

# New Record of the Bigtooth Pomfret *Brama orcini* (Pisces: Bramidae) from Korea

Woo Jun Lee<sup>1</sup>, Jin-Koo Kim<sup>1\*</sup> and Yoshiaki Kai<sup>2</sup>

<sup>1</sup>Department of Marine Biology, Pukyong National University, Busan, 608-737, Korea

<sup>2</sup>Maizuru Fisheries, Research Station, Field Science Education and Research Center, Kyoto University, Maizuru, Kyoto 625-0086, Japan

## Abstract

A single specimen of *Brama orcini* (267.0 mm standard length, SL), belonging to the family Bramidae, was collected by purse seine from Jeju Strait, Korea, in December 2013. The specimen is characterized by having 16 gill rakers, 54 lateral line scales, and 36 vertebrae. *B. orcini* is distinguished from the most similar species, *Brama japonica*, by the number of lateral line scales (52-54 in *B. orcini* vs. 65-75 in *B. japonica*). We propose a new Korean name “Keun-bi-neul-sae-da-rae” for *B. orcini*.

**Key words:** *Brama orcini*, *Brama dussumieri*, *Brama japonica*, Bramidae, mtDNA COI, Korean fish fauna, New record

## 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 5 species in Korea (Kim et al., 2005; Kim et al., 2012). The 5 species in Korea are *Brama japonica* Hilgendorf, 1878, *Pteraclis aesticola* (Jordan & Snyder, 1901), *Pterycombus petersii* (Hilgendorf, 1878), *Taractichthys steindachneri* (Döderlein, 1883), and *Taractes asper* Lowe, 1843. The genus *Brama*, family Bramidae, comprises 8 species worldwide (Mead, 1972; Pavlov, 1991; Moteki, 1995), but only one species, *B. japonica*, is recorded in Korea (Kim et al., 2012). However, the species of *Brama* are difficult to distinguish by external morphology (Mead, 1972). In December 2013, a single specimen of *Brama* was collected from Jeju Strait, Korea, and was identified as *Brama orcini* by both morphological and molecular methods. In this study, we describe the species and add it as a new member of the Korean fish fauna.

## Materials and Methods

A single specimen of *Brama orcini* was collected by a purse seine in Jeju Strait, Korea on 9 December 2013. The following description was made on the basis of this specimen. Counts and measurements followed Hubbs and Lagler (2004) by a vernier caliper to the nearest 0.1 mm. The vertebrae were counted from a radiograph (Softex HA-100, Japan). The specimen was deposited at Pukyong National University (PKU), Korea. Molecular identification of this specimen was performed by a universal primer set VF2 (5'-TCAACCAACCACAAAGA-CATTGGCAC-3') and FishR2 (5'-ACTTCAGGGTGAC-CGAAGAATCAGAA-3') primers, which amplify the mitochondrial DNA (mtDNA) cytochrome c oxidase subunit I (COI) (Ward et al., 2005; Ivanova et al., 2007). Genomic DNA was extracted from muscle tissue using Chelex 100 resin (Bio-Rad, USA). A polymerase chain reaction (PCR) was performed in a total volume 50 µL containing DNA template 5 µL, dNTP 4 µL, 10X buffer 5 µL, Taq polymerase 0.5 µL, reverse primer 1 µL, forward primer 1 µL, and distilled water. PCR was conducted under the following conditions: initial de-

