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**FEASIBILITY AND SAMPLING DESIGN FOR CLOSE-KIN MARK-  
RECAPTURE ANALYSIS OF SILKY SHARKS IN THE EASTERN  
PACIFIC OCEAN**

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## Summary

This document is the final report for project IATTC CKMRfeas (101137231). This project was intended as a pilot study assessing the viability of Close-Kin Mark-Recapture (CKMR) as an assessment tool for silky and hammerhead sharks in the Eastern Pacific Ocean (EPO). The original proposal focused on evaluating DNA quality. However, in keeping with good practices in CKMR design, the project was refocused around simulation testing, particularly as the risk of insufficiently high-quality DNA being available was not substantial enough to warrant an exclusive focus. The project also focused solely on silky sharks, to produce a reliable foundation for one species that can then

be applied to others such as hammerhead sharks. This made it possible to produce estimates of the number of tissue samples that may be needed in order for a CKMR assessment of silky sharks to be viable in the EPO.

A range of simulation tests was conducted, exploring a variety of hypotheses regarding the population size, stock structure, and sampling regime that might be in play. The results suggest that between 9,000 and 30,000 tissue samples collected over a three-year period may be sufficient to produce reliable estimates of silky shark population sizes in the EPO. The recommendation is to err towards larger sample sizes given uncertainty as to the size of the population and the potential impacts of aging error. Rough estimates of sampling costs are included, based on these results and existing knowledge of the costs to collect and process tissue samples. The results also show the value of augmenting CKMR data with information on fishery catches, such as those supported by ABNJ-Tuna 2 project EU grants SI2.827511 ("IATTC- Long-term sampling program for shark catches of artisanal fisheries in Central America – testing of sampling designs Phase I") and SI2.840499 ("IATTC- Extension of Long-term sampling program for shark catches of artisanal fisheries in Central America – testing of sampling designs").

Sampling protocols were also developed in parallel to the simulation exercises, and testing of these protocols began. Several hundred silky shark tissue samples have now been collected from sites in Mexico, Ecuador, and Peru, and the procedures for collecting and storing tissue samples have been refined in the process. The permits needed to export the tissue samples from each country to the United States of America (USA) for processing are also being acquired. Once the samples are shipped, DNA quality tests and initial evaluations of genetic stock structure will be conducted, allowing the sampling design to be refined for full-scale CKMR analysis.

Overall, IATTC CKMRfeas (101137231) has enabled the development of an initial CKMR assessment model which in turn has provided estimates of the number of samples that may be needed in order to estimate various management-relevant quantities, such as adult abundance and fishing mortality rates, using CKMR. Based on these results, it is concluded that a full-scale silky shark CKMR project is viable and should be conducted.

## Introduction

The Inter-American Tropical Tuna Commission (IATTC) is the regional fisheries management organization (RFMO) responsible for the conservation and management of tuna and tuna-like species, associated species and their ecosystems, throughout the Eastern Pacific Ocean (EPO), from Canada, in the north, to Chile, in the south. The IATTC

is constantly working to improve the tools for ensuring sustainable fisheries of tropical tunas and related species in the EPO. Sharks are one such group of species, for which there is a lack of accurate fishery statistics from all significant fisheries, especially the artisanal fisheries of coastal states, thus making it challenging to conduct stock assessments of sharks in the EPO. Therefore, there is a critical need for comprehensive stock assessments of sharks in the region to better inform their management and conservation.

Silky sharks (*Carcharhinus falciformis*) are distributed throughout the EPO and thousands of tons are caught every year by various fishing gears in the region, including as the main shark bycatch species for tuna fisheries and as bycatch and target catch from smaller-scale coastal fishing fleets ([SAC-14-INF-L](#)). These dynamics make it extremely difficult to obtain an accurate estimate of total catches or construct a representative index of abundance, hindering several past efforts by the IATTC staff to develop a conventional assessment of the stock status of this key shark species for the IATTC.

Close-Kin Mark-Recapture (CKMR) (Bravington et al. 2016) is an emerging method uniquely suited to estimating the population status of species such as sharks that are often logistically difficult and costly to monitor and assess using more conventional assessment techniques. The core requirements of CKMR are representative tissue samples from the species in question, and a genomics toolbox capable of calculating the degree of “kinship” between these samples, specifically identifying which tissue samples are, for example, half-sibling pairs (HSPs) or parent-offspring pairs (POPs). While the concept of CKMR has existed for some time, recent advances in genetics have reduced costs of assigning kinship to tissue samples to levels that now make the method feasible for the large population sizes often seen in marine ecosystems. While still emerging, CKMR is now being used in the assessment and management of some marine species around the world, including southern bluefin tuna.

Building upon ongoing IATTC field work data collection efforts under the ABNJ-Tuna 2 project EU grants SI2.827511 (“IATTC- Long-term sampling program for shark catches of artisanal fisheries in Central America – testing of sampling designs Phase I”) and SI2.840499 (“IATTC- Extension of Long-term sampling program for shark catches of artisanal fisheries in Central America – testing of sampling designs”), the objective of this project was to evaluate the feasibility of CKMR for silky and hammerhead shark stocks in the EPO. This project focused exclusively on silky sharks, so that a robust CKMR program can be developed based on the challenges of one species before adapting the silky shark protocols developed through this pilot study for hammerhead sharks in the EPO.

CKMR is a powerful emerging tool for shark assessment, but requires a rigorous study design to ensure that the number and distribution of samples collected are capable of resolving the management questions CKMR is designed to address. It is critical to know,

for example, whether it will be logistically and financially feasible to collect the number of samples required to estimate total population size, and to understand what number and quality of samples may be needed to estimate additional parameters of interest such as population growth rates and stock structure.

