

# The Complete Mitogenome of Longman's Beaked Whale (*Indopacetus pacificus*) (Chordata: Ziphiidae)

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**Abstract.** In this study, we used the next-generation sequencing method to deduce the complete mitogenome of Longman's beaked whale (*Indopacetus pacificus*) for the first time. The nucleotide composition was asymmetric (33.2% A, 27.0% C, 12.8% G, and 27.1% T), with an overall GC content of 39.9%. The assembled mitogenome consisted of 16,341 base pairs (bp) and followed the typical vertebrate arrangement, including 13 protein coding genes, 22 transfer RNAs, two ribosomal RNA genes, and a non-coding control region of the D-loop. The D-loop contains 873 bp and is located between tRNA-Pro and tRNA-Phe. The maximum likelihood phylogenetic tree of 10 cetacean mitogenomes showed that *I. pacificus* is located in the clade with *Hyperoodon ampullatus* and *Berardius bairdii*. The complete mitogenome of the Indo-Pacific beaked whale deduced in this study provides essential and important DNA molecular data for further phylogenetic and evolutionary analyses of cetaceans.

**Key words:** Ziphiidae, Longman's beaked whale, mitogenome, next generation sequencing.

## INTRODUCTION

Longman's beaked whale (*Indopacetus pacificus*) is one of the world's most poorly known whales and is considered one of the rarest of all cetaceans (West *et al.* 2013). It has been known for more than 30 years as a large, unidentified species of beaked whale that inhabits tropical waters of the Pacific and Indian Oceans. It belongs to the family Ziphiidae and is among the least known cetaceans. The genus *Indopacetus* includes only one species, *I. pacificus*, with no

known subspecies.

*Indopacetus pacificus*, also known as the Indo-Pacific beaked whale or tropical bottlenose whale, is restricted to warmer waters of the Pacific and Indian Oceans. It can be found in deep ocean waters, and the color of this whale is poorly known but it is probably of a dark-bluish or black hue. This species has an estimated length of 5.0~5.5 m, a moderately long beak, a relatively flat head, and a distinctive dorsal fin that is low, triangular, and wide-based (Nowak 2003). It has two forward-pointing teeth present at the

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very front of the lower jawbone; each of which is located at the tip of its respective mandible. Only mature males have teeth that erupt (Pitman *et al.* 1999) which indicates sexual dimorphism in this species. Until recently, it was one of the least known species among living toothed whales, and only cryptic information was available on its field characteristics (Afsal *et al.* 2009). Moreover, evidence revealed that fishery interactions and loud anthropogenic sounds may threaten Longman's beaked whale. Even low levels of bycatch might cause unsustainable impacts to this naturally rare cetacean (Taylor *et al.* 2008). It is listed in Appendix II of CITES, and research is needed to determine the impacts of potential threats to this species.

Beaked whales in the Ziphiidae are generally poorly known and have some unresolved taxonomic issues (Burbidge *et al.* 2014). Not much information is known about intraspecific variations in morphology, and many species are very similar in external appearance (Dalebout 2002). Although *I. pacificus* is morphologically distinct from other ziphiid species, significant potential still exists for the misidentification of these animals, both at sea and when stranded. These problems occur due in part to its rarity, remote distribution, and similarity in external form to *Hyperoodon planifrons*, a southern bottlenose whale, as well the overall subtlety of diagnostic features in ziphiids (Dalebout *et al.* 2003). Since very little information is available concerning *I. pacificus*, it is difficult to describe its appearance (Tinker 1988). The aim of this paper was to decode the complete mitogenome of *I. pacificus*, so that a clear molecular structure of this species can be presented.

## MATERIALS AND METHODS

Muscle tissue from a dead stranded *I. pacificus* (voucher no. NMNS011169) was collected in Ilan County, northeastern Taiwan on 23 July 2005. The methods for genomic DNA extraction, library construction, and next-generation sequencing (NGS) followed those described in previous publication (Shen *et al.* 2014). Using commercial software (Geneious V9, Auckland, New Zealand), about 0.004% (912 of 21,026,460) raw NGS reads generated by MiSeq (Illumina, San Diego, CA, USA.) were *de novo* assembled to produce a circular form of the complete mitogenome with

about an average of 14 coverage. To validate the phylogenetic position of *I. pacificus*, we used PHYML 3.0 (Guindon *et al.* 2010) software to construct a maximum-likelihood tree containing complete mitogenomes of seven species derived from four different genera in the Ziphiidae. The pygmy sperm whale (*Kogia breviceps*) (family Kogiidae) and sperm whale (*Physeter macrocephalus*) (family Physetrida) were used as outgroups for tree rooting. Substitution model selection for all mitogenomes was performed using PHYML as implemented in Smart Model Selection (SMS) in PhyML (Lefort *et al.* 2017). The best-fitting model according to the Bayesian information criterion (BIC) was used for the phylogenetic analyses.

