Short Note

A Stranding Record of Omura's Whale (*Balaenoptera omurai* Wada, Oishi, and Yamada, 2003) in the Taiwan Strait, China

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Wada et al. (2003) recognized Omura's whale (Balaenoptera omurai) as a new baleen whale species. It is separated from all extant baleen whale species on the basis of external morphology, osteology, and mitochondrial DNA (mtDNA) data. Sasaki et al. (2006) investigated the evolutionary history of Omura's whale using complete mtDNA sequences and short interspersed repetitive element (SINE) insertion patterns and suggested that this species evolved as an ancient independent lineage that diverged much earlier than the sei whale (Balaenoptera borealis), Bryde's whale (Balaenoptera brydei), and pygmy Bryde's whale (Balaenoptera edeni). Omura's whale resembles the fin whale (Balaenoptera physalus) in external appearance but is much smaller (Wada et al., 2003; Jefferson et al., 2007). The most prominent external feature is the asymmetrical lower jawthat is, the left lower jaw has mostly dark pigmentation, and the right lower jaw is predominantly white (Wada et al., 2003).

Omura's whale is one of the least known baleen whales and is red-listed as "Data Deficient" by the International Union for Conservation of Nature (IUCN) (2008). The initial specimens used to describe B. omurai were eight individual whales from the Solomon and Cocos Islands during the 1970s and one stranded specimen from the Sea of Japan (Wada et al., 2003). The majority of other records come from skeletal specimens in several institutions (Yamada et al., 2006a, 2006b, 2008; Ma et al., 2007). Until 2015, most were from rare live sightings in New Caledonia ("Extraordinarily Rare Whale Sighting," 2012) and Australia ("Omura's Whale," n.d.), and from stranding records in Hong Kong ("Taipo Whale," 2014), Australia, Iran, Mauritania, and Brazil (Jung

et al., 2016; Ottewell et al., 2016; Ranjbar et al., 2016; Cypriano-Souza et al., 2017). The most comprehensive documentation of a genetically confirmed population of living Omura's whales was presented from northwestern Madagascar and included descriptions of basic ecology and behavior (Cerchio et al., 2015).

When a stranded cetacean defies morphological classification, identification via molecular genetics becomes necessary as well as being more precise. The cytochrome oxidase c subunits I (coxI) gene has proved successful in cetacean species identification (George et al., 2011; Viricel & Rosel, 2012; Alfonsi et al., 2013). The cytochrome b (cytb) gene has also been broadly applied for baleen whales' identification, including for bowhead whales (Balaena mysticetus), humpback whales (Megaptera novaeangliae), pygmy Bryde's whales, Omura's whales, and North Atlantic right whales (Eubalaena glacialis) (Rastogi et al., 2004; Ma et al., 2007; McLeod et al., 2008; Sholl et al., 2013). Omura's whale formed a monophyletic lineage with the blue whale (*Balaenoptera musculus*), B. borealis, B. brydei, and B. edeni, and diverged much earlier with B. musculus from B. borealis, B. brydei, and B. edeni. Hence, it can be easily distinguished from other baleen whales by using molecular genetic analysis (Sasaki et al., 2006).

The present study describes an Omura's whale that was stranded on 27 November 2011 on Pingtan Island (25° 35' 05" N, 119° 53' 05" E) along the northwestern coast of the Taiwan Strait, China (Figure 1). Several morphological measurements of this specimen were taken. On the basis of the small number and asymmetric color patterns of the baleen plates, it was originally suspected to be an Omura's whale. For further identification, partial



Figure 1. The present (black triangle) and historical (black circles) stranding locations of Omura's whales (*Balaenoptera omurai*) in Chinese waters; TW07 was without an available location and, thus, unmarked.

fragments of *cox1* and *cytb* genes were amplified, and then sequence similarity searches, diagnostic sites, and phylogenetic analysis were conducted. In addition, 14 other reliable stranding records of Omura's whale along Chinese coastal waters were reviewed to advance the knowledge of this species in this location. External morphometric data were collected following Norris & The Committee on Marine Mammals (1961) and Wang (2012) from the carcass in its original position on the left side (Table 1).

