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First Record of Japanese gonate squid, *Gonatopsis japonicus* Okiyama, 1969 (Mollusca: Cephalopoda: Ganatidae) from Korea waters

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ABSTRACT

To date, the family Gonatidae consists of four genera and a total of 20 species. Two species within Gonatidae, *Berryteuthis* magister and *G. makko*, have been reported in Korean waters so far. In this study, a specimen of gonate squid was collected during DeepSea surveys and was identified as *Gonatopsis japonicus* Okiyama, 1969, which is the first record in South Korea. We provide morphological descriptions and photographs of *G. japonicus*, with the mitochondrial cytochrome c oxidase subunit I gene sequence.

Keywords: New record, *Gonatopsis japonicus*, DeepSea surveys, Korea

INTRODUCTION

The family Gonatidae (Mollusca: Cephalopoda), commonly known as oegopsid oceanic squid, is widely distributed in subpolar and temperate waters, with a bipolar distribution in the arctic-boreal and sub-Antarctic regions, but is absent from subtropical and tropical oceans (Okiyama, 1969; Nesis, 1997; Okutani *et al.*, 1998; Lindgren *et al.*, 2005; Roper *et al.*, 2010; Katugin *et al.*, 2015). Many Gonatidae species start life as paralarvae and juveniles in the upper water levels, but as adults, they descend to deeper waters to mate and spawn (Nesis, 1997; Roper *et al.*, 2010; Katugin*et al.*, 2015). They feed in epipelagic waters until reaching adulthood, after which some species undergo diel vertical migrations. Spent females of genus *Gonatus* and *Gonatopsis* become degenerate and float in deeper layers or at the surface. Gonatidisare crucial prey for many marine animals, and some species, like *Berryteuthis magister*, are commercially fished, with up to 70,000 tonnes harvested annually in the Pacific Ocean and Bering Sea by Russian fisheries (Chuchukalo, 2006; Roper *et al.*, 2010; Katugin *et al.*, 2015). The systematics of Gonatidae remain unclear due to challenges in species identification, especially when specimens are damaged, in early or late life stages, or mutilated by predators, undermining the reliability of distribution and biology data (Katugin *et al.*, 2015).

The family Gonatidae consists of four genera with a total 20 species, including two species in genus *Berryteuthis* (*B. magister* (S. S. Berry, 1913), and *B. magister magister* (S. S. Berry, 1913)), five species in genus *Gonatopsis* (*G. borealis* Sasaki, 1923, *G. japonicus* Okiyama, 1969, *G. makko* Okutani & Nemoto, 1964, *G. octopedatus* Sasaki, 1920, and *G. okutanii* Nesis, 1972), 12 species of genus *Gonatus* (*G. antarcticus* Lönnberg, 1898, *G. berryi* Naef, 1923, G. *californiensis* R. E. Young, 1972, *G. fabricii* (Lichtenstein, 1818), *G. kamtschaticus* (Middendorf, 1849), *G. madokai* Kubodera & Okutani, 1977, *G.*

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middendorffi Kubodera & Okutani, 1981, *G. onyx* R. E. Young, 1972, *G. oregonensis* Jefferts, 1985, *G. pyros* R. E. Young, 1972, *G. steenstrupi* Kristensen, 1981, and *G. ursabrunae* Jefferts, 1985), and one species of genus *Okutania* (*O. anonycha* (Pearcy & G. L. Voss, 1963)) (MolluscaBase, 2024). To data, two species in Gonatidis, *B. magister* and *G. makko*, have been reported in Korean waters (National Institute of Biological Resources, 2024).

In the present study, we newly report a japanese gonate squid, *G. japonicus* Okiyama, 1969 for the first time in Korean waters using morphological diagnosis and partial mitochondrial cytochrome c oxidase I (COI) gene sequence data.