 © 2014 The Korean Society of Fisheries and Aquatic Science

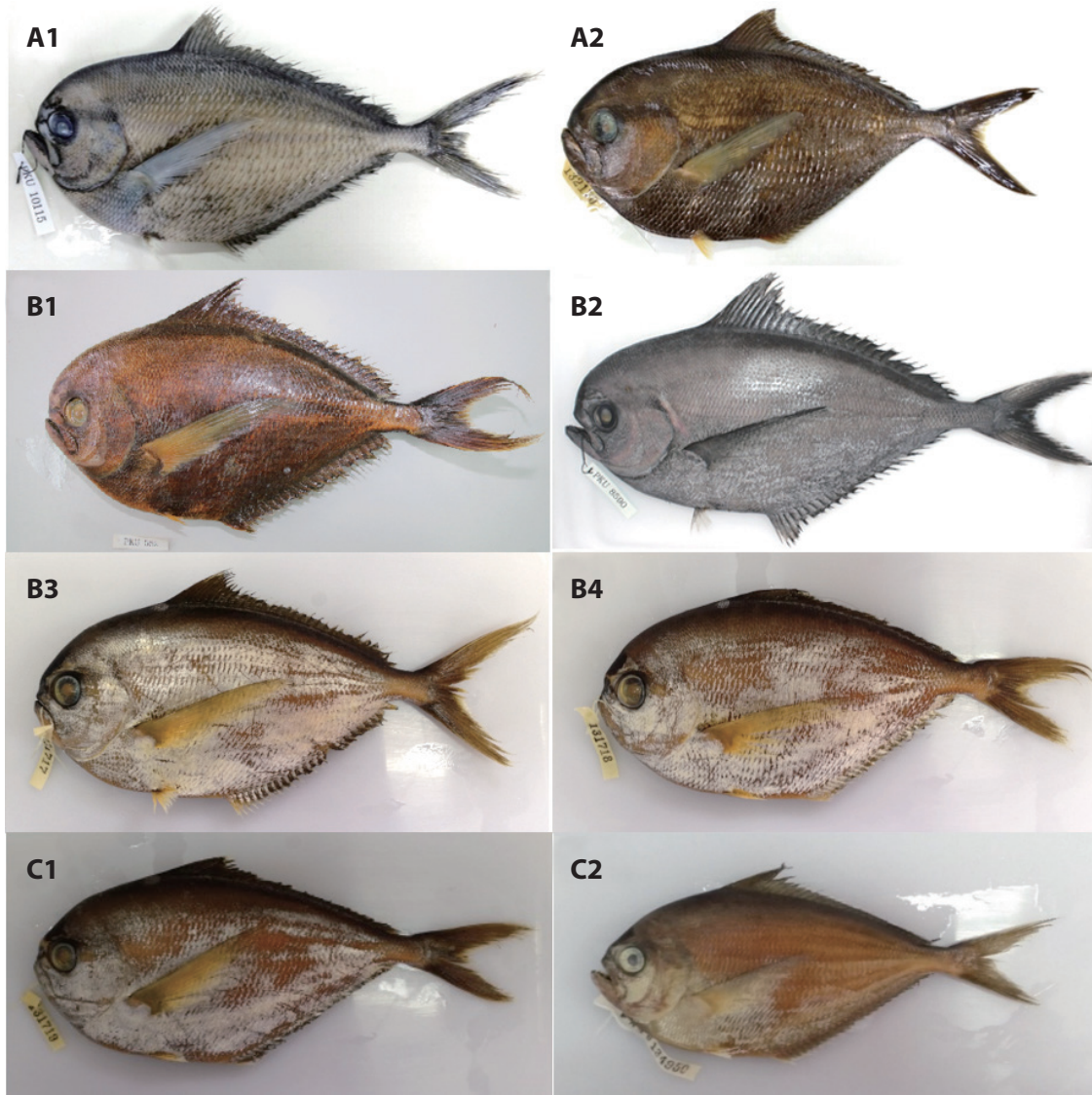
This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/3.0/>) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly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

Received 20 August 2014; Revised 04 September 2014

Accepted 05 September 2014

\*Corresponding Author

E-mail: taengko@hanmail.net



**Fig. 1.** Lateral view of three *Brama* species. (A1) *Brama orcini*, 267.0 mm standard length (SL), PKU 10115; (A2) *Brama orcini*, 188.3 mm SL, FAKU 132170; (B1) *Brama japonica*, 462.0 mm SL, PKU 562; (B2) *Brama japonica*, 446.0 mm SL, PKU 8590; (B3) *Brama japonica*, 198.6 mm SL, FAKU 131717; (B4) *Brama japonica*, 191.4 mm SL, FAKU 131718; (C1) *Brama dussumieri*, 100.1 mm SL, FAKU 133306; (C2) *Brama dussumieri* 137.5 mm SL, FAKU 134950.

