

Molecular and morphological evidence for the taxonomic status of a newly reported species of *Albula* (Albuliformes: Albulidae) from Korea and Taiwan

Hyuck Joon Kwun^a, Jin Koo Kim^{a*}, Ryu Doiuchi^b and Tetsuji Nakabo^c

^aDepartment of Marine Biology, Pukyong National University, Busan 608-737, Korea; ^bFisheries Experimental Station, Wakayama Prefectural Research Center of Agriculture, Forestry and Fisheries, Wakayama 649-3503, Japan; ^cThe Kyoto University Museum, Kyoto University, Kyoto 606-8501, Japan

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To clarify the taxonomic status of five specimens of Albula collected from Korea and Taiwan (Albula sp.), genetic differences among them and other congeneric species were investigated based on mitochondrial DNA cytochrome b sequences. All five specimens of Albula sp. showed identical haplotypes and strongly supported a monophyletic group on phylogenetic analysis. The genetic differences between Albula sp. and ten other species of Albula ranged from 0.100 to 0.164. These values were almost equal to or exceeded the interspecific differences among the latter ten species (0.038–0.206). Morphological comparisons of Albula sp. and another four Indo-Pacific species, A. argentea, A. glossodonta, A. oligolepis and A. virgata, are also presented. Albula sp. could be distinguished from the latter four species in their numbers of pored lateral-line scales, anal fin rays and vertebrae, as well as in several proportional measurements.

Keywords: Albula sp.; bonefish; morphology; mitochondrial DNA; cytochrome b

Introduction

Bonefishes genus Albula Scopoli 1777 (Albulidae: Albuliformes) are distributed globally in tropical and subtropical coastal areas (Hildebrand 1963; Pfeiler et al. 2006; Randall 2005; Nelson 2006). Although Albula had been considered to contain only two species, A. vulpes (Linnaeus, 1758) and A. nemoptera (Fowler, 1911), eight valid species are recognized worldwide. Among them, four species occur in the Indo-Pacific region, A. argentea (Forster in Bloch and Schneider 1801), A. glossodonta (Forsskål, 1775), A. oligolepis Hidaka, Iwatsuki and Randall 2008, and A. virgata (Jordan and Jordan, 1922) (Hidaka et al. 2004, 2008), whereas *A.esuncula* (Garman, 1899) and A. pacifica (Beebe, 1942) are known from the eastern Pacific, and A. nemoptera and A. vulpes from the western Atlantic (Smith 2002; Pfeiler 2008; Pfeiler et al. 2008). Two other species (Albula sp. A-B) have been proposed based on their genetic and distributional characteristics (Colborn et al. 2001; Bowen et al. 2008), their identities are, however, still alive.

In Korea, although Mori (1952) first recorded *A. vulpes* in a checklist of Korean fishes, Kim et al. (2005) regarded the species to be *A. neoguinaica* (Valenciennes in Cuvier and Valenciennes 1847). Kim et al. (2008) then documented the occurrence of a leptocephalus at Jeju Island and analysed its mitochondrial (mt) DNA cytochrome *b* gene (*cyt b*) sequence,

thus identifying the leptocephalus as A. forsteri (Valenciennes in Cuvier and Valenciennes 1847). In Japan, two bonefishes are known to date. A single species, given the scientific name A. vulpes by Matsubara (1955), has been recognized. Aizawa (2000) regarded the species as A. neoguinaica, whereas Hidaka et al. (2004) subsequently considered it to be A. forsteri. A. glossodonta has also been recorded for southern Japan by Hidaka et al. (2004). In China, Zhang (1984) reported a morphological description of A. vulpes from Fujian Province, but A. vulpes is currently known only from the western Atlantic, as noted above. In Taiwan, Shen et al. (1993) reported A. glossodonta, but no subsequent observations have been recorded. In recent years, Hidaka et al. (2008) confirmed A. argentea as valid, synonymizing both A. neoguinaica and A. forsteri with A. argentea, in their taxonomic review. However, Hidaka et al. (2008) did not recognize A. argentea in East Asia, regarding its distribution as restricted to the Philippines and southward. Therefore, the appropriate scientific identities of the species regarded as A. vulpes, A. neoguinaica, or A. forsteri in East Asia are currently unknown.

We collected five Albula specimens from the Northwestern Pacific (Korea and Taiwan). To clarify the taxonomic status of them, we investigated the genetic differences among them and with other species of Albula from throughout the world, on the basis of

^{*}Corresponding author. Email: taengko@pknu.ac.kr

Table 1. List of nucleotide samples in the genus Albula.

