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Northernmost record of *Valenciennea wardii* (Actinopterygii, Gobiiformes, Gobiidae) from Ulleung Island, Northwest Pacific

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Abstract

Valenciennea wardii (Playfair in Playfair et Günther, 1867) often exhibits color variations depending on its habitat. However, owing to its reclusive behavior and low abundance, it is challenging to collect *V. wardii* using fishing gear, and ecological and population genetic studies remain limited. On 11 November 2024, a single specimen of the tropical gobiid fish *V. wardii*, which was previously unrecorded in the waters around the Korean Peninsula, was collected from the coastal waters off Ulleung Island via SCUBA diving. It was analyzed using detailed morphometric and meristic measurements in conjunction with mitochondrial cytochrome c oxidase subunit I (*COI*) sequencing to confirm its taxonomic identity. Morphological analysis revealed distinct characteristics, particularly brown transverse body bands and a black blotch with a white margin on the first dorsal fin, which distinguish it from other closely related species. Genetic analysis showed high similarity to *V. wardii* specimens collected from the South China Sea and Sri Lanka but indicated notable divergence from those collected in the Philippines, suggestive of potential cryptic diversity within the species. This study reports the poleward range expansion of *V. wardii* and proposes the new Korean name "gal-saeg-tti-bok-gi-mang-duk" based on the characteristics of this species having dark brown transverse bands. These records provide concrete evidence for the poleward expansion of this tropical marine fish species and play a crucial role in monitoring the impacts of climate change on marine ecosystems.

Keywords

Gobiidae, northernmost record, Northwest Pacific, Ulleung island, *Valenciennea wardii*, Ward's sleeper

Introduction

Gobiidae (order Gobiiformes) is the most diverse family of fish within Actinopterygii, comprising 167 genera and 1430 species worldwide (Fricke et al. 2025). This family comprises four subfamilies: Kraemeriinae, Ptereleotrinae, Gobiinae, and Microdesminae (see Fricke et al. 2025). The genus *Valenciennea* is a member of the subfamily Gobiinae and was first established by Bleeker (1856), with *Gobius strigatus* Broussonet, 1782 [valid name: *Valenciennea strigata* (Broussonet, 1782)] designated as the type species. This genus comprises 16 species, with only *Valenciennea helsdingenii* (Bleeker, 1858) having been recorded in Korea, whereas 11 species, including this species, have been reported in Japanese waters (Suzuki et al. 2011; Myoung et al. 2014; Suzuki et al. 2016; Nelson

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et al. 2016; MABIK 2023). This genus is characterized by separated pelvic fins, more than 60 longitudinal scales, and a gill opening extending beyond the posterior edge of the preoperculum, which distinguishes it from related genera within Gobiinae (see Hoese and Larson 1994; Nakabo 2013). The majority of the species of this genus are distributed across the tropical and subtropical waters of the Indo-Pacific region (Hoese and Larson 1994). They typically inhabit sandy or muddy substrates, digging burrows and feeding on small invertebrates by sifting sand through their mouths (Hernaman et al. 2009; Kovačić et al. 2018). Additionally, as a monogamous species, adult individuals typically exist in male-female pairs, with the male responsible for guarding the eggs (Reavis 1997).

Valenciennea wardii (Playfair in Playfair et Günther, 1867) is a marine fish species that primarily inhabits tropical waters from the Indian Ocean, including the Red Sea to the western Pacific and its northernmost distribution has previously been recorded in Japanese waters (31°36′N) (Hoese and Larson 1994; Ragul et al. 2024; GBIF 2025). Owing to its wide longitudinal distribution, *V. wardii* often exhibits color variations depending on its habitat, including differences in fin blotches and body bands (Hoese and Larson 1994). Molecular analysis has also identified different lineages in the waters between Sri Lanka and the Philippines (Steinke et al. 2009). However, owing to its reclusive behavior and low abundance, it is challenging to collect *V. wardii* using fishing gear, and ecological and population genetic studies remain limited (Ragul et al. 2021; Ragul et al. 2024).

Recently, new introductions of tropical and subtropical fish species into temperate waters have increasingly been reported in the waters around the Korean Peninsula, particularly along the Tsushima Warm Current regions (Park et al. 2017; Jeong and Kim 2023; Myoung et al. 2023; Kim et al. 2024; Lee et al. 2024). Climate-driven increases in seawater temperatures have been suggested as a major factor contributing to the poleward expansion of tropical marine species (Gervais et al. 2021; Hwang et al. 2024). Therefore, continuous monitoring of tropical fish species is necessary to assess the impact of climate change on fish communities in temperate Korean waters (Kim 2009; Punzón et al. 2021).

