

New Record of *Brama dussumieri* (Pisces: Bramidae) from Korea, as Revealed by Morphological and Molecular Analyses

Woo Jun Lee and Jin-Koo Kim*

Department of Marine Biology, Pukyong National University, Busan 48513, Korea

Abstract

Ten specimens of *Brama dussumieri* (family Bramidae) were collected from waters off Jeju Island, Busan, and Gangneung, Korea, during 2013-2014. The specimens were characterized by having 58-64 lateral line scales and 13-15 gill rakers. An analysis of 567 base pair sequences of mitochondrial DNA cytochrome c oxidase subunit I showed that sequences in our ten specimens are concordant with those of *B. dussumieri* from the USA, India, and Japan, although with slight differences (genetic distance = 0.000-0.018). *Brama dussumieri* was distinguished from the most similar species, *Brama japonica*, by the number of lateral line scales (57-65 in *B. dussumieri* vs. 65-75 in *B. japonica*) and the number of gill rakers (13-15 in *B. dussumieri* vs. 17-20 in *B. japonica*). We propose the new Korean name “Wae-sae-da-rae” for *B. dussumieri* in Korea.

Key words: *Brama dussumieri*, New record, Bramidae, mtDNA COI

Introduction

The family Bramidae in the order Perciformes comprises 7 genera and 22 species worldwide (Nelson, 2006), 6 genera and 10 species in Japan (Hatooka and Kai, 2013), and 4 genera and 6 species in Korea (Kim, 2011; Kim et al., 2012; Lee et al., 2014). The 6 species in Korea are *Brama japonica* Hilgendorf, 1878, *Brama orcini* Cuvier, 1831, *Pteraclis aesticola* (Jordan & Snyder, 1901), *Pterycombus petersii* (Hilgendorf, 1878), *Taractichthys steindachneri* (Döderlein, 1883), and *Taractes asper* Lowe, 1843. Of these, *B. orcini* was the last to be reported as a new member of the Korean fish fauna (Lee et al., 2014).

We collected 10 specimens that looked like *Brama japonica*, in the family Bramidae, from waters off Jeju Island, Busan, and Gangneung, Korea, which we identified as *Brama dussumieri* Cuvier, 1831, based on the taxonomic criteria of Mead (1972), who previously described the morphological characteristics of 6 of 7 genera and 18 of 22 species worldwide. In this study, we also used molecular identification

methods, such as DNA barcoding, to clarify the taxonomic status of cosmopolitan species, such as *B. dussumieri*. This paper presents the first morphological description of *B. dussumieri* from Korea, and elucidates allometric variations occurring among local populations. We propose the new Korean name “Wae-sae-da-rae” for *B. dussumieri* in Korea.

Materials and Methods

Ten specimens of *Brama dussumieri* were collected from waters off Jeju Island, Busan, by purse seine net, and off Gangneung, by set net, during 2013-2014 (Fig. 1). Counts and measurements followed Hubbs and Lagler (2004), with measurements performed to the nearest 0.1 mm using Vernier calipers. Vertebrae were counted from radiographs (Softex HA-100, Japan). The specimens are deposited at Pukyong National University (PKU).

 © 2015 The Korean Society of Fisheries and Aquatic Science

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/3.0/>) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Received 14 May 2015; Revised 25 July 2015

Accepted 27 July 2015

*Corresponding Author

E-mail: taengko@hanmail.net

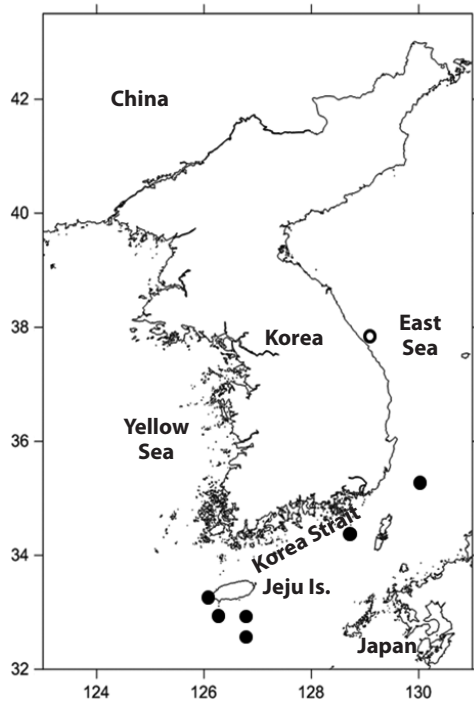


Fig. 1. Map showing the locations of sampling sites of *Brama dussumieri* collected by purse seine (●) and by set net (○).

