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First Record of the Japanese Fluvial Sculpin, *Cottus pollux* (Scorpaeniformes: Cottidae) from Korea

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ABSTRACT Two sculpin specimens (79.3∼100.8 mm standard length) were collected from the upper reach of Deokdongcheon Stream, a tributary of the Hyeongsangang River, in Korea. They were identified as *Cottus pollux* by characteristics such as the absence of palatine teeth, 12∼13 unbranched pectoral fin rays, pelvic fins without obvious bands or spots, and the absence of a blackish band on the head or anterior part of the body. A phylogenetic analysis based on the nuclear *ITS1* gene and mitochondrial *cytb* gene indicated that the specimens formed a clade with Japanese *C. pollux*, supporting the morphological species identification. We propose a new Korean name for the species: "Min-mu-nui-dug-jung-gae"

Key words: Cottidae, *Cottus*, *Cottus pollux*, Japanese fluvial sculpin, first record

INTRODUCTION

The freshwater sculpin genus *Cottus* Linnaeus, 1758 comprises more than 60 species, and its distribution spans from marine to freshwater habitats (Yokoyama and Goto, 2005; Kanno *et al*., 2018). Three species have been reported to inhabit the Korean Peninsula, of which two species [*C. koreanus* (Fujii *et al*., 2005) and *C. hangiongensis* (Mori, 1930)] are widely distributed in Korea (Chae *et al*., 2019), while *C. czerskii* (Berg, 1913) is found only in the Dumangang River (Kim and Park, 2002).

In October 2021, two specimens belonging to the genus *Cottus* were collected during an ichthyofaunal survey in the upper reach of Deokdongcheon Stream, a tributary of the Hyeongsangang River in Korea. The collected specimens were identified as *C. pollux* (Günther, 1873) by characteristics such as the absence of palatine teeth, 12∼13 unbranched pectoral fin rays, pelvic fins without obvious bands or spots, and the absence of a blackish band on the head or anterior part of the body (Goto *et al*., 2002; Nakabo, 2013). Their phylogenetic relationships determined using the nuclear internal transcribed spacer 1 (*ITS1*) gene and mitochondrial cytochrome *b* (*cytb*) gene supported the morphological species identification.

Cottus pollux has not yet been reported in Korea and has been considered endemic to Japan, distributed in Honshu and northwest Kyushu (Hosoya, 2015). This species tends to form separate groups (large, middle, and small egg types) within the species according to egg size (Goto *et al*., 2002; Yoshigou, 2010). Although the small and middle egg types are confused taxonomically, the large egg type is clearly recognized as *C. pollux* (Nakabo, 2013; Hosoya, 2015). Therefore, *C. pollux* is described here as the first official record in freshwater from Korea based on two voucher specimens and the size of its eggs collected from Deokdongcheon Stream.

MATERIALS AND METHODS

Counts and measurements followed to the methods of Hubbs and Lagler (1964), and the voucher specimens are deposited in the specimen storage facility of Soonchunhyang University, Korea. Egg size was measured under a microscope after obtaining eggs by pressing the belly of a female in the field on March 25, 2022, fixing them in 10% formalin, and transporting them to the laboratory.

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Fig. 1. Freshly collected (A) and formalin-preserved (B) *Cottus pollux*, SUC25237 (100.8 mm SL, male), collected from the upper reach of Deokdongcheon Stream, Korea.

For the phylogenetic analysis, genomic DNA was extracted from our specimens and from specimens of *C. koreanus* (SUC23963, collected from Namhangang River), *C. hangiongensis* (SUC569, collected from Baebongcheon Stream), and *C. pollux* (SUC25257~25258, only pectoral fin, collected from Hoamcheon Stream with permission from Korea National Park Service) kept in the storage facility. The primers and protocols from Kanno *et al.* (2018) and Chang *et al.* (2014) were used to amplify the *ITS1* and *cytb* genes. The *ITS1* (505~585 bp) and *cytb* (1,040 bp) gene sequences were aligned using T-Coffee (Notredame *et al.*, 2000) and then used for phylogenetic analysis. A Bayesian inference (BI) tree was conducted for 2,000,000 (*cytb*, 4,000,000) generations using MrBayes 3.2.7 (Ronquist *et al.*, 2012). The evolutionary model was selected using ModelTest-NG (Darriba *et al.*, 2020), and the best model GTR + I was applied for the BI tree reconstructions. The genetic distance of the *cytb* gene was calculated using the *p*-distance with 1,000 bootstrap replications in MEGA X (Kumar *et al.*, 2018).

