Genetics of Aquatic Organisms 10(1), GA934
https://doi.org/10.4194/GA934

PROOF
SHORT PAPER

GENAQUA
GENETICS OF AQUATIC ORGANISMS

Complete Mitogenome of Family Kogiidae (*Kogia breviceps* and *Kogia sima)* from Indian Waters

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How to Cite

Mukundan, L.P., Magesh, M., Ganesan, K., Krishnamoorthy, C., Balan, B., Sebastian, W., Cubelio, S.S. (2026). Complete Mitogenome of Family Kogiidae (*Kogia breviceps* and *Kogia sima)* from Indian Waters. *Genetics of Aquatic Organisms, 10(1), GA934*. https://doi.org/10.4194/GA934

Article History
Received 17 July 2025
Accepted 04 January 2026
First Online 16 January 2026

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Keywords
Kogiid whale
Indian ocean
Mitochondrial genome
Phylogeny
Odontoceti

Abstract

The only two extant species of the genus Kogia, the pygmy sperm whale (*Kogia breviceps*) and the dwarf sperm whale (*Kogia sima*), are a unique find in the world's oceans. This study presents the first complete mitochondrial genomes of *K. breviceps* and *K. sima* from Indian waters. The mitogenomes of *K. breviceps* and *K. sima* were 16,412bp and 16,405bp in length and comprised the standard set of 37 genes. Phylogenetic analysis confirmed the species status and their close evolutionary affinity with the family Physeteridae. This study will provide valuable information for future phylogenetic and population studies on these little-known odontocetes.

Introduction

The pygmy and dwarf sperm whales (*Kogia breviceps* Blainville, 1838 and *Kogia sima* Owen 1866) are among the least understood cetaceans, inhabiting deep offshore waters globally. Their elusive nature and limited research, particularly in the Indian Ocean, make understanding their population structure and genetic diversity challenging (Jefferson et al., 2011). Both species belong to the family Kogiidae and are closely related to the sperm whale (*Physeter catodon*). They are deep-diving specialists feeding primarily on squid. Kogiids are distributed globally across warm-temperate and tropical waters, with *K. sima* thought to favour somewhat warmer habitats than *K. breviceps* (Plon et al., 2023).

Research on Kogiid whales remains limited because they are exceptionally difficult to study in the wild due to their elusive surface behaviour, extended dive times, and predominantly solitary nature. (Ramos et al*.,* 2020). Consequently, information regarding their global distribution, abundance and population structure is primarily derived from stranding incidents and detection during acoustic surveys (McAlpine, 2018; McIvor et al., 2022). Although studies on *Kogia* genetics have been conducted globally, primarily focusing on Atlantic and Pacific populations, the Indian Ocean populations remain largely unexplored (Chivers et al., 2005). Previous studies on *Kogia* phylogeny have relied on short DNA fragments, hindering a comprehensive understanding of species and population boundaries (Shan et al., 2019). Mitochondrial DNA (mtDNA) is a

valuable tool for studying cetacean genetics due to its maternal inheritance, non-recombining nature, and rapid mutation rate (Cui et al*.,* 2017). Complete mitochondrial genomes provide more comprehensive information than partial sequences (Shan et al., 2019). Despite India's diverse cetacean fauna, molecular data, especially complete mitogenomic data, remain scarce (George et al., 2011). This knowledge gap, particularly for lesser-known species like *Kogia*, hinders our understanding of their genetic diversity and evolutionary history in Indian waters.

The study aims to sequence and analyse the complete mitochondrial genomes of *K. breviceps* and *K. sima* from Indian waters. We also conducted a phylogenetic analysis by comparing the protein-coding genes (PCGs) of the Kogiid mitogenomes with PCGs of 20 other Cetacean mitogenomes retrieved from GenBank, in order to gain deeper insights into their evolutionary relationships. This study's results will fill a crucial gap in the understanding of *Kogia* species in the Indian Ocean, offering insights into their evolutionary relationships and informing future conservation strategies.

Materials and Methods

Whale specimens were obtained from strandings along the Tamil Nadu coast, Southeastern India. Specimen collected from Sambai Village, Ramanathapuram District, Tamil Nadu, India (09°30'53''N, 78°54'59''E) on 25-05-2019 was assigned the institute ID: MM011. Another specimen collected from Kumarappan Vayal Fisherman Village, Pudhukottai District, Tamil Nadu, India (09°55'11''N, 79°09'10''E) on 06-07-2021 was assigned the institute ID: MM017. Initial species identification was based on morphological characteristics, following established identification keys (Gill, 1871; Sekiguchi et al., 1992; Wang et al., 2002; McAlpine, 2018). Tissue samples were collected, preserved in ethanol, and stored at -20°C. Genomic DNA was extracted using the DNeasy Blood & Tissue Kit.

