Potential for CKMR to be used to assess shark species of concern in the IOTC area, with reference to scalloped hammerhead sharks

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Abstract

Most assessments of shark species conducted within RFMOs globally are notoriously uncertain. Catch data are typically unreliable and the species are generally not the subject of major sampling programs reserved for high-value target species. To address this major uncertainty, we discuss the potential for close-kin mark recapture (CKMR) to be applied to shark species of concern in the IOTC area and how sampling programs, if carried out at the appropriate scale, could support robust estimation of the spawning stock abundance of sharks. A brief conceptual overview of CKMR is provided, and a summary of a recent design study on scalloped hammerheads in the Australian-Southeast Asian region is provided. This information paper argues that sampling programs and associated logistics required to underpin CKMR estimates of sharks should be initiated. This will require coordination between contracting parties and cooperation on international requirements for sample transportation such as CITES. Sampling is recommended to start as soon as possible, along with coordination of an Indian Ocean tissue bank, for both target and bycatch species of interest.

Introduction

This information paper details the potential for close-kin mark recapture (CKMR) to be used to estimate adult population size of elasmobranch species caught as bycatch within the Indian Ocean.

We first briefly describe CKMR, with reference to previous CKMR studies on shark species, and then provide a summary of a recent CKMR design study that examined sample sizes likely to be required to estimate abundance for scalloped hammerhead shark (*Sphyrna lewini*, SHH), in Northern Australia and-SE Asia. The project arose from Australian state management agencies (Northern Territory, Queensland and Western Australia) having an interest in new methods for understanding SHH status given the species is thought to have undergone significant declines in the region, but the lack of informative data makes robust assessment impossible. This problem is generic to the species (and many other elasmobranch species) across their distribution. Hence, CKMR is of interest as a possible approach to gain new insight of population status of bycatch species caught throughout the Indian Ocean, that are typically difficult to assess using traditional methods.

Overview of CKMR

By examining genetic sequencing data derived from sampled individuals, CKMR uses the prevalence of closely related animals in the samples to determine a fisheries independent estimate of adult breeding abundance (Bravington et al 2016a). Simply put, abundance can be estimated because a small population is likely to contain a higher incidence of closely related individual than a larger population. In this context, “close kin” or “closely related” indicate a set of specific kinship relations, usually parent-offspring pairs (POPs) and half-sibling pairs (HSPs; i.e., two individuals sharing one parent). Other kinship types, such as full-sibling pairs, are less directly useful for CKMR – for the reasons behind this see Bravington et al (2016a).

To give a general flavour of how CKMR works, consider the simplest possible case of a closed, stable population. If m potential parents and n potential offspring are sampled, and k POPs are detected amongst them, then the abundance of adults is estimated by $N = (2mn) / k$. This is equivalent to a Lincoln-Petersen estimator, with the factor of 2 resulting from the fact that every juvenile has 2 potential parents (Bravington et al 2016). Real applications using POPs (e.g. Bravington et al 2016b; Hillary SBT ref) are more complicated than this to account for the realities of population dynamics, demography (maturity onset), catches being removed, and other variables.

Estimation of abundance is possible from HSPs only (e.g. Hillary et al 2018) but there is complexity involved. For two individuals to be HSPs, the unseen parent of the two must have survived from the birth year of the oldest to the birth year of the youngest. This means that HSPs carry information about adult mortality as well as abundance. For more details, see Bravington et al (2016b), Hillary et al (2018) and Patterson et al (2022). Recently, CKMR using only HSPs was used to estimate changes in abundance of whale shark (*Rhincodon typus*) in the Indian Ocean (Pillans et al 2025).

