



Molecular Identification of Delphinids and Finless Porpoise (Cetacea) from the Arabian Sea and Bay of Bengal

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Abstract

The exact number of extant delphinid species from seas around India is still debated and the lack of adequate field keys and reliable inventory has resulted in misidentification of several species. As a part of a project to develop a molecular taxonomy of cetaceans from this region, partial sequences of mtDNA cytochrome b were generated from accidentally caught/stranded delphinids and finless porpoise. Species were identified by phylogenetic reconstruction of sample sequences with the reference sequences available in portals GenBank (NCBI) and the web-based program DNA Surveillance. A comparison was made with the homologous sequences of corresponding species from other seas of the world. Our molecular investigations allowed us to identify five species of cetaceans from Indian coasts, including Delphinus capensis, previously reported as D. delphis. We detected unique haplotypes in Indo pacific humpbacked dolphin (Sousa chinensis; n = 2) and finless porpoise (Neophocaena phocaenoides; n = 12) from Indian coast. On the other hand, some haplotypes were shared with other regional populations in spinner dolphin (Stenella longirostris; n = 16) and bottlenose dolphin (Tursiops aduncus; n = 3). Common dolphins (Delphinus capensis; n = 2) had both unique and shared haplotypes including one highly divergent sequence.

Key words: Delphinids, finless porpoise, mitochondrial DNA, molecular taxonomy, haplotypes

Introduction

Taxonomy is fundamental to conservation efforts of marine mammals and the units on which conservation is based are determined largely by species designation. Ambiguous identification of species can lead to erroneous conclusions, such as loss of genetic variability and unwitting extinction of species. In cetaceans, morphological features are often subtle and difficult to compare because of the rarity of specimens or widespread distributions and regional variation (Reeves *et al.* 2004). Identifying the geographical variants of recognized species of delphinids and phocoenids is even more difficult using the conventional approaches and in this context molecular genetics can provide significant contributions to taxonomic understanding of inter and intra-

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