To confirm species identity, the mitochondrial cytochrome oxidase 1 (COX1) gene was amplified using universal primers LCO1ea (5'-TCGGCCATTTTACCTATGTTCATA-3') and HBCUem (5'-GGTGGCCGAAGAATCAGAATA-3') (Alfonsi et al*.,* 2013), yielding a ~736 bp amplicon. PCR was performed in 50 µL reactions using Platinum SuperFi II DNA Polymerase (Thermo Fisher) with 1x SuperFi II buffer, 2.5 mM $MgCl_2$, 50 ng genomic DNA, and 25 pmol of each primer. Cycling conditions were: 98°C for 30 s, 32 cycles of 98°C for 10 s, 53°C for 10 s, 72°C for 30 s, and 72°C for 5 min. Products were purified and sequenced bidirectionally on a SeqStudio 24 Flex Genetic Analyzer (Applied Biosystems). Sequences were verified against GenBank using BLAST.

Complete mitochondrial genomes were amplified as 14 overlapping fragments using species-specific primers designed from previously published whale mitochondrial sequences available in GenBank. Primer pairs, sequences, and amplicon sizes are listed in Table 1. PCR reactions used 50 µL mix with Platinum

Table 1. List of primers used to amplify the complete mitochondrial genomes of *Kogia breviceps* and *K. sima*

S.No	Oligo Name	Sequence (5'-3')	Approximate size of amplicons
1.	Physet_Kogi_mtDNA_S75F Physet_Kogi_mtDNA_S1474R	5'AAAGGTTTGGTCCCAGCCTTC3' 5'TATCACCAGGCTCGTTAGGCTT3'	1399 bp
2.	Physet_Kogi_mtDNA_S1283F Physet_Kogi_mtDNA_S2775R	5'AAAGCAAAGMTTACCCCTTGTACC3' 5'GAGGGGATTTGAACCTCTGGGTRT3'	1492 bp
3.	Physet_Kogi_mtDNA_S2475F Physet_Kogi_mtDNA_S3927R	5'ATCCTAATGGTGCAGCCGCTAT3' 5'ATTTTCGGGGTATGGGCCCGATA3'	1452 bp
4.	Physet_Kogi_mtDNA_S3679F Physet_Kogi_mtDNA_S5263R	5'GCYCTCTGCATRTGRCACATCTCA3' 5'TTCAATCCTGCCGGGRCTTCT3'	1584 bp
5.	Physet_Kogi_mtDNA_S5022F Physet_Kogi_mtDNA_S6514R	5'AGCCTTCAAAGCYCTAAGCAAGT3' 5'TAGTGRAAGTGRGCKACTACATAG3'	1492 bp
6.	Physet_Kogi_mtDNA_S6230F Physet_Kogi_mtDNA_S7676R	5'CTTTATCGTATGAGCYCACCACAT3' 5'TTTGAGCCRCAGATTTCTGAAC3'	1446 bp
7.	Physet_Kogi_mtDNA_S7436F Physet_Kogi_mtDNA_S8941R	5'TCCCAACATCRGAYTTAAAACCAG3' 5'CCTTGRAAGGTRCTYTCTCGGA3'	1505 bp
8.	Physet_Kogi_mtDNA_S8737F Physet_Kogi_mtDNA_S10228R	5'TGACCCACCARACCCACTCWTACC3' 5'RTCCRATRGCTGCYTCRCAGGCT3'	1491 bp
9.	Physet_Kogi_mtDNA_S9963F Physet_Kogi_mtDNA_S11403R	5'TGATTTCGACTCACTRGACTGTGA3' 5'GTARGGCRAGGTTTGTTAGGCT3'	1440 bp
10.	Physet_Kogi_mtDNA_S11189F Physet_Kogi_mtDNA_S12667R	5'CACAGSYATYCTCATCCAAACC3' 5'GGGTRRAAGCGGAYAAGTAGGA3'	1478 bp
11.	Physet_Kogi_mtDNA_S12373F Physet_Kogi_mtDNA_S13780R	5'CCGCYCTCCARGCAATCCTAT3' 5'RGTTGSTGCRTTGTATAGTTATGG3'	1407 bp
12.	Physet_Kogi_mtDNA_S13563F Physet_Kogi_mtDNA_S15061R	5'AAAACSACAGCCCTCATCCAA3' 5'TGGRTTTGCTGGGGTRTAGTTGT3'	1498 bp
13.	Physet_Kogi_mtDNA_S14888F Physet_Kogi_mtDNA_S16487R	5'GGATCCAACAACCCCMYAGGAAT3' 5'GTGYCATRRGGCTTGTGTCGGA3'	1599 bp
14.	Physet_Kogi_mtDNA_S76F Physet_Kogi_mtDNA_S15055R	5'AYYCTTCCGACCCTGGTTTGGAA3' 5'TRGGRCTGTTGATRTGGGGTCGT3'	15055 bp