Genomic DNA was extracted from muscle tissue using Chelex 100 resin (Bio-Rad, USA), and polymerase chain reaction (PCR) was conducted using universal primer sets VF2 (5'-TCAACCAACCACAAAGACATTGGCAC-3') and FishR2 (5'-ACTTCAGGGTGACCGAAGAATCAGAA-3'), which amplify mitochondrial DNA (mtDNA) cytochrome c oxidase subunit I (COI) (Ward et al., 2005; Ivanova et al., 2007). The PCR was performed on a total volume of 30 μ L of sample, containing 5 μ L DNA template, 4 μ L dNTP, 5 μ L 10X buffer, 0.5 μ L Taq polymerase, 1 μ L reverse primer, 1 μ L forward primer, and distilled water. The PCR was conducted under the following conditions: initial denaturation for 1 min at 95°C, followed by 35 cycles of 1 min at 95°C for denaturation, 1 min at 50°C for annealing, and 1 min at 72°C for extension, with a final extension for 5 min at 72°C. The PCR products were purified using ExoSAP-IT (Biochemical Co., USA) and sequenced using an ABI PRISM Big Dye Terminator v3.1 Ready Reaction Cycle Sequence Kit (Applied Biosystems, USA) on an ABI3730xi DNA Analyzer (Applied Biosystems). The sequence was aligned using ClustalW (Thompson et al., 1994) in BioEdit (ver. 7) (Hall, 1999). A neighbor-joining (NJ) tree (Saitou and Nei, 1987) was constructed using the Kimura two-parameter model (Kimura, 1980) in MEGA 5 (Tamura et al., 2011).

Material examined: PKU 9301 and 9302, 2 specimens, 102.1-153.6 mm standard length (SL), Seogwipo-si, Jeju Island, Korea, 4 July 2013; PKU 9303 and 9304, 2 specimens, 148.7-157.1 mm SL, Seogwipo-si, Jeju Island, Korea, 8 July

2013; PKU 9635, 1 specimen, 162.1 mm SL, Seogwipo-si, Jeju Island, Korea, 13 August 2013; PKU 9884, 1 specimen, 181.1 mm SL, Gangneung-si, Gangwon-do, Korea, 25 September 2013; PKU 10126, 1 specimen, 199.9 mm SL, Geoje-do, Gyeongsangnam-do, Korea, 26 December 2013; PKU 10130, 1 specimen, 200 mm SL, Busan, Korea, 2 January 2014; PKU 10374 and 10375, 2 specimens, 191.3-192.0 mm SL, Seogwipo-si, Jeju Island, Korea, 12 March 2014.

Comparative material examined: *Brama dussumieri*: FAKU 133306, 100.1 mm SL, Kawajiri-misaki, Yamaguchi, Japan, July 2010; FAKU 134950, 137.5 mm SL, Otomi, Fukui, Japan, July 2012. *Brama japonica*: PKU562, Wan-do, Korea, September 2008; PKU8590, Jeju Island, Korea, April 2013. *Brama orcini*: PKU 10115, Jeju Island, Korea, December 2013.

Results and Discussion

Brama dussumieri Cuvier, 1831

(New Korean name: Wae-sae-da-rae) (Fig. 2)

Brama dussumieri Cuvier, 1831: 294 (type locality: eastern Indian Ocean); Mead, 1972: 55 (Indo-Pacific Ocean, Atlantic Ocean); Masuda et al., 1984: 437 (Ryukyu Island and Ogasawara Island, Japan); Robins and Ray, 1986: 354 (USA); Hataoka and Kai, 2013: 908 (Japan).

Brama agassizi Poey, 1860: 204 (type locality: Cuba).

Brama leucotaenia Fowler, 1938: 44 (type locality: Basilan Island, Sulu Archipelago).

Description

Dorsal fin rays, 32-34; pectoral fin rays, 19-20; anal fin rays, 26-29; lateral line scales, 58-64; gill rakers, 13-15; vertebrae, 39-42 (Table 1).

Proportion of measurements as a percentage of SL: head length 24.4-27.1; predorsal length 36.7-40.5; length of dorsal fin base 55.7-60.1; snout to pectoral fin 25.8-27.8; snout to pelvic fin 32.8-38.6; snout to anal fin 50.5-55.4; fork length 108.0-112.9; body depth 45.7-50.7; body width 11.1-13.0; upper caudal fin length 33.6-46.2; lower caudal fin length, 25.3-33.9.

