ASED http://e-ASED.org
Animal Systematics, Evolution and Diversity

Anim. Syst. Evol. Divers. Vol. 29, No. 4: 288-293, October 2013
http://dx.doi.org/10.5635/ASED.2013.29.4.288

New Record of *Sillago sinica* (Pisces: Sillaginidae) in Korean Waters, and Re-identification of *Sillago parvisquamis* Previously Reported from Korea as *S. sinica*

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ABSTRACT

A single specimen of the genus *Sillago*, collected from Gwangyang, Korea, in May 2009, is characterized by XI first dorsal fin spines, 3 or 4 rows of melanophore pattern along the second dorsal fin membrane, and a darkish posterior margin of the caudal fin. Our specimen was identified as *Sillago sinica* reported as a new species; this identification is confirmed by mitochondrial DNA cytochrome oxidase subunit I sequences, which show that our specimen corresponds to *S. sinica* (d=0.000) and differs from the congeneric species *Sillago parvisquamis* (d=0.170). Comparisons of Korean specimens previously reported as *S. parvisquamis* with specimens of *S. sinica* show that the *S. parvisquamis* specimens are actually *S. sinica*. We propose the new Korean name "buk-bang-jeom-bo-ri-myeol" for *S. sinica*.

Keywords: first record, *Sillago sinica*, *Sillago parvisquamis*, re-identification, Sillaginidae, Korea

INTRODUCTION

The family Sillaginidae, order Perciformes, comprise 31 species in three genera worldwide (Nelson, 2006) and 4 species in 1 genus in Korea (Kim et al., 2005; Kwun and Kim, 2010). The Korean species are *Sillago sihama* (Forsskål, 1775); *Sillago japonica* Temminck and Schlegel, 1843; *Sillago parvisquamis* Gill, 1861; and *Sillago aeolus* Jordan and Evermann, 1902. Sillaginid fishes are morphologically similar, which has led to considerable confusion in species-level identifications (Sano and Mochizuki, 1984). A number of recent molecular phylogenetic and phylogeographic studies of cryptic species have been conducted (Kon et al., 2007; Kai et al., 2011), and the family Sillaginidae has been studied by DNA sequencing (Xue et al., 2010). Kwun and Kim (2010) indicated slight morphological differences between Korean and Japanese specimens of *S. parvisquamis*. We closely compared *S. parvisquamis* from Korea (reported by Kwun and Kim, 2010) with *Sillago sinica* specimens reported by Gao et al. (2011) and performed molecular analyses on a single specimen of *S. sinica* collected in Gwangyang, Korea.

MATERIALS AND METHODS

A single specimen of *Sillago sinica* was collected from Gwangyang, Korea on 29 May 2009. After collection, the specimen was fixed in 10% formalin after extraction of muscle tissue, and transferred to 70% ethanol. Muscle tissue was stored in 99% ethanol. The specimen is deposited in the National Institute of Biological Resources (NIBR), Korea. Counts and measurements followed Hubbs and Lagler (2004) with a vernier caliper to the nearest 0.1 mm. The vertebrae were counted from a radiograph (HA-100; Softex, Tokyo, Japan).

Genomic DNA was extracted from muscle tissue using Chelex 100 resin (Bio-Rad, Hercules, CA, USA). Polymerase chain reaction (PCR) was used to amplify the mitochondrial DNA cytochrome oxidase subunit I (COI) using universal

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pISSN 2234-6953 eISSN 2234-8190

primer set (VF2: 5′-TCAACCAACCACAAAGACATTGG CAC-3′ and FishR1: 5′-TACACTTCTGGGTGGCCAAA GAATCA-3′) (Ivanova et al., 2007), with PCR solution containing 5 μL of genomic DNA, 5 μL of 10× buffer, 4 μL of 2.5 mM dNTPs, 1 μL of each primer, 0.5 μL of FR Taq polymerase (Biomedic, Korea), and distilled water to bring the final volume to 50 μL. PCR was performed under the following conditions: initial denaturation was for 2 min at 95°C, followed by 35 cycles of 30 s at 94°C for denaturation, 30 s at 61°C for annealing, and 30 s at 72°C for extension, with a final extension at 72°C for 3 min. The nucleotide sequence was deposited in the DDBJ/EMBL/GenBank databases (accession no. KC708229). The sequence was aligned with ClustalW (Thompson et al., 1994) in BioEdit version 7 (Hall, 1999). The sequences of 4 *Sillago* species (*S. aeolus*, *S. japonica*, *S. parvisquamis*, and *S. sihama*), from the National Center for Biological Information database, were used for the sequence comparison. Also, *Lateolabrax japonicus* (PKU 547; KC708230) was used as an outgroup. The genetic distances were calculated with the Kimura-2-parameter model (Kimura, 1980) in MEGA 5 (Tamura et al., 2011). Neighbor-joining (NJ) tree was constructed in MEGA 5 (Tamura et al., 2011) with 1,000 bootstrap replications.