SuperFi II DNA Polymerase, 1x SuperFi II buffer, 2.5 mM $MgCl_2$, 50 ng DNA, and 25 pmol primers. Cycling conditions were: 98°C for 30 s, 35 cycles of 98°C for 10 s, 52–58°C for 10 s, 72°C for 45 s, and 72°C for 5 min. Amplicon sizes were verified by 1% agarose gel electrophoresis.

Bidirectional Sanger sequencing achieved 2x coverage per amplicon (4x in overlaps). Reads were trimmed to Phred ≥30 (average ~40), with low-quality ends (<Phred 20) clipped, yielding 800–1,000 bp reads. Electropherograms were inspected using Sequence Scanner (Applied Biosystems). Sequences were assembled in Geneious Prime (medium sensitivity, ≤5% mismatches, ≥100 bp overlaps) using reference-guided mapping. No gaps occurred due to >200 bp overlaps, with discrepancies resolved by consensus calling. The resulting sequences were, annotated by aligning with other Odontocete mitochondrial genomes using Geneious Prime (Biomatters Ltd.), the MitoAnnotator pipeline (Iwasaki et al., 2013) and MITOS (Bernt et al., 2013). tRNA genes were annotated by using tRNAscan-SE 2.0 (Chan et al., 2021) with default parameters coupled with ARWEN software (Laslett & Canback, 2008).

To investigate the phylogenetic relationships of *Kogia breviceps* and *Kogia sima* within the family Kogiidae and the infraorder Cetacea, complete mitochondrial genomes of 20 other Cetacean species were retrieved from GenBank. This included members of the families *Physeteridae* (sperm whales), *Delphinidae* (dolphins), *Monodontidae* (belugas and narwhals), *Ziphiidae* (beaked whales), and *Phocoenidae* (porpoises) (Table 2). The mitogenome of *Vulpes lagopus* (NC026529) was used as an outgroup. The 13 protein-coding genes for each species were aligned separately using MAFFT v7 (Katoh & Standley, 2013) under default parameters and then concatenated, excluding the stop codons. The sequences were trimmed manually after visual inspection to remove ambiguous regions. The optimal partition scheme and the evolutionary model for each partition based on codon position were identified using PartitionFinder v2.1.1 (Lanfear et al*.,* 2016). The parameters used were the greedy algorithm, models=all, branch lengths estimated as unlinked and Bayesian information criterion (BIC). Maximum-likelihood (ML) analysis was conducted in RAxML v8.2.12 (Stamatakis, 2014) using the model GTRGAMMA for all partitions and 10000 nonparametric bootstrapping replicates were used to assess the node support. Bayesian phylogenetic analysis was conducted using MrBayes 3.2.7 software (Ronquist et al., 2012) with 10,000,000 generations. The resulting trees obtained from ML and BI analyses were visualized and edited by FigTree v1.4.3 with adjustable settings.

Results and Discussion

The stranded specimens were identified as an adult female of *K. breviceps* (MM011) and a pregnant female of *K. sima* (MM017) based on the identification keys (Gill, 1871; Sekiguchi et al., 1992; Wang et al., 2002; McAlpine, 2018). *K. breviceps* has a smaller, falcate dorsal fin located more posteriorly than *K. sima*, which has a dolphin-like dorsal fin near the midpoint of the back. Additionally, *K. sima* has short longitudinal grooves on the throat, while these grooves are absent in *K. breviceps*. *K. breviceps* also has a longer snout than *K. sima*, as measured by the distance between the tip of the snout and the blowhole. Furthermore, no maxillary teeth are present in *K. breviceps*, whereas *K. sima* has ten pairs of mandibular teeth and two pairs of maxillary teeth. There is no diagnostic difference in colour pattern between the two species. Dorsally, both species are dark grey, and ventrally, they are white.