Body ovate, strongly compressed; head large (24.4-27.1% SL), forehead feebly arched; snout short (5.5-7.3% SL), slightly blunt, mouth strongly oblique; interorbital region convex, anterior nostril round and located at anterior tip of snout, posterior nostril is a slit midway between anterior nostril and orbit; eye elliptical in shape, with horizontal axis shorter than vertical axis; branchiostegal ray number, 7; membrane completely covered by opercular flap; posterior margin of upper jaw extending slightly beyond line vertical to the middle of the pupil; upper jaw protruding more than lower jaw; one row of small conical teeth in upper jaw, one row or two rows of



Fig. 2. Specimen of *Brama dussumieri*, PKU 9302, 154.6 mm standard length (SL), Seogwipo-si, Jeju Island, Korea.

Table 1. Comparison of counts and measurements for *Brama dussumieri* and *Brama japonica*

	<i>B. dussumieri</i>			<i>B. japonica</i>	
	Present study		Cuvier (1831)	Mead (1972)	
	Korea	Japan			Lee et al. (2014)
Number of specimens	10	2		24	2
Standard length (mm)	102.1–200.0	100.1–137.5		20.6–158.0	349.0–359.0
Counts					
Dorsal fin rays	32–34	33–34	3/29	33–35	34–35
Anal fin rays	26–29	27–28	3/21	26–29	28
Pectoral fin rays	19–20	19	19	19–22	21–22
Lateral line scales	58–64	58–59		57–65	71–75
Gill rakers	13–15	-		13–15	19–20
Vertebrae	39–42	40		40–43	40–41
In % of SL					
Predorsal length	36.7–40.5	39.1–39.3		36.1–50.0	36.6–37.0
Prepectoral length	25.8–27.8	27.8–28.2		28.2–32.5	27.5–28.6
Prepelvic length	32.8–38.6	39.5–40.3		38.0–45.3	36.6–38.1
Preanal length	50.5–55.4	49.2–51.1		39.5–47.8	46.6–47.0
Length of dorsal fin base	55.7–60.1	55.7–57.2		49.6–59.8	59.4–60.0
Fork length	108.0–112.9	108.7–110.8		111.5–126.9	110.9–115.6
Body depth	45.7–50.7	49.7–51.3		47.7–62.7	47.0–47.4
Head length	24.4–27.1	26.7–27.6		26.6–35.0	25.5–27.0
Body width	11.1–13.0	11.5–12.9		9.9–18.9	12.0–12.7
Head width	11.0–12.6	12.0–12.1		11.3–20.8	12.4–12.6
Snout length	5.5–7.3	6.6–7.3		5.6–8.3	7.3–7.6
Upper jaw length	12.6–13.6	13.7–14.5		13.8–19.9	12.3–13.4
Eye diameter, horizontal	6.4–8.5	6.3–7.3		7.1–14.5	5.7–6.8
Eye diameter, greatest	6.7–9.7	7.6–7.7		8.1–14.5	5.9–7.0
Pectoral fin length	33.2–40.3	32.6–36.7		30.8–40.8	36.5–41.0
Pelvic fin length	8.6–12.5	8.6–11.4		12.0–30.4	8.4
Upper caudal fin length	33.6–46.2	32.4–60.8		35.6–65.4	29.0–29.8
Lower caudal fin length	25.3–33.9	26.9–37.2		32.2–40.2	29.7–30.8
Origin of pectoral fin to insertion of pelvic fin	9.4–12.0	10.8–11.1		6.6–11.7	9.6–9.9

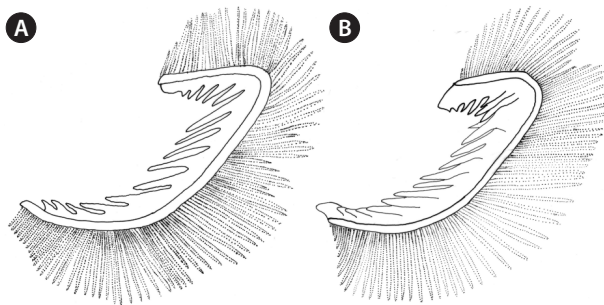


Fig. 3. (A) Gill rakers of *Brama dussumieri*, PKU 10375. (B) Gill rakers of *Brama japonica*, PKU 8590.

teeth in lower jaw, some mid-section teeth markedly large and recurved; dorsal fin originating slightly posterior to base of pectoral fin, reaching anterior caudal peduncle; pectoral fin starts under edge of opercle and reaches to mid body; pelvic fin short, originating on a vertical line slightly posterior to the origin of the pectoral fin; caudal fin strongly forked, length of upper lobe (32.3-46.2% SL) longer than that of lower lobe (25.3-33.9% SL); body and head mostly covered with oblong ctenoid scales; dorsal and anal fins covered with large oblong ctenoid scales.