To that end, the focus of this project was on conducting the simulation studies needed to inform these questions, in keeping with best practices for CKMR project design (Punt et al. 2024). These steps have identified an initial estimate of the number of samples that might need to be collected per year in a full-scale CKMR project for silky sharks. Subsequently, expanded simulation testing was conducted to evaluate the potential robustness of CKMR to alternative hypotheses regarding silky shark population sizes and stock structures in the EPO, along with uncertainty in catch estimates and aging of sampled sharks. A pilot sampling program has also been launched across three countries. The methods and results of this project are described below.

## Methods

A two-part simulation study was conducted to inform the use of CKMR for silky sharks in the EPO. This simulation work focused on providing guidance on the sample sizes (number of tissue samples from individual sharks) that may be required in order for CKMR to provide sufficiently precise and accurate results, as well as sensitivity to the inclusion of catch data and alternative plausible states of stock structure. Parallel to this simulation work, testing began on strategies for collecting tissue samples from silky sharks caught in artisanal fisheries in Mexico, Ecuador, and Peru, as well as for obtaining the permits needed to export these samples to the USA for analysis. Insights that have resulted from this initial sample collection phase are discussed.

### Simulation Testing

A custom age-based Bayesian CKMR model, developed for this project, served as the baseline tool for evaluating the potential of CKMR for silky sharks. This model estimates numbers of sharks at age over time, along with annual fishing mortality rates, natural mortality rates, and maturity at age by fitting to half-sibling (HSP) and parent-offspring (POP) kinship probabilities, with the option to also fit to estimates of total catches with a supplied coefficient of variation (CV). The model assumes that variables such as the slope of the length-inverse Lorenzen mortality function, the weight-at-age function, the Beverton-Holt steepness parameter, the sex ratio, and the selectivity of the fishing fleet are known. These are strong assumptions that will need to be revisited in tactical

applications, but facilitate the task at this stage of testing the general viability of CKMR for silky sharks.

Two different sets of simulation tests were then conducted with this model. In the first, the *internal* test, the Bayesian nature of the model was leveraged to simulate kinship data from the assessment model itself, given pre-defined parameters. The model was then fit to the simulated kinship data, and the relevant quantities estimated by the model were compared to their true values and expressed as either mean absolute percent error (MAPE) or mean percent error (MPE, a measure of bias). In the second simulation exercise, the model was fit to data generated from an entirely separate individual-based model, the *ibm* test, and the relevant quantities estimated by the model were compared to their true values.

The *internal* tests focused on evaluating the sensitivity of the model to the proportion of the population sampled, inclusion and quality of catch data, and relative weighting of different age classes in the tissue sample program. The unfished population sizes were constrained between estimates of the unfished population size of North Pacific shortfin mako sharks at the low end and North Pacific blue sharks at the upper end, and the number of tissue samples collected over a three-year period was varied between 6,000 and 30,000. One set of scenarios was run where no catch data were included, and then three additional scenarios were run where the model included true and unbiased catch data with CVs ranging from 0.1 to 0.5. The efficiency of CKMR models can be affected by the relative weighting of different age groups in the sampling program (Punt et al. 2024). Three different scenarios were assessed, one in which all age groups were weighted equally relative to their relative abundance, one in which sampling focused on younger sharks, and one in which sampling focused on middle-aged sharks. Factorial combinations of these options were run, with the true state of the population in terms of depletion and population trend and all biological parameters held constant.

For the *ibm* tests, a wide range of scenarios was run, focused primarily on stock structure. Twenty-four scenarios were generated with the *ibm* model, ranging in both the size and connectivity of three different sub-populations of silky sharks, with completely isolated populations at one extreme and a panmictic population at the other. Sharks simulated within the *ibm* followed a pattern of imperfect skip reproduction, in which a fixed proportion of the population only reproduces every two years, as opposed to annually, mirroring a dynamic seen in some sharks (Swenson et al. 2024). The CKMR model was then fit to these *ibm* simulations, varying in the number of tissue samples available to the model and whether or not the model was *naive* to the possibility of skip reproduction or tried to account for it by estimating the proportion of the population that pups every two years, in the manner of Swenson et al. (2024).

# Results

## ***Internal*** Test Results

The same general simulated silky shark population was used for each iteration of the model, with the exception that the scale of the population changed under different scenarios, though all trends and values relative to reference points were identical (Figure 1).