Table 2. Cetacean mitogenomes used in the present study to construct the phylogenetic tree

S.No	Superfamily	Family	Species	Accession number
1.	Mysticeti	Balaenidae	*Balaena mysticetus*	AP006472.1 accessed on 13.05.2024
2.	Mysticeti	Balaenidae	*Eubalaena australis*	AP006473.1 accessed on 13.05.2024
3.	Mysticeti	Balaenopteridae	*Balaenoptera acutorostrata*	AP006468.1 accessed on 13.05.2024
4.	Mysticeti	Balaenopteridae	*Balaenoptera bonaerensis*	AP006466.1 accessed on 14.05.2024
5.	Mysticeti	Eschrichtiidae	*Eschrichtius robustus*	AP006471.1 accessed on 14.05.2024
6.	Mysticeti	Neobalaenidae	*Caperea marginata*	AP006475.1 accessed on 14.05.2024
7.	Odontoceti	Delphinidae	*Cephalorhynchus commersonii*	NC060610.1 accessed on 14.05.2024
8.	Odontoceti	Delphinidae	*Cephalorhynchus heavisidii*	NC020696.1 accessed on 14.05.2024
9.	Odontoceti	Kogiidae	*Kogia breviceps*	NC005272.1 accessed on 14.05.2024
10.	Odontoceti	Kogiidae	*Kogia sima*	MH791441.1 accessed on 14.05.2024
11.	Odontoceti	Monodontidae	*Delphinapterus leucas*	NC034236.1 accessed on 14.05.2024
12.	Odontoceti	Monodontidae	*Monodon monoceros*	MT251289.1 accessed on 14.05.2024
13.	Odontoceti	Phocoenidae	*Neophocaena asiaeorientalis*	NC026456.1 accessed on 10.05.2024
14.	Odontoceti	Phocoenidae	*Neophocaena phocaenoides*	MT948062.1 accessed on 10.05.2024
15.	Odontoceti	Phocoenidae	*Phocoena dioptrica*	NC053752.1 accessed on 10.05.2024
16.	Odontoceti	Phocoenidae	*Phocoena phocoena*	MT948111.1 accessed on 10.05.2024
17.	Odontoceti	Physeteridae	*Physeter catodon*	KC312610.2 accessed on 10.05.2024
18.	Odontoceti	Pontoporiidae	*Pontoporia blainvillei*	AJ554060.1 accessed on 14.05.2024
19.	Odontoceti	Ziphiidae	*Berardius bairdii*	NC005274.1 accessed on 14.05.2024
20.	Odontoceti	Ziphiidae	*Hyperoodon ampullatus*	MN536368.1 accessed on 14.05.2024

The mitogenomes of *K. breviceps* and *K. sima* were found to be 16,412bp and 16,405bp in length, respectively, in line with the typical size range for mammalian mitochondrial DNA (mtDNA). The overall structure and gene content of both mitogenomes were conserved, and they contain the typical 37 genes found in vertebrate mitochondrial genomes, including 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs), and a control region (Figure 1). All genes, except for ND6 and eight tRNAs ($tRNA^{Gln}$, $tRNA^{Ala}$, $tRNA^{Asn}$, $tRNA^{Cys}$, $tRNA^{Tyr}$, $tRNA^{Ser}$, $tRNA^{Glu}$ and $tRNA^{Pro}$), were located on the heavy (H) strand (Table 3), a common feature in most vertebrate mitogenomes (Shi et al*.,* 2016).

The protein-coding genes ND1-ND6, ND4L, COX1-COX3, ATP6, ATP8, and CYTB in both species exhibited an arrangement consistent with that found in other cetacean mitochondrial genomes (Kim et al*.,* 2017). This conservation in gene order supports the evolutionary stability of mitochondrial gene arrangements in cetaceans. The nucleotide frequencies in *K. breviceps* were A: 31.4%, T: 25.4%, C: 29.1%, and G: 14.2%, while *K. sima* exhibited similar proportions: A: 31.2%, T: 25.1%, C: 29.3%, and G: 14.3%. This indicates that the average nucleotide composition is biased towards A and T (A+T= 56.8% for *K. breviceps* and 56.3% for *K. sima*) than G and C (G+C= 43.3% for *K. breviceps* and 43.6% for *K. sima*). The lowest frequency among all four bases was observed for G, and this pattern, along with the high A+T content, has been observed in the mitogenome of many vertebrates (Wang et al*.,* 2011; Kim et al*.,* 2017). The AT-skew values for *K. breviceps* and *K. sima* were 10.6% and 10.8%, respectively, indicating a slight bias towards A and T. This AT-rich composition is consistent with other mammalian species and is primarily attributed to mutational and structural asymmetries during replication and repair (Formaggioni et al*.,* 2021; Gomes-dos-Santos et al*.,* 2023).

