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Mitochondrial genome of an Atlantic white shark (*Carcharodon carcharias*)

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ABSTRACT

Here we report the first full mitochondrial genome sequence for a white shark caught in the Atlantic Ocean. The mitochondrial genome is 16,745 bp in length and contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a non-coding control region. The base composition of this mtDNA lineage is A: 30.7%, C: 26.9%, G: 13.8%, and T: 28.6%. In concordance with previous population genetic studies, the Atlantic caught individual forms a separate lineage from individuals caught on either side of the Pacific Ocean.

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Mitochondrial genes exhibit a lower rate of evolution in elasmobranchs (Martin et al. 1992), thus complete mitochondrial genomes may be preferable to using a subset of the mitochondrial genome for identifying intraspecific variation (Feutry et al. 2014). The white shark, *Carcharodon carcharias*, is CITES listed and has been the subject of population genetic studies using the mitochondrial DNA (mtDNA) control region and microsatellite loci (Pardini et al. 2001; Jorgensen et al. 2010; Blower et al. 2012; O'Leary et al. 2015). These studies identified multiple mtDNA lineages but the only full mtDNA genome sequences for white shark come from the Pacific Ocean (off the coast of Taiwan, Chang et al. 2014; off the coast of Mexico, Diaz-Jaimes et al. 2014). We characterize the first full mitochondrial genome sequence for a white shark from another ocean basin, the Atlantic Ocean, in an effort to identify additional areas of the mitochondrial genome that could be exploited for identification of genetic variation in this species.

The individual sequenced in this study (accession number OC130-Cc_H stored at −80 °C at Nova Southeastern University, College of Natural Sciences and Oceanography), was illegally fished off the coast of Delaware, USA in 2007 and confiscated by the National Oceanic and Atmospheric Administration Office for Law Enforcement but made available for this work (see Richards et al. 2013 for additional details). As part of a white shark nuclear genome sequencing project underway in our laboratory, Illumina HiSeq 2500 single end reads, 450 bp in length (produced by overlapping 250 bp reads) were used to assemble the mitochondrial genome. We identified reads from mtDNA by mapping reads to the RefSeq white shark mtDNA genome (NC_022415.1) using Bowtie2 (Langmead & Salzberg 2012). The mtDNA reads were used to produce a mitochondrial genome assembly with the program MITObim v. 1.8 (Hahn et al. 2013). This assembly was annotated using DOGMA (Wyman et al. 2004) as in Diaz-Jaimes et al. (2014) and annotations were confirmed by comparison to the gene annotation for the RefSeq sequence. Gene order followed that of Diaz-Jaimes et al. (2014) and that seen in most vertebrates. Using MUSCLE (Edgar 2004), we conducted pairwise alignments of the Atlantic and two Pacific shark sequences. Additionally, we reconstructed a phylogenetic tree with all RefSeq mitochondrial genomes from members of the Lamnidae (Figure 1) using PHYML (Guindon & Gascuel 2003).

The Atlantic shark sequence (gb: KX389266) is 16,745 bp in length and contains 13 protein-coding, 22 tRNA, and 2 rRNA genes, and a non-coding control region. The Atlantic sequence had a similar level of sequence identity with the Mexican (99.0%) and Taiwanese (98.9%) sequences while the two Pacific sequences are almost identical (99.8%). All subsequent comparisons herein discussed are to the RefSeq (Taiwanese) sequence. There are 174 nucleotide differences between the two genomes. As is the case with all of the lamnid sequences, *Cox1* has a GTG start codon in all three white shark sequences.