SYSTEMATIC ACCOUNTS

Order Perciformes
Family Sillaginidae

[1]*_Sillago sinica_ Gao and Xue in Gao, Ji, Xiao, Xue, Yanagimoto and Setoguma, 2011

(new Korean name: Buk-bang-jeom-bo-ri-myeol)
(Table 1, Fig. 1)

Sillago sinica Gao and Xue in Gao, Ji, Xiao, Xue, Yanagimoto and Setoguma, 2011: 256, figs. 1, 3F (type locality: coastal waters of East China Sea, China).

Sillago parvisquamis (non Gill): Kwun and Kim, 2010: 109, figs. 2B, 3B (Korea).

Material examined. NIBR-P0000019930 (previously PKU2043), 1 specimen, 157.0 mm in standard length (SL),

Table 1. Comparison of meristics and morphometrics of *Sillago sinica* and *S. parvisquamis*

Characters	*S. sinica*			*S. parvisquamis*
No. of specimens	1	53	6	2
Registration number	NIBR-P0000019930	OCU_FEL100348–100399, OCU_FEL100403–100404	CNUC 27077, CNUC 28569–28573	FAKU 68748, FAKU 86827
Standard length (mm)	157.0	92.3–175.0	133–165	194.5–196.5
Counts				
Dorsal fin rays	XI-I, 22	X–XI-I, 21–22	X–XI-I, 21–22	XII-I, 22
Anal fin rays	II, 23	II, 21–23	II, 22–23	II, 23
Lateral line scales	79	–	78–79	77–79
Transverse scales	7	7–8	7	7
Vertebrae	38	37–39	37–38	39
Measurements				
In % of standard length				
Head length	25.2	24.7–29.8 (27.0)	25.4–27.0 (26.2)	25.2–27.1 (26.1)
Body depth	14.1	11.3–18.4 (15.4)	11.9–13.9 (13.1)	13.9–16.3 (15.1)
Predorsal length	30.4	–	31.3–33.0 (31.7)	31.4–32.9 (32.1)
Preanal length	51.7	–	48.5–52.8 (50.5)	50.6–53.0 (51.8)
Prepelvic length	27.8	–	26.5–29.4 (28.2)	27.0–29.0 (28.0)
In % of head length				
Snout length	42.9	33.2–45.1 (40.4)	41.7–45.1 (43.2)	41.2–41.4 (41.3)
Eye diameter	15.7	15.4–22.7 (18.7)	14.4–17.8 (16.0)	16.5–18.0 (17.3)
Interorbital width	22.0	19.0–28.1 (22.8)	24.5–28.6 (26.3)	22.6–25.5 (24.0)
Caudal peduncle depth	28.5	19.3–30.0 (24.8)	22.5–27.3 (25.5)	21.4–23.5 (22.4)
1st dorsal spine length	51.5	–	40.2–60.8 (51.1)	57.1–60.4 (58.8)
1st dorsal ray length	39.1	–	23.9–43.7 (34.3)	41.5–44.9 (43.2)
2nd anal spine length	18.2	–	18.5–21.7 (19.8)	24.2–25.1 (24.7)
1st anal ray length	29.8	–	25.2–30.8 (28.3)	36.5–38.3 (37.4)
Pectoral fin length	69.9	–	63.6–72.3 (66.8)	49.6–55.9 (52.8)
Pelvic fin length	49.2	–	44.7–50.6 (47.2)	51.5–58.8 (55.1)
Reference	Present study	Gao et al. (2011)	Kwun and Kim (2010)	Kwun and Kim (2010)

