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PHYLOGEOGRAPHY OF THE *HEXANCHUS GRISEUS*, INFERRED FROM THE MTDNA CONTROL REGION.

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Abstract

The mtDNA control region has been sequenced for 129 specimens of *Hexanchus griseus*. Significant genetic differences were noted between the Pacific Ocean and the Eastern Atlantic Ocean (including the Mediterranean), giving clear indication of population heterogeneity between Oceans.

Keywords: *Elasmobranchii, Malta Trough, Aegean Sea, Valencia Trough*

Introduction

Hexanchus griseus is a cosmopolitan shark that is found to occur in various areas around the globe, including the Mediterranean Sea [1, 2]. It is one of the largest Mediterranean sharks, but little is known about its biology and distribution. IUCN has assessed this species as Nearly Threatened on a global scale [3], while in the past year its status on a regional scale, has been downgraded from Nearly Threatened to Vulnerable [4, 5].

Methodology

This study looked into the genetic structure of this shark, using the complete mtDNA control region as a molecular tool to identify subtle differences between 129 individuals originating from different geographical origins, with the main focus being the Mediterranean Sea population. The control region was amplified using newly designed primers, and it was sequenced through the use of five sequencing reactions.

Results and Discussion

The first genetic differences noted were based on the length of the control region. The number of VNTRs varied between locations, but since the mutation processes leading to the formation of VNTRs are different from the other point mutations noted in the control region, then their data was not used in this phylogeographic study. A total of 1258bp were analysed, and exhibited 14 polymorphic sites, with the maximum genetic difference between specimens being that of 1%. The haplotypic diversity noted was 0.743 ± 0.023 , while the nucleotide diversity was 0.0015 ± 0.0010 . The mean pairwise difference between individuals was 1.943 ± 1.110 , and had a Ti/Tv of 1.75, while three indels were also recorded.

Nested clade phylogeographical analysis and the phylogenetic tree (Figure 1) for the control region has shown that there are no sharing of haplotypes between distant locations. In fact, specimens from the Pacific Ocean formed a clade which is distinct from that noted in the Atlantic Ocean (including the Mediterranean Sea), and so the greatest genetic divergence was noted between these two Oceans. Moreover no haplotypes were shared between the North-eastern Atlantic Ocean and the South-eastern Atlantic Ocean. On the other hand Mediterranean specimens do share a haplotype with the North Atlantic Ocean, indicating recent divergence between these two locations.

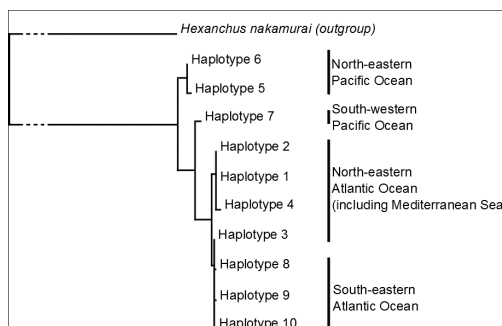


Fig. 1. A phylogram based on Maximum Likelihood analysis of the control region (1258bp) of *Hexanchus griseus* (haplotypes 1 - 10).

It can be concluded that even though this shark is a cosmopolitan species, still its population is subdivided into groups that are genetically different from each other. This stresses the need for conservation measures to tackle each group separately.

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