## DESCRIPTION AND REMARKS

The complete mitogenome of *I. pacificus* consists of 16,341 base pairs (bp) (GenBank accession no.: KY364702). The nucleotide composition was asymmetric (33.2% A, 27.0% C, 12.8% G, and 27.1% T) with an overall GC content of 39.9%. The D-loop contained 873 bp and was located between transfer (t)RNA-Pro and tRNA-Phe.

The protein coding, and ribosomal (r)RNA and tRNA genes of the mitogenome were predicted using the DOGMA (Wyman *et al.* 2004), ARWEN (Laslett and Canback 2008), and MITOS (Bernt *et al.* 2013) tools. Some ambiguous annotations were manually inspected by BLAST against closely related species. Four of 13 protein-coding genes (PCGs) terminated with incomplete stop codons of T- - (*COX1* and *ND4*). Other PCGs terminated with either TAA or TAG. The longest one was the *ND5* gene (1821 bp) among all PCGs, whereas the shortest was the *ATP8* gene (198 bp). The *12S* rRNA (1046 bp) and *16S* rRNA (2692 bp) genes were located between tRNA-Phe and tRNA-Leu (UAA) and were separated by tRNA-Val. Figure 1 illustrates the schematic map of the 16,341-bp mtDNA of *I. pacificus*.

Table 1 shows length distributions of 13 PCGs, two rRNAs, and the D-loop region among ten cetacean mitogenomes examined in this study. A length variation was not shown in the *cytochrome B*, *ND6*, *ND5*, *ND4*, *ND4L*, *ATP6*, or *COI* genes. The most variable DNA length was among the D-Loop regions and ranged