This study reports a novel occurrence of tropical *V. wardii* collected from Ulleung Island using morphological and molecular analyses, including detailed morphological descriptions. In addition, we document the northernmost distributional record of *V. wardii* in response to climate change.

Materials and methods

Sampling. A single specimen of *Valenciennea wardii* was collected during a SCUBA diving survey from the sandy bottom at a depth of approximately 25 m on the eastern coast of Ulleung Island using a hand net (Fig. 1). The collection site was compared with the historical records of the

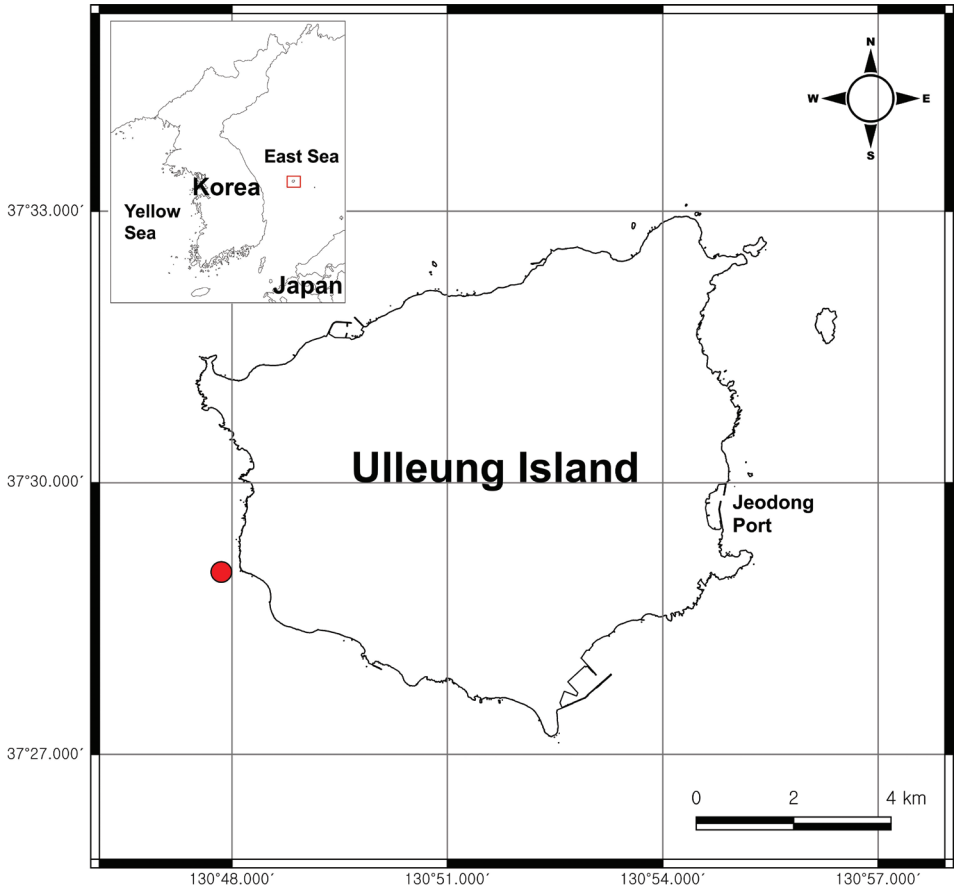

Figure 1. Map showing the sampling area of *Valenciennea wardii* from Republic of Korea.

species registered in the Global Biodiversity Information Facility (GBIF 2025) and other studies (Ragul et al. 2024; Rathnasuriya et al. 2021; Shea and To 2018). Immediately after capture, the morphological and meristic characteristics of the specimens were determined following the methods described by Hoese and Larson (1994) and Nakabo (2013). For the molecular analysis, a portion of the right pectoral fin was preserved in 99% ethanol. In the laboratory, the specimens were fixed in 15% formalin for 1 week, rinsed with freshwater for 3 days, and preserved in 70% ethanol for long-term storage. Specimens were deposited at the National Institute of Fisheries Science, Fisheries Resources Research Center (NIFS_FRRC). In addition, to determine their current occurrence in relation to water temperature, surface water temperature data on a monthly basis from 2012–2024 around Ulleung Island was collected from a marine meteorological buoy located 18 km east of Jeodong Port (southwestern Ulleung Island).