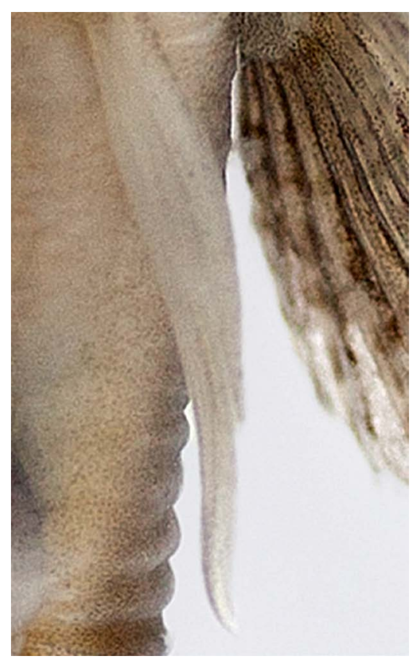

Fig. 2. Pelvic fin of *Cottus pollux*, SUC25237 (100.8 mm SL, male), collected from the upper reach of Deokdongcheon Stream, Korea.

TAXONOMIC ACCOUNTS

***Cottus pollux* Günther, 1873**
(New Korean name: Min-mu-nui-dug-jung-gae)
(Fig. 1~2; Tables 1~2)

Cottus pollux Günther, 1873: 240 (type locality: River in Otarranai, Japan); Nakabo, 2002: 1525 (Japan).
Cottus hilgendorfii: Döderlein, 1884: 208 (Tokyo, Japan); Watanabe, 1960: 121 (Japan); Okada, 1961: 699 (Japan).

Fig. 3. Habitat of *Cottus pollux* in the upper reach of Deokdongcheon Stream, Korea.

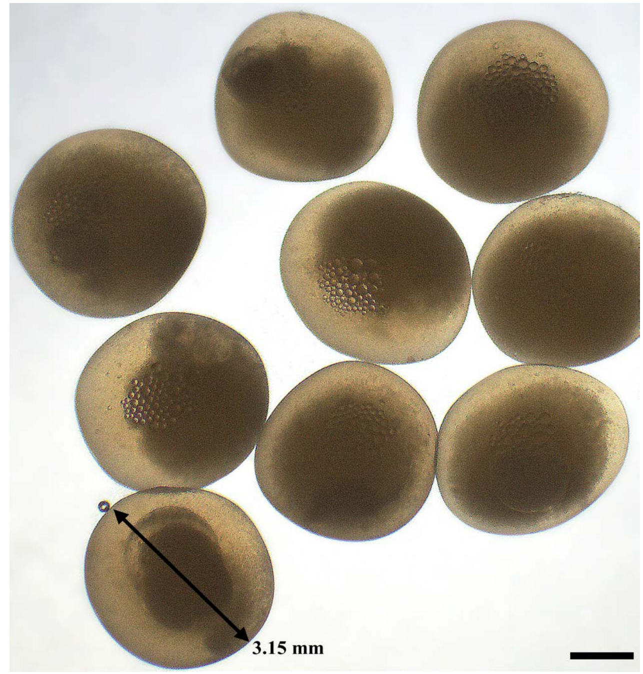

Fig. 4. Egg size of *Cottus pollux* from the upper reach of Deokdongcheon Stream, Korea. Bar indicates 1 cm.

Cottus nozawae: Watanabe, 1960: 119 (Japan); Okada, 1961: 693 (Japan); Zhang *et al*., 2016: 193.
Cottus japonicus: Okada, 1961: 699 (Japan).

