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Short Note

Genetic Diversity and Preliminary Phylogeographic Analysis of the Longman's Beaked Whale (*Indopacetus pacificus*) in the Western Tropical Indian Ocean

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Beaked whales (Ziphiidae) are among the least known cetaceans, primarily due to their offshore habitat and deep diving behavior. To date, 24 species are known to exist around the globe (Committee on Taxonomy of the Society for Marine Mammalogy, 2026), but the rate at which species have been discovered has increased substantially over the past few decades (e.g., Reyes et al., 1991; Dalebout et al., 2002; Yamada et al., 2019; Carroll et al., 2021). Molecular methods have provided evidence for cryptic speciation and supported the description of at least two new species in the last 10 years, including the Ramari's beaked whale (*Mesoplodon eueu*; Carroll et al., 2021) and the Sato's beaked whale (*Berardius minimus*; Yamada et al., 2019). Information about the ecology, population structure, distribution, and behavior of beaked whales has also increased (Hooker et al., 2019). However, there have been disproportionate efforts toward a small number of species, such as goose-beaked whales (*Ziphius cavirostris*), northern bottlenose whales (*Hyperoodon ampullatus*), and dense-beaked whales (*Mesoplodon densirostris*), whereas most other species have received less attention due to their more cryptic nature and less predictable presence (e.g., Gowans & Whitehead, 2001; Foley et al., 2021; Barlow et al., 2025).

The Longman's beaked whale (*Indopacetus pacificus*), also known as the tropical bottlenose whale, is one of the least known beaked whale species around the globe, and likely one of the rarest, despite a large body size and a relatively widespread distribution across the tropical and subtropical waters of the Indo-Pacific region (Anderson et al., 2006; Pitman, 2009; Fisher et al., 2022). Although initially included in the genus *Mesoplodon*, Moore (1968) proposed to place this species in a new genus, *Indopacetus*, based on morphological differences; this was later confirmed with genetic evidence (Dalebout et al., 2003). Although distributed across the Indo-Pacific region, Longman's beaked whales are thought to be more common in the western Indian Ocean than elsewhere within their known range (Anderson, 2005; Anderson et al., 2006; Pitman, 2009). They are mainly found in lower slope and abyssal plain habitats in groups ranging from one to 40 individuals (Anderson et al., 2006). To date, there is limited information on the population structure, phylogeography, and genetic diversity of this species, and only a few control region sequences have been generated from samples collected in stranding events (Dalebout et al., 2003; Garrigue et al., 2016).

In November 2021, an expedition was conducted to assess the occurrence of blue whales (*Balaenoptera musculus*) and other cetaceans off the northern islands of Seychelles (see details of sampling in Stafford et al., 2023). The expedition consisted of vessel-based visual surveys that were conducted in slope habitats (500 to 2,000 m) and abyssal plains (< 2,000 m) off the northern portion of the Mahé Plateau. On 9 November 2021, a group of 80 to 100 Longman's beaked whales was observed (4° 22' 55.2" S, 56° 34' 1.2" E), and a small vessel was deployed to collect skin and blubber biopsy samples using a 79.4 kg draw weight crossbow with Finn Larsen bolts and tips (7 × 40 mm; Ceta-Dart, Copenhagen, Denmark). Samples were preserved in 90° ethanol. DNA was extracted from tissue samples using the DNAeasy tissue and blood DNA extraction kit from Qiagen (Hilden, Germany). DNA purity and concentration were evaluated using a NanoDrop™ 2000c Spectrophotometer (Thermo Fisher Scientific, Abingdon, Great Britain). A 500-base pair (bp) fragment of the mitochondrial DNA control region (CR) was amplified from both samples

using primers from Caballero et al. (2007). PCR products were cleaned using magnetic beads and sequenced in both forward and reverse directions on an ABI 3730 Genetic Analyzer (Hatfield Marine Science Center, Newport, OR, USA).

Obtained sequences were manually edited and aligned using *Geneious Prime*, Version 2023.0.1 (Biomatters LTDA, Auckland, New Zealand) to generate consensus alignments. Previously published or available sequences from Genbank were downloaded and aligned with the sequences generated in this study using *MacClade* (Maddison & Maddison, 2000), and haplotypes were identified. A haplotype network was constructed using the statistical parsimony methodology as implemented in the software *TCS*, Version 1.21 (Clement et al., 2000). This method estimates an unrooted tree, providing a 95% plausible set for all sequence type linkages within the tree and considering gaps as a fifth character state. Haplotype (h) and nucleotide (π) diversity calculations were performed in the program *Arlequin*, Version 3.5.1 (Excoffier & Lisher, 2010). Since sample sizes from different geographic locations were so small (one or two sequences), no population structure analysis could be conducted.