Morphological analysis. Morphological measurements and meristic counts were performed according to the methods described by Hoese and Larson (1994) and Nakabo (2013). Eight meristic counts and twenty-six body part measurements were conducted using a stereoscopic microscope (SZH16; Olympus, Tokyo, Japan) and an image analysis system (Mosaic 2.0; Fuzhou Tucsen Photonics, Fuzhou, China). Body size measurements were expressed as percentages of the standard length (SL).

Molecular analysis. Total DNA was extracted from the pectoral fin using the GeneAll Exgene Clinic SV DNA extraction kit (GeneAll, Seoul, Korea). The mitochondrial DNA (mtDNA) cytochrome oxidase subunit I (*COI*) region was amplified for molecular analysis using the VF2 primer (5′-TCA ACC AAC CAC AAA GAC ATT GGC AC-3′) and FishR2 primer (5′-ACT TCA GGG TGA CCG AAG AAT CAG AA-3′) (Ward et al. 2005). PCR was performed under the following conditions: initial denaturation at 95°C for 5 min; 35 cycles of denaturation at 94°C for 30 s, annealing at 52°C for 30 s, and extension at 72°C for 1 min; final extension at 72°C for 7 min. DNA sequences were obtained using an ABI 3730XL DNA Analyzer (Applied Biosystems, Inc., Foster City, CA, USA) with an ABI BigDye Terminator Cycle Sequencing Ready Reaction Kit v3.1. The obtained sequences were registered with the National Center for Biotechnology Information (NCBI) under Accession No. PQ896806. The obtained DNA sequences were registered with the National Center for Biotechnology Information (NCBI) under accession number NIFS_FRRC_2 (PQ896806). For sequence comparison, the sequences were aligned using ClustalW (Thompson et al. 1994) in BioEdit version 7 (Hall 1999) along with 10 species of the genus *Valenciennea* and one outgroup species registered in NCBI and the Barcode of Life Data System (BOLD). Genetic distances for species identification were calculated using the Kimura-2-parameter model (Kimura 1980) in MEGA6 (Tamura et al. 2013), and a neighbor-joining tree was constructed with 1000 bootstrap replicates.

The nucleotide sequence used for genetic comparison is as follows: *Valenciennea wardii* (KT718531, MF415130, FJ584232, FJ584233), *Valenciennea helsdingenii* (FJ584196), *Valenciennea strigata* (KP194902), *Valenciennea muralis* (Valenciennes, 1837) (FJ584205), *Valenciennea sexguttata* (Valenciennes, 1837) (FJ584217), *Valenciennea longipinnis* (Lay et Bennett, 1839) (OQ386776), *Valenciennea puellaris* (Tomiyama, 1956) (FJ584208), *Valenciennea immaculata* (Ni, 1981) (PP089099), *Valenciennea parva* Hoese et Larson, 1994 (JQ350414), *Valenciennea persica* Hoese et Larson, 1994 (MT076642), and *Pherallodus indicus* (Weber, 1913) (MT053042).

Results

Gobiidae Cuvier, 1816
Valenciennea Bleeker, 1856

Valenciennea wardii (Playfair in Playfair et Günther, 1867)

English common name: Ward's sleeper

New Korean name: 갈색띠복기망둑 [gal-saeg-tti-bok-gi-mang-duk]

Fig. 2; Table 1

Valenciennea wardii (Playfair in Playfair et Günther, 1867).—Hoese and Larson 1994: 63 (Japan, Vietnam, Thailand, Maldives, Sudan, Western Australia, Gulf of Aden, Egypt).—Randall and Egmond 1994: 65 (Seychelles).—Allen et al. 2003: 152 (Papua New Guinea).—Allen and Adrim 2003: 61 (Indonesia).—Randall 2005: 558 (New Caledonia).—Nakabo 2013: 1508 (Japan).—Choi et al. 2013: 445 (Micronesia).—Lin et al. 2016: 75 (East China Sea).—Prokofiev 2016: 814 (Vietnam).—Shea and To 2018: 3 (Hong Kong).—Fricke et al. 2019: 292 (Papua New Guinea).—Ragul et al. 2024: 63 (India).

Specimen observed. Voucher number NIFS_FRRC_2, standard length 26.44 mm, collected from eastern coast of Ulleung Island (37°29′01″N, 130°47′54″E), at a depth of 24 m, bottom water temperature 21°C, using a hand net, 11 November 2024.