Korean name: [1]*북방점보리멸

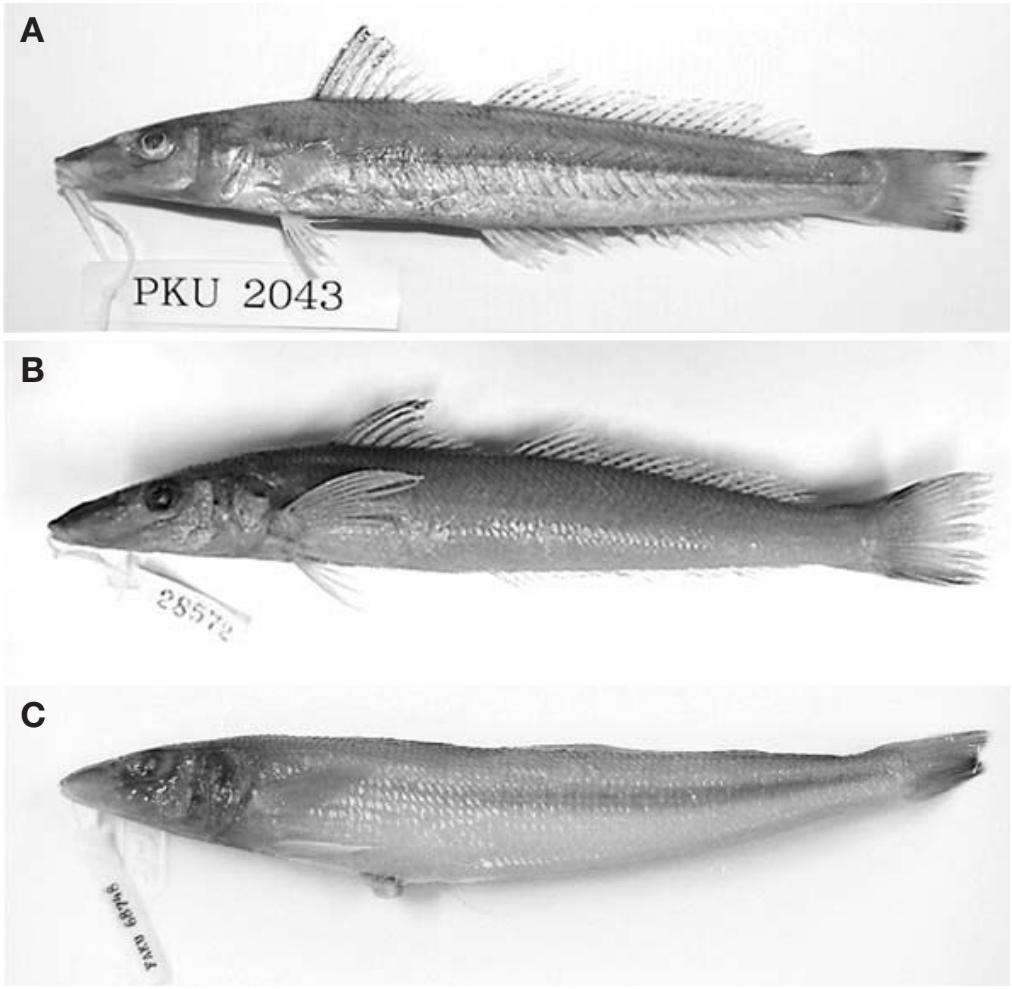

Fig. 1. A, *Sillago sinica*, NIBR-P0000019930 (previously PKU 2043); B, *Sillago sinica*, preserved specimen, CNUC 28572; C, *Sillago parvisquamis*, preserved specimen, FAKU 68748.

Gwangyang, Korea, 29 May 2009; collected by Kwun HJ and Kim JK.