Sequences were successfully generated from the two samples collected in Seychelles and deposited in Genbank with Accession Number PZ180027. Nine sequences (haplotypes) were downloaded from Genbank from samples collected from Japan (Accession Number LC841881, Miyako island, Okinawa; AN AB572012, Kagoshima, Sendai; Kitamura et al., 2013; Kobayashi et al., 2021), Taiwan (AN KY364702), New Caledonia (AN KP892561; Garrigue et al., 2016), the Maldives (AN AY162439, Felijhu Atoll; Dalebout et al., 2003), South Africa (AN AY162438, Sodwana Bay, Natal; AN AY162437, Blythesdale Beach, Natal; Dalebout et al., 2003), Somalia (AN AY162436, Danane; Dalebout et al., 2003), and Australia (AN AY162435, Mackay, Queensland; Dalebout et al., 2003). Access to an additional sequence obtained from an individual stranded in Hawai'i was not possible (West et al., 2013), preventing us from including it in this analysis.

In the 447 bp consensus alignment, seven haplotypes were identified among all samples ($n = 16$; Table 1 & Figure 1), and the frequency of each haplotype was determined based on previously published information (see Table 1 for additional information). The two samples from Seychelles shared the same haplotype as the sample from the Maldives (H2). The samples from Taiwan ($n = 2$) and New Caledonia ($n = 5$) also shared the same haplotype (H4). All other samples had five unique haplotypes. In the haplotype network (Figure 1), haplotype H1, identified in two samples from Natal, South Africa, appeared to be the most ancestral haplotype, from which haplotypes H2, H3, and H4 were derived, with one nucleotide difference between them. The most divergent haplotype was identified in the sample from Queensland, Australia, with three nucleotide changes when compared to H3. The overall species haplotype diversity (h) was 0.791 ± 0.08, and the overall species nucleotide diversity (π) calculated to date was $0.62\% \pm 0.04$.

Results presented herein are still preliminary and limited by small sample size but provide an

Table 1. Six variable sites over 447 base pairs (bps) of the mtDNA control region of *Indopacetus pacificus* define seven haplotypes. Haplotype frequencies and geographic origin of samples identified with a particular haplotype are also presented. The symbol "." indicates a match to the initial haplotype variable sites, and "?" indicates missing data.

Variable sites								
mtDNA control region (447 bps)								
Haplotype	65	68	96	103	316	436	Haplotype frequency	Geographic origin of samples
H1	T	G	A	T	?	?	2	Natal, South Africa
H2	.	.	G	.	C	T	3	Maldives and Seychelles
H3	.	.	.	C	T	?	1	Somalia, East Africa
H4	.	.	G	.	C	C	7	New Caledonia and Taiwan
H5	C	.	.	C	T	C	1	Okinawa, Japan
H6	.	A	G	.	C	C	1	Kagoshima, Japan
H7	.	.	.	C	?	?	1	Queensland, Australia
Total number of samples							16	