Morphological description. Body slender and elongated, tapering towards caudal region. Eyes positioned close together across dorsal midline. Snout protruding, with tip of upper jaw extending beyond lower jaw. Posterior end of maxilla reaching midpoint of eye. Gill opening extending below middle of preopercle. Body covered with ctenoid scales, with scaleless pectoral fin base. Dorsal fins separated; first dorsal fin with spines only, and second dorsal fin comprising one spine and several soft rays. Spine tips of dorsal fin soft and curved backward. Dorsal fin margin rounded. Second dorsal fin origin located anterior to anal fin origin. Tip of pectoral fin reaching anal fin origin. Caudal fin rounded with a tapered tip (Fig. 2C). Pelvic fins separated (Fig. 2D). Meristic counts and body part measurements of *Valenciennea wardii* shown in Table 1.

Table 1. Measurements and counts of *Valenciennea wardii*.

Character	Presently reported study	Bleeker 1858	Hoese and Larson 1994	Ragul et al. 2024
	South Korea	Zanzibar	Indo-Pacific	India
Measurements in absolute values [mm]				
Total length	34.46	8.89	—	—
Standard length (SL)	26.44 (n = 1)	—	50–91 (n = 22)	62.3 (n = 1)
Measurements in relative values [%SL]				
Head length	32.6	—	27.7–32.5	29.8
Head width	16.9	—	—	12.1
Head depth	18.3	—	—	13.8
Eye diameter	8.7	—	5.4–7.5	5.1
Flesh interorbital width	8.2	—	—	—
Bony interorbital width	2.1	—	—	—
Snout length	8.3	—	9.4–14.0	9.5
Upper-jaw length	14.4	—	12.2–14.5	8.7
Body depth at pelvic fin origin	16.6	—	—	17.2
Body depth at anal fin origin	16.3	—	18.2–20.0	17.6
Caudal peduncle length	18.7	—	—	19.1
Caudal peduncle width	3.8	—	—	6.0
Caudal peduncle depth	10.4	—	—	11.1
First pre-dorsal length	37.3	—	—	36.1
Second pre-dorsal length	57.1	—	—	57.4
Preanal length	57.8	—	—	57.9
Prepectoral length	33.3	—	—	32.3
Prepelvic length	32.9	—	—	32.2
First dorsal fin base	21.9	—	—	21.7
Second dorsal fin base	25.5	—	—	26.9
Anal fin base	23.5	—	—	24.1
Third dorsal spine length	20.9	—	17.1–22.4	—
Fourth dorsal spine length	20.8	—	16.9–20.1	—
Pectoral fin length	28.4	—	—	27.1
Pelvic fin length	20.7	—	—	19.7
Caudal fin length	27.4	—	25.7–29.5	29.1
Counts				
Dorsal fin rays	VI–I, 12	VI–I, 12	VI–I, 11–12	VI–I, 12
Pectoral fin rays	20	—	19–22	20
Pelvic fin rays	I, 5	—	—	—
Anal fin rays	I, 12	I, 12	I, 11–12	I, 12
Segmented caudal fin rays	17	—	17 (5)	16
Branched caudal rays	13	—	13 (5)	14
Longitudinal scales	84	95	70–88	78
Transverse scales	21	—	19–25	24

Coloration. Head light brown, with diagonal reddish stripe crossing pupil. Yellow stripe running obliquely from upper jaw across posterior edge of preopercle to gill region, bordered by black-edged blue stripe above. Body light grey, bearing three dark brown transverse bands that widen posteriorly. Black blotch extending from dorsal fin membrane to dorsal surface of caudal peduncle, positioned between second and third brown transverse bands and near posterior end of caudal peduncle. Round black spot present between fourth and sixth spines of first dorsal fin, bordered with white. Dorsal fin margin white. White blotches extending from body to midsection of dorsal fin membrane. Anal fins with white and light orange edges bordered with black. Pectoral fin membranes transparent with light brown rays. Pelvic fins entirely white, with faint yellowish tinge in middle. Caudal fin with prominent black spot near upper tip and faint dark yellow spot at base. Caudal fin base white, transitioning to yellow towards posterior. Tips of soft rays from upper to middle sections of caudal fin were white (Fig. 2).

Molecular analysis. A 596 bp mtDNA *COI* sequence was obtained and compared to 10 species of the genus *Valenciennea* (*V. wardii*, *V. sexguttata*, *V. strigata*, *V. helsdingenii*, *V. parva*, *V. muralis*, *V. longipinnis*, *V. puellaris*, *V. persica*, and *V. immaculata*) registered in the NCBI and BOLD databases. *V. wardii* collected from the Ulleung Island in the East Sea (otherwise known as the Sea of Japan) showed a genetic distance of 0–0.012 from individuals from Taiwan, the South China Sea, and Sri Lanka, and a distance of 0.044 from an individual from the

