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Demografia histórica do tubarão-azul entre o Atlântico e o Mediterrâneo

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Resumo
Durante a última Idade do Gelo e os períodos interglaciais, as mudanças climáticas e as flutuações do nível oceânico alteraram as distribuições e isolaram as populações de vários organismos marinhos. Analisando o DNA mitocondrial do tubarão-azul, *Prionace glauca*, entre o Atlântico e o Mediterrâneo, o presente estudo tem como objetivo avaliar como esses períodos influenciam sua demografia histórica.

Palavras-chave: *Prionace glauca*; DNA mitocondrial, Inferência Bayesiana, Transição do Pleistoceno Médio-Inferior.

Historical demography of the blue shark between the Atlantic and Mediterranean

Abstract
During the last Ice Ages and Interglacial periods, climatic changes and sea-level fluctuations altered the range distributions and isolated populations of several marine organisms. Analyzing the mitochondrial DNA of the blue shark, *Prionace glauca*, among the Atlantic and the Mediterranean, the current study aims to evaluate how these periods influence its historical demography.

Keywords: *Prionace glauca*, Mitochondrial DNA, Bayesian inference, Early-Middle Pleistocene Transition.

Introduction

The Earth has undergone a general climate cooling that began some 45 million years ago (Mya) in the Eocene Epoch. The Pliocene (5.3 Mya) and Pleistocene (2.6 Mya) saw the continuation of this cooling which culminated in the recent glaciation events. The planet enters on a period of 41-ky oscillations of climate from late Pliocene through to the Mid-Pleistocene (0.9 Mya) when the periodicity became 100-ky [1]. These major swifts produced the later glacial and interglacial ages resulting in a global scale climatic change with high fluctuation in temperature, humidity, and sea-levels over these periods affecting the range distribution and forming physical barriers for their dispersal [2].

Currently, fishing activity plays a major role in declines for numerous marine species [3]. Among the most affected species are sharks, millions of individuals are caught yearly [4] boosted by the high demand and economic value for their fins [5]. Nevertheless, sharks

remain a data deficient group with gaps regarding knowledge about their population structure, life-histories, recent and long-term demographic histories.

The blue shark, *Prionace glauca* considering the importance and substantial catches of blue sharks, several important gaps in their biological knowledge remains unsolved, including information related to their demographic history. Genetic data have been collected aiming to provide information about important demographic parameters and processes relevant to conservation, such as the estimation of effective population size (N_e) and its fluctuation over time [6].

Objectives

The main objective is to evaluate the demographic history of the blue shark, *Prionace glauca* between the Atlantic and Mediterranean through the analysis of mitochondrial DNA control region sequences.

Material and Methods

There were used *Prionace glauca* sequences of the mitochondrial DNA control region from Brazil accounting for 34 haplotypes deposited in the GenBank® database (Accession Nos. KY994016 - KY994042, MH085076 - MH085080, MH806840, MH806841) and the haplotype sequences from the Atlantic ocean (Accession Nos. KY923141-KY92319) [7] and from Mediterranean (Accession Nos. MG545732-MG545901) [8]. Sequences alignment was performed by the MUSCLE algorithm [9] in Geneious R11.1.5 [10]. The phylogenetic was built using BEAST v1.10.4 on XSEDE [11,12] running Markov chain Monte Carlo (MCMC) for 500 million iterations and 10% of burn-in. The best-fit nucleotide substitution model GTR+I+G (p-inv=0.68, gamma=0.25) was selected by jModelTest 2.1.10 on XSEDE [12,13] adopting an uncorrelated lognormal relaxed clock model [14] and the Birth-Death process as priors. The model convergence, effective sample size (ESS) and 95% of highest posterior density (HPD) intervals were all calculated by TRACER v1.7.1 [15]. The calibration using the *P. glauca*'s first occurrence around 4.5±0.5 (3.6-5.3) Mya [16] and the divergence time among *P. glauca* and silky shark, *Carcharhinus falciformis*, set as outgroup, dated around 50.0±2.5 (45.1-54.9) Mya [17]. The Bayesian skyline plots [18] were built using BEAST v1.10.4 on XSEDE running MCMC for 500 million iterations and 10% of burn-in adopting a strict clock model and a piecewise-constant skyline model as priors. The plot construction, model convergence, ESS and 95% of HPD intervals were all calculated by TRACER v1.7.1.

Results

The Bayesian phylogenetic inference (Figure 1) evidence a coalescent event dated 4.29 Mya during the Early Pliocene (5.3-3.6 Mya) resulting in the formation of two haplogroups among the Atlantic and Mediterranean oceans. The Bayesian skyline plot (Figure 2) demonstrates a smooth expansion from the effective population size from Pliocene and Pleistocene with an accentuated expansion occurring after 1 Mya until 250 Kya during the Early-Middle Pleistocene Transition (EMPT).