Color when fresh. Head and body silvery, but slightly darker dorsally; pectoral and pelvic fins translucent; dorsal and anal fin dark.

Color after fixation. Head and body mainly grayish brown, but margin of upper jaw, inner pectoral fin base, and orbital rim black; fin color same as when fresh.

Distribution

Tropical regions of all oceans (Mead, 1972), Ryukyu Is. and Ogasawara Is., Japan (Hatooka and Kai, 2013), and waters off Jeju Island, Busan, and Gangneung, Korea (present study).

Remarks

The specimens in the present study were identified as belonging to the genus *Brama*, based on the following morphological characteristics: dorsal fin originating behind the head, over base of pectoral fin, with most elements of the dorsal and anal fins branched, both fins moderately stiff, and with fins erect and covered with ctenoid scales (Mead, 1972). Our specimens were very comparable to those described in other references (Mead, 1972; Hatooka and Kai, 2013), in terms of most counts and measurements. The specimens were identified as belonging to *B. dussumieri*, based on numbers of gill rakers (13-15) (Fig. 3, Table 1, 2), vertebrae (39-42) (Table 3), lateral line scales (58-64) (Table 4), and the distance between the origin of the pectoral fin base and the insertion of the pelvic fin base (<12% SL). However, the specimens were different from those in other references based on prepectoral length, preanal length, and upper jaw length (Table 1); these differences may represent local variations, as mtDNA COI sequences were well matched among local populations. We compared a 567-base pair mtDNA COI sequence in Korean *B. dussumieri* with that of *B. dussumieri* from distant areas (USA, India, and Japan). The sequences in 10 specimens from this study corresponded well with the sequences in specimens from the USA, India, and Japan (genetic distance, $d = 0.000-0.018$), but differed dramatically from sequences in Korean *B. japonica* ($d = 0.154-0.168$) (Fig. 4). Korean and Japanese *B. dussumieri* differed from congeneric species in the western and eastern Atlantic and East Pacific Oceans in length of the pelvic fin and head width. The specimens from Korea and Japan exhibit a shorter pelvic fin and narrower head width than those from the Atlantic Ocean and East Pacific Ocean (Fig. 5; Mead, 1972); also representing local variation. *Brama dussumieri* is most similar to *B. japonica* and *B. orcini*; however, the three species are easily distinguished by the number

Table 2. Number of gill rakers in *Brama dussumieri*, *Brama japonica*, and *Brama orcini*

		Gill rakers							
		13	14	15	16	17	18	19	20
<i>B. dussumieri</i>	Present study (Korea)	1	4	5	-	-	-	-	-
<i>B. japonica</i>	Present study (Korea)	-	-	-	-	-	-	1	1
<i>B. orcini</i>	Present study (Korea)	-	-	-	1	-	-	-	-

Table 3. Number of vertebrae in *Brama dussumieri*, *Brama japonica*, and *Brama orcini*

		Vertebrae						
		37	38	39	40	41	42	43
<i>B. dussumieri</i>	Present study (Korea)	-	-	1	4	3	1	-
	Present study (Japan)	-	-	-	2	-	-	-
	Mead (1972)	-	-	-	3	13	10	1
<i>B. japonica</i>	Present study (Korea)	-	-	-	1	1	-	-
<i>B. orcini</i>	Present study (Korea)	1	-	-	-	-	-	-