This baleen whale was a male as indicated by the upward genital aperture and a penis (Figures 2A & 2B). Most of its epidermis had fallen off, and only some black debris remained on the left lower jaw (Figure 2A). The tongue overflowed from its mouth. There were no apparent traumatic injuries, and the cause of death remains unknown. There were 60 to 66 throat pleats that reached beyond the navel (Figure 2C). The interior of the baleen was yellowish-white. The exterior was trim and discrepant in that the left baleen row was all black, while the anterior one-fifth to one-fourth of the right side presented as yellowish-white (Figure 2D). There were 217 to 218 pairs of short, broad baleen plates; and most of these plates were bi-colored except the anterior right baleen (Figure 2D). The flippers were small and slender at the anterior one-third of the body length (BL)

(Figure 2E). The dorsal fin was falcate, rising at a gradual angle at the posterior one-third of BL (Figure 2F). The flukes were broad with an obvious notch (Figure 2G). A pair of nipples appeared at both sides of the posterior end of the genital slit (Figures 2B & 2H). In light of the small number and asymmetric color patterns of the baleen plates, this specimen was initially suspected to be an Omura's whale.

The cytb gene was amplified with prim-CBMYSTF1/CBMYSTR (Ma et ers al.. 2007; McLeod et al., 2008). The cox1 gene BOCOIF amplified using primers was (5'-GGTCAACAAATCATAAAGATATTGG-3') and HCO2198 (George et al., 2011). All Polymerase Chain Reactions (PCRs) were performed following Ma et al.'s (2007) method. The PCR products were directly sequenced in both directions. After being edited by *BioEdit*, Version 7.2.5 (Hall, 1999), cox1 and cytb genes were 659bp and 526bp in length, respectively. Repeated DNA samples were consistent. Sequences were assigned to Genbank accession numbers KP230447 and KP230448, respectively. Sequence significant alignments of *cox1* and *cytb* sequences by *Basic* Local Alignment Search Tool (BLAST; https:// blast.ncbi.nlm.nih.gov/Blast.cgi) were all referred to baleen whales. Both displayed 99 to 100% similarity with Omura's whale sequences, while the other closest neighboring species showed 93 to 96% identity. When the cox1 sequence was submitted to BOLD Systems (Ratnasingham & Hebert, 2007), it matched to an Omura's whale (BOLD: AAF3211; Genbank accession number AB201257) with 100% similarity of placement at species level. When submitted to Witness for Whales (Mysticetes, Version 4.3; CytB Database) (Ross et al., 2003), our cytb sequence clustered with a Bryde's whale (Solomon Islands) haplotype with 100% bootstrap support in a neighborjoining tree analysis, and it was identical to the specimen BeneWP2.HY in the genetic distances analysis. BeneWP2.HY was an early sequence of Omura's whale from Solomon Islands that were previously referred to as a pygmy Bryde's whale (AF146392) (Yoshida & Kato, 1999), although it was ultimately determined to be an Omura's whale (Wada et al., 2003).

All sequences of Omura's whale on Genbank were collected referring to complete mtDNA (AB201256 & AB201257), *cox1* gene (KM233839 & KX254410), and *cytb* gene (AF146392, AF398371, EF103940, KM233837 & KX254409). The other baleen species sequences were downloaded as well, and there were Antarctic minke whale (*Balaenoptera bonaerensis*) (AP006466), common minke whale (*Balaenoptera acutorostrata*) (AP006468), gray whale (*Eschrichtius*)