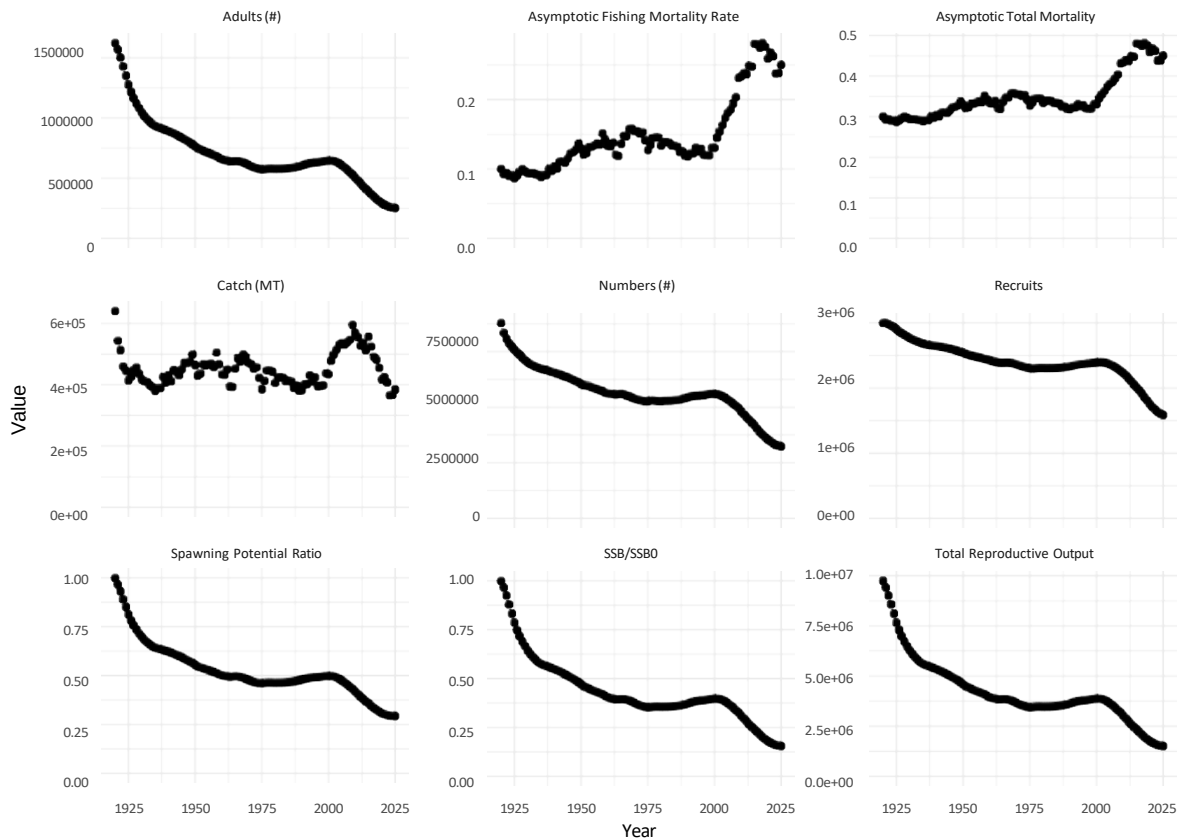


Figure 1: Time series of true simulated values used to generate kinship data.

Total population sizes in the most recent year of the simulations ranged from a low of 1,078,718 to a high of 21,574,358. The effective proportion of the population sampled in a given year was a function of the number of tissue samples and the absolute size of the population. Values ranged from a high of roughly 0.93% of the population per year to a low of 0.01% (Figure 2).

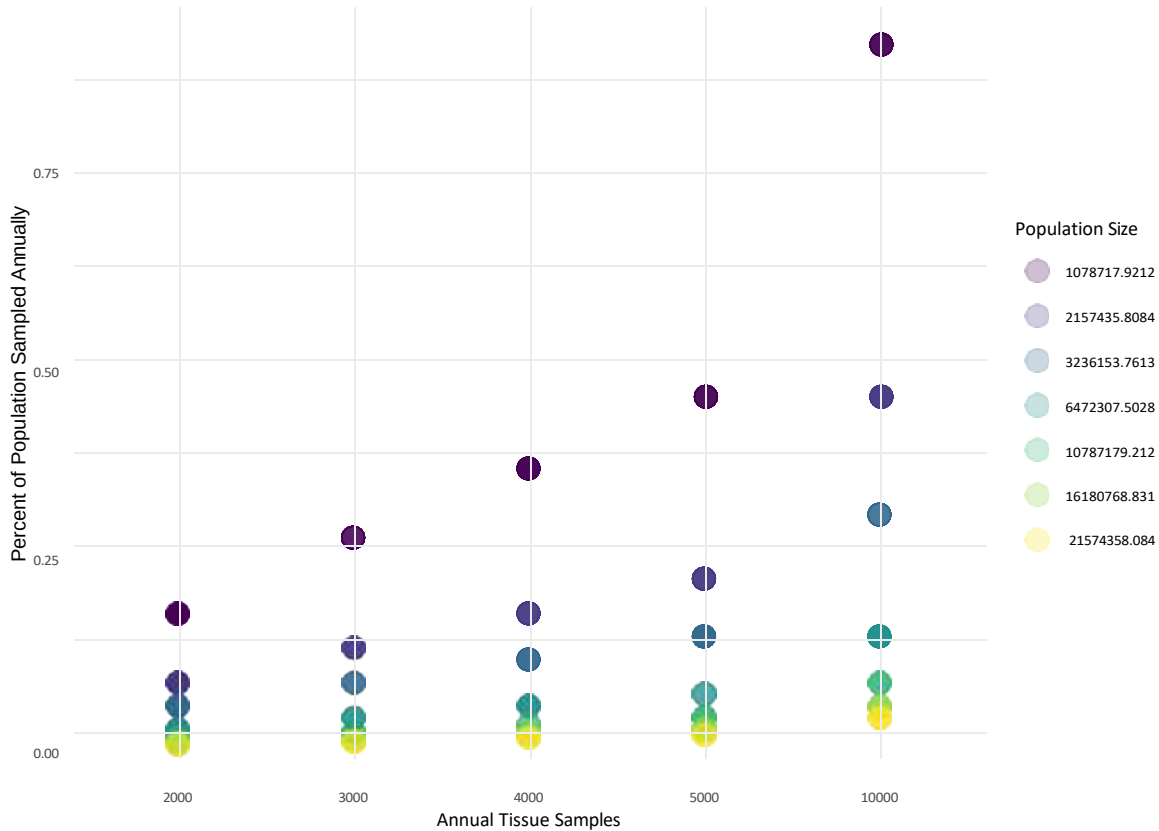


Figure 2: Percent of population sampled annually as a function of total population size and number of annual tissue samples.

Figure 3 shows an example fit to the data to illustrate the functionality of the model. The model provides estimates as far back as the earliest observed birth dates in the model, with much greater uncertainty in years with fewer observed births. In this particular simulation the model was fit to both kinship data and catch data.

Figure 4 shows the distribution of MAPE in population-level parameters as a function of the number of annual tissue samples collected and the total population size. Focus-ing first on population traits over the last five years, there was a wide range in the ability of the model to accurately estimate different parameters. As is to be expected with CKMR, the model performed best at estimating adult abundance and total repro-ductive output (TRO). As the model only indirectly estimates abundance of juveniles, estimates of total numbers were more error-prone than those of adults. The model was worse at estimating values relative to reference points, with spawning potential ratio (SPR) estimated slightly better than spawning stock biomass (SSB) relative to unfished spawning stock biomass (SSB0). Error rates in fishing mortality were often the highest among this subset of variables.