Description. Counts and measurements are shown in Table 1. Body elongated, slightly compressed, and head tapering. Mouth small, terminal, and snout long. Body depth low, and dorsal margin of head slightly sloping. Eyes normal and located middle of the head, and cheek large. Posterior tip of maxilla not reaching to anterior margin of eye, and upper jaw projecting beyond lower jaw. Single row of conical teeth on both jaws. Two pairs of nostrils located in front of eyes. Interorbital region flat and covered with scales. Lateral line extending to caudal fin base with a slight curvature along middle of body. Body and head covered with ctenoid scales; cheek covered with both ctenoid and cycloid scales; only small scales on base of caudal fin. Posterior margin of preopercle serrated. Opercle with a small spine. Two dorsal fins that appear contiguous but completely separated; origin of first dorsal fin located posterior to origin of pelvic fin; origin of second dorsal fin located vertically above origin of anal fin. Second dorsal spine longest, and others gradually became shorter. Pectoral fin slender. Origin of pelvic fin located vertically above lowest base of pectoral fin, and pelvic fin rays shorter than pectoral fin rays. Caudal fin slightly emarginate but nearly truncate.

Coloration. When fresh, body is yellowish-green dorsally and silver-white ventrally. Darkish brown band on snout, gradually fading posteriorly. Two dorsal fins with transparent membranes; first fin darkish anteriorly and second fin with 3 or 4 rows of dusky spots. Pectoral fin pale yellow; pelvic fin white; anal fin membrane transparent with small irregular black spots; caudal fin yellowish with darkish posterior lobe. After fixation, body is bright yellow and silvery white from upper base of the pectoral fin to the ventral side. A single faint stripe is present along middle of body.

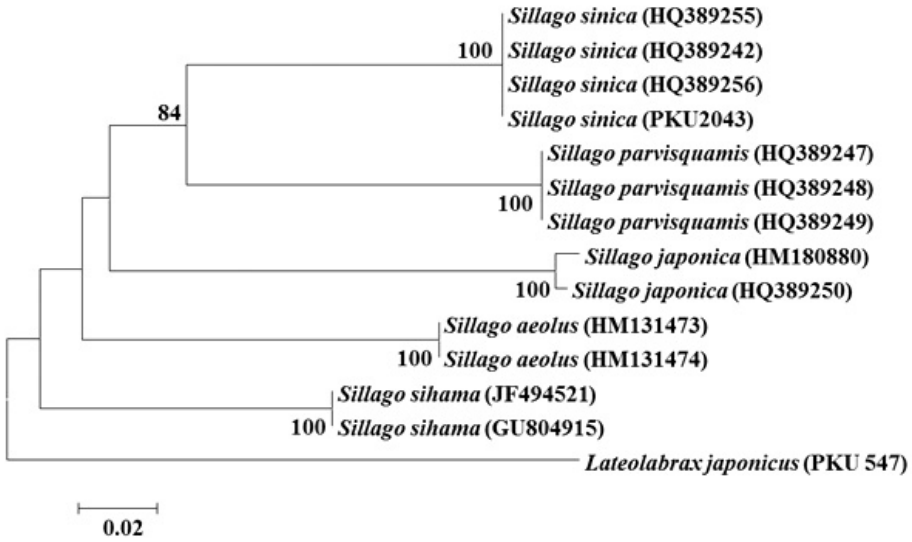

Fig. 2. Neighbor-joining (NJ) tree for cytochrome oxidase subunit I gene sequences of 4 Sillaginidae species. The NJ tree was constructed under the kimura 2-parameter (K2P) model using *Lateolabrax japonicus* as an outgroup. *Sillago sinica* (PKU 2043) indicate present specimen (NIBR-P0000019930). Bar indicates genetic distance of 0.02.