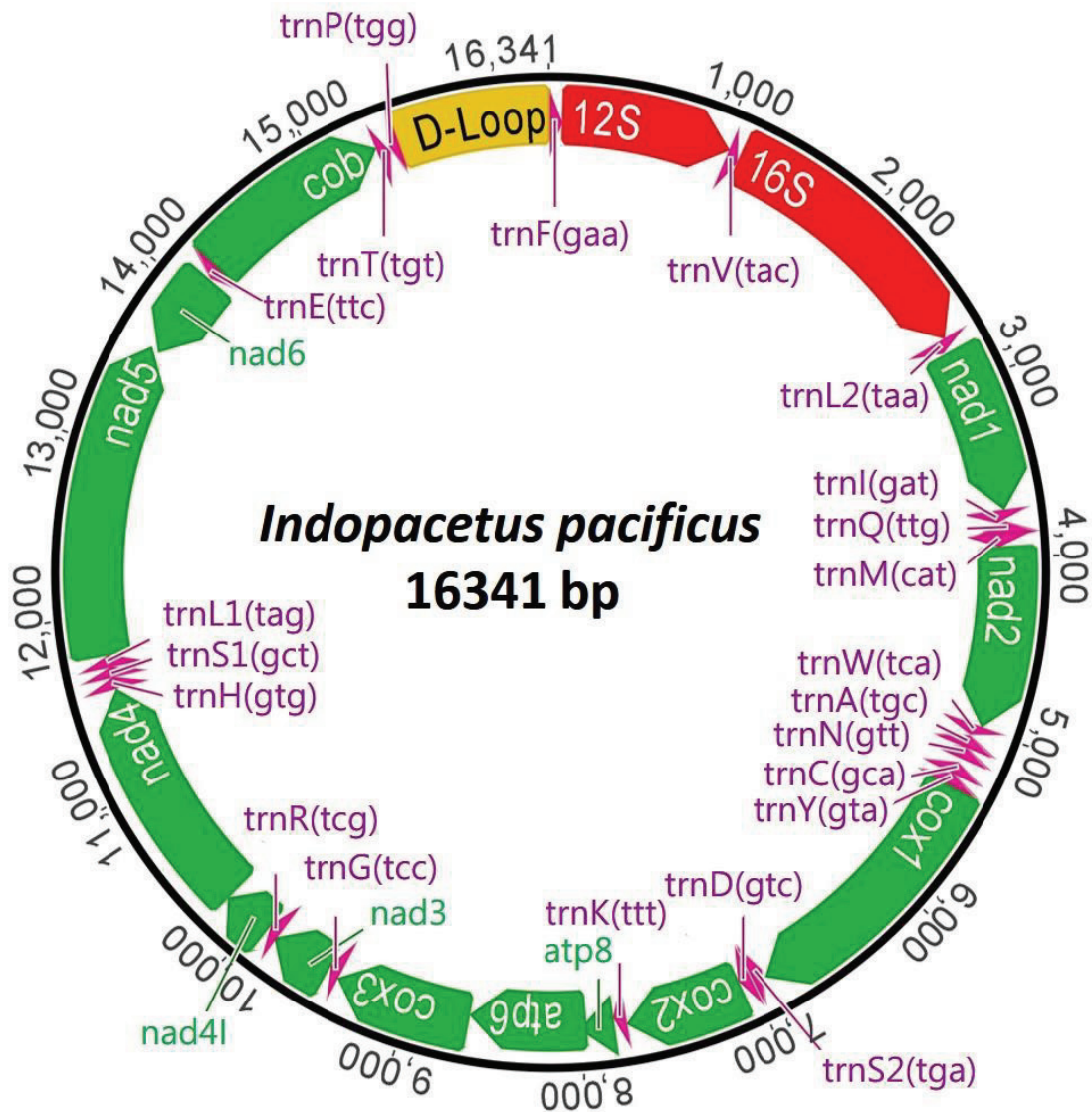


Fig. 1. Schematic map of the 16,341-bp mtDNA of *Indopacetus pacificus*. Green-colored sections represent 13 protein-coding genes: seven subunits of complex I (nd); one subunit of complex III (cob); three subunits of cytochrome c oxidase (cox); and two subunits of ATP synthase (atp6 and atp8). 12S and 16S ribosomal RNA are in red-colored sections; 22 transfer RNAs are identified at their positions; and the non-coding control region is in the brown-colored section.

from 870 bp of *M. ginkgodens* to 954 bp of *P. macrosaphalus*. In addition, DNA sequence divergences were calculated as p-distances (Nei and Kumar 2000) of the 13 PCGs, two rRNAs, and D-loops among the ten mitogenomes examined. Table 2 shows the overall mean p-distance and standard error (SE) of each gene or DNA fragment. Among them, 12S rRNA and 16S rRNA were the two least variable genes, and the D-Loop region was the most divergent fragment of the ten cetacean mitogenomes.

The maximum-likelihood phylogenetic tree (Fig. 2) shows that *I. pacificus* is located in the clade with *Hyperoodon* and *Mesoplodon*. It is not a sister species with *Mesoplodon* (Dalebout *et al.* 2004) nor *Ziphius* (Morin *et al.* 2017), a genus that was previously thought to be closely related to *I. pacificus*. Our results shed some light on relationships among the four genera of the Ziphiidae, and further research is needed to clarify ziphiid phylogeny. In conclusion, the complete mitogenome of *I. pacificus* was decoded

