Short Note

First Record of Omura's Whale (*Balaenoptera omurai*) in the Beibu Gulf, China

Supplementary Material

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Supplementary Material S1

A partial fragment of the mtDNA cytochrome c oxidase subunit 1 (*cox1*) was amplified and sequenced using primers Lco1ea 5'-TCGGCCATTTTACCTATGTTCATA-3' and Hbcuem 5'-GGTGGCCGAAGAATCAGAATA-3' (Alfonsi et al., 2013). The partial cytochrome b (*cytb*) gene was amplified and sequenced using primers L14724 5'-TGACTTGAARAACCAYCGTTG-3' and H15387 5'-GAATGGGATTATGTCTATGT-3' (Viricel & Rosel, 2012). The mitochondrial control region (D-loop) was amplified and sequenced using primers Ce-CRF 5'-GAATTCCCCGGTCTTGTAAACC-3' and Ce-CRR 5'-TCTCGAGATTTTCAGTGTCTTGCTTT-3' (Hoelzel et al., 1991).

For phylogenetic analyses, we selected all previously published sequences of the three different mtDNA markers (two partial coding sequences, *cox1* gene, 700 bp; the *cytb* gene, 640 bp; and D-loop region, 938 bp) for Omura's whales (*Balaenoptera omurai*) from GenBank sequences. The other baleen whale species sequences (including Balaenopteridae + Eschrichtiidae + Neobalaenidae) were extracted from the complete mitochondrial gene or genome. The pygmy right whale (*Caperea marginata*) was used as an outgroup. We chose one sequence of *cox1* and *cytb* and two sequences of D-loop for each species (except for the Omura's whale). For the D-loop region, 50 gaps were removed from the original alignment obtained by using *ClustalW*, resulting in an 882-nucleotide-long final alignment.

The two subspecies of Bryde's whale (*Balaenoptera edeni*) have been previously recognized as two individual species: *Balaenoptera edeni brydei* was the Bryde's whale (*Balaenoptera brydei*) and *Balaenoptera edeni edeni* was the pygmy Bryde's whale (*Balaenoptera edeni*). So, when the sequences of the two subspecies were obtained from GenBank, their species' names were retained to be consistent with GenBank.

Supplementary Material S2

The *cox1* sequence submitted to the BOLD Systems matched to *Balaenoptera omurai* reference sequences with 100% similarity (BOLD: AAF3211; GenBank Accession Numbers KP230448, AB201257, NC_007937, and AB201256). The DNA Surveillance analysis results showed the present specimen sequences clustered with *B. omurai* reference sequences for both D-loop (Figure S1A) and the *cytb* (Figure S1B) with high bootstrap support (100%).

All published sequences of the three different mtDNA markers (*cox1* gene, *cytb* gene, and D-loop) for Omura's whales were obtained from GenBank. Some short sequences were removed from the alignment due to being covered by long sequences. The D-loop alignment was trimmed to the length of 402 bp from 12 sequences. In total, there were five haplotypes with five variable sites. The 20 Madagascar samples with only one sequence represented one single haplotype [KT582064]. Seven sequences from two specimens from Korean coastal waters [MG877683 and MG877682], two from the Sea of Japan [AB201256 and AB201257], one from Chinese coastal waters [AF398372], one from the offshore of West Africa [KM233838], and one from the western coast of Australia [KT757371] matched one common haplotype. Another haplotype was defined from the sequences of specimen BBG01 [MK676071] and BOM-2011-11-29 [MN422218] (Xu et al., 2017) from the Chinese coast. The last two haplotypes were obtained from the sequences of a specimen from the Solomon Islands [AB116096] and a specimen from the Cocos Islands [AB116097], respectively.

The *cytb* gene alignment was trimmed to the length of 444 bp from six sequences. In total, there were four haplotypes with three variable sites. One common haplotype was defined from sequences of two specimens from Chinese coastal waters [KP230447 and EF103940] and one specimen from the Sea of Japan [AB201257]. Another haplotype was defined from the sequence of specimen BBG01 [MK676069] from Chinese coastal waters. The other two haplotypes were obtained from sequences of the specimens from the South Atlantic Ocean [KX254408] and Sea of Japan [AB201256], respectively.

The *cox1* gene alignment was trimmed to the length of 516 bp from seven sequences. In total, there were three haplotypes with two variable sites. One common haplotype was defined from sequences of five specimens, including two from Chinese coastal waters [KP230448 and MK676070], two from the Atlantic Ocean [KX254410 and KM233839], and one from the Sea of Japan [AB201257]. Another haplotype was defined from the sequence of the specimen from Korean coastal waters [KP993089]. The last haplotype was obtained from the sequence of the specimen from the Sea of Japan [AB201256].