Materials examined. Two specimens: SUC25237, 100.8 mm standard length (SL); SUC25238, 79.3 mm SL; Amgok-dong, Gyeongju-si, Gyeongsangbuk-do, Korea, 14 October 2021, collected by B.H. Yun and M.S. Sung.
Diagnosis. *C. pollux* is clearly distinguished from *C. koreanus* and *C. hangiongensis*, reported to inhabit Korea, by the absence of bands or spots on the pelvic fin. It is distinguished from other congeners by the following combination of characteristics: absence of palatine teeth; 1 spine preopercle; 12~14 unbranched pectoral fin rays; 15~18 second dorsal fin rays; absence of a blackish band on the head or anterior part of the body (Nakabo, 2013).
Description. Tables 1~2 gives counts and measurements. Body cylindrical, slightly compressed. Caudal peduncle robust and thick. Head large, slightly flattened vertically. Snout short and blunt. Mouth terminal; maxilla extending to point below middle of pupil; upper jaw slightly longer than lower jaw; villiform teeth in moderate bands on jaws and prevomer; palatines toothless. Eye relatively large and close to upper margin of head; interorbital space narrow and slightly concave. Single preopercular spine, simple, slightly curved upward. First dorsal fin originating above upper end of gill opening. Second dorsal fin originating just behind first dorsal fin, its origin sometimes connected by membrane to first dorsal fin; basal length of second dorsal fin slightly longer than that of anal fin. Pectoral fin large and unbranched rays, its distal tip reaching anal fin origin. Pelvic fin extending posteriorly to anus (in a mature male). Anal fin originating below base of second ray of second dorsal fin. Caudal fin slightly rounded, all rays unbranched, except for interior nine rays. No scales on body surface; skin smooth. Lateral line beginning at upper tip of gill opening and extending to base of caudal fin; slightly curved downwards near insertion of second dorsal fin.
Color when fresh. Ground color of head and body yellowish brown; irregularly scattered small light and dark spots laterally; two dark brown polygonal patterns under second dorsal fin. All fins yellowish-white, except for distal margin of first dorsal fin (mature male); all fin rays with obvious or unclear black spots, except for pelvic fin; no pattern on pelvic fin. Distinct dark brown blotch on caudal fin base.
Color after preservation. Nearly same as when fresh, except olive-brown on head and body, and small light lateral spots disappeared.
Distribution. Known from Japan: Honshu and northwest Kyushu (Hosoya, 2015). In Korea, only from Deokdongcheon and Hoamcheon Streams in Gyeongju-si, Gyeongsangbuk-do to date (Byeon and Lee, 2017; present study).
Habitat and ecological notes. Both specimens were collected from Deokdongcheon Stream where the bottom had a high ratio of boulders and cobbles, and the water depth and current velocity were 20~60 cm and 0.27~0.89 m/s,