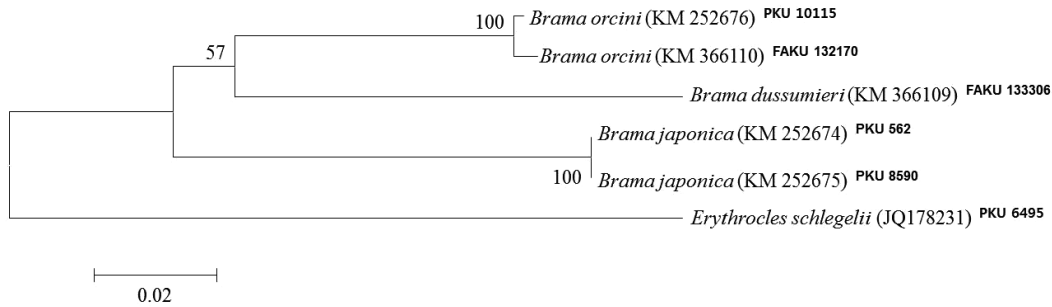
naturation for 1 min at 95°C, followed by 35 cycles of 1 min at 95°C for denaturation, 1 min at 50°C for annealing, and 1 min at 72°C for extension, with a final extension at 72°C for 5 min. The PCR products were purified using ExoSAP-IT (Biochemical Co., USA). The PCR products were sequenced with the ABI PRISM BigDye Terminator v3.1 Ready Reaction Cycle Sequence Kit (Applied Biosystems, USA) on an ABI3730xi DNA Analyzer (Applied Biosystems). The sequence was aligned with ClustalW (Thompson et al., 1994) in BioEdit (ver. 7) (Hall, 1999). A neighbor-joining (NJ) tree (Saitou and Nei 1987) was constructed by the Kimura two-parameter model (Kimura, 1980) and in MEGA 5 (Tamura et al., 2011).

## Results and Discussion

### *Brama orcini* Cuvier, 1831

(New Korean name: Keun-bi-neul-sae-da-rae) (Fig. 1)

*Brama orcini* Cuvier, 1831: 295 (type locality: eastern Indian Ocean); Mead, 1972: 72 (Indo-Pacific, East Pacific); Eschmeyer et al., 1983: 336 (USA); Masuda et al., 1984: 159 (Ryukyu Is. and Ogasawara Is., Japan); Smith, 1986: 634 (South Africa); Anderson et al., 1998: 24 (Maldives); Mundy, 2005: 375 (Hawaiian Archipelago); Hatooka and Kai, 2013: 908 (Sagami Bay, Ryukyu Is. and Ogasawara Is., Japan).



**Fig. 2.** Neighbor-joining tree constructed by the mitochondrial DNA COI sequences for three *Brama* species, with one outgroup *Erythrocles schlegelii*. Numbers at branches indicate bootstrap probabilities in 1,000 bootstrap replications. Bar indicates genetic distance of 0.02.

## Material examined

PKU10115, 267.0 mm standard length (SL), collected by a purse seine, Jeju Strait, (126°46'E, 33°53'N), 9 December 2013 (Fig. 1, A1).

## Comparative material examined

***Brama orcini*:** FAKU 132170, 188.3 mm SL, Sagami Bay, Japan (Fig. 1, A2), ***Brama japonica*:** PKU562, 395 mm SL, Wan-do, September, 2008 (Fig. 1, B1); PKU8590, 349.0 mm SL, Jeju Island, April, 2013 (Fig. 1, B2); FAKU 131717-131719, 191.4-198.6 mm SL, Nohara, Maizuru, Japan (Fig. 1, B3-4), ***Brama dussumieri*:** FAKU 133306, 100.1 mm SL, Kawajiri-misaki, Yamaguchi, Japan, July, 2010 (Fig. 1, C1); FAKU 134950, 137.5 mm SL, Otomi, Fukui, Japan (Fig. 1, C2).

## Description

Dorsal fin rays 34; pectoral fin rays 20; anal fin rays 29; lateral line scales 54; gill rakers 16; vertebrae 36 (Table 1).

Body ovate, strongly compressed; body depth very high (51.2% in SL); head large, forehead slightly arched; snout short (7.6% in SL), slightly blunt; mouth strongly oblique, 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 the upper jaw, irregular rows of teeth in the lower jaw, some mid section of teeth markedly large; eyes large (7.0% in SL), oblique and oval shaped; interorbital region convex; one pair of nostrils, round and located at anterior tip of snout; dorsal fin starts above posterior to origin of pectoral fin, end above the slightly anterior caudal peduncle; head and body completely covered with large oblong ctenoid scales; dorsal and anal fins covered with small scales; pectoral fin starts under edge of opercle and reaches to mid body; pelvic fin relatively short, and originating on vertical line posterior to the origin of the pectoral fin; caudal fin strongly forked, length of upper lobe (36.6% in SL)

greater than that of lower lobe (31.6% in SL).

