6	7	8	9
1. <i>C. abbreviata</i>									
2. <i>C. caribaea</i>	21.4								
3. <i>C. galea</i>	0.7	21.2							
4. <i>C. meyendorffii</i> 1	24.8	25.5	25.0						
5. <i>C. meyendorffii</i> 2	25.2	25.9	25.4	1.1					
6. <i>C. mira</i>	19.4	24.5	18.8	25.9	26.4				
7. <i>C. pulchella</i>	19.7	18.7	19.9	21.0	21.6	21.6			
8. <i>C. richardi</i>	19.2	19.2	19.4	21.9	22.5	22.1	15.4		
9. <i>C. violacea</i> 1	20.5	23.2	19.9	24.3	25.0	17.2	23.0	21.7	
10. <i>C. violacea</i> 2	21.6	23.7	21.0	25.0	25.7	18.5	22.6	22.6	10.0

highly influenced by climate change, which can lead to shifts in their geographic ranges, range contractions, and even local extinctions. The *Coralliophila* species are closely associated with coral reef ecosystems, where the majority of this group is known to interact closely with scleractinian corals. Given the global shifts in coral reef distribution patterns caused by rising sea temperatures, which significantly affect the primary habitats of *Coralliophila* species, it is necessary to pay attention to the changes in species diversity and distributional patterns of *Coralliophila* species from Korean waters.

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