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Information on a CSIRO close-kin design study for shortfin mako (*Isurus oxyrhincus*) in the Indian Ocean

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Contents

1 Abstract

Shortfin mako shark has a wide distribution which includes CCSBT statistical areas. Given this overlap in space, for the information of the CCSBT we are including a brief overview of a CSIRO project for the Indian Ocean Tuna Commission (IOTC) that is (1) conducting an updated look at stock structure in the Indian Ocean (2) considering statistical design and logistical aspects influencing the feasibility of using close-kin mark recapture to estimate spawning stock abundance of shortfin mako in the Indian Ocean.

2 Introduction and Background:

Like all pelagic sharks which interact with high-seas fisheries, the global population status of shortfin mako (SMA) shark (*Isurus oxyrhincus*) is highly uncertain. Following concern about declines, the species was listed under Appendix II of CITES in 2019. The species is captured as bycatch in pelagic fisheries globally and its spatial distribution in the Indian Ocean includes CCSBT statistical areas. Additionally, the shortfin mako is considered to have a high vulnerability to longlining gear (Murua et al., 2018) and its life history makes it vulnerable to declines. A recent surplus production model-based assessment for the Indian Ocean conducted by Coelho et al (2024) using the JABBA framework (Winkler et al 2018) indicated that the species is currently overfished and subject to overfishing. This assessment found that a reduction on the TAC of 40% of current catches is required to prevent further declines in the Indian Ocean population (Coelho et al 2024).

While the JABBA assessment is the current best state of knowledge of SMA population status in the Indian Ocean, there are many uncertainties which limit ongoing ability to track the population status. Application of the JABBA approach to SMA in the Atlantic has been problematic with the models being unable to account for conflicting catch trajectories (de Bruyn et al 2017).

3 Project approach

In 2023, CSIRO initiated a study to examine the feasibility and likely sample requirements for applying Close kin mark recapture (CKMR) to estimate abundance of the spawning population of SMA in the Indian Ocean. The CKMR approach compares sequencing data from a collection of sampled individuals to look for closely related individuals. Typically, these are parent-offspring pairs, or those which share a parent (half sibling pairs). This information is used to estimate the abundance of the spawning population as the rate of detection is related *ceteris paribus* to the reproductive output of the mature population (CKMR scoping doc for IOTC).

The CKMR approach has been used to overcome limitations on estimates of abundance of both target fisheries for species such as SBT (Bravington et al 2016) and school shark (Thomson et al 2020). The technique has also been applied to non-target shark species in conservation settings (Hillary et al 2018; Patterson et al 2022).

Before initiating a CKMR study, it is advisable to aggregate available information on the population under consideration into a model-based framework (Bravington et al, 2016) which allows for quantitative appraisal of the effect of design parameters (e.g. number of tissue samples, duration of sampling).

4 Project Scope

The project is set to deliver to the IOTC in late 2025 and has tuned age-structured population models to be consistent with the population status provided by Corelho et al (2024) using available life history and demographic data for the species in the Indian Ocean along with IOTC catch series used in the JABBA assessment. Various sampling scenarios will be considered to evaluate the likely number of samples and duration of sampling programs required to obtain abundance estimates at a useable level of accuracy (e.g. CVs < 15%). Due to the absence of large adults in catch, the project will primarily consider sampling of juveniles and therefore population inference based on half-sibling pair data.

The project has also obtained contemporary and legacy tissue samples (Corrigan et al., 2018) of SMA from sites around the Indian Ocean and beyond (Atlantic and Pacific) to review the stock structure of the species based on SNP based methods (e.g. Feutry et al 2023; Nicolic et al 2020).

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