Species	Locality	Accession number	Voucher number PKU 3394			
Albula sp.ª	Korea	HM119396				
Albula sp. ^a	Taiwan	HM119397-119400	ASIZP0067114, ASIZP0067133 ASIZP0067192, ASIZP0067194			
Albula esuncula ^{c,e}	Panama	AF311760	ALB40			
	Mexico	EF602158	A8			
Albula forsteri ^b	Korea	EU555519	NIBR-P0000002382			
Albula glossodonta ³	Hawaii	AF311768, AF311769	ALB61, ALB62			
Albula nemoptera ^c	Brazil	AF311754, AF311755	ALB22, ALB23			
Albula oligolepis ^c	Indo-Pacific	AF311770, AF311773	ALB77, ALB88			
Albula pacifica ^d	Mexico	DQ272658, DQ272659	A15, A16			
Albula neoguinaica ^e	Fiji	AF311765	ALB54			
Albula virgata ^c	Hawaii	AF311764	ALB47			
Albula vulpes ^c	Caribbean	AF311753, AF311771	ALB1, ALB7			
Albula sp. A ^{c,e}	California	AF311758	ALB35			
	Mexico	EF602156	AL05			
Albula sp. B ^c	Atlantic	AF311751, AF311756	ALB10, ALB28			

^a Present study; ^b Kim et al. (2008); ^c Colborn et al. (2001); ^d Pfeiler et al. (2006); ^e Pfeiler et al. (2008).

their mtDNA cyt b sequences. We also compared the morphological characters of Albula sp. with those of four congeneric species from the Indo-Pacific region reported by Hidaka et al. (2004, 2008).

Materials and methods

Genomic DNAs were extracted from the muscle tissues of the fish using 10% Chelex 100 Resin (Bio-Rad, Hercules, CA). The polymerase chain reaction (PCR) was used to amplify the mitochondrial DNA cyt b gene using primers H14803 (5'-TGCTAGGGTTGTGTT-TAATT-3') (Pfeiler et al. 2006) and albula-L (5'-GTCT CCAAGAAGGTTAGG-3'). PCR was conducted on a

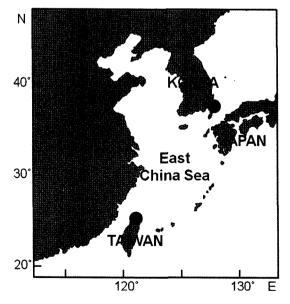


Figure 1. Sampling area (•) of Albula sp.

thermal cycler (ABI 2720 Thermal Cycler, Foster City, CA), with PCR solutions containing 5–10 µl of genomic DNA, 2.5 µl of 10X PCR buffer, 2 µl of 2.5 mM dNTPs, 1 µl of each primer, 0.2 µl of FR Tag DNA polymerase (Biomedic, Korea) and 25 µl of distilled water. The PCR proceeded under the following conditions: initial denaturation at 94°C for 3 min, 30 cycles of denaturation at 94°C for 1 min, annealing at 50°C for 1 min, and extension at 72°C for 1 min, and a final extension at 72°C for 10 min. The amplification products of the target DNA were checked with agarose gel electrophoresis. The samples were purified using the Corebio™ Duo-PCR Purification Kit (Core Bio System Co. Ltd, Korea). DNA was sequenced on an ABI 3730XL Sequencer (Applied Biosystems Inc., Foster City, CA) using the ABI PRISM® BigDye™ Terminator v3.0 Ready Reaction Cycle Sequencing Kit (Applied Biosystems Inc., Foster City, CA). The nucleotide sequence data reported here have been submitted to the DDBJ/EMBL/GenBank nucleotide sequence databases (accession numbers HM119396-HM119400). For the molecular comparisons, we obtained the mtDNA cyt b sequences of other Albula species (Table 1) and two outgroups (Elops saurus and Pterothrissus gissu) from the NCBI (National Center for Biological Information) database.

Mitochondrial DNA cyt b sequences were checked and aligned using BioEdit ver. 7 (Hall 1999), and the genetic distances were calculated according to the Kimura two-parameter model (Kimura 1980) using MEGA4 (Tamura et al. 2007). Phylogenetic trees were inferred with the neighbour-joining (NJ) and maximum-likelihood (ML) methods. NJ analysis was conducted with the Kimura two-parameter model and

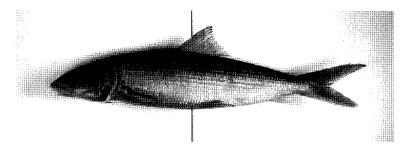


Figure 2. Albula sp., PKU3394, 350.1 mm SL, Gijang, Busan, Korea.