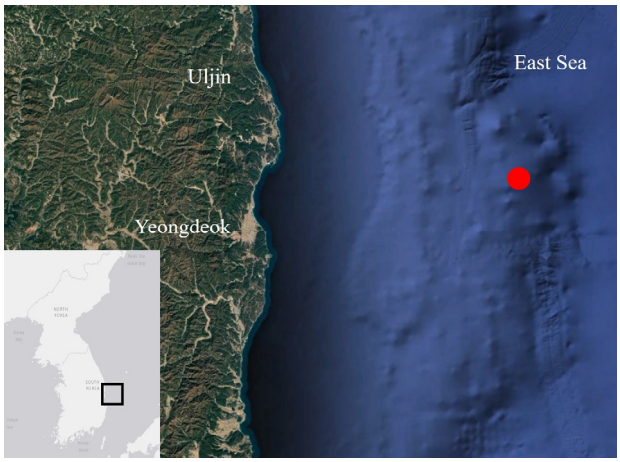

Fig. 1. Map showing the sampling area of *Gonatopsis japonicus* in East Sea.

MATERIALS AND METHODS

A specimen of *G. japnicus* was collected during DeepSea surveys in the offshore waters of Gyeongsangbuk-do, 30 April 2024, by research ships of the National Institute of Fisheries Science (NIFS) using a standard bottom trawl haul (Fig. 1). After being transported to the National Marine Biodiversity Institute of Korea (MABIK), a portion of the tissue was sampled for molecular analysis using absolute ethanol, then preserved in 5% formalin for 24 hours, and finally transferred to 99% ethyl alcohol for long-term storage. The morphological features of the specimen were photographed using a DSLR camera (Nikon D800, Japan), after which the fixed specimen was deposited at the MABIK. Total genomic DNA was extracted from the tissue of the fixed specimen using the E.Z.N.A Mollusc DNA Kit (Omega Co., Norcross, GA) according to the manufacturer's instructions. Partial fragment of the mitochondrial COI gene was amplified using the primer set LCO1490 and HCO2198 (Folmer *et al.*, 1994). For PCR reactions, TOPsimple™ DryMIX-nTaq (Enzynomics, South Korea) was used and the thermal cycling conditions were set as follows: an initial denaturation at 95℃ for 2 minutes, followed by denaturation at 95℃ for 30 seconds, annealing at 47℃ for 30 seconds, extension at 72℃ for 1 minute, and a final extension at 72℃ for 5 minutes. The denaturation, annealing, and extension steps were repeated 35 cycles. Pairwise genetic distances were calculated using the Kimura 2-parameter (K2P) distance (Kimura, 1980) with MEGA 11 program (Tamura *et al.*, 2021).

SYSTEMATIC ACCOUNTS

Class Cephalopoda Cuvier, 1795 두족강

Subclass Coleoidea Bather, 1888 초형아강

Superorder Decapodiformes R. E. Young, Vecchione & Donovan, 1998 십완상목

Order Oegopsida A. d'Orbigny, 1845 개안목

Family Gonatidae Hoyle, 1886 갈고리흰오징어과

Genus Gonatopsis Sasaki, 1920 향오징어속

***Gonatopsis japonicus* Okiyama, 1969 (Fig. 2)**

북태평양갈고리흰오징어

Gonatopsis japonicus Okiyama, 1969: 19–32, text figs. 1–4, pl. I–III. Roper *et al.*, 2010: 216–217, fig. 241

Type locality: the northern region of the Japan sea (41°02'N, 138°11'E) (Okiyama, 1969).

Habitat: surface to 1,000 m and on the bottom at 400 to 2,000 m (Roper *et al.*, 2010).

Distribution: North Pacific; Japan, and Korea (East Sea, this study).

Material examined: 1 specimen (MABIK MO00186702), Gyeongsangbuk-do offshore (East Sea), Korea, 36°38'21.1"N 130°1'13.74"E, 1,000 m, 30 April 2024, M-H Shin.

Measurement: See Table 1.