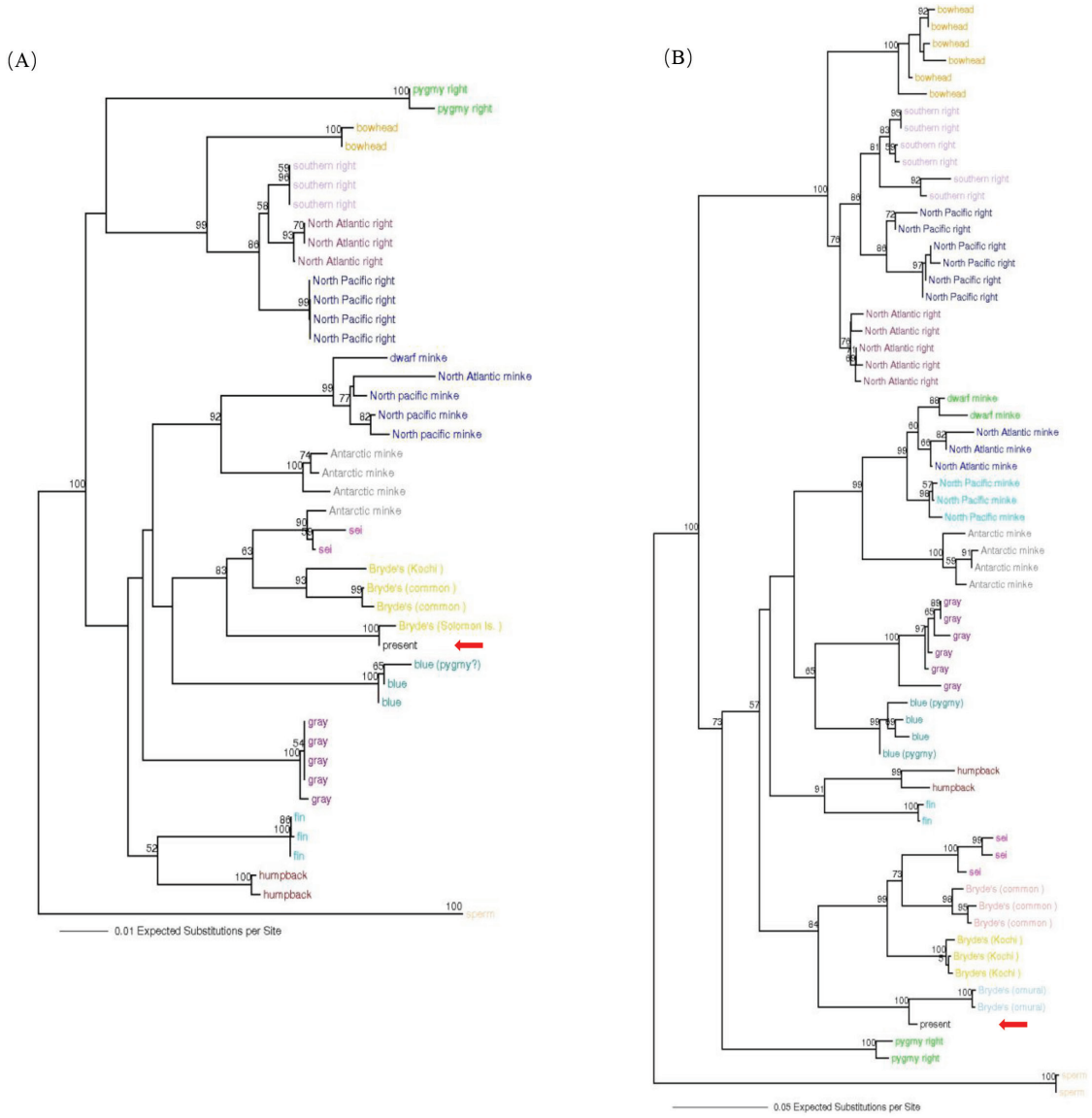

Figure S1. DNA Surveillance trees showing high bootstrap support (100%) grouping Omura's whale BBG01 (labeled as "present" with red arrow) with the reference sequences of *Balaenoptera omurai* (Bryde's [omurai] or [Solomon Islands]): (A) NJ tree based on cytochrome b query and reference sequences of all recognized mysticetes; and (B) NJ tree based on control region query and reference sequences of all recognized mysticetes. Bootstrap values based on 1,000 replicates.

Figure S2. The photos of the stranded Omura's whale were provided by the fisherman who first found it on the beach.

Literature Cited for Supplemental Material

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