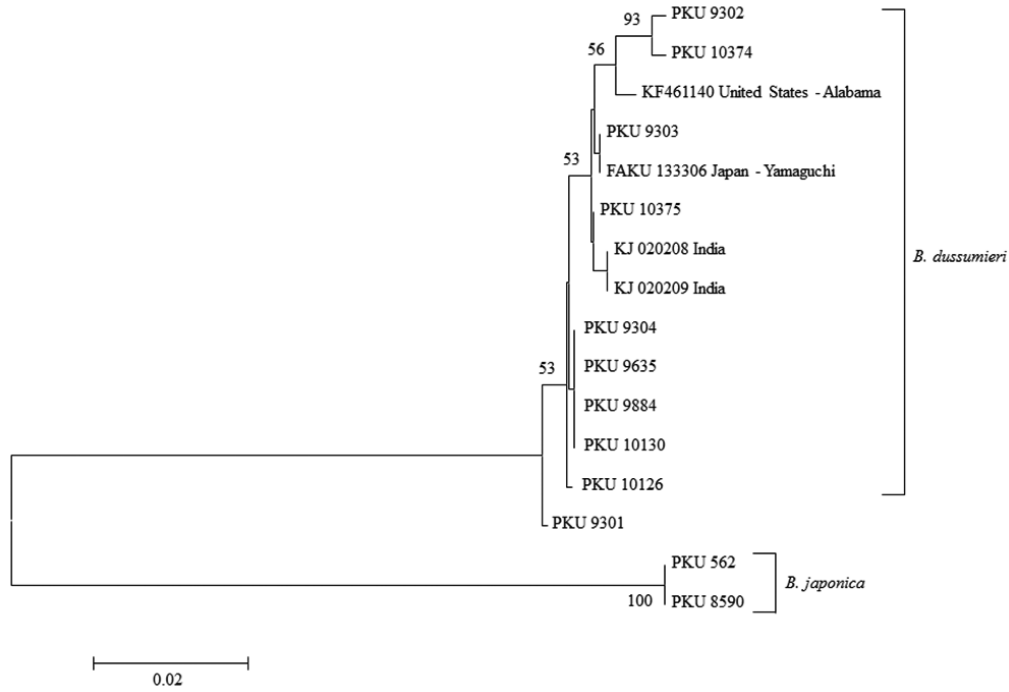


Fig. 4. Neighbor-joining tree for *Brama dussumieri* and *Brama japonica* specimens, constructed from a 567-base pair mitochondrial DNA COI sequence. Numbers at branches indicate the bootstrap probabilities in 1000 bootstrap replications. Scale bar indicates a genetic distance (d) of 0.02.

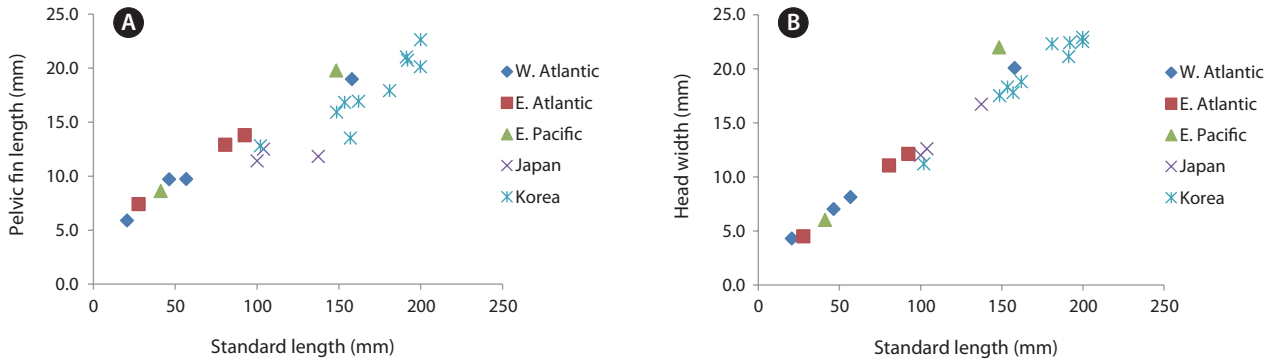


Fig. 5. (A) Relationship standard length (SL) and pelvic fin length in *Brama dussumieri*. (B) Relationship standard length (SL) and head width in *Brama dussumieri*.

Table 4. Number of lateral line scales in *Brama dussumieri*, *Brama japonica*, and *Brama orcini*

		Lateral line scales																					
		54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
<i>B. dussumieri</i>	Present study (Korea)	-	-	-	-	1	2	-	2	1	3	1	-	-	-	-	-	-	-	-	-	-	-
	Present study (Japan)	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>B. japonica</i>	Present study (Korea)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
<i>B. orcini</i>	Present study (Korea)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

of gill rakers (13-15 in *B. dussumieri* vs. 17-20 in *B. japonica* vs. 12-16 in *B. orcini*), number of lateral line scales (57-65 in *B. dussumieri* vs. 65-75 in *B. japonica* vs. 52-54 in *B. orcini*), and distance between the origin of the pectoral fin base and the insertion of the pelvic fin base (< 12% SL in *B. dussumieri* and *B. japonica* vs. > 12% SL in *B. orcini*) (Mead, 1972; Hatooka and Kai, 2013). We propose the new Korean name “Wae-sae-da-rae” for *B. dussumieri*, because of its relatively small size (maximum length: 22.5 cm SL; Pavlov, 1991) as compared to that of congeneric species.