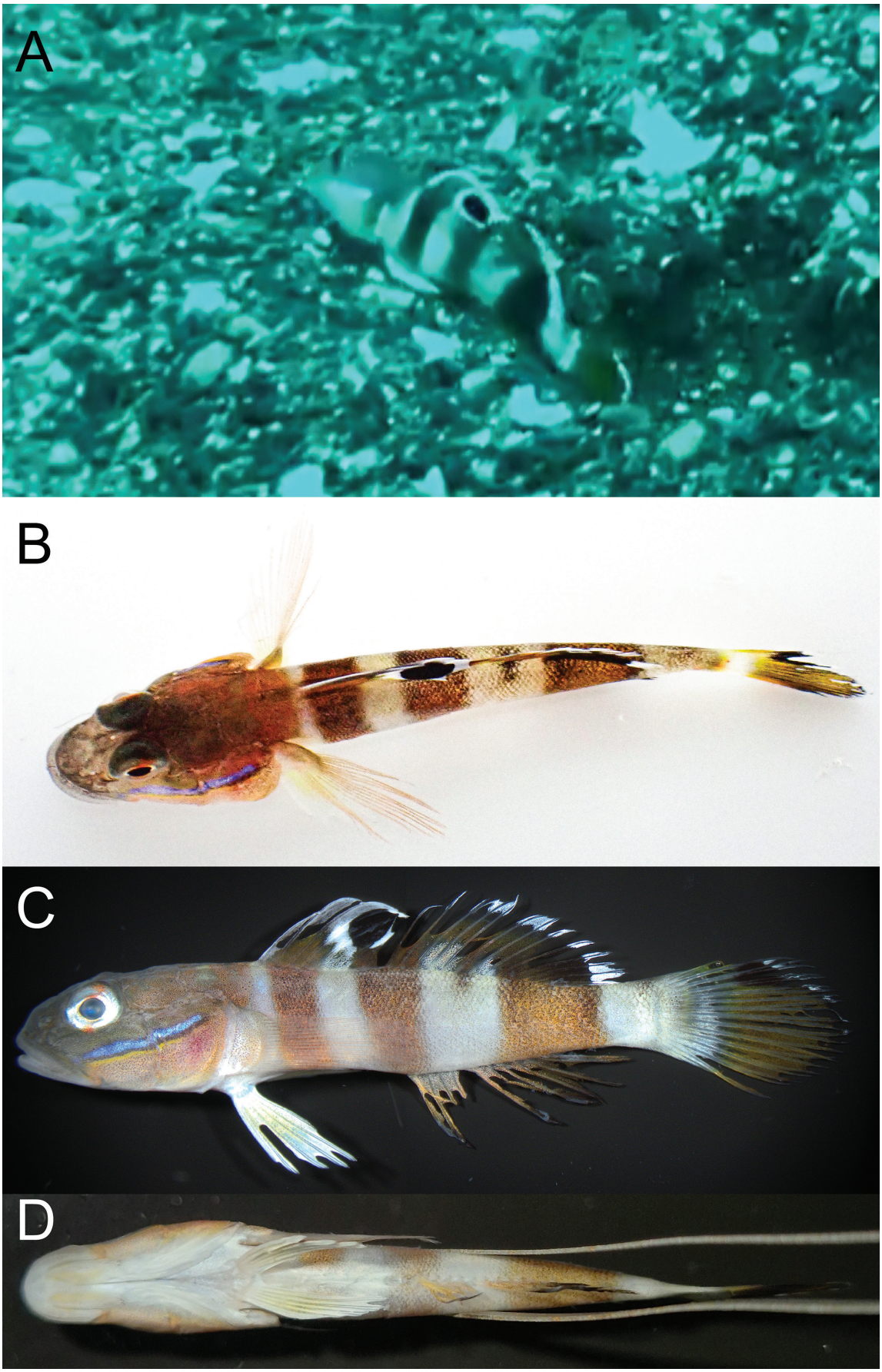

Figure 2. *Valenciennea wardii*, NIFS_FRRC_2 (26.44 mm SL), the Ulleung Island, Republic of Korea, November 11, 2024. **A** in-situ underwater image; **B** dorsal view; **C** lateral view; **D** ventral view.

Philippines. The genetic distance from other *Valenciennea* species ranged between 0.169 and 0.244, confirming species-level differentiation (Fig. 3).

Seawater temperature. In 2024, the highest water temperature (28.6°C) was recorded in August, while the lowest (11.8°C) was recorded in February. The annual mean water temperature in 2012, as well as the average temperatures during the summer (August) and winter (February) season were 1.9°C, 1.2°C, and 2.2°C higher compared to those in 2012, respectively (Fig. 4). Water temperature has shown an increasing trend over the past decade (2012–2024).