1000 bootstrap replications using MEGA4 (Tamura et al. 2007). ML analysis was conducted with the K81uf + I+G model, determined with Modeltest 3.7 (Posada and Crandall 1998; Posada and Buckley 2004),

with 100 bootstrap replications using PAUP 4.0b10 (Swofford 2002).

Counts were made according to Rivas and Warlen (1967) and measurements were made according to

Table 2. Meristic and morphometric characters of genus Albula.

	Albula sp.ª	Albula argentea ^b	Albula oligolepis ^b	Albula virgata ^b	Albula glossodonta ^c 28	
Number of specimens	5	30	36	39		
Standard length (mm)	62.8-350.1	49-308	73-589	85-322	65-530	
Counts						
Dorsal fin	18	17-18	17–19	17-18	17-18	
Pectoral fin	16–18 (17.6)	16–18	17-19	17 - 18	17-19	
Pelvic fin	10	10	10	10 - 11	9-10	
Anal fin	9	8	7–9	8	7-8	
Pored lateral line scales	77–80 (78.5, $n = 2$)	68-74	61–65	63-67	66-70	
Scales above lateral line	9 (n = 4)	8-9	7.5-8	9-10	8–9	
Scales below lateral line	6-7 (6.3, n=4)	5–6	6	6-6.5	5–6	
Predorsal scales	25 (n=1)	17-24	18-25	22-26	21-23	
Branchiostegal rays	13–15 (14.4)	12-15	12-15	13-14	12-14	
Gill rakers	16 (n = 1)	17-25	16-22	18-21	18-23	
Vertebrae	77–78 (77.4)	71–74	64–66	65-68	67-69	
Measurements in% SL						
Body depth	16.6-22.0 (19.1)	16-25	18-23	18-22	16-31	
Predorsal length	48.8-52.7 (50.7)	48-54	46-53	48-52	47-53	
Prepectoral length	29.4-33.6 (31.4)		******	_	_	
Prepelvic length	61.3-63.4 (62.4)	58-62	58-65	57-62	57-64	
Preanus length	73.1–75.3 (74.3)	71-74	68-76	68-74	67–74	
Depth of caudal peduncle	6.7–7.3 (6.9)	7–9	78	7–8	7–9	
Length of caudal peduncle	11.8–13.4 (12.7)	9-13	9-12	11-12	9-13	
Length of dorsal base	15.7–18.5 (16.8)	15-18	12-17	15-17	14 - 17	
Length of anal base	5.5-7.4 (6.5)	5-8	5-6	5-6	5-6	
Length of longest dorsal ray	16.9–18.9 (17.9)	17-19	14-19	17-20	17-22	
Length of longest anal ray	6.5–10.3 (9.0)	8-10	7-14	9-10	8-10	
Length of pectoral fin	16.4–17.2 (16.7)	15–18	14-17	16–18	15-19	
Length of pelvic fin	12.7–13.8 (13.3)	13-15	12-14	13–16	12-15	
Head length	28.8-35.8 (33.5)	28-32	28-32	26-31	28-30	
Snout length	11.9–12.7 (12.3)	10-12	11-13	10-12	9-13	
Postorbital length of the head	14.3–16.2 (15.1)	12–15	12–14	11-14	10–13	
Suborbital width	2.5-4.4 (3.4)	2-4	3	2-3	2–4	
Interorbital width	7.1–8.4 (7.7)	9-13	9-12	7-11	6-8	
Length of eye	3.8-8.4 (6.9)	5-10	4–8	5-8	5–9	
Length of upper jaw	11.6–14.6 (13.3)	10-12	10-13	9-12	8-11	
Length of mandible	9.6-12.9 (11.5)	7-10	7-11	7–9	_	

Table 2 (Continued)

	Albula sp.ª	Albula argentea ^b	Albula oligolepis ^b	Albula virgata ^b	Albula glossodonta ^c	
Preoral length	2.6-3.9 (3.4)			_		
Length of last dorsal fin ray	6.3-7.8 (6.9)	6-8	5-8	6–8	6–8	
Length of last anal fin ray	5.6-7.0 (6.2)	48	57	5-7	5-7	
Body width	9.9-14.3 (11.7)	11–15	10-15	10-14	8-14	
Preanal fin length	83.7-85.7 (84.4)	84-87	83-88	80-87	8087	
Upper caudal fin lobe length	23.9-26.6 (25.5)	27-31	23-30	26-31	27-35	
Lower caudal fin lobe length	22.5-26.0 (24.5)	25-29	20-28	25-29	26-31	
Width of mouth	7.2-8.2 (7.6)	7–11	7–10	8–10	_	
Maxillary depth	2.0-3.2 (2.8)	2-4	2-5	2–4	_	

^a Present study; ^b Hidaka et al. (2008); ^c Hidaka et al. (2004).