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

**Color after fixation.** Head and body grayish yellow, but black dorsally; fin color same as when fresh.

## Distribution

Indo-Pacific, and East Pacific oceans, southeast Africa between 30°N and 30°S (Mead, 1972; Last and Moteki, 2001), Sagami Bay (Numazu, Shizuoka), Ryukyu Is. and Ogasawara Is., Japan (Hatooka and Kai, 2013) and Jeju Strait, Korea (present study).

## Remarks

The present specimen collected from Jeju Strait, belongs to the genus *Brama*, dorsal fin originating behind head, over base of pectoral fin, the most of the elements in dorsal and anal fin branched, and both fins moderately stiff, erect and covered with ctenoid scales (Mead, 1972). The present specimen agreed well with the description of Mead (1972), who investigated the holotype and non-type specimens of *B. orcini*, in the numbers of lateral line scales (54), and gill rakers (16), and the distance between the origin of the pectoral fin base and the insertion of the pelvic fin base exceeding 12% SL. Other counts and measurements were consistent with those of a previous study of this species (Mead, 1972; Hatooka and Kai, 2013), except for the number of vertebrae: 36 in the present specimen vs. 38-40 in Mead (1972) vs. 37-40 in Hatooka and Kai (2013). The further study is required to reveal whether morphological difference between Korean and Japanese specimens of *B. orcini* is regional variations. Also, *B. orcini* is distinguished from the congeneric species *B. japonica* and *B. dussumieri* by the number of gill rakers (12-16 in *B. orcini* vs. 17-20 in *B. japonica* vs. 13-15 in *B. dussumieri*), the number of lateral line scales (52-54 in *B. orcini* vs. 65-75 in *B. japonica* vs. 57-65 in *B. dussumieri*), the distance between the

origin of the pectoral fin base and the insertion of the pelvic fin base, expressed in terms of SL (greater than 12% in *B. orcini* vs. less than 12% in *B. japonica* and *B. dussumieri*) and in head length (HL) (greater than 42% in *B. orcini* vs. less than 42% in *B. japonica* and *B. dussumieri*), and shape of the forehead arch (more strongly arched in *B. japonica* than in *B. orcini*) (Mead, 1972; Hatooka and Kai, 2013; Present study) (Fig. 1 A1-2, B1-4). To identify the species more accurately, we analyzed a total of 557 base pairs of the mtDNA COI sequence. The mtDNA COI sequence in the Korean *B. orcini* corresponded well with that of the Japanese *B. orcini* (genetic distance,  $d = 0.005$ ), and differed considerably from that of the Korean

*B. japonica* ( $d = 0.118$ ) and the Japanese *B. dussumieri* ( $d = 0.120$ ). Accordingly, we identified our specimen as *B. orcini*, based on both morphological and molecular characteristics. We propose the new Korean name “Keun-bi-neul-sae-da-rae” for *B. orcini*, because the species has relatively large scales as compared with those of congeneric species.

## Acknowledgments

This research was supported by the Marine Biodiversity Institute of Korea (MABIK).