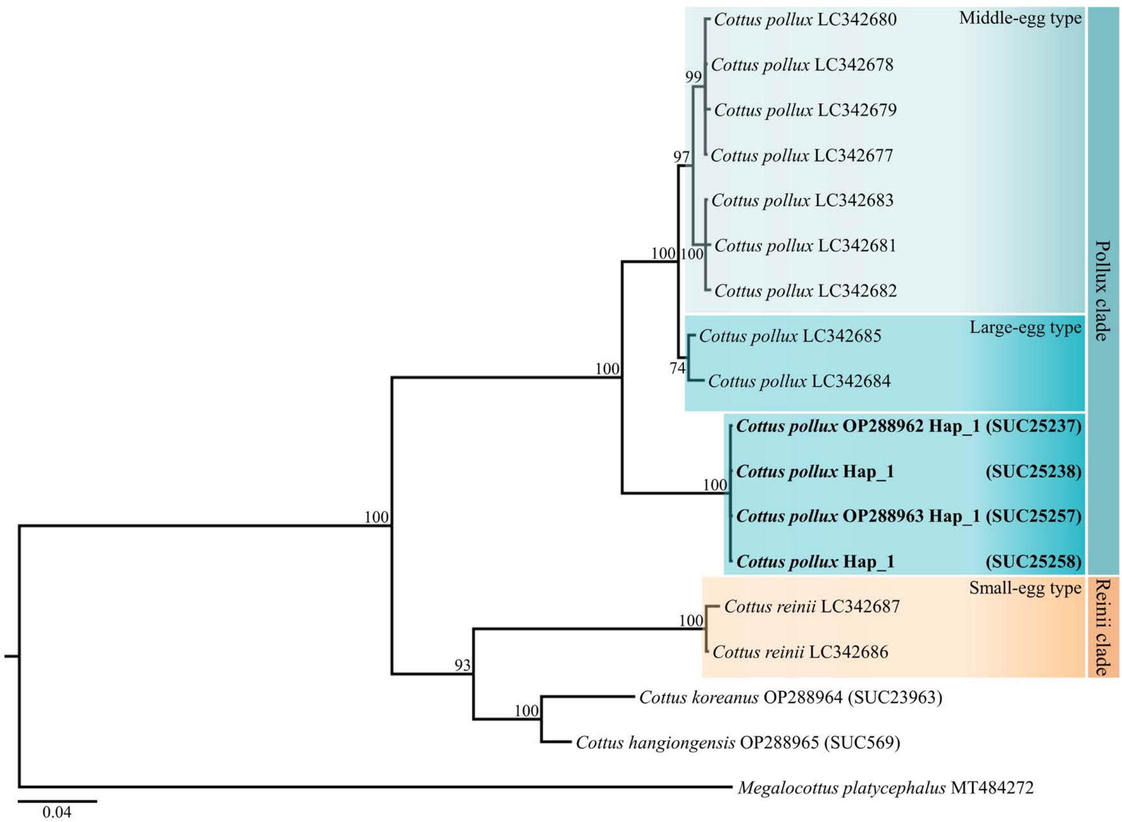

Fig. 5. Phylogenetic tree of the genus *Cottus* obtained from Bayesian inference analyses of the *ITS1* gene. Posterior probabilities are shown at the base of each node. The GenBank accession numbers or study institution voucher numbers are given after the scientific names. Bold font indicates *C. pollux* collected from Gyeongju-si, Gyeongsangbuk-do, Korea. Hap, haplotype.

respectively (Fig. 3). *C. pollux* has a fluvial life history and the egg size obtained from a female was 3.0±0.12 mm (n=30, Fig. 4).

Remarks. The two specimens collected from Deokdongcheon Stream, Korea in this study were easily identified as members of the genus *Cottus*, based on the following characters: dorsal surface of head without processes or bony ridges, uppermost preopercular spine simple and curved upward, dorsal fin separated with spinous and rays (Girard, 1850; Kim, 1997). From southern Far East Asia, seven *Cottus* species (*amblystomopsis*, *czerskii*, *hangiongensis*, *koreanus*, *nozawae*, *pollux*, and *reinii*) have been recognized to date. Of these, the present specimens agreed well with the original description of *C. pollux* (Günther, 1873) in having smooth skin, no spines on the head except on the preoperculum, lateral line reaching the caudal fin, and 13 anal fin rays (Table 1). However, there was a slight difference in the number of dorsal fin rays (IX, 19 in original description vs. VIII~IX, 17 in Korean specimens), but this could be due to differences in the examination method or individual variation. The number of the dorsal fin rays of the present specimens are included in the number of the dorsal fin rays reported after Yoshigou (2010) had counted many Japanese specimens (VII~X, 14~18 in Japanese specimens). Therefore, we identified our specimens as *Cottus pollux*.

Of the species occurring in southern Far East Asia, *C. pollux* differs from *C. amblystomopsis* (Schmidt, 1904) and *C. nozawae* (Snyder, 1911) in the presence of unbranched rays on the pectoral fin, from *C. czerskii* in the absence of palatine teeth, from *C. koreanus* and *C. hangiongensis* in the absence of bands or spots on the pelvic fin, and from *C. reinii* (Hilgendorf, 1879) in the absence of blackish bands on the head or anterior part of the body (Fujii *et al.*, 2005; Nakabo, 2013; Saveliev and Kolpakov, 2018). Therefore, *C. pollux* is easily discriminated from its seven congeners distributed in southern Far East Asia by the above diagnostics.

Previously, Byeon and Lee (2017) confirmed the habitat of *C. koreanus* for the first time in a stream (Oshipcheon Stream) flowing into the East Sea south of Samcheok, Korea. These individuals were described as differing from

