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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the whitetip reef shark *Triaenodon obesus* from the British Indian Ocean Territory Marine Protected Area

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ABSTRACT

We present the first mitochondrial genome of *Trianenodon obesus* from the Chagos Archipelago in the British Indian Ocean Territory (BIOT) Marine Protected Area. The mitogenome was 16,702 bp in length and consisted of 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and a non-coding control region (D-loop). GC content was at 38.9%. The control region was 1064 bp in length. This mitogenome for the BIOT MPA *T. obesus* differed from the previously published *T. obesus* genome by 15 bp and the differences include a 2 bp insertion and 13 single nucleotide polymorphisms distributed across the mitogenome in the BIOT MPA sequence. Whole mitogenome sequence of *T. obesus* from the Chagos archipelago presented here fills existing gaps in genetic information on marine species from the BIOT MPA and provides additional tools for species specific assessments as to the effectiveness of MPA management. In addition, methods presented here lay the framework for genetic studies in remote locations with limited infrastructure.

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The Whitetip Reef Shark (*Triaenodon obesus*) is a small requiem shark with distinct white tips on its dorsal and caudal fins, and a dark gray-brown dorsal region that fades to light on the ventral side. The whitetip reef shark has a wide distribution in the Pacific and Indian Oceans. It typically lives along the bottom in clear, shallow waters surrounding coral reefs and has been reported at depths of 1,083 feet (330 m) (Smale 2019). Whole mitochondrial genomes improve the resolution of population genetic estimates and provide tools to study sub-populations of species. Here, we sequenced the complete mitochondrial genome of *T. obesus* collected from the Chagos Archipelago, British Indian Ocean Territory Marine Protected Area (BIOT MPA) (Latitude: 05.7731°S; Longitude: 071.2974°E).

The specimen was stored at the Hopkins Marine Station, Stanford University in 70% ethanol (Sample Accession # 020002232503). DNA was extracted from the muscle biopsy of an individual mature male and the mitochondrial genome was sequenced on the MinION sequencer using published methods (Johri et al. 2019; Dunn et al. 2020; Johri et al. 2020; Johri et al. 2020; Johri et al. 2020). 302,000 Fast5 files obtained from sequencing were converted to FASTQ files, and processed as described in (Johri et al. 2019), resulting in a contig of 165 reads. The mitogenome contig was then annotated as described in (Johri et al. 2020) and checked for accuracy by comparison with annotated Carcharhinidae mitochondrial genomes from GenBank including that of *Triaenodon obesus* (Genbank: NC_026287.1).

To assess the phylogenetic position of *T. obesus*, a maximum likelihood (ML) tree was generated in GeneiousVR version 8.1.9 (Kearse et al. 2012). Sixteen complete mitochondrial genomes, consisting of fifteen carcharhiniforms and two hexanchiformes, were obtained from GenBank. These sequences were aligned and phylogenetically assessed using methods described in (Johri et al. 2020).

The mitochondrial genome of *Trianenodon obesus* (GenBank: MN943497) was 16,702 bp in length and consisted of 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and a non-coding control region (D-loop). GC content was at 38.9%. All PCGs started with ATG and all PCGs ended with an incomplete stop codon, which are likely completed by post-transcriptional polyadenylation (Ojala et al. 1981).The control region was 1064 bp in length. This mitogenome for the BIOT MPA *T. obesus* differed from the published *T. obesus* genome (16700 bp, Genbank: NC_026287.1) (Chen et al. 2016) by 15 bp. Differences include a 2 bp insertion and 13 single nucleotide polymorphisms distributed across the mitogenome in the BIOT MPA sequence compared to NC_026287.1. Bayesian analysis (Figure 1) shows that *T. obesus* resides within the clade representing the family Carcharhinidae. Whole mitochondrial genome sequence of *T. obesus* from the Chagos archipelago presented here fills existing gaps in genetic information from the BIOT MPA. In addition, the data presented

