



The complete mitochondrial genome of the endangered great hammerhead shark, *Sphyrna mokarran*

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ABSTRACT

We present the first mitochondrial genome sequence of the great hammerhead shark, *Sphyrna mokarran*. This species is of considerable conservation concern throughout its global distribution, and currently listed as Endangered on the IUCN Red List. The mitochondrial genome is 16,719 bp in length with 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a non-coding control region. The gene arrangement is congruent with other shark and most vertebrate species. This *S. mokarran* mitogenome provides a genomic resource for assisting with population studies and conservation efforts for this highly depleted species.

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The great hammerhead shark, *Sphyrna mokarran* (Sphyrnidae), is an elasmobranch of considerable conservation concern (Endangered: International Union for the Conservation of Nature (IUCN) Red List) (Denham et al. 2007). The slow life-history traits of this shark coupled with commercial overexploitation for its high value fins has resulted in substantial population declines throughout much of its distribution. Due to the slower evolutionary rate of mitochondrial genes in elasmobranchs compared to other vertebrates, complete mitochondrial genome sequences can offer greater resolution than single gene studies when examining the population structure and phylogeny of elasmobranchs (Feutry et al. 2014; Martin et al. 1992). This higher resolution can be critical in elucidating evolutionary significant units for management and conservation purposes (Feutry et al. 2015). Here we present the first characterization of the whole mitochondrial genome of the great hammerhead shark to assist in future population genetic, conservation and phylogenetic assessments.

The specimen sequenced was a male shark sampled in 2010 off the Florida Keys, USA (geospatial coordinates: 24.36667, -82.41666). A fin clip sample (accession number OC-226) is stored in 100% ethanol at Nova Southeastern University, College of Natural Sciences and Oceanography. DNA was extracted from the fin clip using a QIAGEN DNeasy Blood & Tissue Extraction Kit (Qiagen Inc., Valencia, CA) and amplified in four fragments via long PCR using KAPA HiFi HotStart ReadMix PCR (Kapa Biosystems, Boston, MA). Amplicons were purified with QIAGEN QIAquick Gel

Extraction Kit and Agencourt[®] AMPure XP beads (Beckman Coulter Life Sciences, Indianapolis, IN). Libraries were prepared for sequencing on an Illumina MiSeq system with paired-end reads (2x250 bp) using a Nextera XT DNA Library Preparation Kit. Fastq files were trimmed using the Minoche protocol (Eren et al. 2013). A *de novo* assembly was created with Velvet 1.1 (Zerbino 2010), and the single ambiguity seen resolved by performing a subsequent assembly with Bowtie2 (Langmead & Salzberg 2012) using the consensus sequence from Velvet as the reference index. This final assembly was annotated using MitoAnnotator (Iwasaki et al. 2013).

The mitochondrial genome of the great hammerhead shark (gb: KY464952) is 16,719 bp long containing 13 protein-coding, 22 tRNA, and 2 rRNA genes, and 1 non-coding control region. The nucleotide base composition is: 31.6% A, 25.6% C, 13.0% G, 29.8% T. The *COI* gene began with the alternative start codon GTG. The *COII* and *ND4* genes contained incomplete stop codons. A MUSCLE alignment was performed in Geneious[®] 7.1.9 (<http://geneious.com>, Kearse et al. 2012) with the four other published Sphyrnidae mitochondrial genomes (*Eusphyra blochii*: NC_031812.1, *Sphyrna lewini* RefSeq: NC_022679.1, *Sphyrna tiburo* RefSeq: NC_028508.1, *Sphyrna zygaena* RefSeq: NC_025778.1), using the blacktip reef shark, *Carcharhinus melanopterus*, mitochondrial genome as the outgroup (RefSeq: NC_024284.1). The order of genes on the great hammerhead mitochondrial genome is congruent with the other Sphyrnidae sharks. A Bayesian tree (Figure 1) was created with default parameters in MrBayes 3.2 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003)