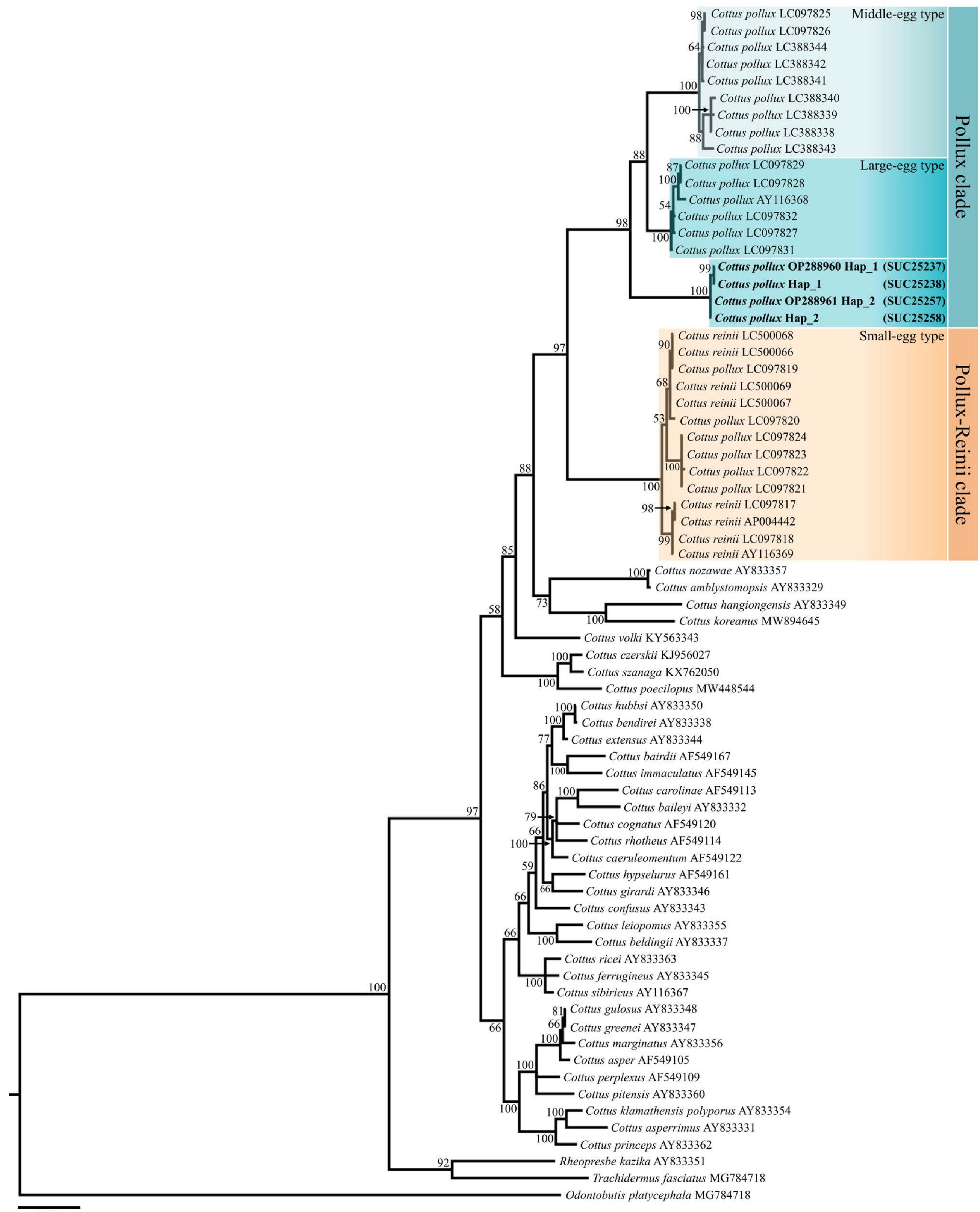

Fig. 6. Phylogenetic tree of the genus *Cottus* obtained from Bayesian inference analyses of the *cytb* gene. Posterior probabilities are shown at the base of each node. The GenBank accession numbers or study institution voucher numbers are given after the scientific names. Bold font indicates *C. pollux* collected from Gyeongju-si, Gyeongsangbuk-do, Korea. Hap, haplotype.

Table 1. Comparison of the major morphological characteristics between Korean and Japanese specimens of *Cottus pollux*