Stages of CKMR studies

Typically, CKMR studies have several components:

1. **Sampling design:** Consideration of the suitability of a particular candidate species for CKMR and, if possible, implementation of a statistical design study. The latter is a modelling exercise which uses available information of potential population size and stock structure, catch data and demographic information to determine the number of samples required to obtain a

sufficiently precise estimate of abundance and potentially population changes (e.g. Hillary et al 2021; Patterson and Bessell-Browne, 2025; Patterson et al 2025). For large populations (e.g. shortfin mako in the Indian Ocean) required samples are in the 1000s (Patterson and Bessell-Browne, 2025).
Note that for many sharks of conservation concern, there is simply no data available with which to perform a thorough design study. Thus, in several cases, such as white sharks (Hillary et al, 2018), grey nurse sharks (Bradford et al 2025 et al), whale sharks (Pillans et al 2025) and speartooth sharks (Patterson et al 2022), the population sizes were considered to be sufficiently small that work commenced on obtaining samples and conducting CKMR studies without an initial design. For widespread species with large population sizes and at least some level of catch history and/or assessment, a design study is recommended.

2. **Investigation of logistical feasibility:** Typically, this requires detailed discussion with potential sampling providers to determine whether sufficient samples can be obtained. This step would consider in-country catch data to determine the reported catch of the species and any country specific aspects such as regulations on sample collection, non-retention measures and general availability of the species. This aspect also needs to consider international agreements such as CITES and the associated permitting requirements. While these can be considerable, studies such as Pillans et al (2025), which obtained CITES permission for shipping whale shark samples from various Indian Ocean countries to Australia for extraction and sequencing, show that these aspects are not insurmountable.
3. **Genetic exploration and assay design:** This requires exploratory sequencing of a small number of samples (~100) for discovery of Single Nucleotide Polymorphisms (SNPs) which are most informative on relatedness for the species in question.
4. **Sequencing of samples and quality control:** This step sequences all samples using the SNPs discovered in the previous step to create the data required for CKMR. Quality control protocols, which investigate whether there is potential for contamination, failed sequencing, etc., are applied to compile a "clean" sequencing dataset suitable for CKMR.
5. **Kin-finding:** Using the clean sequencing dataset, statistical pairwise comparison of sequencing results from all samples is conducted to identify kin-pairs of interest (e.g., POPs and HSPs).
6. **CKMR modelling:** Lastly, models are fit to the kinship data, i.e., the number of kin-pairs detected and the number of comparisons made. The data typically also contain covariates such as age, maturity, likely maternity/paternity, etc. Statistical estimation of population models based on the kin data and associated covariates proceeds similarly to stock assessment model estimation (Bravington et al., 2016a). Depending on the spread of ages present in the samples (and hence their birth years), the data can estimate abundance through time and can also provide estimates of total mortality and other parameters of interest (Patterson et al, 2022; Hillary et al 2012).

Feasibility of CKMR for scalloped hammerhead in the Australian-SE Asian region

After initial scoping, a project funded by the Australian Fisheries Research and Development Corporation (FRDC) was developed to address the question of what scale of sampling program would be required to provide a useful estimate of adult abundance. This requires consideration of the likely size of the SHH population, the connectivity of different stocks, and the demographics of the species (maturity, fecundity and mortality schedules). The project was led by CSIRO with data and provision of expertise from Northern Territory Agriculture and Fisheries and Western Australia Department of Primary Industries and Regional Development.

Scalloped hammerhead shark is a listed species under the Convention on the Conservation of Migratory Species of Wild Animals (CMS) and listed under CITES Appendix II. The species is caught as bycatch in commercial fisheries in Northern Australia and in shark control programs in Eastern Australia. While assessments have been conducted (Leigh 2015; Saunders et al 2023), the accuracy of these is limited by highly uncertain catch and effort data.

Aims/objectives

Primary aims of the project were to:

1. Evaluate the ability for CKMR to provide abundance estimates for SHH based on potential sampling programs.
2. Evaluate the robustness of CKMR to model misspecification given uncertainty about spatial structuring of SHH populations and investigate how spatial allocation of sampling might address potential biases.
3. Use the design modelling to determine whether sampling in a single jurisdiction (the Northern Territory) could produce informative abundance estimates.

Methodology

To address these objectives, the project used individual-based simulation models to simulate populations with "SHH-like" demographics. These models incorporated age- and sex-specific movement, mating and mortality processes, with parameters based on best-available information in the literature. Given uncertainty in the spatial structure of SHH in the Australia-SE Asia region, several scenarios were considered with varying levels of connectivity. The simulated populations were also tuned to available catch at age data, so that simulated sampling programs would focus on ages that tend to appear in current catches (overwhelmingly juveniles).