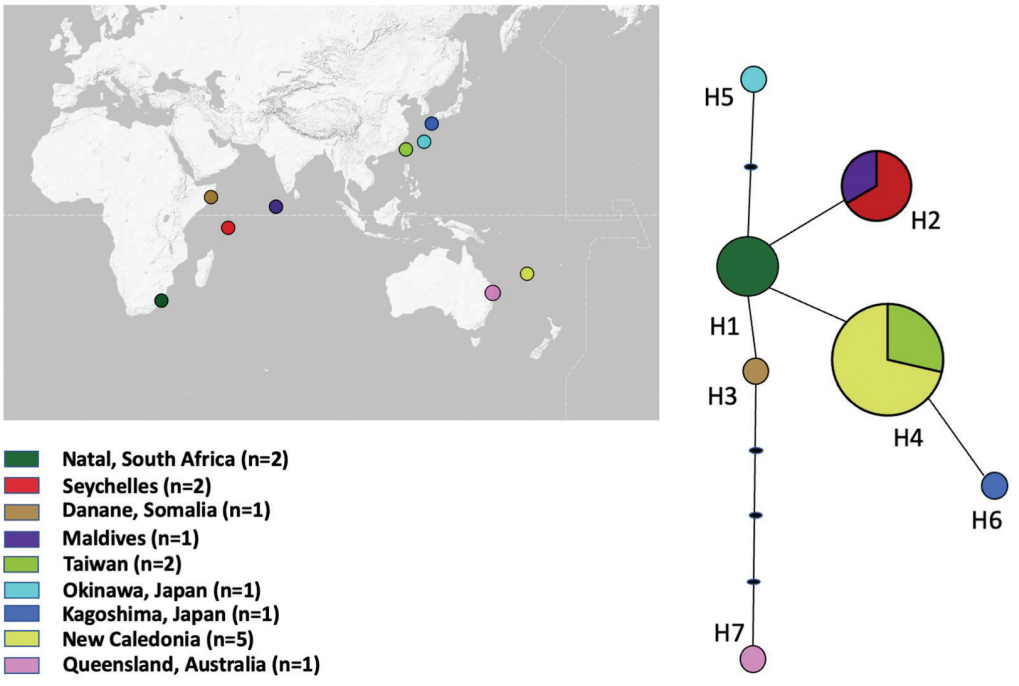


Figure 1. *TCS* haplotype network of Longman's beaked whale (*Indopacetus pacificus*) mtDNA control region haplotypes (447 bps). The size of the circles represents the frequency of the haplotype, and the black dots represent the number of mutational steps between haplotypes.

initial investigation on the mitochondrial genetic diversity of Longman's beaked whales in the western tropical Indian Ocean and allow for comparisons with other beaked whale species (Table 2). Haplotype diversity (h = 0.791 ± 0.08) calculated for Longman's beaked whales is similar to or higher than that of other species studied to date (Dalebout et al., 2005, 2006; Kitamura et al., 2013; Thompson et al., 2016; Table 2), suggesting high levels of genetic diversity in this species. In a previous study by Garrigue et al. (2016), the haplotype identified in animals from New Caledonia (southwestern Pacific) was considered the same as the haplotype found in the Maldives when 226 bps of the mtDNA control region were compared. In this study, we compared a longer fragment of 447 bps, which allowed separation of the haplotype found in samples from New Caledonia and Taiwan (H4) from the haplotype identified in the samples from the Maldives and Seychelles (H2). Nucleotide diversity (π = 0.62% ± 0.04) estimated from all samples studied to date for this species was also similar to those found in other ziphiids, ranging in the mid-values of those reported for five other species with larger sample sizes (Table 2). This difference may be attributable to our smaller sample size and the longer gene region we analyzed, compared to the shorter mtDNA control region examined in previous studies (e.g., Dalebout et al., 2005). However, care must be taken when conducting these comparisons, particularly as the total sample size is limited to 16 individuals throughout the Indo-Pacific region.

Although conducting a full phylogeographic analysis for this species was beyond the scope of this study, it is interesting to find mtDNA control region haplotypes being shared in samples collected in some distant regions—for example, between samples from Taiwan and New Caledonia—which may indicate limited population structure in this species, similar to what was found in Gray's beaked whale (*Mesoplodon grayi*) in the South Pacific (Thompson et al., 2016). Longman's beaked whales have been regularly observed in the western Indian Ocean region, particularly in the Maldives, in Seychelles, and in the Mozambique Channel (Anderson et al., 2006). Additional efforts are encouraged to collect samples in these regions to further investigate the population structure, genetic and genomic diversity, and evolutionary ecology of Longman's beaked whales.

Table 2. Distribution, sample sizes, mtDNA control region sequence size studied (in base pairs [bps]), haplotype (*h*), and nucleotide (π) diversities (± standard deviation [SD]) estimated for beaked whales (Ziphiidae) around the globe

Species	Sample size (*n*)	Sample distribution	mtDNA control region fragment length (bp)	Haplotype diversity (*h*)	Nucleotide diversity (%) (π)	Reference
Indopacetus pacificus	16	Indo Pacific and Pacific Ocean	447	0.791 ± 0.080	0.62 ± 0.040	This study
Ziphius cavirostris	87	Worldwide	290	0.926 ± 0.010	1.27 ± 0.723	Dalebout et al., 2005
Hyperoodon ampullatus	183	North Atlantic Ocean	434	0.510 ± 0.030	0.14 ± 0.001	Dalebout et al., 2006
Berardius bairdii	64	Japan	431	0.565 ± 0.060	0.46 ± 0.004	Kitamura et al., 2013
Berardius bairdii	39	North Pacific	431	0.610 ± 0.060	0.67 ± 0.003	Kitamura et al., 2013
Berardius arnuxii	2	Japan	431	1.000 ± 0.500	0.23 ± 0.003	Kitamura et al., 2013
Mesoplodon grayi	94	Australia and New Zealand	530	0.963 ± 0.007	0.87 ± 0.478	Thompson et al., 2016

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CRediT Co-Author Contributions

Writing – Original Draft: SC and JK; *Writing – Review & Editing:* SC and JK; *Conceptualization:* SC and JK; *Investigation:* SC and JK; *Methodology:* SC; *Formal Analysis:* SC; *Project Administration:* JK; *Funding Acquisition:* JK

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