The complete mitochondrial genome of a gray reef shark, *Carcharhinus amblyrhynchos* (Carcharhiniformes: Carcharhinidae), from the Western Indian Ocean

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The complete mitochondrial genome of a gray reef shark, *Carcharhinus amblyrhynchos* (Carcharhiniformes: Carcharhinidae), from the Western Indian Ocean

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**ABSTRACT**

We present the mitochondrial genome sequence of a gray reef shark, *Carcharhinus amblyrhynchos* (Bleeker 1856), a coral reef associated species. This is the first mitogenome for this species from the western Indian Ocean. The mitogenome is 16,705bp in length, has 13 protein-coding genes, 2 rRNA genes and a non-coding control region, and demonstrates a gene arrangement congruent with other shark and non-vertebrate species. This mitogenome provides a genomic resource for assisting with population, evolutionary and conservation studies for the gray reef shark, which is increasingly under threat from fisheries.
The Seychelles *C. amblyrhynchos* mitogenome sequence (gb: MT663280) is 16,705 bp in length with a gene order identical to that of other sequenced *Carcharhinus* species and typical of most vertebrates, with 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a non-coding control region (D-loop). Nucleotide composition leaned to an A+T bias with 31.5% A, 25.2% C, 13.1% G, and 30.1% T. The ND2, ND3, ND4, COII, and CYTB genes contained incomplete stop codons. The Seychelles *C. amblyrhynchos* shark had 99.9% identity to the two Chagos *C. amblyrhynchos* individuals. The Seychelles shark contained 23 substitutions compared to Chagos individual (MT104515) sequenced by the Oxford Nanopore system, 10 substitutions compared to Chagos individual (MT093205) sequenced using the Illumina HiSeq system, and five substitutions (with two occurring in the control region) compared to both Chagos *C. amblyrhynchos* individuals. The maximum likelihood analysis is consistent with the results of Dunn et al. (2020), clustering *C. amblyrhynchos* with *C. albimarginatus* and *C. falciformis* (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

Mitogenome data supporting this study are openly available in GenBank at: https://www.ncbi.nlm.nih.gov/nuccore/MT663280.

The raw Illumina sequence reads are available from the NCBI SRA database: https://www.ncbi.nlm.nih.gov/sra/SRX8934594

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**Figure 1.** Maximum likelihood tree based on the GTR + I + G model of evolution and 1000 bootstraps. The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches for all nodes where the support is >75%. The Seychelles *C. amblyrhynchos* mitogenome (MT663280) placement is shown in bold.