

Genetic and distribution data of the bramble shark *Echinorhinus brucus* (Bonnaterre, 1788) and the prickly shark *Echinorhinus cookei* Pietschmann, 1928 to better reconstruct their conservation status

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Elasmobranch species show low resilience in relation to anthropogenic stressors such as fishing efforts, loss of habitats, and climate change. In this sense, the elasmobranch populations appear to be at risk of extinction in many cases. Despite conservation researchers making efforts to implement knowledge, the information on the biology, reproduction, distribution, or genetic structure of some species is still scattered, often caused by the occurrence of species in inaccessible habitats. *Echinorhinus brucus* is a deep benthic shark evaluated as “Endangered” on which little information is available, particularly about its geographical range and genetic structure, while *E. cookei* is listed as “Data Deficient”. *Echinorhinus brucus* belongs to the Echinorhinidae family, and its unique congeneric species is *E. cookei*. The main morphological diagnostic characteristic of both species is the presence of denticles with different shapes and patterns on the derma. In the present paper, mitochondrial COI and NADH2 sequences were retrieved from both *E. brucus* and *E. cookei* species, and analyses were conducted by applying different models of phylogenetic inference. Sequences of *E. brucus* captured in the Indian Ocean (IOS) did not cluster with the Atlantic *E. brucus* counterparts (AOS) but instead with *E. cookei* sequences; the different models showed an overlapping tree topology. Concurrently, a review of the historical and recent captures of the two species was carried out. The worldwide distribution of *E. brucus* excludes the Pacific Ocean area, where *E. cookei* occurs, and is characterised by presumably current local extinctions in the North Sea and the western Mediterranean Sea. The dataset describes two definite areas of significantly high abundance of *E. brucus* located in the Atlantic Ocean (Brazil) and the Indian Ocean (India). These areas suggest zones for conservation plans, especially considering the two lineages identified through molecular approaches.