Sample no.	BOM-2011-11-29					
Sex	Male					
Condition of specimen	Epidermis has been removed					
Number of throat grooves between flippers	60-66					
Number of baleen plates	217	^{rl} , 218 ^r				
Length of baleen	157 cm	^L , 162 cm ^R				
Body length (BL)	715 cm	100%				
Length, tip of upper jaw to gape	131 cm ^L	18.3%				
Length, tip of upper jaw to center of eye	141 cm ^L	19.7%				
Length, tip of upper jaw to external auditory meatus	$180 \text{ cm}^{\text{L}}$	25.3%				
Length, tip of upper jaw to anterior insertion of flipper	211 cm ^L	29.5%				
Length, tip of lower jaw to midpoint of umbilicus	440 cm	61.5%				
Length, tip of lower jaw to midpoint of genital aperture	484 cm	67.7%				
Length, tip of lower jaw to center of anus	524 cm	73.3%				
Length, tip of lower jaw to posterior extremity of throat creases (direct)	451 cm	63.1%				
Length, notch to center of anus	180 cm	25.2%				
Length, notch to midpoint of genital aperture	224 cm	31.3%				
Length, notch to midpoint of umbilicus	283 cm	39.6%				
Length, notch to dorsal fin tip	276 cm	38.6%				
Center of eye to angle of gape (direct)	11.5 cm ^L	1.6%				
Center of eye to external auditory meatus (direct)	40.5 cm ^L	5.7%				
Eye height	1.5 cm ^L	0.2%				
Eye length	16 cm ^L	2.2%				
Length, mammary slits	4 cm ^L , 4.5 cm ^R	0.6%, 0.6%				
Length, genital slit	44 cm	6.1%				
Length, anal opening	7 cm	1%				
Length, flipper (anterior insertion to tip)	94 cm ^L	13.1%				
Length, flipper (axilla to tip)	75.5 cm ^L	10.6%				
Width, flipper (maximum)	23.5 cm ^L	3.3%				
Height, dorsal fin (fin tip to base)	16.5 cm	2.3%				
Length, dorsal fin base (subjective)	31 cm	4.3%				
Width, flukes (tip to tip)	146.5 cm	20.5%				
Distance from nearest point on anterior border of flukes to notch	41.5 cm	5.8%				
Depth of notch between flukes (if none, so state)	10 cm	1.4%				

 Table 1. Morphological measurements of an Omura's whale (Balaenoptera omurai) stranded on the northwestern coast of the Taiwan Strait, China, on 27 November 2011

Note: Values labeled "L" were taken on the left side, and values labeled "R" were taken on the right side.

robustus) (AP006471), B. edeni (AB201258), B. brydei (AP006469), B. borealis (AP006470), B. physalus (X61145), B. musculus (X72204), and M. novaeangliae (AP006467). Multiple sequence alignment was conducted in MEGA6 using the ClustalW option (Tamura et al., 2013). Cox1 and cytb genes remained 659bp and 478bp, respectively. For diagnostics, 12 (cox1) and eight (cytb) sites could distinguish Omura's whale from other species (Table 2), and there were nine (cox1) and

five (*cytb*) sites among them coincident with the "pure" characteristic attributes for Omura's whale identified by Viricel & Rosel (2012). The diagnostic sites in our sequences definitely indicated that this mysticete was an Omura's whale.

The pygmy right whale (*Caperea marginata*) (AP006475) was used as an outgroup. Neighborjoining and maximum likelihood trees were built using the Kimura 2-parameter model by *MEGA6* with 1,000 bootstraps (Kimura, 1980; Felsenstein, 1985; Saitou & Nei, 1987). Four gene trees had the same topology; hence, a neighbor-joining tree of the *cytb* gene was presented (Figure 3).

Our *cytb* sequence clustered with other Omura's whale sequences as a monophyletic group with 100% bootstrap support. Omura's whale formed a



Figure 2. Morphological appearance of an Omura's whale stranded on the northwestern coast of the Taiwan Strait, China, on 27 November 2011: (A) overall view of ventral side; (B) the exposed penis, with arrows pointing to nipples; (C) throat pleats reaching posterior beyond the navel; (D) exterior view of baleen (above is upper right baleen); (E) left flipper; (F) dorsal fin; (G) flukes; and (H) a pair of nipples.

Table 2. Diagnostic sites of *cox1* and *cytb* genes for Omura's whale within the family Balaenopteridae. The sequence spanned from nucleotide position 5409 to 6067 and 14192 to 14669; nomenclature according to the complete Omura's whale mitochondrial genome (AB201256) (Sasaki et al., 2006).

<i>cox1</i> (659bp)										<i>cytb</i> (478bp)												
		1	2	2	3	3	4	5	5	6	6	6	6			3	3	3	4	4	4	
	8	4	2	4	0	8	8	4	8	0	4	5	5	4	6	2	4	5	3	4	6	
Species	8	5	6	7	4	5	4	7	0	1	9	5	8	6	9	3	9	5	8	4	8	
B. edeni	C	G	С	Т	А	С	Т	G	А	Т	А	А	С	G	С	С	G	С	С	С	Т	
B. brydei	.						С															
B. borealis	Т						С	А														
B. bonaerensis							С	А							А							
B. acutorostrata		А					С	А														
B. physalus	.						С	А														
B. musculus	.						С	А														
M. novaeangliae					G		С	А														
B. omurai AB201256	G	Т	Т	С	G	Т	Α	С	С	С	${G}$	${G}$	Т	Α	Т	Т	Α	Т	Т	Т	С	
B. omurai AB201257	G	Т	Т	С	G	Т	Α	С	С	С	${G}$	${G}$	Т	Α	Т	Т	A	Т	Т	Т	С	
B. omurai KM233839	G	Т	Т	С	G	Т	Α	С	С	С	${G}$	${G}$	Т	Α	Т	Т	Α	Т	Т	Т	С	EF103940
KP230448	G	Т	Т	С	G	Т	Α	С	С	С	G	G	Т	Α	Т	Т	Α	Т	Т	Т	С	KP230447