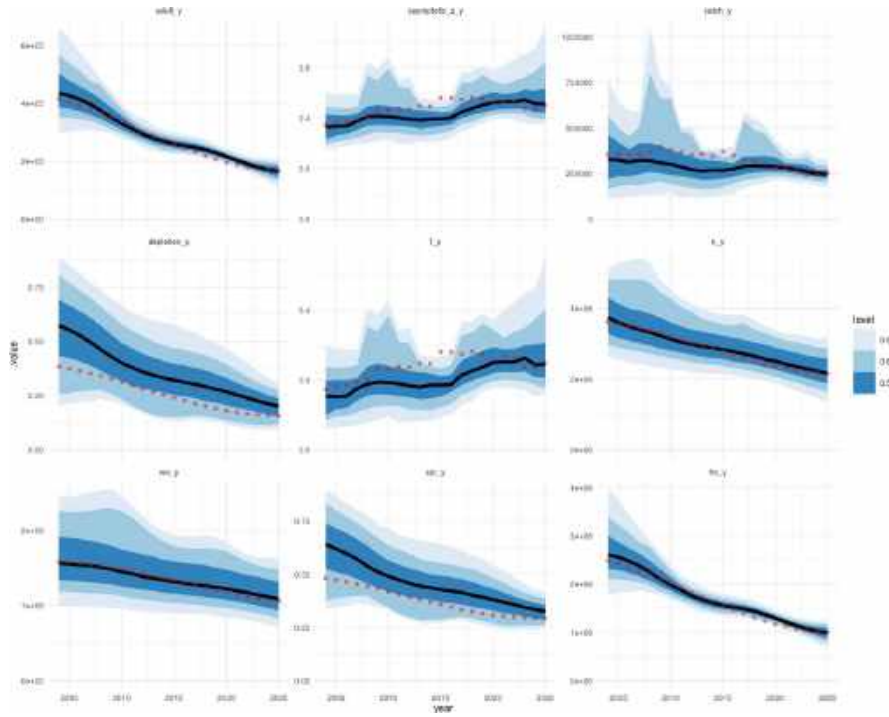


Figure 3: Example true values (red points) and posterior distributions from a single simulation fit.

Figure 5 shows the same set of results but with bias (MPE) rather than MAPE. Adult abundance and TRO were both unbiased at higher sample sizes, with positive biases at lower sample sizes (consistent with CKMR theory). The model tended to overestimate both SPR and SSB/SSB0 even at high sample sizes.

Overall, 10,000 samples per year were generally sufficient to achieve MAPE values in adult abundance and reproductive output below 50%. However, this encompasses a wide range of population sizes. For smaller populations of roughly 1 to 2 million individuals, collecting as few as 3,000 samples per year was generally sufficient to reach these levels of accuracy.

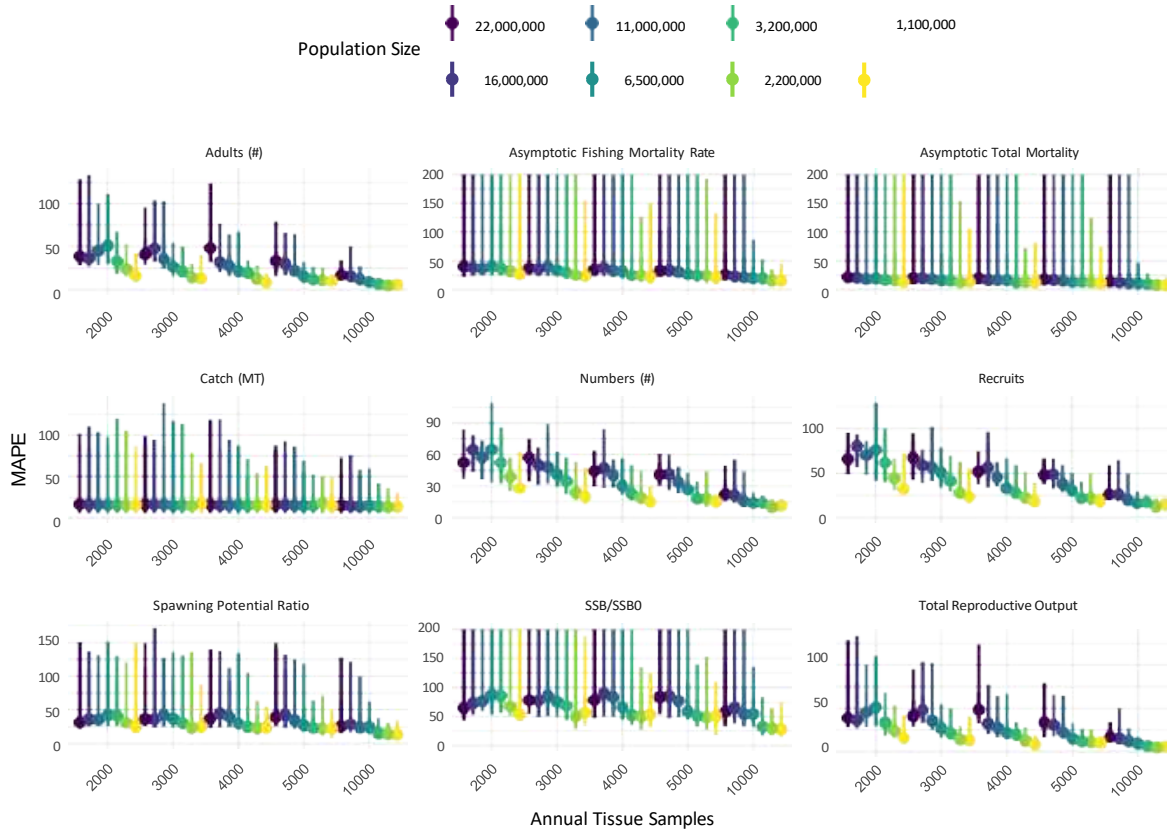


Figure 4: Distribution of MAPE as a function of annual tissue samples (x-axis) and recent population size (color). Y-axis values capped at 200%.

