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# New Record of Juvenile *Sigmops gracilis* (Pisces: Gonostomatidae) from Jeju Island, Korea, Revealed by DNA Barcoding

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## Abstract

A juvenile of the slender fangjaw, *Sigmops gracilis* Günther, 1878 (Stomiiformes: Gonostomatidae) was collected from Jeju Island, Korea, and identified by DNA barcoding. This species is characterized by its large curved mouth and the presence of 11 dorsal fin rays and 28 anal fin rays. During the juvenile stage, the species is distinguished from other gonostomatid species by the position of the origin of the dorsal fin, which is located at the 7th-8th ray of the anal fin. The Korean name "Sol-ni-ael-tung-i" is proposed for this species.

**Key words:** *Sigmops gracilis*, Gonostomatidae, Pisces, DNA barcoding, Korea, First report

## Introduction

Worldwide, the family Gonostomatidae (order Stomiiformes) consist of 23 species in 5 genera (*Banapartia*, *Cyclothone*, *Gonostoma*, *Margrethia*, and *Sigmops*). These genera are distributed in the Indian, Atlantic, and Pacific oceans (Nelson, 2006), and they comprise most abundant fish group in the mesopelagic and bathypelagic zones (Nakabo, 2002). In particular, the genus *Cyclothone* has the greatest abundance of individuals (Froese and Pauly, 2012). Based on difficulties in the taxonomy of *Gonostoma* species, including non-monophyly, the genus was divided into two genera (*Gonostoma* and *Sigmops*) based on molecular phylogeny (Miya and Nishida, 2000). At present, four *Sigmops* species (*S. bathyphilus*, *S. ebelingi*, *S. gracilis*, and *S. longipinnis*) are considered valid (Froese and Pauly, 2012). No members of this family have previously been reported from Korean waters, possibly because of their very deep habitat. However, in this study, we report the first occurrence of a juvenile of a Gonostomatidae species in Korea, based on DNA barcoding. We describe its morphological and molecular characteristics and provide a new Korean name for the species.

## Materials and Methods

### Sample collection

In February 2012, a juvenile of a Gonostomatidae species was collected at a depth of 100 m at Jeju Island, Korea (32.54°N, 126.05°E) in a RN80 net (mouth opening 0.8 m, mesh size 0.33 mm). The specimen was fixed in 99% EtOH and later deposited at the National Institute of Biological Resources (NIBR-P 0000018076), Korea.

### DNA extraction, PCR, and sequencing

Total DNA was extracted from the eyeball of the specimen using 10% Chelex 100 resin. Polymerase chain reaction (PCR) was used to amplify the mitochondrial DNA cytochrome oxidase subunit I (mtDNA COI) gene using the previously reported PCR primers VF2 (5′-TCA ACC AAC CAC AAA GAC ATT GGC AC-3′) and FishR1 (5′-TAC ACT TCT GGG TGG CCA AAG AAT CA-3′) (Ivanova et al., 2007). The

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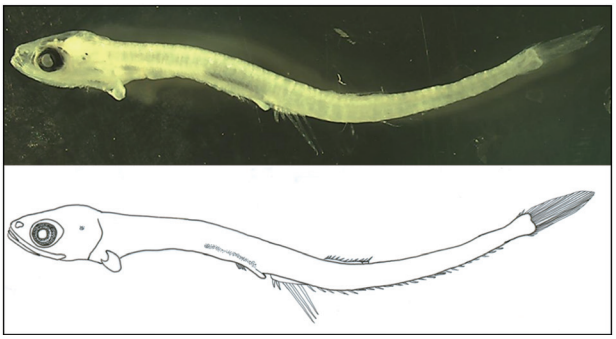

**Fig. 1.** *Sigmops gracilis* Günther, 1878, NIBR-P0000018076, 12.6 mm in standard length.

PCR conditions were as follows: initial denaturation at 94°C for 2 min, 35 cycles of denaturation at 94°C for 30 s, annealing at 50°C for 40 s, extension at 72°C for 1 min, and a final extension at 72°C for 10 min.