Eight overlaps with a total length of 74bp and 73bp were observed in the mitogenomes of *K. breviceps* and *K. sima,* respectively, which makes the mitochondrial genome compact. A 56bp nucleotide sequence was dispersed in ten intergenic spacers within the mitogenome of *K. breviceps*, ranging in size from 1 to 32bp. In the case of *K. sima* mitogenome, a 59bp nucleotide sequence was distributed in 12 intergenic

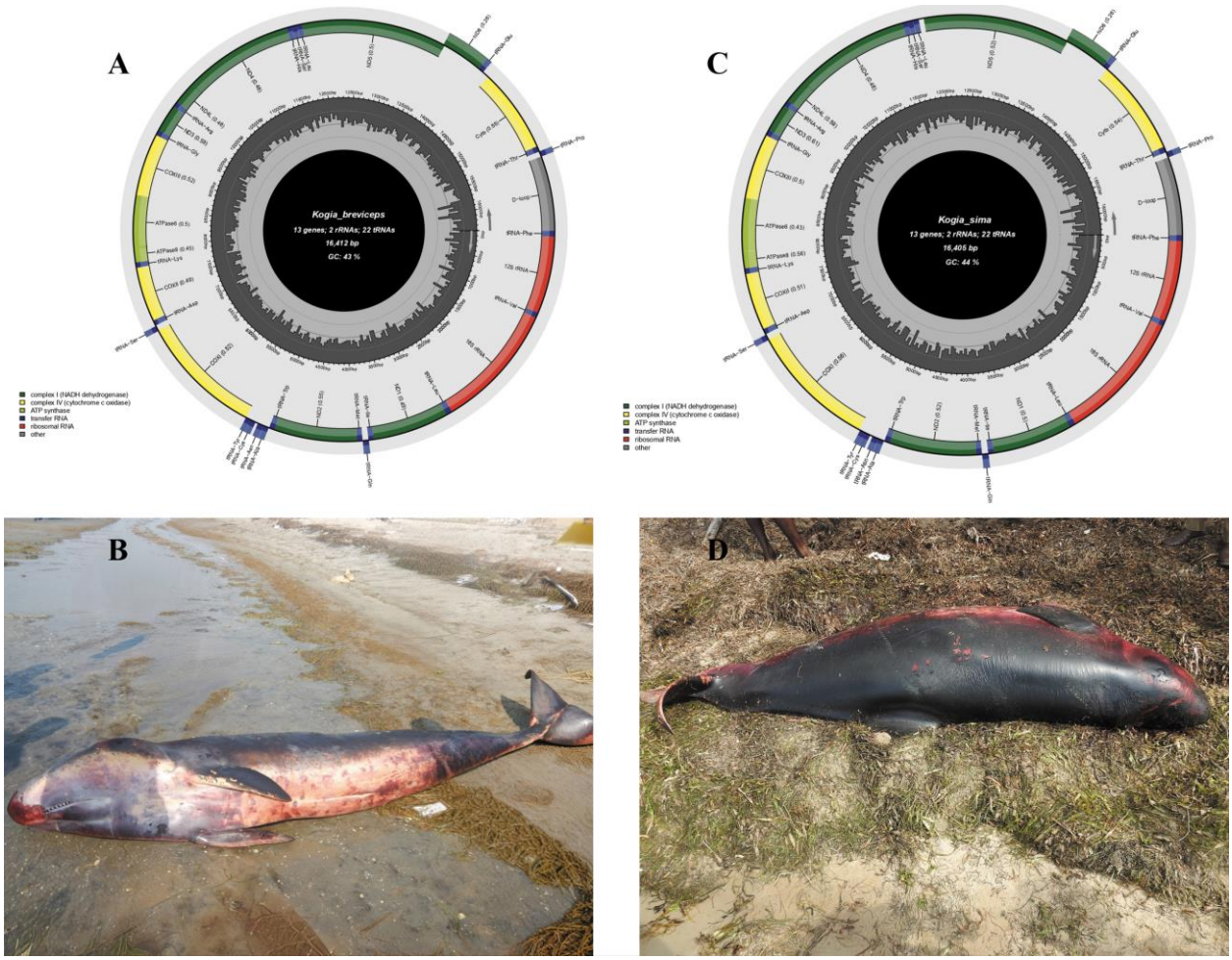

Figure 1. (A & C) Illustrate the mitochondrial gene organization of the pygmy sperm whale (*Kogia breviceps*) (Accession no: PV738932, specimen ID: MM011) and dwarf sperm whale (*Kogia sima*) (Accession no: PV738933, specimen ID: MM017). Genes encoded on the light and heavy strands are depicted inside and outside the circular map, respectively. The inner grey ring represents the GC content. (B & D) represents images of the stranded specimens of *K. breviceps* and *K. sima*.