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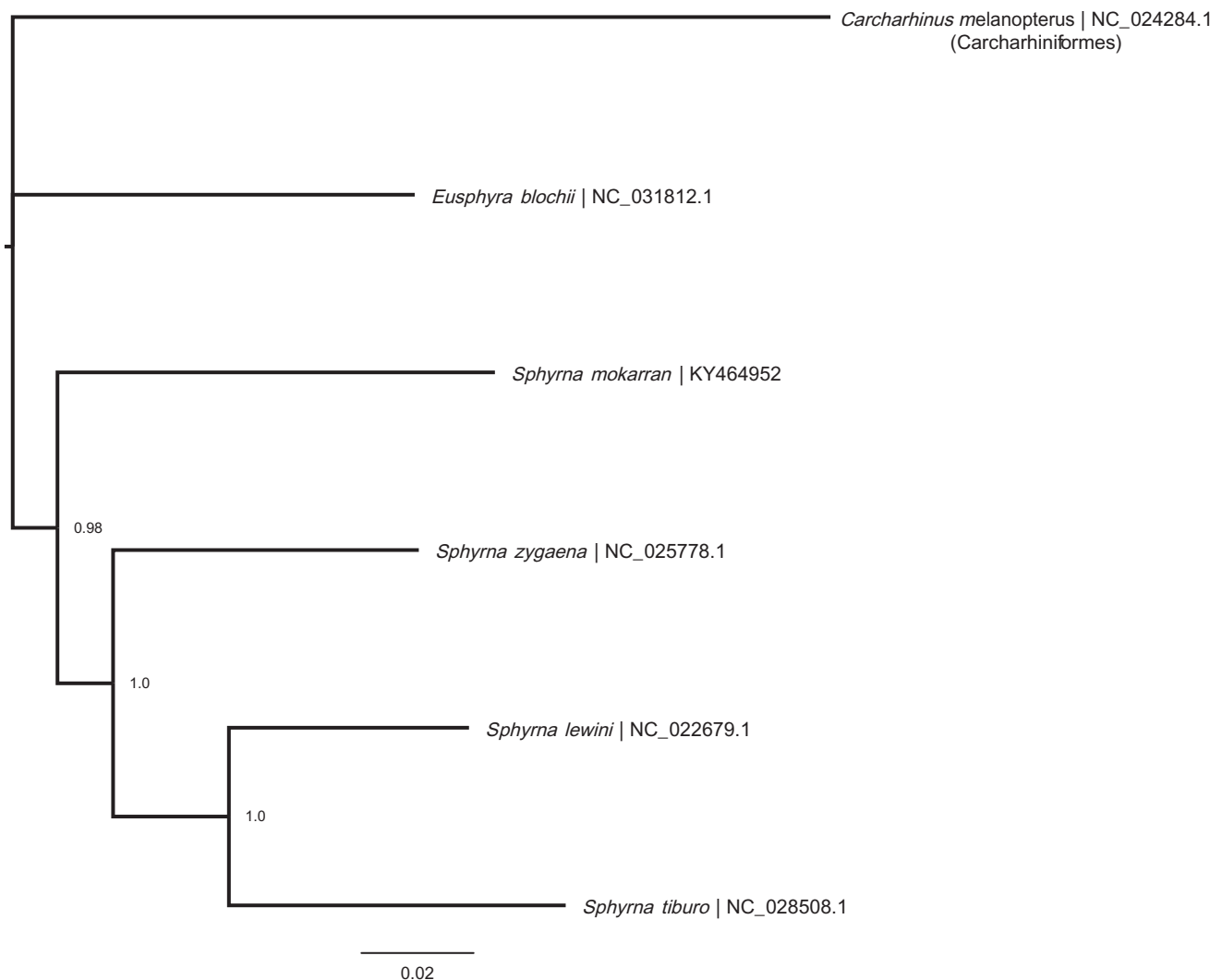


Figure 1. Bayesian tree depicting the five available Sphyrnidae mitogenomes with a Carcharhiniformes shark species (*Carcharhinus melanopterus*) as the outgroup. NCBI RefSeq numbers, branch lengths and posterior probability of the clades are shown.

and the best substitution model (GTR + I) determined by the Bayesian Information Criterion in JModelTest2.1.7 (Darriba et al. 2012).

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Disclosure statement

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