The simulations produced virtual datasets that were then provided to relatively simple CKMR estimation models. These models estimate initial adult abundance (at the start of the study period) and population growth and mortality rates, from which a trend in abundance could be inferred. By running many simulations, error statistics can be calculated empirically from the set of independent estimates obtained (negating the need for distributional assumptions).

Results/key findings

The accuracy and precision of the adult abundance estimates varied greatly between the scenarios considered, but many met or exceeded our benchmark for concluding sampling was adequate—namely to achieve unbiased abundance estimates with a coefficient of variation (CV) less than 20%. Under the assumption of a true adult population size of ~33,000 animals (based on life history and estimated catch levels), and assuming limited connectivity of adults between Northern Territory (NT), Eastern Australian (EA) and Indonesian (Indo) stocks, sampling 500 individuals (assumed to be juveniles) from NT and 200 from each of EA and Indo annually over a 3-5 year period was sufficient to estimate abundance. If sampling did not occur in all regions, the abundance estimates became biased. Subject to the same true adult population size, but assuming that SHH in these three regions have high connectivity through movement of adults, then unbiased and sufficiently precise estimates could be attained with half the sample numbers, i.e., 250 juveniles from NT and 100 from each of EA and Indo annually over 5 year period (3 years was no longer adequate).

Implications

The Patterson et al (2025) SHH design study, which focused on SE-Asian and Australian stocks, is clearly not directly transferable to the IOTC context. However, the results of this study indicate that CKMR will be viable for estimating the abundance of SHH populations. Further, for SHH and other species of management and conservation concern such as oceanic whitetip and shortfin mako, CKMR is likely the only feasible method available that will provide sufficiently accurate information on abundance and trend. This is not an instant process, but the results from our SHH (Patterson et al, 2025) and mako shark (Patterson and Bessell-Browne, 2025) design studies indicate that 5-year sampling periods should yield informative results that would vastly improve our current knowledge of these species.

CKMR will also provide information on spatial population structuring by sex, and the samples can be used for updating and refining genetic understanding of the species.

On the assumption that there will be ongoing interest in SHH, which seems likely given the CMS and CITES provisions, the findings of our Australian study indicate sampling should commence at a level of at least 500 samples per year for 3 or more years. A similar design study can be conducted for SHH (or other species of interest) in the Indian Ocean, with the main inputs required being:

- Some idea of current catches and, if possible, catch history
- Relevant population demographics (i.e. fecundity, maturity, and reasonable assumptions regarding mortality)
- Spatial structuring or general age/sex specific movement patterns

Importantly, the Patterson et al (2025) study indicated that unless the population was well mixed, which seems unlikely given background knowledge of the population structuring, sampling within a single sub-stock (i.e., NT only) is likely to lead to biased or inaccurate results. Therefore, samples should be collected across the range of the species. For SHH in the Indian Ocean, this does indicate a need for an international sampling program, which should be centrally coordinated. Initiation of a coordinated international program, especially with the requirements to adhere to CITES and within-country export processes, and noting the varying levels of infrastructure and capability among areas and nations that will interact with the species, is going to require significant time and effort. Nevertheless, wherever samples can be collected, we would argue strongly that it should begin as soon as possible. We know that sampling will be beneficial and starting sample collection and storage procedures in preparation for a larger program is guaranteed to be prudent. Additionally, sampling and archiving of tissue samples for bycatch species such as sharks is complementary to sampling of target tuna and neritic species. There is, therefore, opportunities for sampling programs to coordinate and store samples in an Indian Ocean Tissue Bank which are being actively scoped under IOTC activities at present. Such a sampling program could also facilitate improved collection of other biological samples (size, maturity, hard parts etc).