Discussion

The morphological characteristics of the *Valenciennea wardii* specimen collected from the Ulleung Island were slightly different in longitudinal scale counts (84 vs. 95) from the original description (Playfair and Günther 1867), but this falls within the range previously reported for *V. wardii* (i.e., 70–88; Hoese and Larson 1994). Other meristic characteristics and external morphological features matched well with the original description. In particular, the black spots on the first dorsal fin and three brown

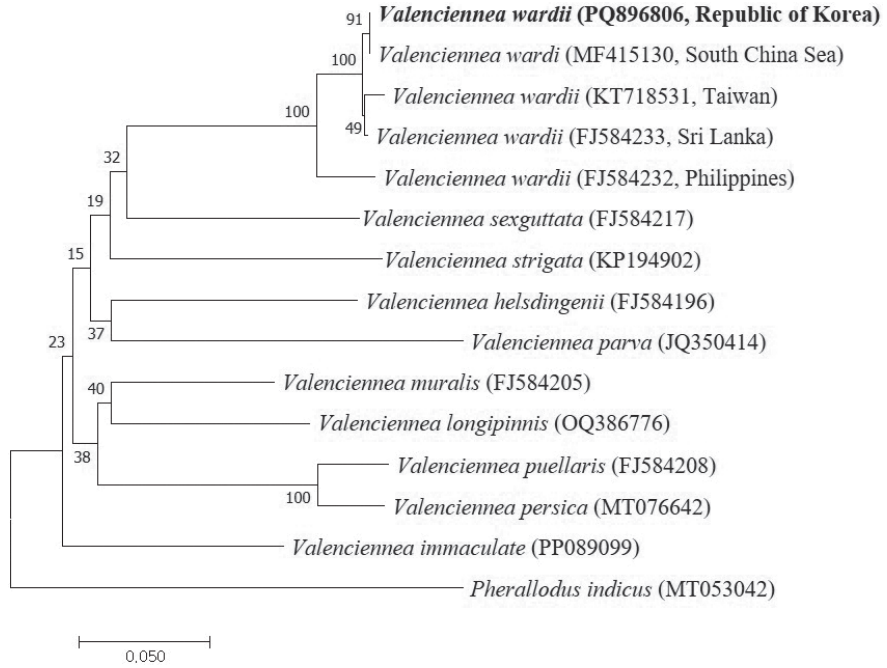

Figure 3. Neighbor joining tree based on partial mitochondrial DNA COI region, showing the relationships among 10 species of genus *Valenciennea* and 1 outgroup *Pherallodus indicus*. The tree was constructed using the Kimura 2-parameter model and 1000 bootstrap replications The parentheses indicate the NCBI accession number while the superscript indicates sampling site of *Valenciennea wardii*. The bottom bar indicates a genetic distance of 0.05.

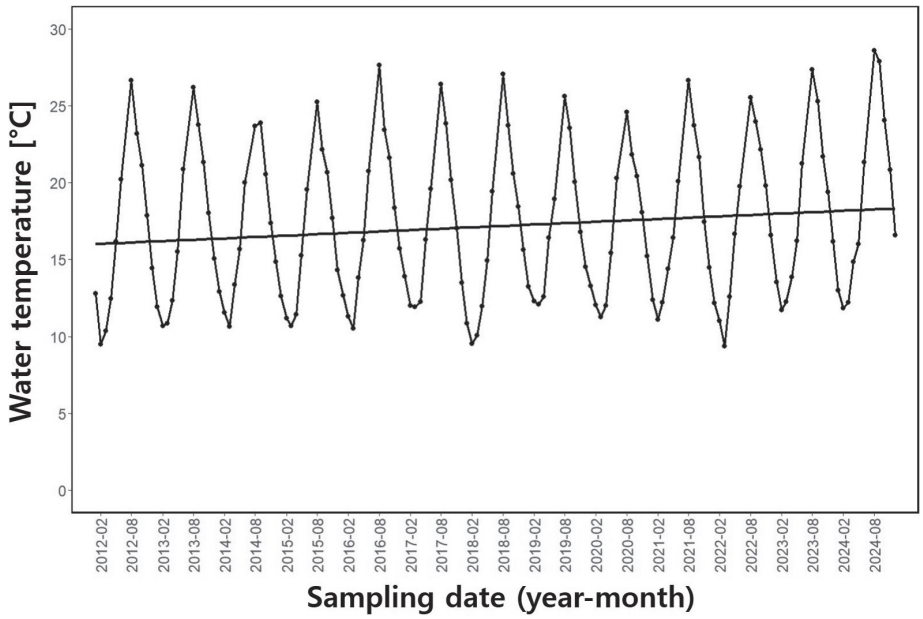

Figure 4. Long-term changes (2012–2014) in monthly mean sea surface temperature around the Ulleung Island.