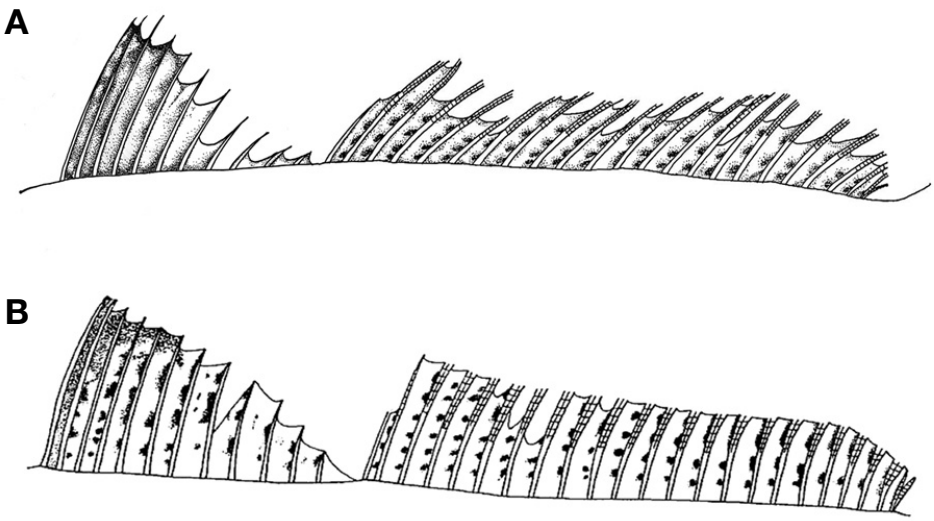

Fig. 3. Dorsal fin showing the melanophore distribution pattern of *Sillago* species. A, *Sillago sinica*, NIBR-P0000019930 (previously PKU 2043); B, *Sillago parvisquamis* (Sano and Mochizuki, 1984: 141, fig. 3B).

MtDNA COI analysis. A total of 550 bp of mitochondrial DNA cytochrome oxidase subnit I (mtDNA COI) were obtained from our specimen and the base pair sequence was then compared with those of four Sillaginidae species. The sequence from our specimen corresponds exactly to that of *S. sinica* (d=0.000) but differs from that of *S. parvisquamis* (d=0.170), which is a morphologically similar species. The sequence from our specimen also shows significant departures from those of *S. sihama* (d=0.190), *S. aeolus* (d=0.193), and *S. japonica* (d=0.216). A NJ tree shows that the present specimen corresponds to *S. sinica* (bootstrap value, 100%) (Fig. 2).

Distribution. *Sillago sinica* is distributed in China (East China Sea, Yellow Sea, and Bohai Sea) (Gao et al., 2011) and Korea (South Sea) (present study).

Remarks. The specimen in this study was identified as *S. sinica*, a new species recently reported by Gao et al. (2011) as having XI first dorsal fin spines, 38 vertebrae, a second

dorsal fin with 3 or 4 rows of dusky spots, and a caudal fin with a darkish posterior margin (Table 1, Fig. 3). The specimen is morphologically very similar to *S. parvisquamis*, but is distinguishable from *S. parvisquamis* by the number of first dorsal fin spines (XII−XIII in *S. parvisquamis*) and the melanophore pattern on the second dorsal fin membrane (5−6 rows in *S. parvisquamis*) (Sano and Mochizuki, 1984; Gao et al., 2011). Also, *Sillago sinica* is distributed in Asia including China and Korea, whereas the congeneric species *S. parvisquamis* is distributed in the South China Sea, Japan, and Taiwan (Shao and Chang, 1978; McKay, 1985, 1992; Hayashi, 2002). In addition, our mtDNA COI analysis showed that our specimen corresponds to *S. sinica* (genetic distance, d=0.000), whereas it differs from *S. parvisquamis* (d=0.170) and *S. sihama* (d=0.190). In the past, the slight morphological variations between the species were considered as regional variations. Recently, however, a number of studies have revealed that these are cryptic species, based on molecular markers (Kon et al., 2007; Ji et al., 2011; Kai et al., 2011; Kwun et al., 2011). Similarly, Kwun and Kim (2010) identified this specimen as *S. parvisquamis* based on some meristic characters and having several rows of dark spots on second dorsal membrane. In addition, they considered morphological differences between Korean and Japanese specimens of *S. parvisquamis* as regional variations, and suggested that molecular investigations of the two groups should be conducted to confirm their species identifications. In present study, we confirmed that *S. parvisquamis* collected in Korea by Kwun and Kim (2010) is *S. sinica*. If *S. parvisquamis* is found in Korea in the future, considerable confusion may result it the same Korean name is used to describe both *S. parvisquamis* and *S. sinica*. Therefore, we propose the new Korean name "buk-bang-jeom-bo-ri-myeol" for *S. sinica*, based on its areal distribution in the East China Sea and Yellow Sea.

ACKNOWLEDGMENTS

We thank Dr. Jong-Young Park (Chonbuk National University, Korea), Dr. Yoshiaki Kai (Kyoto University, Japan) for the loan of the comparative species. This research was supported by the project on survey and excavation of Korean indigenous species of the National Institute of Biological Resources (NIBR) under the Ministry of Environment, Korea.

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Received April 10, 2013
Revised October 1, 2013
Accepted October 5, 2013