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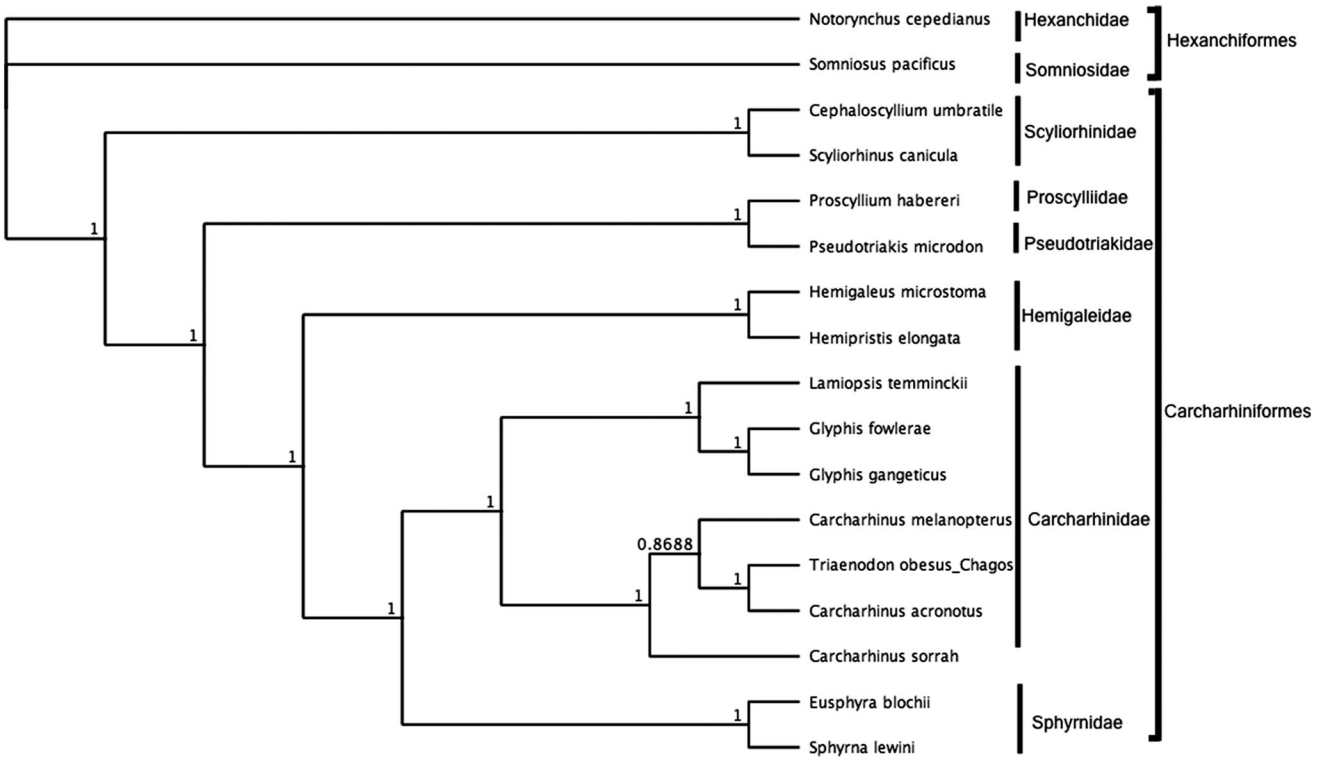

Figure 1. Bayesian estimate of phylogenetic position of *Triaenodon obesus* within the order Carcharhiniformes based on the complete mitochondrial genome. Members of the order Hexaniformes served as the outgroup. Families are indicated by vertical lines and orders by square brackets. Numbers at nodes are posterior probabilities. GenBank Accession Numbers: *Notorynchus cepedianus* (AB560489.1); *Somniosus pacificus* (AB560492.1); *Cephaloscyllium umbratile* (KT003686.1); *Scyliorhinus canicula* (Y16067.1); *Proscyllium habereri* (KU721838.1); *Pseudotriakis microdon* (AB560493.1); *Hemipristis elongata* (KU508621.1); *Hemigaleus microstoma* (KT003687.1); *Lamiopsis temminckii* (KT698048.1); *Glyphis fowlerae* (KT698049.1); *G. gangeticus* (KT698040.1); *Carcharhinus melanopterus* (KJ720818.1); *C. sorrah* (KF612341.1); *C. acronotus* (KF728380.1); *Triaenodon obesus_Chagos* (MN943497); *Eusphyra blochii* (KU892590.1); *Sphyrna lewini* (JX827259.1).

here alongwith our previously published work in the Chagos archipelago (Ferretti et al. 2018; Dunn et al. 2020; Tickler et al. 2019; Johri et al. 2020) will enable species specific assessments of top predators in the BIOT MPA and provide metrics to assess the effectiveness of MPA management. Last, methods described here lay the framework for future molecular studies in study sites with limited laboratory infrastructure.

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Disclosure statement

Authors declare no conflict of interest.

Author contributions

SJ contributed to concept, sequencing, bioinformatics and wrote the manuscript with comments from ED, TC, RS and BB, TC and RS contributed to sampling, ED provided laboratory support and BB contributed the sample and concept of the manuscript. All authors edited the manuscript.

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Data availability statement

Data which support the findings of this study are openly accessible in Genbank with the reference accession number MN943497.1 at DOI: https://www.ncbi.nlm.nih.gov/nuccore/MN943497.1

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