Acknowledgments

The authors are grateful to anonymous reviewers for valuable advice and suggestions for improvement of the paper. We are deeply indebted to Dr. Y. Kai (FAKU) for his donating the tissue sample of the comparative species. This research was supported by the project on Institute of Marine Bio-resources of Marine-Bio Technology Programme under the Ministry of Oceans and Fisheries, Korea.

References

- Cuvier G and Valenciennes A. 1831. Histoire naturelle des poissons. Tome septième. Livre septième. Des Squamipennes. Livre huitième. Des poissons à pharyngiens labyrinthiformes. F. G. Levrault, Paris, FR.
- Fowler HW. 1938. Proceedings of the United States National Museum v. 85:44, Fig. 15
- Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl Acids Symp Ser 41, 95-98.
- Hatooka K and Kai Y. 2013. Bramidae. In: Fishes of Japan with pictorial keys to the species. 3rd ed. Nakabo T, ed. Tokai Univ Press, Tokyo, Japan.
- Hilgendorf FM. 1878. Über das Vorkommen einer Brama-Art und einer neuen Fischgattung Centropholis aus der Nachbarschaft des Genus Brama in den japanischen Meeren. Sitzungsberichte der Gesellschaft Naturforschender Freunde zu Berlin 15, 1-2.
- Hubbs CL and Lagler KF. 2004. Fishes of the Great Lakes Region. Revised ed. University of Michigan Press, Ann Arbor, MI, USA.
- Ivanova NV, Zemlak TS, Hanner RH and Hebert PDN. 2007. Universal primer cocktails for fish DNA barcoding. Mol Ecol Notes 7, 544-548.
- Jordan DS and Snyder JO. 1901. Descriptions of nine new species of fishes contained in museums of Japan. J Coll Sci Imperial Univ Tokyo 15, 301-311.
- Kim BJ. 2011. Fish species of Korea. In: National List of Species of Korea: Vertebrates. National Institution of Biological Resources, ed. National Institution of Biological Resources, Incheon, KR.
- Kim BJ, Kim JK, Ryu JH and Park JT. 2012. First reliable record of the sickle pomfret, *Taractichthys steindachneri* (Bramidae: Perciformes) from Korea. Korean J Ichthyol 20, 230-233.
- Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol 16, 111-120.
- Lee WJ, Kim JK and Kai Y. 2014. New record of the bigtooth pomfret, *Brama orcini* (Pisces: Bramidae) from Korea. Fish Aquat Sci 17, 497-501.
- Lowe RT. 1843. Notices of fishes newly observed or discovered in Madeira during the years 1840, 1841, and 1842. Proc Zool Soc Lond 1843, 81-95.
- Masuda H, Amaoka K, Araga C, Uyeno T and Yoshino T. 1984. The fishes of the Japanese Archipelago. Tokai Univ Press, Tokyo, JP.
- Mead GW. 1972. Bramidae. Dana Report 81, 1-166.
- Nelson JS. 2006. Fishes of the world. 4th ed. John Wiley and Sons Inc., NJ, USA.
- Pavlov YP. 1991. Information on morphometrics and ecology of pomfrets of the genus *Brama* inhabiting the southeastern Pacific Ocean. J Ichthyol 31, 120-123.
- Poey F. 1858. Memorias sobre la historia natural de la Isla de Cuba 2, 1-96.
- Robins CR and Ray GC. 1986. A field guide to Atlantic coast fishes of North America. Houghton Mifflin Company, Boston, USA.
- Saitou N. and Nei M. 1987. The Neighbor-Joining Method – a new method for reconstructing phylogenetic trees. Mol Biol Evol 4, 406-425.
- Steindachner F. and Döderlein L. 1883. Beiträge zur Kenntniss der Fische Japan's. (I.). Denkschriften der Kaiserlichen Akademie der Wissenschaften in Wien, Mathematisch-Naturwissenschaftliche Classe 47, 211-242.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M and Kumar S. 2011. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28, 2731-2739.
- Thompson JD, Higgins DG and Gibson TJ. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucl Acids Res 22, 4673-4680.
- Ward RD, Zemlak TC, Innes BH, Last PR and Hebert PDN. 2005. DNA barcoding Australia's fish species. Phil Trans Biol Sci 360, 1847-1857.