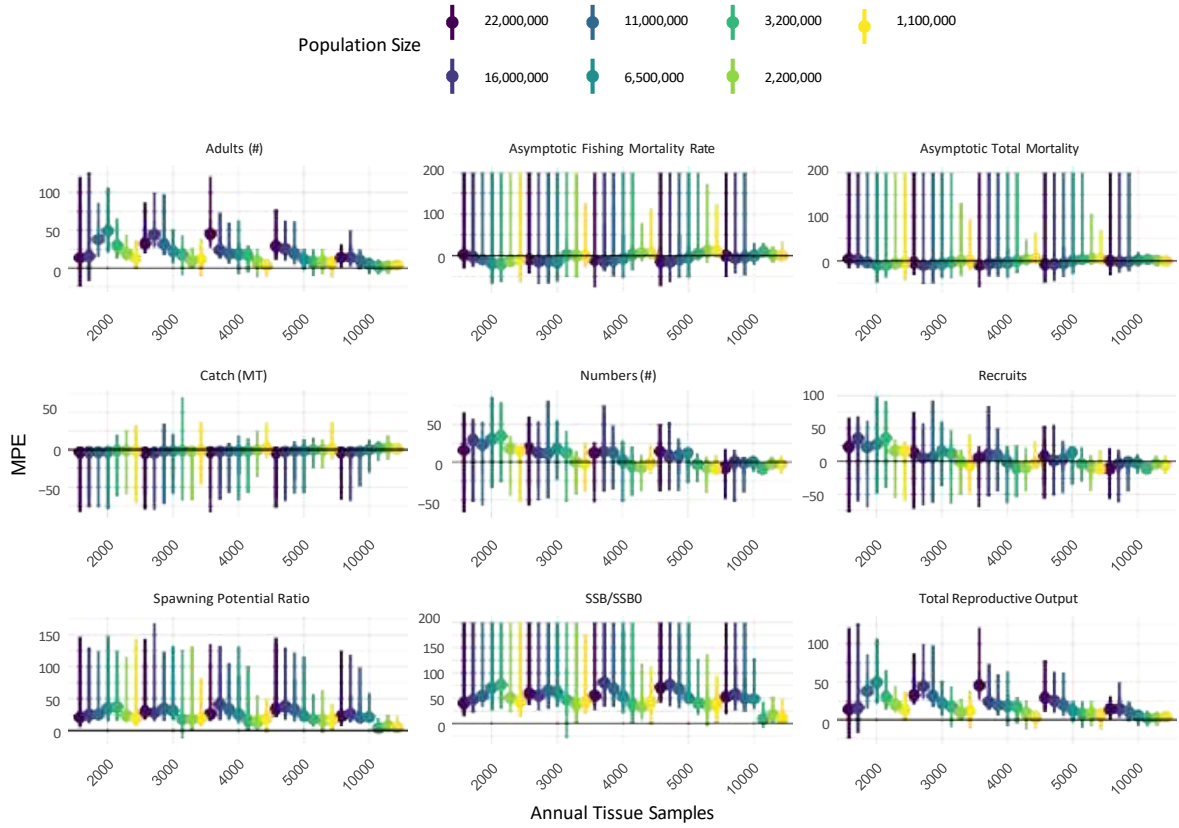


Figure 5: Distribution of MPE as a function of annual tissue samples (x-axis) and recent population size (color). Y-axis values capped at 200%.

Figure 6 and Figure 7 show the performance of the model in terms of MAPE and MPE for constant parameters. With higher sample sizes the model was able to correctly estimate both fecundity parameters and natural mortality.