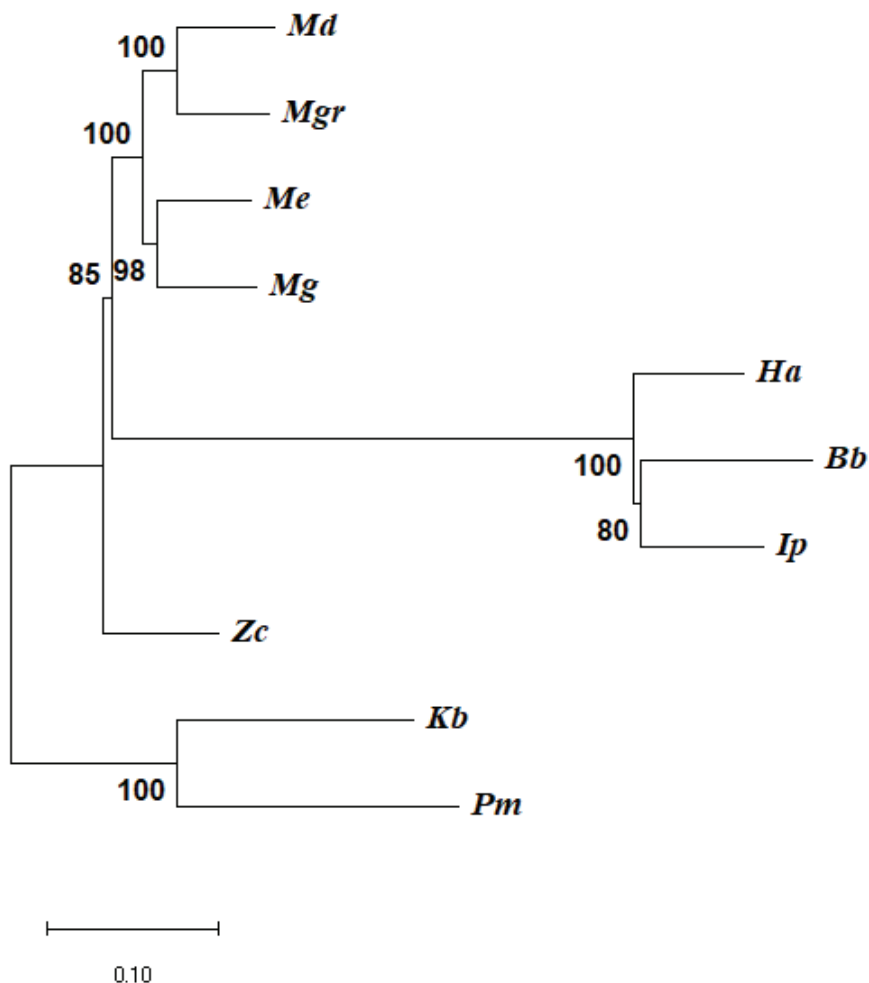


Fig. 2. Molecular phylogeny of *Indopacetus pacificus* and other related species in the Ziphiidae based on the complete mitogenome. The complete mitogenomes of additional species were downloaded from GenBank, and the phylogenetic tree was constructed by the maximum-likelihood method with the best-fitting model GTR+G and the computed approximate likelihood ratio test (SH-like branch supports). GenBank accession numbers for tree construction are listed as follows: *Ip*, *Indopacetus pacificus* (KY364702); *Me*, *Mesoplodon europaeus* (KC776688); *Mg*, *Mesoplodon ginkgodens* (KR534596); *Md*, *Mesoplodon densirostris* (KF032860); *Mgr*, *Mesoplodon grayi* (KF981442); *Bb*, *Berardius bairdii* (AJ554057); *Pm*, *Physeter macrocephalus* (AJ277029); and *Kb*, *Kogia breviceps* (AJ554055).

for the first time in this study and provides essential and important DNA molecular data for further phylogenetic and evolutionary analyses of cetaceans.

#### Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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# 朗氏喙鯨(*Indopacetus pacificus*) (Chordata: Ziphiidae)的完整粒線體基因體組成

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本研究利用次世代定序技術首次成功獲得朗氏喙鯨(*Indopacetus pacificus*)的完整粒線體DNA序列。本種粒線體基因體的核 酸組成爲非對稱性，其組成爲33.2% A, 27.0% C, 12.8% G, 及27.1% T，整體的GC組成是39.9%。經組裝後的粒線體基因體共有 16,341鹼基對。如同典型的脊椎動物一樣，本種的粒線體DNA環狀結構的基因排列組合包含13個蛋白質編碼基因(protein coding genes), 22個轉移核糖核酸(transfer RNAs)基因, 2個核糖體核糖核酸(ribosomal RNAs)基因及一個非編碼區域的控制區(non-coding control region of the D-loop，以下簡稱D-loop)。D-loop共有873 鹼基對，座落於 tRNA-Pro與 tRNA-Phe之間。以最大似然分析分法建構10種齒鯨之粒線體基因體分子親緣樹發現，朗氏喙鯨與北瓶鼻鯨(*Hyperoodon ampullatus*)和貝氏喙鯨(*Berardius bairdii*)被歸類於同一個支系中。本研究完整組裝朗氏喙鯨的粒線體基因體，提供重要的DNA分子訊息可做爲鯨類的親緣關係及演化分析的素材。

關鍵詞：喙鯨科，朗氏喙鯨，粒線體基因體，次世代定序