	Korean specimens	Japanese specimens			
	Present study	Günther (1873)	Yoshigou (2010)		
			Large-egg type	Middle-egg type	Small-egg type
Standard length (mm)	79.3~100.8 (n = 2)	114.3 (n = 2)	45.8~119.7 (n = 48)	41.3~105.7 (n = 49)	66.3~102.8 (n = 9)
Dorsal fin rays	VIII~IX, 17	IX, 19	VII~X (VIII~IX), 14~18 (16~17)	VII~X (VIII~IX), 16~18 (17~18)	VIII~IX (VIII), 17~18 (18)
Anal fin rays	13	13	12~14 (12~13)	12~14 (13)	12~13 (13)
Pectoral fin rays	12~13	–	12~14 (13)	14~16 (15)	16~17 (16)
Gill rakers	5~6	–	4~7 (5~6)	4~7 (5~6)	5~7 (6)
In % of standard length					
Body depth	20.3~20.7 (20.5)	–	13.1~19.4 (16.0)	14.1~19.2 (16.7)	17.8~21.0 (19.7)
Head length	29.9~32.4 (31.1)	–	26.8~32.6 (29.7)	27.6~32.8 (30.5)	29.0~32.3 (30.6)
Snout length	7.5~8.5 (8.0)	–	6.6~9.2 (8.0)	7.3~9.7 (8.5)	8.1~9.9 (8.8)
Eye diameter	7.5~8.2 (7.9)	–	6.1~9.2 (7.6)	6.1~9.3 (7.8)	6.8~8.1 (7.6)
Postorbital length	17.3	–	13.6~18.5 (16.2)	14.0~18.3 (16.3)	16.4~18.1 (17.0)
Interorbital width	3.9~4.3 (4.1)	–	2.3~4.1 (3.4)	2.7~5.1 (3.7)	3.2~4.4 (3.6)
Upper jaw length	13.2~16.8 (15.0)	–	9.6~15.0 (11.7)	9.1~13.4 (11.1)	7.9~12.8 (11.1)
Length of snout to origin of 1st dorsal fin	33.7~33.9 (33.8)	–	30.4~35.4 (32.5)	31.1~36.2 (33.1)	30.6~34.6 (32.0)
Length of snout to origin of 2nd dorsal fin	54.2~54.7 (54.4)	–	50.4~57.8 (54.8)	51.2~57.5 (54.7)	49.8~54.2 (52.1)
Length of snout to insertion of pelvic fin	28.0~30.3 (29.1)	–	23.1~31.0 (27.5)	24.5~33.5 (29.2)	28.1~35.0 (31.7)
Length of snout to origin of anal fin	56.4~57.3 (56.8)	–	53.1~61.6 (57.7)	52.2~61.0 (57.2)	53.2~59.0 (56.8)
Caudal peduncle depth	8.9~9.1 (9.0)	–	7.8~10.6 (9.1)	7.3~9.5 (8.4)	9.5~10.9 (10.3)
Caudal peduncle length	15.1~17.6 (16.3)	–	15.3~19.8 (17.8)	15.7~20.7 (18.4)	17.6~20.5 (19.2)
Basal length of 1st dorsal fin	22.0~22.8 (22.4)	–	19.7~27.1 (23.6)	19.7~25.8 (22.5)	19.4~22.3 (20.6)
Basal length of 2st dorsal fin	36.2~38.7 (37.5)	–	35.0~41.7 (37.9)	34.2~40.5 (37.8)	37.3~40.6 (39.0)
Basal length of anal fin	26.0~29.7 (27.8)	–	22.5~28.4 (25.5)	22.6~30.0 (26.0)	24.8~28.8 (26.3)
Pectoral fin length	25.6~26.0 (25.8)	–	23.1~28.8 (25.9)	23.9~28.8 (25.8)	24.8~27.2 (26.1)
Pelvic fin length	21.2~25.4 (23.3)	–	13.9~21.3 (18.3)	16.3~20.4 (18.0)	18.5~21.1 (19.8)
Caudal fin length	19.2~21.5 (20.3)	–	18.4~24.7 (21.3)	16.8~23.2 (20.0)	19.5~21.8 (20.6)
In % of head length					
Snout length	25.2~26.2 (25.7)	–	23.1~29.6 (26.8)	24.4~30.8 (27.7)	26.8~31.6 (28.9)
Eye diameter	23.2~27.5 (25.3)	–	20.3~30.6 (25.6)	19.9~30.1 (25.7)	23.3~27.7 (25.0)
Postorbital length	53.5~58.0 (55.7)	–	50.2~60.1 (54.6)	47.5~58.1 (53.4)	52.3~58.3 (55.8)
Interorbital width	13.1~13.3 (13.2)	–	7.4~13.8 (11.3)	8.8~16.0 (12.2)	10.3~13.6 (11.8)
Upper jaw length	44.3~51.8 (48.0)	–	33.1~50.8 (39.5)	30.1~44.9 (36.4)	27.4~40.9 (36.1)
Upper jaw width	54.9~61.2 (58.0)	–	37.1~72.8 (50.8)	36.5~59.4 (44.9)	47.3~55.7 (52.1)

Table 1. Continued

	Korean specimens		Japanese specimens		
	Present study	Günther (1873)	Yoshigou (2010)		
			Large-egg type	Middle-egg type	Small-egg type
Caudal peduncle depth	28.0~29.7 (28.9)	–	25.4~36.8 (30.7)	24.7~31.5 (27.5)	30.3~35.9 (33.6)
Pectoral fin length	79.1~87.1 (83.1)	–	81.3~96.7 (87.4)	75.8~95.6 (84.5)	82.3~89.0 (85.6)
In % of Body depth					
Caudal peduncle depth	42.9~44.7 (43.8)	–	52.0~66.1 (57.3)	44.9~58.3 (50.3)	50.0~55.2 (52.2)
Body width	87.0~89.3 (88.1)	–	70.8~89.3 (80.4)	69.4~83.2 (74.8)	67.4~78.7 (73.4)
In % of Caudal peduncle depth					
Caudal peduncle length	169.4~194.1 (181.7) 51.5~59.0 (55.3)*	–	40.8~61.0 (51.3)	38.5~59.5 (45.8)	50.3~57.0 (53.5)
Caudal peduncle width	56.1~59.9 (58.0)	–	45.7~58.8 (52.4)	38.2~50.0 (45.4)	37.6~42.9 (39.8)
In % of Eye diameter					
Interorbital width	47.5~57.4 (52.5)	–	26.8~64.5 (44.7)	34.5~72.2 (47.9)	41.7~57.7 (47.4)