Conclusion

The uncertainty regarding the status of SHH stocks will not resolve with current data collection methods, and interest and scrutiny due to interactions with the species seems unlikely to abate. To address the challenges posed by current conservation concerns and listings, new approaches will be required that can deliver information needed for certification of sustainability initiatives, to ensure that export permits are granted, etc. All of the above points to the need to initiate low-cost sampling programs in collaboration with key industry bodies and operators.

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References:

Bradford RW, Harasti D, Westlake EL, Thomson R, Feutry P, Baylis S, Mayne B, Anderson C, Hillary R, Gunasekera R, Butcher P, Louden B, Gallen C, Patterson, TA (2025). Eastern grey nurse shark, *Carcharias taurus*, population abundance and trend. Report to the National Environmental Science Program. CSIRO Environment, Hobart, Tasmania.

Bravington MV, Skaug HJ, Anderson EC. Close-Kin Mark-Recapture. STATISTICAL SCIENCE. 2016a May 1:259-74.

Bravington, M.V., Grewe, P.M. and Davies, C.R., 2016b. Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture. *Nature communications*, *7*(1), p.13162.

Hillary, R.M., Bravington, M.V., Patterson, T.A. *et al.* Genetic relatedness reveals total population size of white sharks in eastern Australia and New Zealand. *Sci Rep* **8**, 2661 (2018). https://doi.org/10.1038/s41598-018-20593-w

Hillary R, Tremblay-Boyer L, Williams A, Hill NJ, Preece AL. Indian Ocean Yellowfin tuna Close-Kin Mark Recapture Design Study. Working Paper; 2021.

Hillary R, Preece A, Davies CR, Bravington MV, Eveson JP, Basson M. Initial exploration of options for inclusion of the close-kin data into the SBT operating model. In Scientific Committee report (OMMP workshop) CCSBT-ESC/1208/21. Commission for the Conservation of Southern Bluefin Tuna 2012.

Leigh, G.M. (2015). Stock assessment of whaler and hammerhead sharks (Carcharhinidae and Sphyrnidae) in Queensland. Queensland Government Department of Agriculture and Fisheries. URI: https://era.dpi.qld.gov.au/id/eprint/5146/1/Stock%20assessment%20of%20whaler%20and%20hammerhead%20sharks%20%28Carcharhinidae%20and%20Sphyrnidae%29%20in%20Queensland.pdf

Patterson TA & Bessell-Browne P (2025a) Evaluation of potential close-kin mark recapture sampling designs for Indian Ocean shortfin mako shark IOTC Working Party on Ecosystems and Bycatch, September 2025, IOTC-2025-WPEB21(AS)-42

Patterson TA, Feutry P, Gunasekera R, Burns C, Bessell-Browne P, Baylis S (2025b) Consideration of sampling requirements and logistics for close-kin mark recapture and a reappraisal of potential for stock structure in Indian Ocean shortfin mako shark. Working paper, IOTC Working Party on Ecosystems and Bycatch, September 2025, IOTC-2025-WPEB21(AS)-41

Patterson TA, Hillary RM, Kyne PM, Pillans RD, Gunasekera RM, Marthick JR, Johnson GJ, Feutry P. Rapid assessment of adult abundance and demographic connectivity from juvenile kin pairs in a critically endangered species. Science Advances. 2022 Dec 21;8(51):eadd1679.

Patterson TA, Eveson, JP, Baylis S, Tremblay-Boyer L, Usher M, Braccini M. (2025) Understanding the feasibility of close kin mark recapture for Scalloped Hammerhead in Australia, SE Asia and the Western Pacific. Final Report FRDC Project: 2023-068, 2025

Pillans RD, Patterson TA, Hillary RM, Feutry P, Donovan A, Baylis S. (2025) CSIRO briefing to DCCEEW on Indian Ocean whale shark abundance estimates https://cites.org/sites/default/files/documents/E-CoP20-Inf-021.pdf

Saunders, T., Braccini, M., Wortmann, J., Buckworth, R.C., Helmke, S., Peddemors, V., Roelofs, A.J., Johnson, G., Usher, M. and Newman, S.J. (2023) Stock status of Scalloped Hammerhead (*Sphyrna lewini*) in Australian waters. Contact an author for access.