Note: Dot (.) indicates identical nucleotide with *B. edeni*. Sites in shadow are identified as "pure" characteristic attributes (Viricel & Rosel, 2012). Sites in italic are identified as diagnostic sites in this note.

basal branch in the clade that included *B*. *borealis*, *B*. *edeni*, and *B*. *brydei*.

Jr. & K. Robertson, pers. comm., 26 October 2016) by its control region sequence.

Discussion

Omura's Whale in Chinese Waters

The literature published since 1990 concerning Omura's whale in Chinese waters has been reviewed. Altogether, including our specimen, there were 15 stranded mysticetes positively identified as Omura's whale (Table 3).

The Rui'an specimen (CH01) was originally suggested to belong to B. edeni off the Solomon Islands using *cytb* gene and its control region (AF398371 & AF398372) (Yang et al., 2002). Subsequently, the Solomon Islands' specimens were named as B. omurai (Wada et al., 2003), and Rosel & Wilcox (2014) noted that both sequences were misidentified as B. edeni on Genbank. The Yuhuan specimen (CH02) was identified by Tadasu K. Yamada with external appearance and skeletal morphology (Wang et al., 2006). A vertebra sample (CH03) was identified based on cytb gene (EF103940) (Ma et al., 2007). Seven specimens (TW01-07) were confirmed based on skeletal morphology by Yamada et al. (2006b). Wang (2012) confirmed both specimens (CH04 & CH05) with examination of their skeletons. Wang also described a juvenile (CH06) from its external and skeletal morphology. The Omura's whale that stranded in Hong Kong (HK01) was matched to a Japanese haplotype (AB116095) (R. L. Brownell, In most baleen whales, there are male nipples rudimentary or developed—in the fetus or in both the fetal and postnatal whale (Clarke, 2005). Male nipples were documented in pygmy right, bowhead, common minke, blue, fin, sei, and humpback whales but were absent in the gray, Bryde's, northern right, and southern right whales (Clarke, 2005). Until our observation, there has been no reference in the literature regarding male nipples in Omura's whale; this male specimen had a pair of exposed nipples posterior to its penis (Figures 2B & 2H).

As a relatively newly described baleen whale, not much information is available about wild individuals or populations of Omura's whale. Also, there are limited external morphological measurement data. It is commonly accepted that the external appearance of Omura's whale resembles that of fin whales in many respects, except for the low number of baleen plates (Wada et al., 2003; Jefferson et al., 2007; Cerchio et al., 2015). Omura's whale has the fewest plates per side among *Balaenoptera* spp., with 181 to 223 baleen plates per side (Table 4), and could be considered a species characteristic for Omura's whale (Wada et al., 2003; Jefferson et al., 2007).



Figure 3. Neighbor-joining tree based on *cytb* (478bp) gene was built in *MEGA6*. Scale bar represents the evolutionary distance using the Kimura 2-parameter model with a gamma distribution (shape parameter = 0.1656). Bootstrap values are shown above branches.

There were 60 to 66 ventral grooves between the flippers and three obvious extra grooves above the left pectoral fin for our specimen (Figure 2E). This number was much less than in the Japanese holotype (Table 4) (Wada et al., 2003). A broad range of the number of ventral grooves, 65 to 95, had been documented for living Omura's whales from northwest Madagascar (Cerchio et al., 2015). The specimens from Iran, Mauritania, Brazil, and Yuhuan (CH02) were consistent with the Madagascan population (Wang et al., 2006; Cerchio et al., 2015; Jung et al., 2016; Ranjbar et al., 2016; Cypriano-Souza et al., 2017). The Dongshan specimen (CH04) was an exception with much fewer grooves (Huang & Liu, 2000). The number of throat grooves in Omura's whale appeared highly variable but, overall, remained small, which might be ascribed to one or two factors. First, counting might be conducted in different locations on the body by different observers; consistency in the counting location was not found in the literature. Alternatively, individual variation exists between different Omura's whales or regional populations.