## DNA analysis

The DNA was sequenced using an ABI 3730XL sequencer and an ABI PRISM BigDye Terminator v3.0 Ready Reaction Cycle Sequencing Kit (Applied Biosystems Inc., Foster City, CA, USA). For comparison we obtained mtDNA COI sequences for gonostomatid species from the National Center for Biological Information (NCBI) database, including *Gonostoma elongatum* (EU148179-81), *S. bathyphilus* (EU148178*), S. longipinnis* (GQ860360), and *S. gracilis* (AB016274). *Sebastes pachycephalus* was used as an outgroup. The mtDNA COI sequences were aligned using BioEdit version 7. Genetic distances were calculated with the Kimura 2-parameter model using the software MEGA 5. A neighbor-joining tree with 1000 bootstrap replications was constructed using MEGA 5.

## Morphological analysis

Counts and measurements followed the methods of Nakabo (2002), and each body part was measured to the nearest 0.1 mm using the Active measure program (Korea). Morphological identification followed Okiyama (1988) and Ozawa and Katayama (2003).

## Results and Discussion

### *Sigmops gracilis* Günther, 1878 (Table 1, Fig. 1)

(Korean name: Sol-ni-ael-tung-i)

*Gonostoma gracile* Günther, 1878 (type locality: south of Japan); Yamamoto in Okamura et al. 1982: 73; Fujii in Masuda et al. 1984: 45.

*Sigmops gracile* Miya and Nishida 2000: 385; Nakabo 2002: 308; Shinohara et al. 2005: 404.

*Sigmops gracilis* Mecklenburg et al. 2002: 213; Ozawa and Katayama 2003: 197; Fedorov et al. 2003: 43.

#### Morphological description

Counts and proportional measurements for the *Sigmops gracilis* juvenile are presented in Tables 1 and 2, respectively. Fin rays: dorsal fin rays, 11; anal fin rays, 28; pectoral fin rays, 9; pelvic fin rays, 8. Body proportions as a percentage of standard length (SL): head length, 18; body depth at pectoral base, 7; preanus length, 47; preanal length, 48; anal fin base length, 41; location of dorsal fin origin, 57; dorsal fin base length, 12. Proportion as a percentage of head length: eye diameter, 37.

Body moderately compressed and elongate. Head moderate and eyes round. Eye diameter longer than the snout length. Body depth uniform except at the caudal peduncle. Mouth very large with hooked teeth, with the posterior tip of the upper jaw reaching to the posterior border of the eye. Notochord flexion complete and all fins develop at their fixed locations. Pelvic and pectoral fins small. Anus not attached to anal fin base, but very close to it. Origin of dorsal fin below the 7th-8th anal fin ray. Anal fin base length much longer than the dorsal fin. Melanophores developed on lateral occipital and dorsal gut. Photophores not observed.

#### Molecular identification

A mtDNA COI sequence of 499 base pairs (bp) derived from the eyeball of the Gonostomatidae juvenile was compared with sequences from other gonostomatid species and an outgroup. The smallest genetic distance was between the juvenile and *S. gracilis* (0.002), and the distances to other members of the same genus (*S. longipinnis* and *S. bathyphilus*) were much greater (0.210 and 0.231, respectively). Therefore, the juvenile collected that was collected in the present study

**Table 1.** Comparison of meristic characters of *Sigmops gracilis* and three *Sigmops* species

| | *S. gracilis*[*] | *S. gracilis*[†] | *S. bathyphilum*[‡] | *S. ebelingi*[§] | *S. longipinnis*[¶] |
|---|---|---|---|---|---|
| | Juvenile | Adult | Adult | Juvenile | Juvenile |
| Dorsal fin rays | 11 | 11-14 | 12-14 | 12-14 | 13-14 |
| Anal fin rays | 28 | 27-30 | 22-24 | 26-29 | 26-29 |
| Pectoral fin rays | 9 | 9-10 | 10-11 | 9-13 | 11-13 |
| Pelvic fin rays | 8 | 7-8 | 7-8 | 8 | 7-8 |

[*]Present study; [†]Nakabo (2002); [‡] Richards (2006); [§]Watson (1996), [¶]Ozawa and Katayama (2003).