**Table 1.** Comparison of counts and measurements of *Brama orcini* and the comparative species

	<i>Brama orcini</i>				<i>Brama japonica</i>		<i>Brama dussumieri</i>
	Present study		Mead (1972)		Present study		Present study
	PKU 10115	FAKU 132170	Holotype		PKU 562, 8590	FAKU 131717, 131718, 131719	FAKU 133306, 134950
Number of specimens	1	1	1	20	2	3	2
Standard length (mm)	267.0	188.0	34.4	30.0-298.0	349.0-359.0	191.4-198.6	100.1-137.5
Counts							
Dorsal fin rays	34	34	34	33-36	34-35	32-34	33-34
Anal fin rays	29	28	28	28-30	28	27	27-28
Pectoral fin rays	20	19	21	20-22	21-22	19	19
Lateral line scales	54	54	-	52-54	40-41	66-67	58-59
Gill rakers	16	-	16	12-16	19-20	-	-
Vertebrae	36	37	34	37-40	40-41	40-41	40
In % of SL							
Predorsal length	38.2	40.5	48.8	36.8-39.9	36.6-37.0	38.3-39.8	39.1-39.3
Length of dorsal fin base	58.2	53.8	52.6	49.3-58.6	59.4-60.0	58.1-58.4	55.7-57.2
Snout to pectoral fin	28.2	28.5	32.3	28.2-35.0	27.5-28.6	27.1	27.8-28.2
Snout to pelvic fin	39.8	41.4	45.6	38.2-50.8	36.6-38.1	38.3-36.9	39.5-40.3
Snout to anal fin	55.9	47.4	62.8	44.8-50.0	46.6-47.0	53.5-60.6	49.2-51.1
Fork length	109.6	109.5	120.9	110.0-125.0	110.9-115.6	110.1-110.7	108.7-110.8
Body depth	51.2	50.1	68.0	47.8-68.3	47.0-47.4	46.9-47.3	49.7-51.3
Head length	26.2	28.5	33.3	25.5-33.3	25.5-27.0	25.1-26.1	26.7-27.6
Body width	11.9	11.1	16.3	9.7-14.1	12.0-12.7	13.3-13.6	11.5-12.9
Head width	10.7	12.3	16.3	10.9-17.8	12.4-12.6	12.2	26.7-27.6
Snout length	7.6	6.9	-	5.6-8.2	7.3-7.6	7.0-7.1	6.6-7.3
Upper jaw length	13.6	14.9	17.2	13.4-17.9	12.3-13.4	13.1-13.6	13.7-14.5
Eye diameter, horizontal	6.0	6.5	11.3	6.4-12.5	5.7-6.8	6.7	6.3-7.3
Eye diameter, greatest	7.0	7.3	11.3	7.2-12.5	5.9-7.0	7.6-7.8	7.6-7.7
Upper caudal fin length	36.6	28.4	-	32.0-42.8	29.0-29.8	32.6-33.4	32.4-60.8
Lower caudal fin length	31.6	31.4	-	30.2-36.0	29.7-30.8	22.2-30.1	26.9-37.2
Origin of pectoral fin to insertion of pelvic fin	12.5	12.4	16.0	13.0-16.3	9.6-9.9	9.9-10.3	10.8-11.1
In % of HL							
Origin of pectoral fin to insertion of pelvic fin	47.7	43.5	-	35.5	38.9	38.1-41.2	40.1-40.4



## References

- Anderson RC, Randall JE and Kuitert RH. 1998. Additions to the fish fauna of the Maldive Islands. Part 2: New records of fishes from the Maldive Islands, with notes on other species. *Ichthyol Bull Smith Inst Ichthyol* 67, 20-32.
- 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.
- Eschmeyer WN, Herald ES, Hammann H. 1983. Pacific Coast Fishes. Houghton Mifflin Co, Boston, MA, USA.
- 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, JP.
- 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.
- Kim IS, Choi Y, Lee CL, Lee YJ, Kim BJ and Kim JH. 2005. Illustrated Book of Korean Fishes. Kyo-Hak Publishing Co., Seoul, KR.
- 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.
- Last PR and Moteki M. 2001. Bramidae. In: FAO Species Identification Guide for Fishery Purposes. The Living Marine Resources of the Western Central Pacific. Vol. 5. Bony fishes part 3 (Menidae to Pomacentridae). Carpenter KE and Niem VH, ed. FAO, Rome, 2824-2836.
- 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.
- Moteki M, Fujita K and Last PR. 1995. *Brama pauciradiata*, a new bramid fish from the seas off tropical Australia and the Central Pacific Ocean. *Japan J Ichthyol* 41, 421-427.
- Mundy BC. 2005. Checklist of the fishes of the Hawaiian Archipelago. *Bishop Mus Bull Zool* 6, 1-703.
- Nelson JS. 2006. Fishes of the World. 4th ed. John Wiley and Sons Inc., NJ, USA.
- Saitou N and Nei M. 1987. The Neighbor-Joining Method – a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4, 406-425.
- Smith MM. 1986. Bramidae. In: Smiths' Sea Fishes. Smith MM and Heemstra PC, eds. Johannesburg, S Afr.
- 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, Zemlac TC, Innes BH, Last PR and Hebert PDN. 2005. DNA barcoding Australia's fish species. *Phil Trans Biol Sci* 360, 1847-1857.