Description: Mantle cylindrical and slender, with

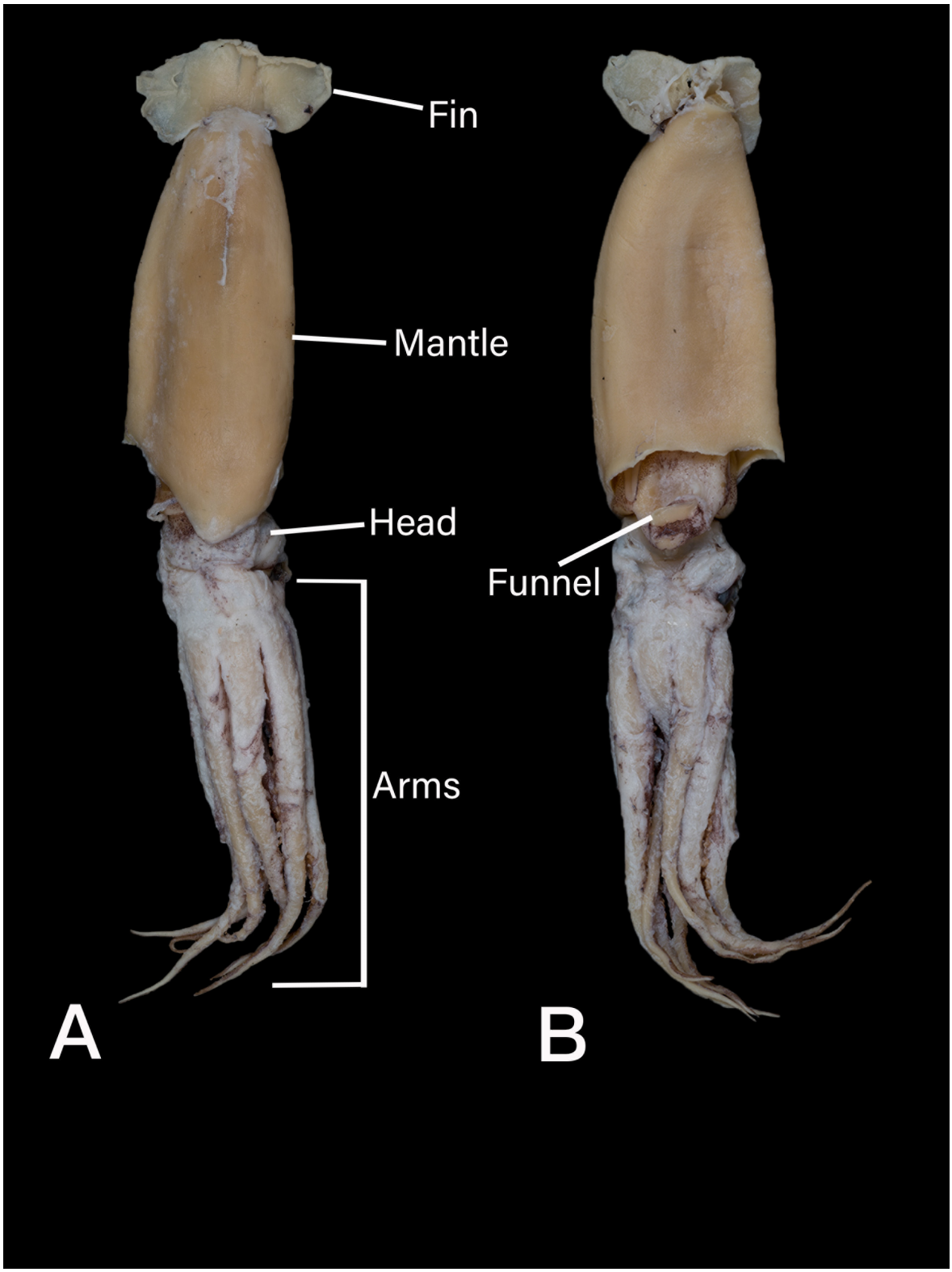

Fig. 2. *Gonatopsis japonicus* Okiyama, 1969. A. dorsal view; B. ventral view.

Table. 1. External measurements and number of suckers of *Gonatopsis japonicus*

Characters	Measured value (mm)	No. of suckers
Total length (mm)	154.82	-
Mantle length (mm)	63.51	-
Mantle width (mm)	27.19	-
Fin length (mm)	18.49	-
Fin width (mm)	32.92	
Arm length Right I (mm)	61.56	27
Arm length Right II (mm)	67.69	28
Arm length Right III (mm)	69.57	27
Arm length Right IV (mm)	67.87	24
Arm length Left I (mm)	60.73	26
Arm length Left II (mm)	72.23	25
Arm length Left III (mm)	74.69	22
Arm length Left IV (mm)	40.43	27

Table. 2. Pairwise genetic distances (%) within 8 species of thegenus *Gonatopsis* based on the mitochondrial DNA COI gene sequences (658bp) using the K2P model