spacers, also ranging in size from 1 to 32bp. In both the mitogenomes, the longest spacer was located between the $tRNA^{Asn}$ and the $tRNA^{Cys}$, which is typically identified as the origin of the light strand replication in mitogenomes (Zhang et al., 2014; Cui et al., 2017).

Complete mitochondrial genomes containing multiple genes have been shown to enhance the reliability of phylogenetic interpretations, thereby providing a more accurate resolution of an organism's higher-level relatedness (Miya & Nishida, 2000). Both Bayesian inference (BI) and Maximum Likelihood (ML) phylogenetic methods using all the 13 protein-coding genes produced congruent topologies, confirming the monophyly of the family Kogiidae (Figure 2). The specimens from the Indian Ocean showed a close relationship to *K. breviceps* (NC005272) and *K. sima* (MH791441), confirming their identification. The phylogenetic tree also demonstrated that the family Kogiidae is closely related to the family Physeteridae (*Physeter catodon*), consistent with previous studies (Shan et al., 2019). The superfamilies Mysticeti (baleen whales) and Odontoceti (toothed whales, including sperm whale) were clearly separated into distinct clades, and the topologies of all the selected ingroups resolved into their respective families, affirming well-established cetacean phylogenetic relationships (Arnason et al*.,* 2004).

Because morphological examinations during fishery interactions, sightings and strandings have failed to resolve inter and intra-specific variations for Kogiid species (Aneesh et al., 2019), it is important to create strong genomic data from the Indian Ocean in order to avoid their misidentification. Genetic research on cetaceans in Indian waters has so far been restricted to analyses of partial mitochondrial DNA sequences (George et al*.,* 2011; Kundu et al*.,* 2024; Kumar et al., 2025). This study reports the first complete mitochondrial genomes of *K. breviceps* and *K. sima* from Indian waters, bridging the existing gap in genetic information for the Indian Ocean and contributing

Table 3. Characteristics of the complete mitochondrial genomes of *Kogia breviceps/K. sima*