Rivas and Warlen (1967), Hubbs and Lagler (2004) and Hidaka et al. (2008). Measurements were made with a Vernier caliper to the nearest 0.1 mm, and all data were then converted to percentages of the standard length (SL). The number of dorsal fin rays, anal fin rays, vertebrae and teeth patch were taken from radiographs (X' Pert-MPD system, Netherlands; SOFTEX M60, Japan; SOFTEX HA-100, Japan). The last two dorsal and anal fin rays were counted separately and the hypural bone was included in the number of vertebrae, following Rivas and Warlen (1967).

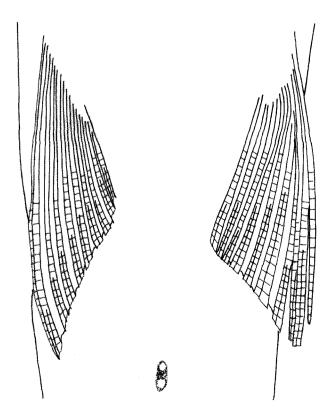


Figure 3. Magnification of abdominal area of *Albula* sp. Showing the pelvic fin that extends to the anterior margin of the anus.

Materials examined

PKU 3394, one specimen, 350.1 mm SL, 35°11′N 129°13′E, Sirang-ri, Gijang-gun, Busan, Korea, 31 October 2007, caught by J. K. Kim with a set net (Figures 1, 2). ASIZP 0067114, one specimen, 62.8 mm SL; ASIZP 0067193, one specimen, 69.1 mm SL; ASIZP 0067192, one specimen, 71.8 mm SL; ASIZP 0067194, one specimen, 96.2 mm SL, 25°2′N 121°65′E, Wanli, Taipei County, Taiwan, 15 June 2006, caught by D. F. Lee with a hook and line.

Results and discussion

A total of 524 base pairs (bp) of mtDNA cyt b sequences were obtained from the five specimens of Albula sp. and compared with those of other Albula species and two outgroups (E. saurus and P. gissu). All five specimens of Albula sp. had identical haplotypes. Albula sp. showed a biased nucleotide base composition, in that cytosine was least represented and thymine most represented (A = 19.5%, C = 19.3%, G = 22.5%, and T = 38.7%). Of the 524 bp sequences for eleven Albula species, 217 nucleotide sites were variable and 180 were parsimoniously informative. The Kimura twoparameter distances (d) ranged from 0.038 to 0.206 among the eleven Albula species. Albula sp. showed the lowest d value (0.100) with Albula sp. B and the highest d value (0.164) with Albula oligolepis (Table 3). The genetic distances (d) between Albula sp. and the other nine Albula species were 0.100-0.164, which are equal to or exceed the interspecific differences among the latter ten congeneric species (0.038-0.206) (Table 3). The NJ tree suggested eleven lineages, including the clade containing Albula sp., which was supported by a bootstrap value of 100% (Figure 4), and the ML tree also supported the monophyly of Albula sp. with a bootstrap value of 100% (Figure 5). These findings indicate that the Albula specimens represent a species distinct from the other congeneric species.

Table 3. Interspecific genetic divergence among 11 Albula species with two outgroups based on mtDNA cyt-b sequences.

	Species	1	2	3	4	5	6	7	8	9	10	11	12	13
1	Albula sp.							,						
2	Albula argentea*	0.162												
3	Albula esuncula	0.105	0.169											
4	Albula glossodonta	0.137	0.198	0.124										
5	Albula nemoptera	0.134	0.186	0.145	0.193									
6	Albula oligolepis	0.164	0.083	0.163	0.183	0.193								
7	Albula pacifica	0.135	0.168	0.147	0.189	0.041	0.167							
8	Albula virgata	0.154	0.038	0.168	0.206	0.183	0.080	0.166						
9	Albula vulpes	0.126	0.188	0.113	0.076	0.165	0.175	0.144	0.191					
10	Albula sp. A	0.125	0.175	0.057	0.147	0.175	0.169	0.154	0.185	0.131				
11	Albula sp. B	0.100	0.194	0.125	0.130	0.137	0.183	0.122	0.185	0.113	0.128			
12	Elops saurus	0.354	0.369	0.334	0.348	0.383	0.376	0.379	0.383	0.342	0.334	0.369		
13	Pterothrissus gissu	0.347	0.363	0.335	0.300	0.341	0.346	0.342	0.359	0.320	0.342	0.329	0.240	

^{*}Including Albula forsteri and Albula neoguinaica.