transverse bands on the body are typical characteristics of *V. wardii*, which can be distinguished from *V. alleni*, *V. decora*, *V. helsdingenii*, *V. longipinnis*, *V. muralis*, *V. sexguttata* (a black spot on or near the tip of the first dorsal fin but lacking the three brown transverse bands), and nine other species in the genus *Valenciennea* (no black spots on the dorsal fin and no brown horizontal stripes) (Fig. 2, Hoese and Larson 1994; Nakabo 2013). In addition, the current specimen showed significantly higher body part ratios for head length (32.6% SL vs. 29.8% SL), head width (16.9% SL vs. 12.1% SL), head depth (18.3% SL vs. 13.8% SL), and eye diameter (8.7% SL vs. 5.1% SL), compared to previously recorded specimens (Ragul et al. 2024). These differences may be attributed to the differences in body size between the specimens in the present study (26.44 mm SL) and previous (62.3 mm SL) studies, because the relative size of the head and eyes decreases, and the head becomes more depressed as fish size increased (Choo and Liew 2006; Table 1).

Owing to the wider geographical distribution of *V. wardii*, this species often shows color variation depending on its habitat (Hoese and Larson 1994). In addition, genetic differences of over 5% in the mtDNA *COI* region were observed between populations from the waters of Sri Lanka and the Philippines (Steinke et al. 2009), suggesting the presence of distinct lineages in these regions. In the neighbor-joining (NJ) tree constructed in this study, the Ulleung Island specimen exhibited close genetic distances (0–0.012) to individuals from Taiwan, the South China Sea, and Sri Lanka but a greater difference (0.044) from the individual from the Philippines. These results suggest that *V. wardii* in Korean waters belongs to a different lineage from that in the Philippines (Fig. 3). Genetic differences of more than 2% in the mtDNA COI region could be indicative of cryptic species within *V. wardii* (see Hebert et al. 2003; Ward 2009). The average genetic distance of the mtDNA region is reported to be approximately 7.93% within genera and 15.46% within families of teleost fishes (Ward et al. 2005). Therefore, future population genetic studies, including specimens from various regions, such as the Red Sea, are suggested to further elucidate the genetic diversity and population structure of *V. wardii*.

The latitudinal distribution range of *V. wardii* extends from 31°36′N to 21°42′S (Hoese and Larson 1994; Ragul et al. 2024; GBIF 2025). In comparison with previous records, this study confirmed a new northernmost record (37°29′01″N) for the species (Fig. 5). The poleward expansion of the distributional ranges of marine species is likely to be influenced by climate-driven global warming and changes in ocean currents in temperate waters (Son et al. 2020; Rutledge 2021; Esposito et al. 2021; Imamura et al. 2022; Hasan et al. 2022; Jeong and Kim 2023; Cardoso et al. 2024). These expanding habitat ranges may have initially been driven by eggs and larvae transported by warm oceanic currents, which are now able to survive during the winter owing to elevated sea temperatures (Booth et al. 2007; Gervais et al. 2021). When tropical and subtropical fish species are introduced into temperate waters, intensive competition with native species may occur, ultimately affecting the biodiversity within marine

