

Close genetic relatedness of whale sharks (*Rhincodon typus*) in the Indo-Pacific region

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Background

The whale shark (*Rhincodon typus*) is a prominent species in Cenderawasih Bay. Its recent association with moored lift-net fisheries there has led to an increase in tourism that facilitates encounters for human snorkelers and SCUBA divers with the sharks. This association has also supported opportunities for research to discover various elements of their biology, ecology, movements and genetics. An understanding of the genetic composition of the sharks in Cenderawasih Bay and their relationships with whale sharks elsewhere in the Indian Ocean and Western Pacific Ocean is important for their conservation and to help design marine protected areas.

Approach

Skin samples from whale sharks in Cenderawasih Bay were collected with modified hog ear notch pliers and small biopsy tips. The samples were preserved in 96% ethanol and stored at 4°C in the laboratory until DNA extraction. The DNA template was amplified for the cytochrome oxidase I (COI) gene. The nucleotide composition and genetic diversity (polymorphisms, haplotypes, and nucleotides) were analyzed. The results from whale sharks in Cenderawasih Bay were compared with those available in Genbank for nearby areas of the Indian and Western Pacific oceans with the neighbor-joining method. Evolutionary distances and haplotype networks were calculated.

Results

Seven haplotypes were detected among the 31 whale sharks sampled in Cenderawasih Bay, for a haplotype diversity (Hd) of 0.1871 (variance = 0.00859, s.d. = 0.093). The nucleotide diversity (π) was 0.00244 (± 0.0013) and the values for theta were 0.75094 per shark and 0.00722 per site. The neighbour-joining tree for individual whale sharks from Cenderawasih Bay and other regions appeared to be closely related to each other. They also appeared to be closely related to whale sharks sampled elsewhere in the Indian and Western Pacific oceans (Chi-square, Chi2: 3.620, df: 5, p: 0.605). Haplotype one has highest frequency (37 individuals), one haplotype has two individuals, and six other haplotypes each have one individual. The three last haplotypes have just one individual, respectively. The whale sharks that we sampled in Cenderawasih Bay had low genetic diversity (haplotype, nucleotide and polymorphic).

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Conclusion

31 whale sharks in Cenderawasih Bay were very closely related, and these sharks were closely related to whale sharks elsewhere in the Indian and Western Pacific oceans. The extent of movements among reproductive sharks in this large region is unknown as is the frequency and magnitude of mating among sharks from these different areas. Further research is needed to monitor the long-term movements of sharks within and among regions, particularly reproductively mature males and females, to help design conservation plans for whale sharks and the habitats that they might depend on for feeding and reproducing.

Keywords: Cenderawasih Bay, haplotype diversity, nucleotide diversity, Coral Triangle