Our molecular analysis revealed that *Albula* sp. does not correspond to the leptocephalus from Jeju Island, Korea, identified as *A. forsteri* by Kim et al. (2008). Instead, the mtDNA *cyt* b sequence of the leptocephalus from Jeju Island (GenBank accession number EU555519) corresponds to that of *A. neoguinaica* from Fiji (GenBank accession number

AF311765; Colborn et al. 2001, d = 0.004), indicating that the leptocephalus from Jeju Island may be A. argentea, a senior synonym for A. neoguinaica, as the northernmost record of the species. In the present study, we have confirmed that there are two species of Albula in Korea, A. argentea and Albula sp., apart from the species regarded as A. neoguinaica sensu Kim

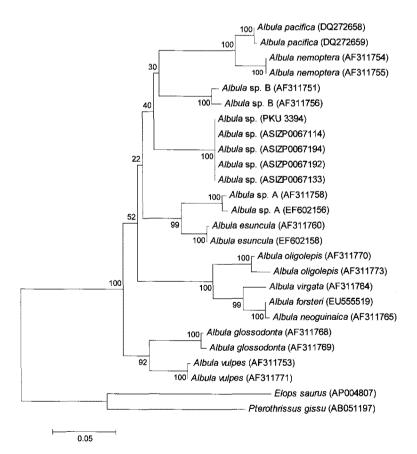


Figure 4. NJ-tree showing relationships among *Albula* species including *Albula* sp. Numbers at branches indicate bootstrap probabilities in 1000 bootstrap replications. Bar indicates genetic distance of 0.05.

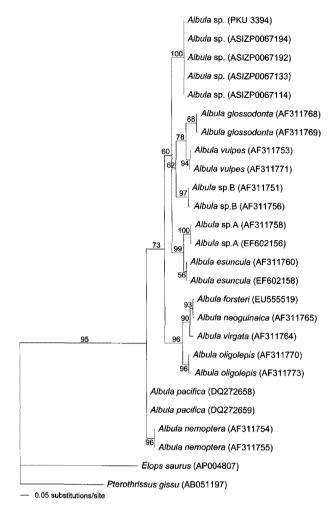


Figure 5. ML-tree showing relationships among *Albula* species including *Albula* sp. Numbers at branches indicate bootstrap probabilities in 100 bootstrap replications. Bar indicates substitutions/site of 0.05.

et al. (2005). The scientific names of these species are inappropriate according to this molecular analysis, showing that the species of *Albula* have been taxonomically confused.

In morphology, one Korean *Albula* specimen corresponded to the four Taiwan *Albula* specimens in the following morphological diagnostic characters suggested by Hidaka et al. (2008); the number of vertebrae 77–78, lower jaw pointed, and posterior tip of pelvic fin reaching to anterior margin of anus. Therefore, we regarded five specimens of *Albula* sp. to be same species because of their identical morphological features.

Albula sp. is very similar to A. argentea sensu Hidaka et al. (2008) in having a pelvic fin that extends to the anterior margin of the anus (Figure 3), but it is distinguishable by its numbers of anal fin rays (nine in Albula sp. vs. eight in A. argentea), pored lateral-line scales (77–80 vs. 68–74, respectively) and vertebrae (77–78 vs. 71–74, respectively; Table 2). In its body

measurements, Albula sp. also differs from A. argentea in the percentage caudal peduncle depth (6.7%–7.3% SL in Albula sp. vs. 7.0%–9.0% SL in A. argentea; Table 2). Albula sp. is distinguishable from A. glossodonta by the shape of its lower jaw (lower jaw pointed in Albula sp. vs. rounded in A. glossodonta), the number of vertebrae (77–78 vs. 67–69, respectively), and the number of pored lateral-line scales (77–80 vs. 66–70, respectively; Table 2). Albula sp. is also distinguishable from A. oligolepis and A. virgata by its number of vertebrae (77–78 in Albula sp. vs. 64–66 in A. oligolepis and 65–68 in A. virgata) and pored lateral-line scales (77–80 vs. 61–65 and 63–67, respectively; Table 2).

As a result of above, we believe that *Albula* sp. may be an undescribed species from the Indo-Pacific. However, further research, such as comparing type specimens of the other congeneric species, is needed for clarifying their taxonomic status confidently.

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