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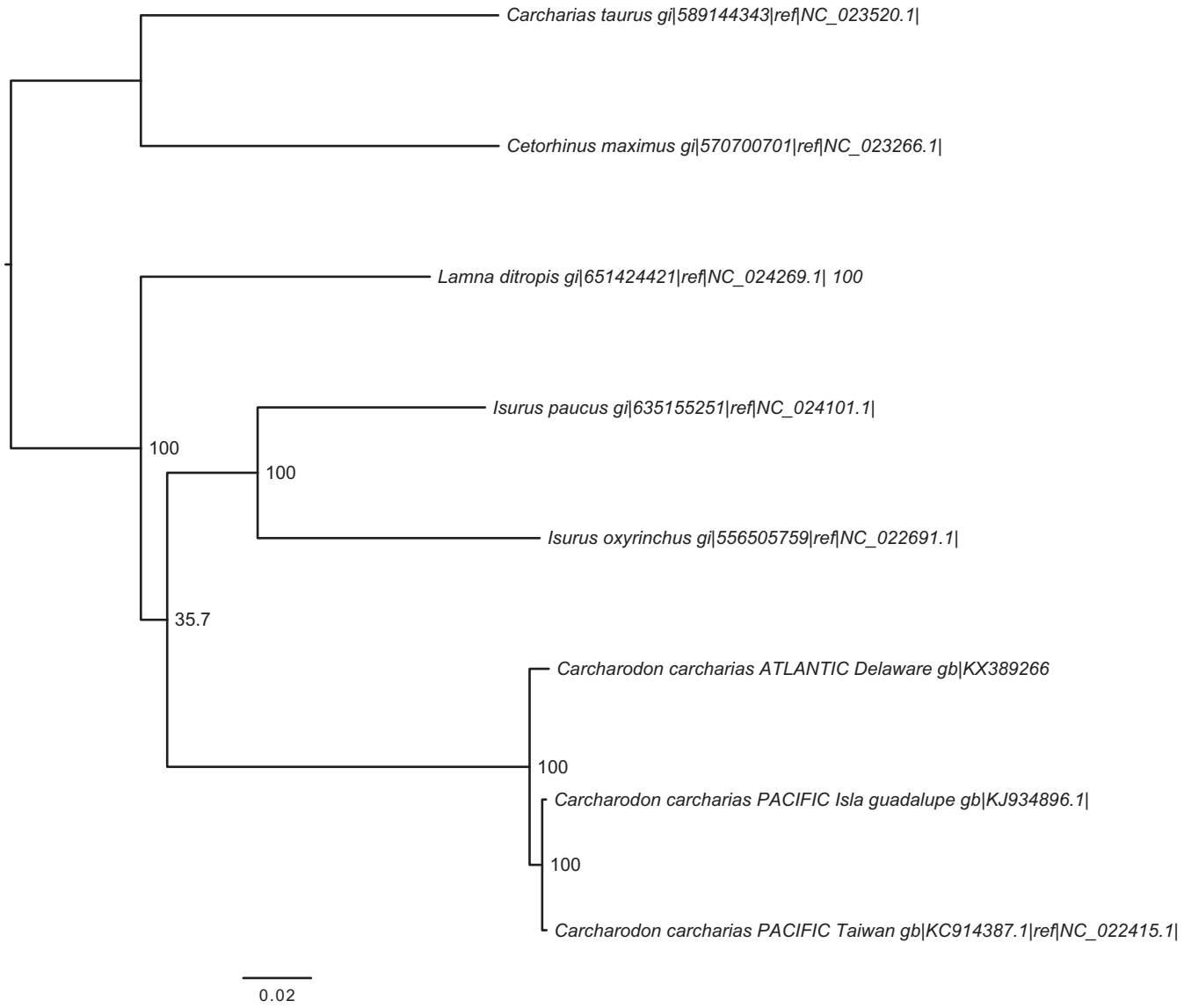

Figure 1. We used MUSCLE to align the mtDNA genome sequences from all members of the Lamniformes present in RefSeq along with the three white shark sequences. Sequences from *Cetorhinus maximus* and *Carcharias taurus* were included as an outgroup. This alignment was then used to produce a Maximum Likelihood Tree with the PHYML plugin for Geneious using the GTR + G model of evolution and 1000 bootstraps. Support values are displayed on a scale of 1 to 100 for the 1000 bootstraps and the root of the tree was placed at the base of the split between the Lamnidae and the two outgroup species. Each label includes the species name and identifying GI and RefSeq numbers for the sequence used. The two previously published white shark sequences from Mexico and Taiwan clustered together and were sister to the Atlantic caught individual used in this study.

The phylogeny depicts the Atlantic sequence as a separate lineage from the Mexican and Taiwanese lineages.

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Disclosure statement

We have no conflicts of interest to report and the authors are solely responsible for the content and writing of this paper.

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