*Proportion of caudal peduncle depth in caudal peduncle length (presumed to be an error in the calculation formula).
The values in parentheses are means (measurements) or common values (counts).

the Hangang River *C. koreanus* population (Byeon *et al.*, 1995) in terms of a shorter head length (male; 20.9~30.8 SL in Hoamcheon Stream vs. 27.0~31.4 in Hangang River), pelvic fin length (13.3~21.3 vs. 23.1~31.2), pectoral fin length (20.7~28.3 vs. 24.3~29.2), and mouth width (48.6~63.5 HL vs. 61.7~69.7). These morphological characteristics mostly agreed with the measurement data of individuals from the Deokdongcheon Stream found in the present study (Table 2). However, Byeon and Lee (2017) compared only the counts and measurements, which are quantitative characteristics, and did not consider the presence of spots on the pelvic fin, the diagnostic character of *C. pollux*, so it is thought that they were recognized as *C. koreanus*. We found no bands or spots on the pelvic fin in the *C. koreanus* population reported by Byeon and Lee (2017). Therefore, it is reasonable to recognize this and we judged its population as *C. pollux*.

Cottus pollux tends to form separate groups within the species according to egg size (Goto *et al.*, 2002; Yoshigou, 2010). This is indicative of the ecological characteristics and associations of freshwater sculpins, i.e., the large egg type (LE; egg size, 2.5~3.7 mm) has a fluvial life history, whereas the middle (ME; 2.2~2.8 mm) and small (SE; 1.8~2.4 mm) egg types have an amphidromous life history (Kanno *et al.*, 2018). Recently, *C. pollux* SE was considered synonymous with *C. reinii* (egg size, 1.8~2.4 mm), which is a sister species in the *C. pollux* species group, due to the low level of genetic differentiation (Goto *et al.*, 2015; Dolganov and Saveliev, 2022). Regarding *C. pollux* ME, a study case that is genetically close to *C. pollux* LE but assigns it as *Cottus* sp. due to a different life history has also been reported (Hosoya, 2015). Yoshigou (2010) performed a morphological analysis of the *C. pollux* species (Table 1). Regarding the measurement data, our two specimens had a large overlap with the Japanese *C. pollux* species group, so there was no noticeable difference. However, regarding the count data, the number of pectoral fin rays (12~13 in Korean specimens vs. 12~14 in Japanese LE vs. 14~16 in ME vs. 16~17 in SE) differed fairly clearly between our specimens and the *C. pollux* species group. In addition, regarding body color, only *C. pollux* LE reportedly lacks a blackish band on the head or anterior part of body. In conclusion, the *C. pollux* specimens from Deokdongcheon Stream observed in this study were confirmed to belong to *C. pollux* LE based on the fluvial life history, 2.8~3.2 (mean 3.0 ± 0.12, $n = 30$) mm egg size, 12~13 pectoral fin rays, and no blackish band on the head or anterior part of the body.

In the BI tree using the nuclear *ITS1* gene and mitochondrial *cytb* gene, our specimens formed a clade

Table 2. Comparison of the major morphological characteristics of Korean *Cottus pollux*