Gene	Position		Size (Bp)	Codon		Strand	Trna	Spacer(+)
	From	To		Start	Stop		Anticodon	/Overlap(–)
$tRNA^{Phe}$	1/1	73/73	73/73			H/H	GAA/GAA	0/0
12S rRNA	74/74	1045/1045	972/972			H/ H		0/0
$tRNA^{Val}$	1046/1046	1112/1112	67/67			H/H	TAC/TAC	0/0
16S rRNA	1113/1113	2693/2688	1581/1576			H/H		1/1
$tRNA^{Leu}$	2695/2690	2769/2764	75/75			H/H	TAA/TAA	0/2
ND1	2772/2767	3728/3722	957/956	ATG/ATG	TAA/TAA	H/H		-1/0
$tRNA^{Ile}$	3728/3723	3796/3791	69/69			H/H	GAT/GAT	-2/-1
$tRNA^{Gln}$	3794/3789	3869/3864	76/76			L/L	TTG/TTG	1/1
$tRNA^{Met}$	3871/3866	3939/3934	69/69			H/H	CAT/CAT	0/0
ND2	3940/3935	4983/4978	1044/1044	ATA/ ATA	TAG/TAG	H/H		-1/-1
$tRNA^{Trp}$	4982/4977	5050/5045	69/69			H/H	TCA/TCA	5/5
$tRNA^{Ala}$	5056/5051	5124/5119	69/69			L/L	TGC/TGC	1/1
$tRNA^{Asn}$	5126/5121	5199/5194	74/74			L/L	GTT/GTT	32/32
$tRNA^{Cys}$	5232/5227	5298/5293	67/67			L/L	GCA/GCA	0/0
$tRNA^{Tyr}$	5299/5294	5364/5359	66/66			L/L	GTA/GTA	1/1
COX1	5366/5361	6916/6911	1551/1551	ATG/ATG	AGA/AGA	H/H		-5/-5
$tRNA^{Ser}$	6912/6907	6980/6975	69/69			L/L	TGA/TGA	7/7
$tRNA^{Asp}$	6988/6983	7055/7050	68/68			H/H	GTC/GTC	0/0
COX2	7056/7051	7739/7734	684/684	ATG/ATG	TAA/TAA	H/H		3/3
$tRNA^{Lys}$	7743/7738	7809/7804	67/67			H/H	TTT/TTT	0/1
ATP8	7811/7806	8011/8006	201/201	ATG/ATG	TAG/TAG	H/H		-40/-40
ATP6	7972/7967	8652/8647	681/681	ATG/ATG	TAA/TAA	H/H		-1/-1
COX3	8652/8647	9436/9431	785/785	ATG/ATG	TA/TA	H/H		0/0
$tRNA^{Gly}$	9437/9432	9505/9500	69/69			H/H	TCC/TCC	0/0
ND3	9506/9501	9852/9847	347/347	ATA/ATA	TA/TA	H/H		0/0
$tRNA^{Arg}$	9853/9848	9921/9916	69/69			H/H	TCG/TCG	0/0
ND4L	9922/9917	10218/10213	297/297	GTG/ATG	TAA/TAA	H/H		-7/-7
ND4	10212/10207	11589/11584	1378/1378	ATG/ATG	T/T	H/H		0/0
$tRNA^{His}$	11590/11585	11658/11653	69/69			H/H	GTG/GTG	0/0
$tRNA^{Ser}$	11659/11654	11718/11713	60/60			H/H	GCT/GCT	1/1
$tRNA^{Leu}$	11720/11715	11789/11784	70/70			H/H	TAG/TAG	0/0
ND5	11781/11776	13610/13605	1830/1830	ATA/ATA	TAA/TAA	H/H		-17/-17
ND6	13594/13589	14121/14116	528/528	TTA/TTA	TA/TAA	L/L		0/0
$tRNA^{Glu}$	14122/14117	14190/14185	69/69			L/L	TTC/TTC	4/4
CYTB	14195/14190	15336/15329	1142/1140	ATG/ATG	AGA/AGA	H/H		0/0
$tRNA^{Thr}$	15337/15330	15406/15398	70/69			H/H	TGT/TGT	0/-1
tRNAPro	15407/15398	15473/15465	67/68			H/H	TGG/TGG	0/0
Control region	15474/15466	16412/16406	939/941			H/H		0/0

valuable data to the regional cetacean genetic repository. The present study fills a critical gap in our understanding of Kogiidae genetics in the Indian Ocean, a region where strandings are rare (Aneesh et al., 2019) and cetacean population dynamics remain poorly understood. The genetic data obtained from these stranded individuals offer a valuable baseline for future research on population genetics, conservation management, and phylogeography in the Indian Ocean.

Conclusions

The newly sequenced complete mitochondrial genomes of the pygmy and dwarf sperm whales from Indian waters represent a significant contribution to the genetic database for these elusive species. The phylogenetic analysis confirmed the species identity of the Indian specimens and placed them within the broader evolutionary context of the Kogiidae family. This genomic resource will aid in resolving taxonomic ambiguities, improving species identification, and promoting the conservation of these rare cetaceans. While the conservation status of *Kogia* species is challenging to assess due to their elusive nature and deep-water habitats, the increasing number of strandings along the Indian coast may indicate shifts in distribution patterns or potential threats from human activities. Future research should combine genetic data with ecological information to better understand the population structure, migration patterns, and threats facing *Kogia* species in the Indian Ocean.

Data Availability

The complete mitochondrial genome sequences of *Kogia breviceps* and *Kogia sima* obtained in this study have been deposited in GenBank under accession numbers PV738932 (*K. breviceps,* specimen ID: MM011) and PV738933 (*K. sima,* specimen ID: MM017).