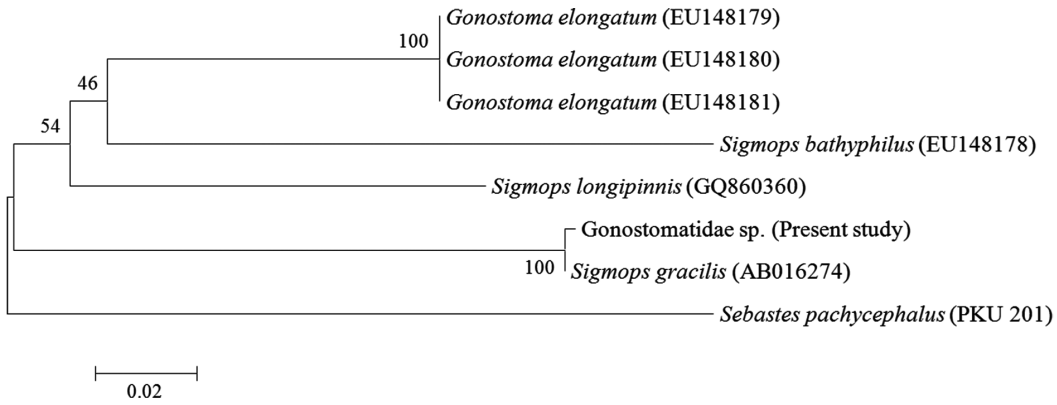


**Fig. 2.** Neighbor joining tree based on partial mitochondrial DNA cytochrome oxidase subunit I sequences, showing the relationships among juvenile of Gonostomatidae sp., four gonostomatids, and one outgroup (*Sebastes pachycephalus*). The tree was constructed using the K2P model and 1,000 bootstrap replications. The bar indicates a genetic distance of 0.02.

was identified as *S. gracilis* (Fig. 2).

**Distribution**

Alaska (Mecklenburg et al., 2002), China (Yang et al., 1996), Japan (Masuda et al., 1984), Kuril Islands (Mecklenburg et al., 2002), Taiwan (Shao, unpublished data), and Korea (present study).

**Remarks**

Juveniles of *S. gracilis* are distinguished from other gonostomatid juveniles by the position of the origin of the dorsal fin (Richards, 2006), which is located at the 7th-8th ray of the anal fin. Juveniles of *S. gracilis* are very similar to those of *G. elongatum*, but these species are distinguished at the photophore stage: *G. elongatum* has a photophore on the opercle at 8.0 mm SL, while *S. gracilis* has a photophore on the operculum at 15.5 mm SL (Okiyama, 1988). The juvenile specimen (12.6 mm SL) examined in the present study did not have a photophore, which is consistent with *S. gracilis*. The *S. gracilis* juvenile was distinguished from the congeneric species *S. bathyphilus* and *S. longipinnis* by the absence of melanophores on the caudal peduncle and the middle of the lateral body, respectively (Ozawa and Katayama, 2003). Juveniles of *S. ebelingi* are distinguished from those of *S. gracilis* by the location of the origin of the dorsal fin (Richards, 2006). According to Kawaguchi and Marumo (1967), *S. gracilis* is the most abundant fish group from 300 to 700 m depth in the Pacific Ocean. The water depth in the survey area in the present study was 100 m, suggesting that juveniles of *S. gracilis* are distributed in shallower depths than adult. The new Korean name "Sol-ni-ael-tung-i" is proposed for this species.

**Table 2.** Comparison with the proportional measurements of *Sigmops gracilis* and *Sigmops longipinnis* juveniles

| | *S. gracilis* | | *S. longipinnis* |
|---|---|---|---|
| | **Present study** | **Okiyama (1988)** | **Ozawa and Katayama (2003)** |
| Standard length (mm) | 12.6 | 10.3 | 17.0 |
| Standard length (%) | | | |
| Head length | 18 | 20 | 18-20 |
| Body depth at pectoral base | 7 | 11 | 18-21 |
| Body depth at caudal peduncle | 3 | 8 | 7-8 |
| Preanus length | 47 | 49 | 48-53 |
| Preanal length | 48 | 50 | 52-55 |
| Anal fin base length | 41 | 41 | 35-43 |
| Predorsal length | 57 | 61 | 55-60 |
| Dorsal fin base length | 12 | 12 | 11-15 |
| Head length (%) | | | |
| Eye diameter | 37 | 38 | 25 |

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