	Present study	Byeon and Lee (2017)	
	Deokdongcheon Stream	Hoamcheon Stream	
	Male	Male	Female
Standard length (mm)	79.3~100.8 (n=2)	- (n=17)	- (n=17)
Dorsal fin rays	VIII~IX, 17	V~IX, 15~18	V~IX, 15~18
Anal fin rays	13	12~14	12~14
Pectoral fin rays	12~13	12~13	12~13
Pelvic fin rays	I, 3	I, 4	I, 4
In % of standard length			
Body depth	20.3~20.7 (20.5)	16.8~24.1 (21.3)	15.2~24.3 (21.2)
Body width	18.0~18.1 (18.1)	14.9~26.3 (20.1)	27.0~31.4 (27.3)
Head length	29.9~32.4 (31.1)	20.9~30.8 (24.9)	19.2~27.3 (22.2)
Length of snout to origin of 1st dorsal fin	33.7~33.9 (33.8)	28.1~45.5 (35.1)	25.0~37.8 (33.3)
Length of snout to origin of anal fin	56.4~57.3 (56.8	46.2~64.8 (55.8)	45.7~59.3 (54.1)
Caudal peduncle length	15.1~17.6 (16.3)	11.4~18.3 (12.3)	11.2~18.9 (13.9)
Caudal peduncle depth	8.9~9.1 (9.0)	7.8~14.5 (10.9)	6.2~14.3 (9.9)
Anal fin length	14.8~15.9 (15.4)	9.4~17.2 (12.6)	8.9~17.5 (10.2)
Pelvic fin length	21.2~25.4 (23.3)	13.3~21.3 (17.6)	12.8~18.7 (15.8)
Pectoral fin length	25.6~26.0 (25.8)	20.7~28.3 (24.8)	18.9~25.4 (21.5)
In % of head length			
Eye diameter	23.2~27.5 (25.3)	11.2~28.4 (23.0)	16.7~29.3 (23.6)
Mouth width	53.5~58.0 (55.7)	48.6~63.5 (57.2)	48.9~62.9 (54.7)
Snout length	25.2~26.2 (25.7)	28.7~33.2 (31.8)	25.8~34.1 (30.3)

The values in parentheses are means.

with Japanese *C. pollux*, supporting the morphological species identification (Figs. 5, 6). The fish in *Cottus* (SUC25257~25258) collected in Hoamcheon Stream reported by Byeon and Lee (2017) were also in this clade, strongly suggesting they are *C. pollux*. In addition, the abovementioned complexity of the *C. pollux* species group according to egg size is reflected in the *cytb* gene BI tree (*ITS1* lacked sequence data) with two major clades (Fig. 6): the Pollux and Pollux-Reinii clades. The *p*-distances of the *cytb* gene between Korean and Japanese *C. pollux* ranged from 0.070 to 0.073, which was slightly higher than the range of *p*-distances generally seen at the level of intraspecific genetic variation (Baker and Bradley, 2006; Kim *et al*., 2006). This may be because the environment that they inhabit did not significantly affect the morphological changes. Alternatively, given the ecological characteristics of *C. pollux* inhabiting the upper reach of streams, it may be due to limited gene flow between geographically different populations (Yu *et al*., 2014; Baek *et al*., 2018; Chen *et al*., 2022).

Cottus pollux is a derivative of the amphidromous species *C. reinii* and appears to have adapted well to freshwater environments due to the long-term closure of the Korea Strait (Dolganov and Saveliev, 2022). In particular, the discovery of *C. pollux* in Deokdongcheon and Hoamcheon Streams suggests that their common ancestor spread not only to Japan but also to Korea during the Pleistocene when the Korea Strait opened (Yokoyama and Goto, 2005; Goto *et al*., 2015). Therefore, it is considered that an accurate grasp of the distribution of *C. pollux* in Korea will be a very important clue for identifying the lineage and evolution of the fish genus *Cottus* in southern Far East Asia.

A new Korean name, "Min-mu-nui-dug-jung-gae", is proposed here for *C. pollux*. It reflects the absence of bands or spots on the pelvic fin, in contrast to *C. koreanus* and *C. hangiongensis*, which are presently reported to inhabit Korea.

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한국산 둑중개과(쏨뱅이목) 첫기록종, *Cottus pollux*

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요 약 : 대한민국 경상북도 경주시 암곡동 형산강 지류인 덕동천 상류에서 둑중개과 (Cottidae) 둑중개속 (*Cottus*)에 속하는 어류 2개체 (표준체장 79.3~100.8 mm)를 채집하였다. 이들은 구개골에 이빨이 없는 점, 가슴지느러미의 기조가 분지되지 않고 기조수가 12~13개인 점, 배지느러미에 뚜렷한 반점이나 무늬가 없는 점, 그리고 머리 또는 몸 앞쪽에 검은색 띠가 없는 점 등에서 *C. pollux*로 동정되었다. 또한, 핵 DNA의 *ITS1* 유전자 영역과 미토콘드리아 DNA의 *cytb* 유전자 영역을 이용한 분자계통학적 분석 결과, 본 표본은 일본산 *C. pollux*와 동일한 유전적 clade를 형성하여 상기 형태학적 특징에 의한 종 동정 결과를 뒷받침하였다. 신한국명으로는 대한민국에 분포하는 둑중개 및 한둑중개와 달리 배지느러미에 반점이나 무늬가 없는 형태적 특징에 따라 '민무늬둑중개'를 제안한다.

찾아보기 낱말 : 둑중개과, 둑중개속, *Cottus pollux*, Japanese fluvial sculpin, 첫기록