The dorsal fin of our specimen was small and similar to the Iranian and Brazilian specimens (Ranjbar et al., 2016; Cypriano-Souza et al., 2017; see Table 4). The specimens from Japan, Australia, and New Caledonia had strongly falcate and hooked dorsal fins rising at a steep angle in the leading edge (Wada et al., 2003; Jefferson et al., 2007; Ottewell et al., 2016). While the present specimen and the Madagascan Omura's whale both displayed a falcate dorsal fin, they showed a more gradual slope in the fin's angle (Figure 2F) (Cerchio et al., 2015). Discrepancies in the dorsal fin shape of Omura's whales could be likely attributed to a developmental or individual variation that was described in the Madagascan population (Cerchio et al., 2015; Ranjbar et al., 2016).

Molecular identification of the present specimen was more reliable compared with morphological classification. The present study identified more diagnostic sites than Viricel & Rosel's (2012) that were sufficient to distinguish Omura's whale within the *Balaenoptera* spp. Our phylogenetic result concurred with Sasaki et al. (2006) that Omura's whale was an ancient independent lineage that was easily distinguished from other similar-in-appearance baleen whales via molecular genetic analysis.

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Acct#	Stranding location	Stranding date	BL (body weight)	Sex	Specimen type	Reference		
CH01	Rui'an City, Zhejiang Province	Nov. or Dec. 1994	5.95 m (~2,000 kg)	?	Tissue (muscle) (genetic)	Yang et al., 2002; Zhou, 2004; Rosel & Wilcox, 2014		
CH02	Yuhuan County, Zhejiang Province	16 Dec. 2001	5.70 m (~1,500 kg)	F	Complete skeleton	Wang et al., 2006		
CH03	Zhanjiang City, Guangdong Province	Feb. 2005	?	?	Vertebra	Ma et al., 2007		
TW01	Pingtung County, Taiwan	5 Nov. 1990	?	?	Incomplete skeleton	Yamada et al., 2006b		
TW02	Tainan County, Taiwan	11 Feb. 1997	5.54 m	М	Whole skeleton and baleen plates	Yamada et al., 2006b		
TW03	Miaoli County, Taiwan	5 March 1997	5.13 m	М	Whole skeleton and baleen plates	Yamada et al., 2006b		
TW04	Taipei Country, Taiwan	8 May 1997	8.00-9.00 m	М	Incomplete skeleton	Yamada et al., 2006b		
TW05	Taoyuan Country, Taiwan	1 Dec. 1998	6.54 m	М	Whole skeleton and baleen plates	Yamada et al., 2006b		
TW06	Hualien Country, Taiwan	27 Jan. 2004	5.95 m	F	Whole skeleton and soft tissues	Yamada et al., 2006b		
TW07	?	?	?	?	Incomplete broken skeleton	Yamada et al., 2006b		
HK01	Hung Shek Mum, Plover Cove Country Park, Taipo, Hong Kong	29 March 2014	10.8 m (~25 t)	F	Whole skeleton	"Taipo Whale," 2014		
CH04	Dongshan County, Fujian Province	12 Dec. 1991	6.85 m (~2.5 t)	М	Skeleton and baleen	Huang & Liu, 2000; Wang, 2012		
CH05	Nanri Island, Fujian Province	29 Aug. 2008	6 m (~3 t)	?	Skeleton	Wang, 2012		
CH06	Zhangpu County, Fujian Province	Nov. 2009	3.90 m	?		Wang, 2012		
CH07	Pingtan Island, Fujian Province	27 Nov. 2011	7.15 m	М	Muscle and skin	Present study		

Table 3. Stranding records of Omura's whales in Chinese coastal waters

Note: Acct# = account number, BL = body length, CH = Chinese mainland, TW = Taiwan, and HK = Hong Kong; "?" marks unavailable information.