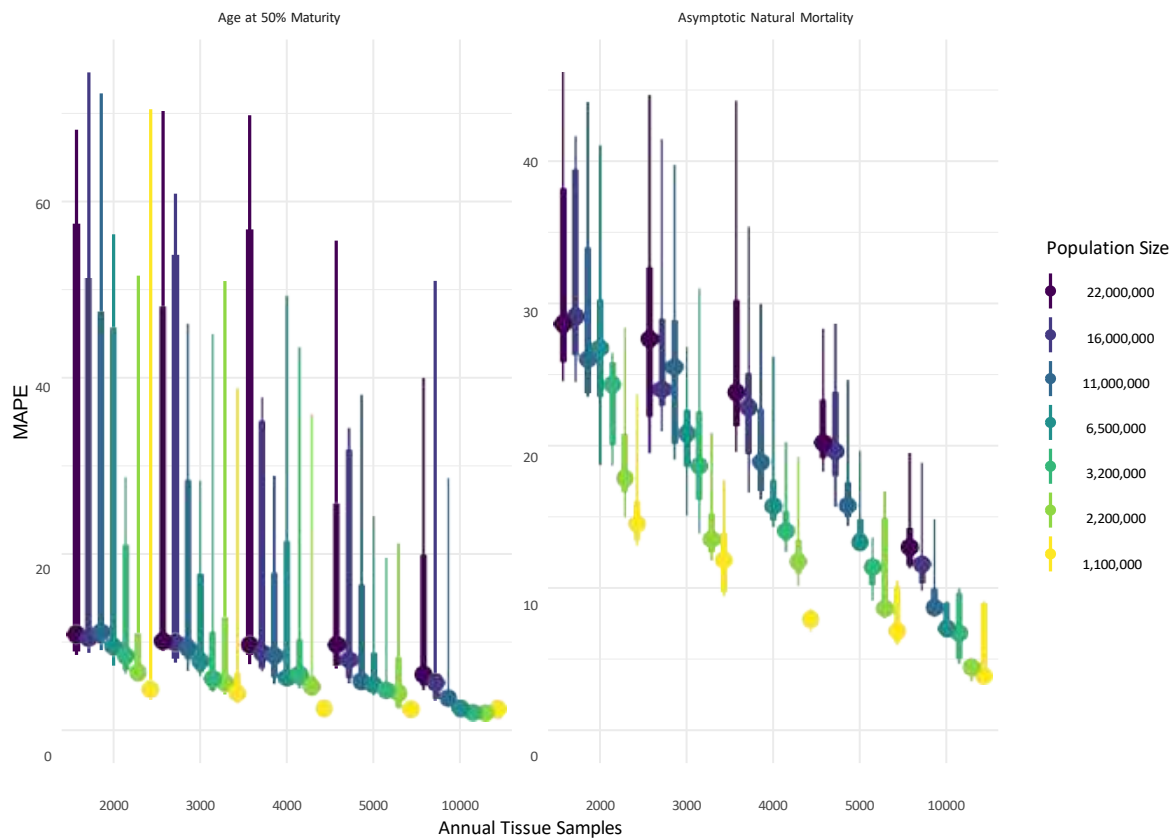


Figure 6: Distribution of MAPE in fecundity and mortality parameters as a function of annual tissue samples (x-axis) and recent population size (color).

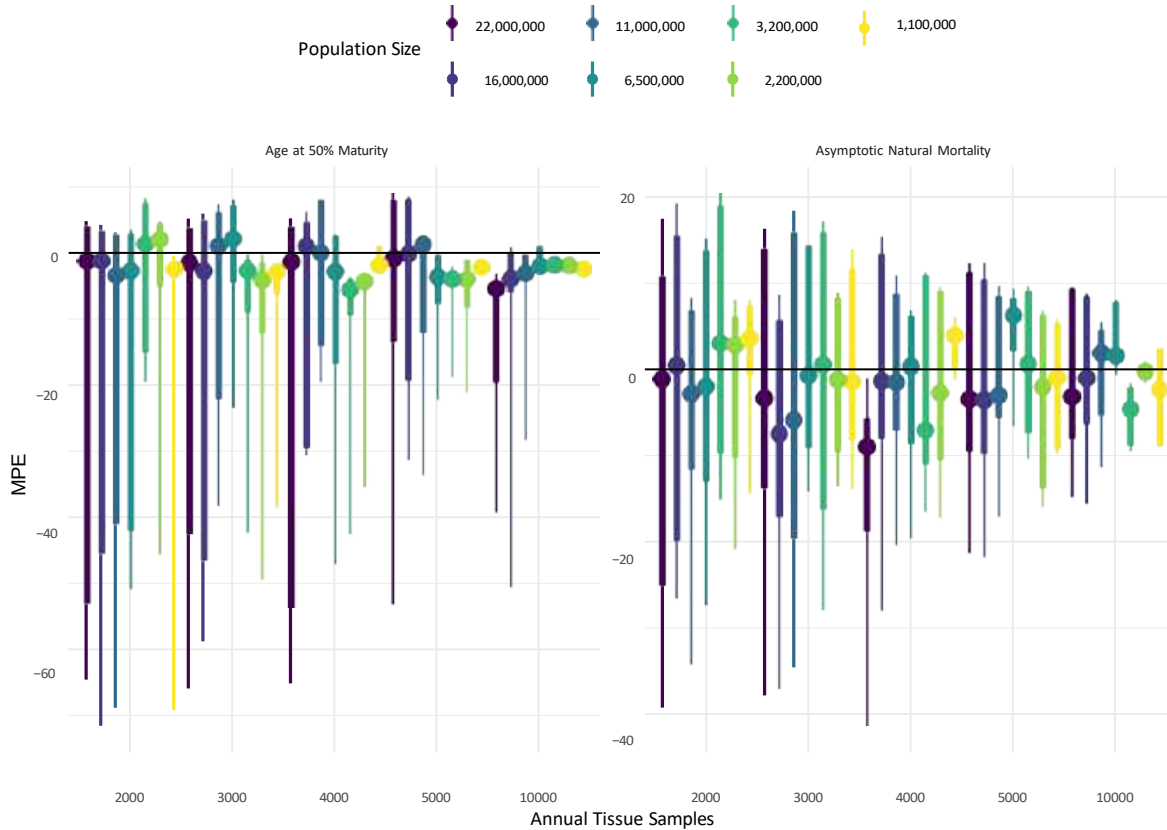


Figure 7: Distribution of MPE in fecundity and mortality parameters as a function of annual tissue samples (x-axis) and recent population size (color).

Along with sample sizes, the influence of relative weighting of different age groups in the tissue sample collection process was also examined. Focusing on the population-level parameters, results were relatively insensitive to the weighting of age groups in the sampling process. Differences in performance as a function of age group weighting were generally modest. Oversampling the youngest age groups relative to their distribution in the catch produced slightly better results in some cases than equal weighting or targeting middle-aged individuals (Figure 8).

Lastly, the influence of having access to catch data of varying quality over the last five years was tested. In order to isolate the effect of catch data, only simulations with the median number of annual tissue samples (4,000) and the median population size (6,500,000) are presented. The MAPE at these median values was then examined as a function of catch data, ranging from having no catch data over the last five years of the program to three levels of certainty over the catch values.

Having access to catch data, even with a high assumed CV, generally substantially reduced MAPE in estimated population-level parameters, most notably for fishing mor-