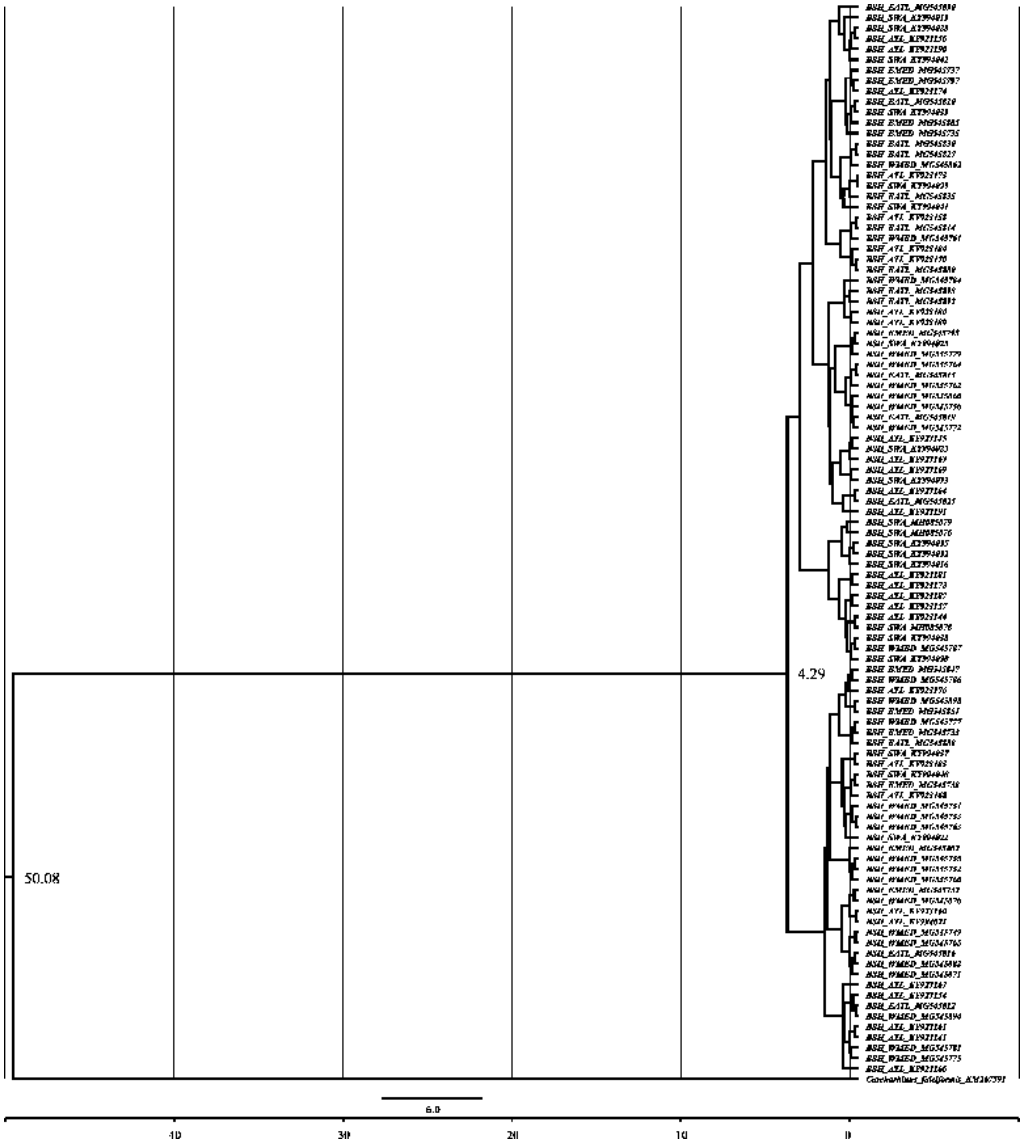


Figure 1. Bayesian phylogenetic inference built with 101 haplotypes from Prionace glauca. Numbers exhibit the node ages in millions of years.

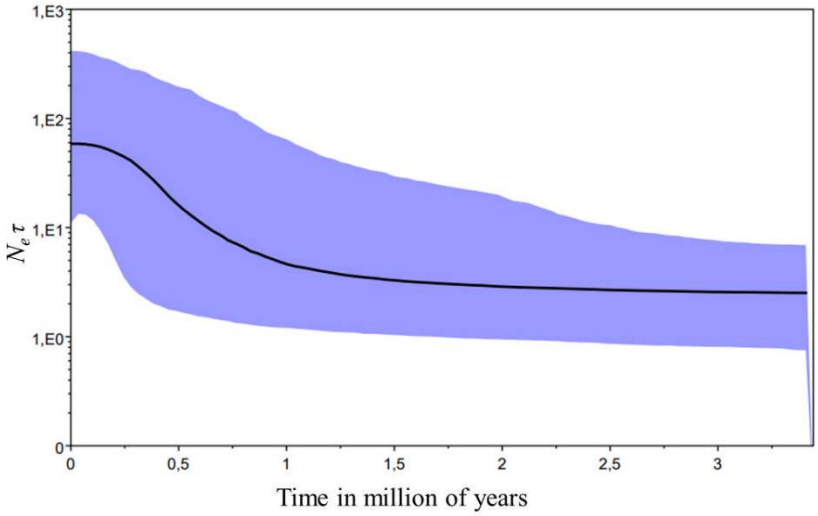


Figure 2. Bayesian skyline plot. The x-axis is in units of million years ago (Mya) in the past, and the y-axis is equal to the product of the effective population size and the generation length in years (τ). The thick solid line is the median estimate, and the dashed lines show the 95% highest posterior density (HPD) region limits.

Discussion

The EMPT (1.2-0.5 Mya) represents a major episode in Earth history. Low-amplitude 41-ka obliquity-forced climate cycles of the earlier Pleistocene were replaced progressively by high-amplitude 100-ka cycles. These changes were accompanied by substantially increased global ice volume and climate transformations, particularly the increasing severity and duration of ice ages and great sea-levels changes have had a profound effect on biota and seascape.

The Bayesian phylogenetic inference demonstrates the existence of two haplogroups between the Atlantic and Mediterranean that diverged at 4.29 Mya. These groups could have formed during these periods of climatic change and were isolated from each other with a secondary contact. The Bayesian skyline plot shows an increase in the effective population size during the EMPT, an indication of changes in the species range distribution.

Conclusions

During the Pliocene, Prionace glauca splits into two haplogroups between the Atlantic and the Mediterranean and during the Early-Middle Pleistocene Transition the groups have an increase in the effective population size mostly due to massive climatic changes and sea-levels fluctuations that change its range distribution, but currently, the groups inhabit the same environment.

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