No.	Species	1	2	3	4	5	6	7	8
1	*Gonatopsis japonicus* (This study)								
2	*Gonatopsis japonicus* (KT429709)	0.15							
3	*Gonatopsis japonicus* (KT429710)	0.15	0.00						
4	*Gonatopsis japonicus* (KT429711)	0.15	0.00	0.00					
5	*Gonatopsis japonicus* (KT429712)	0.15	0.00	0.00	0.00				
6	*Gonatopsis borealis* (KT429708)	11.93	11.89	11.91	11.91	11.91			
7	*Gonatopsis octopedatus* (MZ848533)	8.38	8.51	8.52	8.52	8.52	10.39		
8	*Gonatopsis makko* (KT429700)	14.29	14.64	14.67	14.67	14.67	10.24	12.71	

straight sides in the anterior half, gradually tapering to a sharp point at the posterior end. Integument soft, thin, and muscular. Fin large and thin, slightly longer than wide, about half the length of the dorsal mantle. Head short, broader than the mantle opening, with a deep and distinct excavation for the funnel. Eyes like semilunar opening. Funnel small, dorsal pad inverted V-shaped. Beaks darkly pigmented; upper beak acutely pointed rostrum and a rather obtuse jaw angle; lower beak less noticeable. Arms sturdy and firm, approximately half the length of the dorsal mantle, with the ventral arms being noticeably shorter.

Remarks: Okutani, 2017 noted that *G. japonicus*, as referred to by Okiyama, 1965, is likely to be the immature stage of *G. makko*. And in the genus Gonatopsis, identifying species based on their morphological features is often difficult due to several reasons, such as high morphological similarities, overlapping habitats, and the fact that many specimens are damaged by trawl nets or partially mutilated by predators (Okiyama, 1965; Roper *et al.*, 2010; Oleg *et al.*, 2015). Oleg *et al.*, 2015 suggested that mitochondrial COI gene barcoding is an effective method for identifying species within the family Gonatidae.

In this study, we determined a partial mitochondrial COI gene sequence of *G. japonicus* (Appendix) and *p*-distances were calculated by constructing a sequence alignment based on COI gene sequences from eight individuals of four *Gonatopsis* species (Table 2). The analysis revealed that intra-specific *p*-distances within the genus *Gonatopsis* ranged from 14.67%. The intra-specific

p-distance for *G. japonicus* was 0.15%, which was observed between individuals from Japan and South Korea. The inter-specific p-distance for *G. japonicus* ranged from 8.38% (compared to *G. octopedatus*, MZ848533) to 14.67% (compared to G. makko, KT429700).

In this study, we follow the Korean name for *G. japonicus*, which was suggested by Shin *et al.* 2024 as '북태평양갈고리흰오징어', and apply it accordingly.

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Appendix

Appendix. 1. The mitochondrial cytochrome c oxidase subunit I (COI) partial sequence of *Gonatopsis japonicus* (658bp).

> *Gonatopsis_japonicus* _mtDNA_COI_sequence

TACATTATATTTTATCTTTGGTATTTGAGCAGGTCTGCTAGGAACCTCCCTAAGCCTAATAATTCGAACTGAATTGGGACAAC
CTGGCTCTCTACTAAACGACGATCAACTCTATAACGTTGTAGTCACAGCCCACGGATTTATCATAATTTTTTTTTTAGTAATAC
CTATTATAATTGGGGGATTTGGTAATTGACTTGTTCCCTTAATACTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAAT
ATAAGATTTTGATTATTACCCCCTTCCCTAACACTATTATTAGCCTCTTCAGCTGTCGAAAGAGGGGCTGGTACAGGRTGAAC
AGTTTACCCCCCTCTTTCTAGTAATTTATCTCATGCAGGCCCCTCAGTTGATTTAGCTATTTTTTCTCTACATTTAGCAGGAGT
ATCCTCTATTCTAGGAGCCATCAATTTTATTACTACAATTTTAAATATACGATGAGAAGGYTTACAAATAGAACGACTACCTCT
CTTTGCTTGATCTGTGTTTATTACCGCAATTTTGTTACTTTTATCACTTCCTGTTCTAGCCGGAGCTATTACTATACTATTAAC
TGACCGAAACTTCAATACAACCTTTTTTGACCCAAGGGGGGGAGGGGATCCTATCCTATACCAACACCTATTC