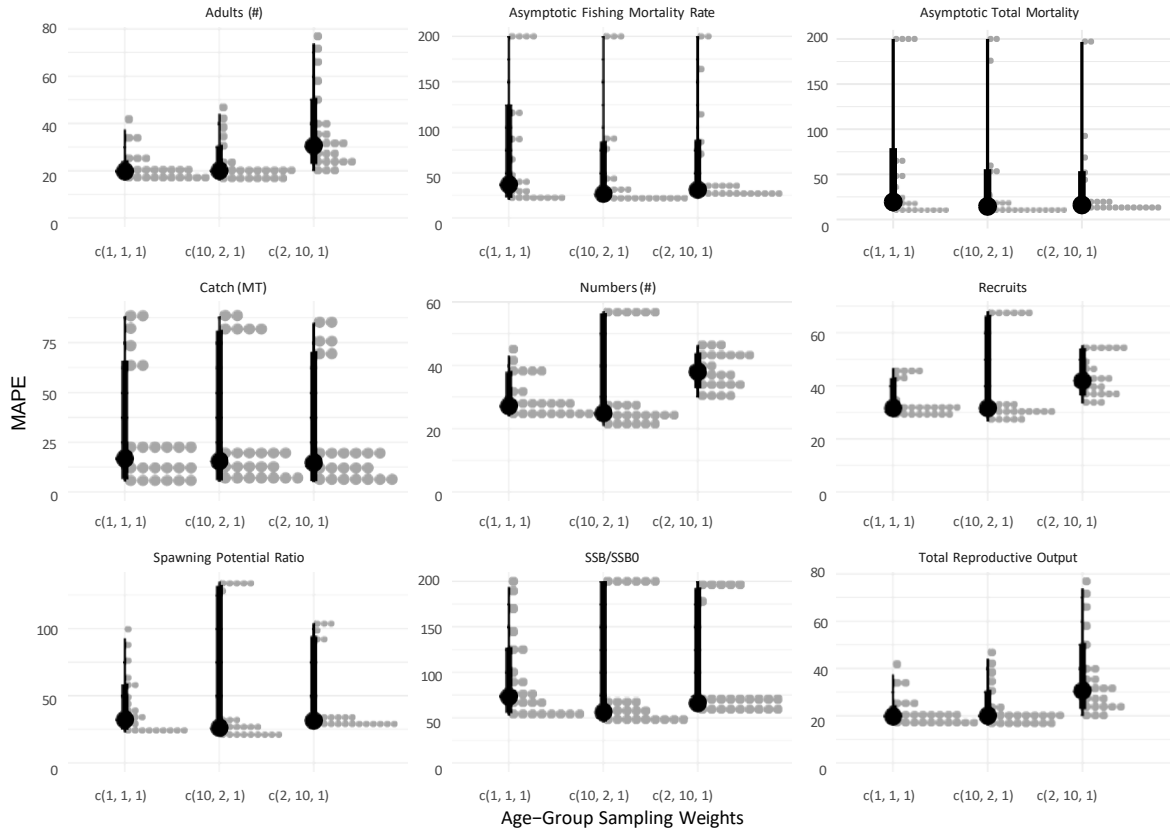


Figure 8: Distribution of MAPE as a function of age-weighting in the sampling protocol (x-axis). Results are only from simulations with median population size and annual sample sizes for visual clarity.  $c(1,1,1)$  indicates equal weighting of all age groups.  $c(10,2,1)$  reflects priority sampling of younger sharks.  $c(2,10,1)$  prioritizes sampling of middle-aged sharks. Y-axis values capped at 200%.

tality rates, as is to be expected, but also for absolute adult abundance (Figure 9). This simulation process highlights the importance of concurrent work being conducted by the IATTC with support from the EU (ABNJ-1 and ABNJ-2) to enable estimation of total catches of silky sharks in the EPO from both commercial and artisanal sources (SAC-16-INF-W and SAC-14-INF-L).

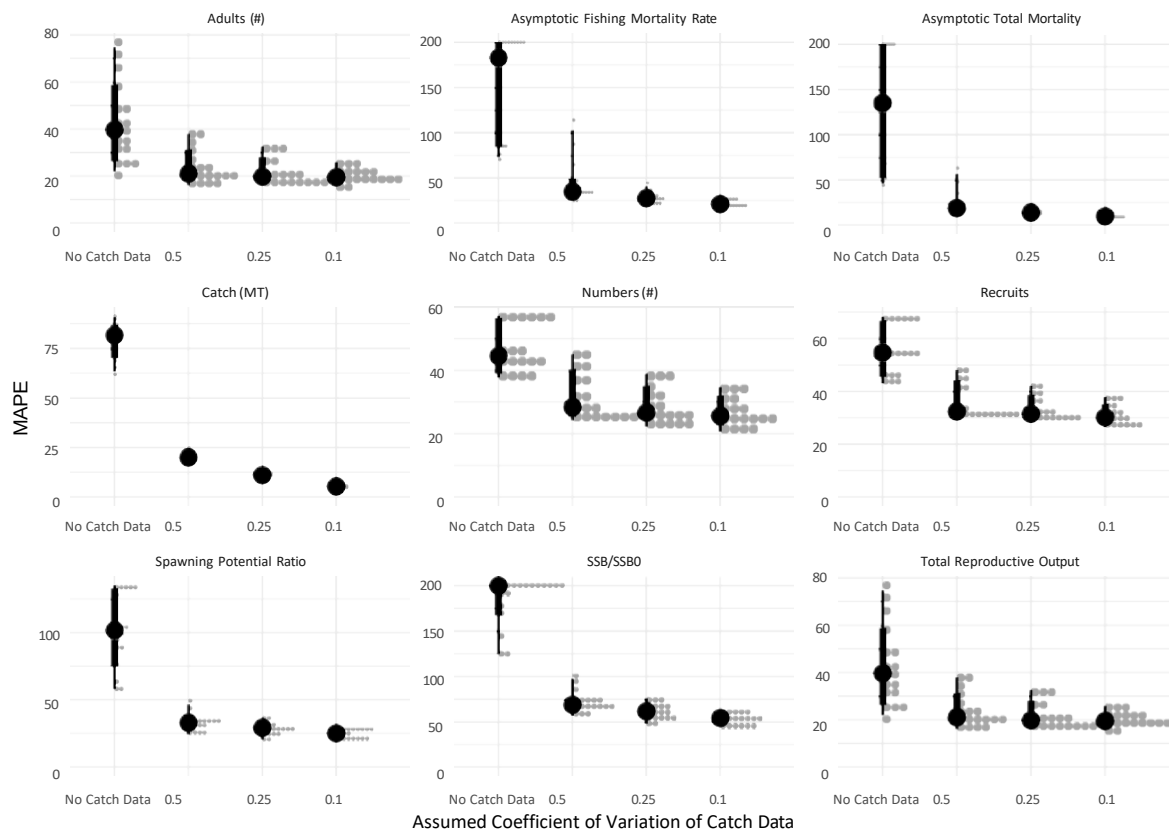


Figure 9: Distribution of MAPE as a function of presence and assumed coefficient of variation (CV) of catch data over the last five years of the study. Y-axis values capped at 200%.