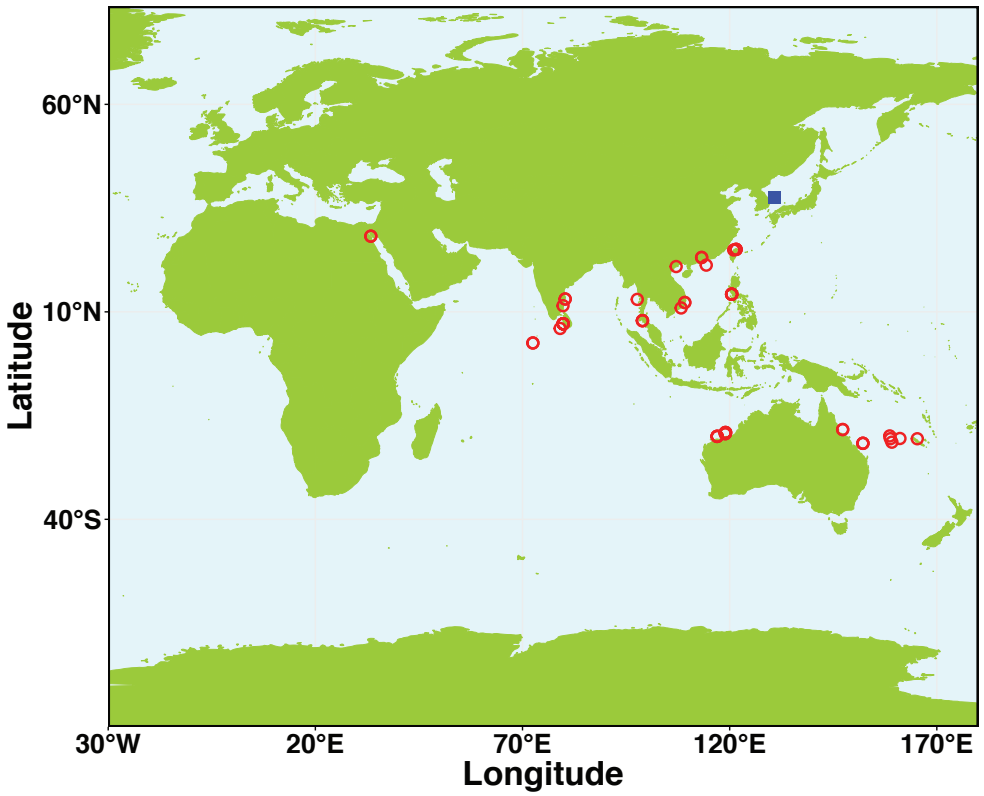

Figure 5. Map showing distribution records of *Valenciennea wardii*. Red dots indicate historical records. Blue square indicates the new record off the Ulleung Island, Republic of Korea.

ecosystems (Taylor and Figueira 2021). Therefore, continuous monitoring of the occurrence of previously unrecorded tropical fish species is essential for accurately assessing changes in marine biodiversity.

Since the 1980s, sea surface temperatures in Korean waters have steadily increased, and this trend is particularly evident in the East Sea (Park et al. 2019). Over the past 12 years, water temperatures around the Ulleung Island have continuously increased, with the 2024 annual average sea temperature rising by approximately 1.9°C overall and by 3.1°C during winter compared to 2012 (Fig. 4). The Ulleung Island has long been recognized as a region influenced by warm ocean currents (i.e., the Tsushima Warm Current), which can provide additional habitat for tropical and subtropical fish species originating from warmer southern waters, such as the Jeju Island (Nakazono 2002; Jung et al. 2014; Myoung et al. 2017; Park et al. 2017). According to Cho et al. (2025), the *Turbo sazae* H. Fukuda, 2017 (Gastropoda), inhabiting Jeju Island expanded its distribution by moving northward along ocean currents such as the Tsushima Warm Current and established populations along the eastern coast of Korea and Dokdo, located east of Ulleung Island. When tropical species are introduced into temperate waters, they often experience low ambient temperatures, which can lead to high mortality during the winter season (Booth et al. 2007; Figueira et al. 2009; Figueira and Booth 2010). The optimal habitat temperature of *V. wardii* is known to be between 22 and 27°C (Froese and Pauly 2024), but the winter sea temperature of the Ulleung Island (which drops below 10°C) is not conducive to the survival of the species in this region. Lower water temperatures can lead to physiological survival limitations for warm-water fish species, including reduced feeding, limited swimming ability, osmotic imbalance, and consequently increased mortality (Hurst 2007; Eme and Bennett 2008). Although the physiological survival mechanism of this species in a specific temperature range is unclear, it experienced a low water temperature shock that could affect its survival. During the additional SCUBA diving survey conducted in winter (1 March 2025), no individuals of this species were found at the study site. However, if winter sea temperatures rise continuously due to ongoing climate change, it may facilitate their survival in the waters around Ulleung Island throughout the year. Research on the settlement of tropical and subtropical fish in temperate waters should continue through consistent monitoring.

This study reports the first occurrence of *V. wardii* in Korean waters and provides fundamental data for its inclusion in the National List of Marine Species. The addition of new species plays a crucial role in asserting national sovereignty over marine biodiversity and in providing the necessary scientific evidence (MABIK 2023). Accordingly, based on the distinctive morphological feature of dark brown transverse bands, we propose the Korean name “gal-saeg-tti-bok-gi-mang-duk” for *V. wardii*. Furthermore, the northernmost occurrence of *V. wardii* reported in this study will serve as essential baseline data for evaluating the impact of climate change on temperate marine ecosystems and will help predict changes in biodiversity and environmental shifts driven by climate change.

Acknowledgments

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