In 655bp of the *cox1* gene, we identified two haplotypes in five specimens. The present specimen shared an identical haplotype with others from Japan, Brazil, and Mauritania (Sasaki et al., 2006; Jung et al., 2016; Cypriano-Souza et al., 2017). Another haplotype with a C-T transition discrepancy was in a Japanese specimen (Sasaki et al., 2006). In 369bp of the *cytb* gene, there were two haplotypes in 12 specimens. Eleven Omura's whale specimens shared a single haplotype, while one Japanese specimen had another haplotype with one G-A transition (Yoshida & Kato, 1999; Yang et al., 2002; Sasaki et al., 2006; Ma et al., 2007; Jung et al., 2016; Cypriano-Souza et al., 2017). The numbers of haplotypes and nucleotide substitutions

are small in Omura's whale. It is possible that Omura's whale has low genetic diversity as suggested for a living population from northwestern Madagascar (Cerchio et al., 2015). Low genetic diversity likely reflects small population size for this species, which is of conservation concern.

As for Omura's whale in China, all carcasses were mainly distributed along the southeast coast of China, including Zhejiang, Fujian, and Guangdong Provinces and Taiwan. Except for two records in the South China Sea, all others appeared in the East China Sea, particularly concentrated in the Taiwan Strait (see Figure 1). There were 12 stranded cases in winter through early spring (i.e., November to March). Considering a likely

Sample no.	Location	BL	No. of ventral grooves	No. of baleen plates	Dorsal fin (height, length, or description)	Reference		
BOM-2011-11-29	Pingtan	715 cm	60-66	217 ^L , 218 ^R	16.5 cm (2.3%), 31.0 cm (4.3%)*	Present study		
?	Madagascar	?	65-95	?	Strongly falcate, rising at a gradual slope	Cerchio et al., 2015		
QE22.09.2007	Iran	397 cm	82	204 ^R	7.5 cm (1.9%), 18.0 cm (4.5%)*; strongly falcate and more consistently backswept	Ranjbar et al., 2016		
Holotype (NSMT-M32505)	Japan	1,103 cm	80-90	208 ^L , 203 ^R	Falcate and very hooked, rising at a steep angle	Wada et al., 2003; Jefferson et al., 2007		
NRIFSF7	Solomon	960 cm	?	181-190 ^r	?	Wada et al., 2003		
WAM M63349	Western Australia	568 cm	?	?	Very hooked, rising at a steep angle; small but noticeably falcate (abruptly)	Ottewell et al., 2016		
?	Australia	?	?	?	Consistent with Bryde's whale rather than fin whale	"Omura's Whale," n.d.		
?	New Caledonia	?	?	?	Somewhat erect and hooked	"Extraordinarily Rare Whale Sighting," 2012		
MauBs_2013_11_03	Mauritania	398 cm	>70	?	Small, fairly triangular	Jung et al., 2016		
BRA_2010_09_10	Brazil	416 cm	65	?	12 cm (2.9%), 26 cm (6.25%)*; small and slightly falcate	Cypriano-Souza et al., 2017		
CH01	Rui'an	595 cm	?	223 ^R	?	Yang et al., 2002; Zhou, 2004		
CH02	Yuhuan	570 cm	74	246 ^L , 246 ^R	20 cm (3.5%), 60 cm (10.5%)*; falcate and slightly hooked	Wang et al., 2006		
CH04	Dongshan	685 cm	45	>200	?	Huang & Liu, 2000; Wang, 2012		
CH06	Zhangpu	390 cm	?	212	8 cm (2.0%, height)*	Wang, 2012		

 Table 4. Morphologic characters of Omura's whales

Note: BL = body length and "?" marks unavailable information. *Percentage indicates measured value of BL. Values labeled "L" were taken on the left side, and values labeled "R" were taken on the right side.

distribution for this species in the Sea of Japan and the Solomon Islands, as well as a presence in Zhe-Min Coastal waters and the South China Sea Warm Current (SCSWC) in the Taiwan Strait, it is likely that Omura's whales migrate through the Taiwan Strait and its adjacent waters. Omura's whale strandings have been observed somewhat regularly since 1990 in Chinese waters (Table 3). Compared with other occasional single specimens recorded in Mauritania, Iran, and Brazil, the South Chinese coastal waters might represent a potentially important habitat for Omura's whale (Jung et al., 2016; Ranjbar et al., 2016; Cypriano-Souza et al., 2017). Despite the current specimen and other Omura's whale stranding records, little is known about this species' biology and ecology in Chinese waters. We recommend field surveys should be undertaken to facilitate collection of pertinent information related to abundance and distribution of this elusive species to ensure appropriate conservation management.

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