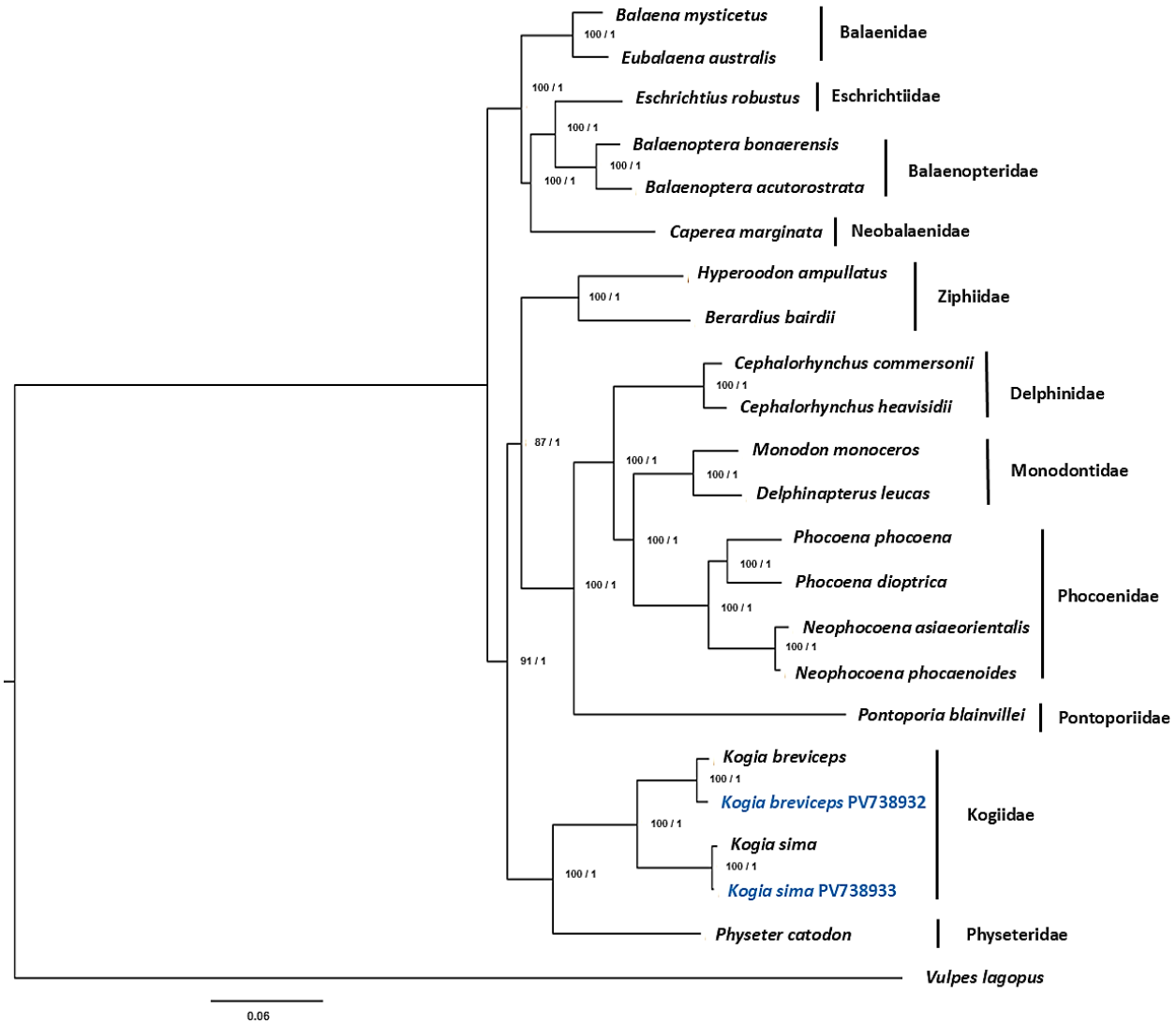

Figure 2. Phylogenetic tree inferred from the nucleotide sequences of 22 Cetacean species. The mitogenome of *Vulpes lagopus* was used as an outgroup. The numbers at the nodes show the bootstrap values/Bayesian posterior probabilities. The sequences for *Kogia breviceps* (Accession no: PV738932, specimen ID: MM011) and *Kogia sima* (Accession no: PV738933, specimen ID: MM017) were generated in this study.

Ethical Statement

The biological material for this work was obtained from dead stranded animals and thus no ethical approval is essential.

Funding Information

Financial support for this work was provided by the Ministry of Earth Sciences, Government of India, through the national scheme "PRITHVI."

Author Contribution

Conceptualization, Methodology, approving the final version to be published: WS, SSC; Writing- Original draft preparation: LM; Data curation, Software: LM, BB; Writing – Review & Editing, sample collection, Resources: MM, KG, CK.

Conflict of Interest

The authors declare that they have no known competing financial or non-financial, professional, or personal conflicts that could have appeared to influence the work reported in this paper.

Acknowledgements

The authors are grateful to the Secretary, Ministry of Earth Sciences, New Delhi and Head, CMLRE, Kochi, for the invaluable encouragement and support provided throughout this research. Furthermore, we are grateful to the officials of the Tamil Nadu Forest Department, for their assistance in providing the necessary biological materials.

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