I SIMPÓSIO BRASILEIRO DE IDENTIFICAÇÃO MOLECULAR DE ESPÉCIES

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Genetic divergence patterns in the 12S and 16S rDNA regions applied to the identification of sharks

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The consumption of shark meat has become more widespread and popular mainly driven by Asian consumption of shark fins. Moreover, the high prices charged by trade promoted the capture of sharks in almost all seas, leading several fish stocks to a collapse. The development of molecular tools applied to species identification has been shown of great importance, especially for quantifying the exploitation of natural populations, evaluating and monitoring trade in endangered species and for the certification of processed products, adding value to their marketing. The nucleotide composition of the 12S rRNA gene region, passing through the tRNA-Valine gene to the 16S rRNA gene permit to identify polymorphic sites among species and design primers for simultaneous multiplex-PCR and restriction enzymes for PCR-RFLP. This study evaluated the genetic diversity of seven shark species [*Squatina* sp. (n = 3), *Sphyrna mokarran* (n = 2), *S. lewinii* (n = 2), *S. tudes* (n = 4), *S. zygaena* (n = 3), *Isurus oxyrinchus* (n = 4) and *Negaprion brevirostris* (n = 1)] to assess the feasibility of developing species-specific molecular markers. The sequences were aligned using the program BioEdit© amounting 1702 base pairs and compared by genetic differences Mega©. We used only sequences with a similarity degree above 98% among individuals. The greatest genetic divergence between species was 0.194 (330 mutations) found in the comparison of *Squatina* sp. and *S. mokarran*, and the smallest genetic divergence found was in the order of 0.043 (73 mutations), detected in the comparison of *S. mokarran* and *S. zygaena*. On the other hand the intraspecific divergence was low, ranging from 0 to 0.006. As the value of divergence between species was high and between specimens was low, it is suggested that discrimination of shark species through genetic markers using the 12S-16S region is feasible. The DNA libraries that are being developed can be used globally for identification of sequences in addition to allowing the design of species-specific molecular markers. These identification methods are already being applied in the Laboratório de Biologia e Genética de Peixes (UNESP-Botucatu) to evaluate shark fishing in the Sao Paulo State coast and in the identification of the species to which belong shark fins arrested by IBAMA, generating data for monitoring fisheries and conservation of the species.

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