## ***ibm*** Test Results

The full set of diagnostics presented for the *internal* tests is available for the *ibm* results, but for the sake of brevity this section focuses on a qualitative assessment of the sensitivity of the estimation model to violations of its core assumptions, namely population structure and skip reproduction.

The results show that the estimation model is generally able to estimate the adult population size even in cases with skip reproduction and spatial population structure (Figure 10), albeit with potentially higher levels of error. The model's ability to estimate total adult abundance was relatively insensitive to the presence of unaccounted-for spatial stock structure. When configured to do so, the model is able to account for skip reproduction, but if skip reproduction is present and the model ignores it, the model overestimates adult abundance. This is consistent with the basic mechanics of CKMR; the model assigns a probability greater than zero that some individuals may be half-siblings that in fact have zero probability of being half-siblings due to the reproductive interval. As a result, the model interprets the lack of half-siblings as being indicative of a larger population size than actually exists.

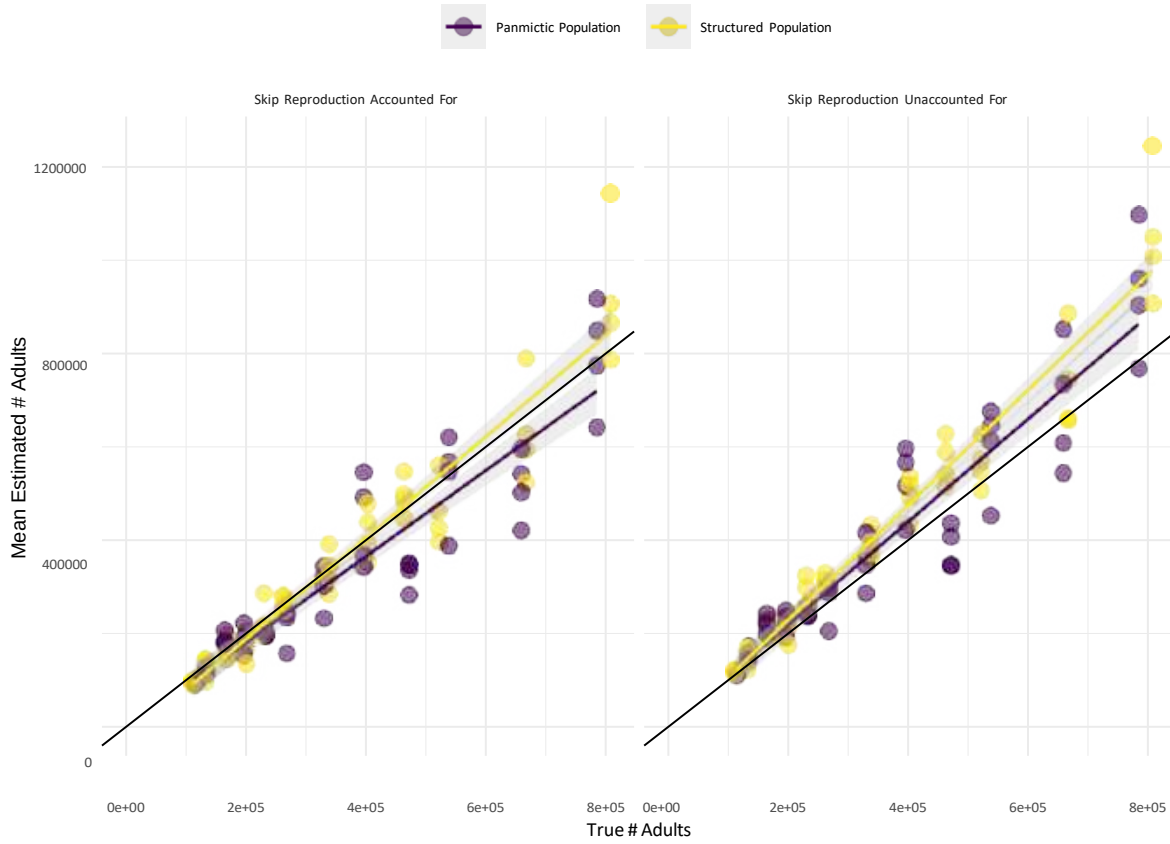


Figure 10: True number of individual-based model (ibm) simulated adults (x-axis) plotted against mean estimated number of adults (y-axis). Color indicates whether the simulated ibm population had spatial stock structure, and panel whether or not the estimation model attempted to account for the presence of skip reproduction.

## Aging Error

Being able to accurately age individuals is important to a successful CKMR study, particularly if processes such as fecundity and mortality of mature individuals vary meaningfully with age or length, and if trends in population size over time are desired. In addition, in most cases ages cannot be directly observed, and instead must be inferred based on more easily measured variables such as length.

Talwar et al. (2025) developed a conceptual model and summary of the state of knowledge of silky shark population dynamics and biology in the EPO. This work showed that there is evidence of size/age dependent fecundity in silky sharks, emphasizing the need for accurate ages. They also found substantial variation in the estimated length-at-age relationship for silky sharks in the EPO, depending on the particular study or region in question (Figure 11).

As a final complication, sharks are available to sampling technicians in the artisanal fleets in a wide range of processed states, ranging from whole sharks to headed and gutted trunks. While DNA samples can be taken from all of these conditional on suitable preservation of the tissue, work is needed to determine accurate methods for assigning ages to processed sharks. The sensitivity of the CKMR model to aging error is currently being explored, and work has begun on integrating aging error directly into the CKMR model.

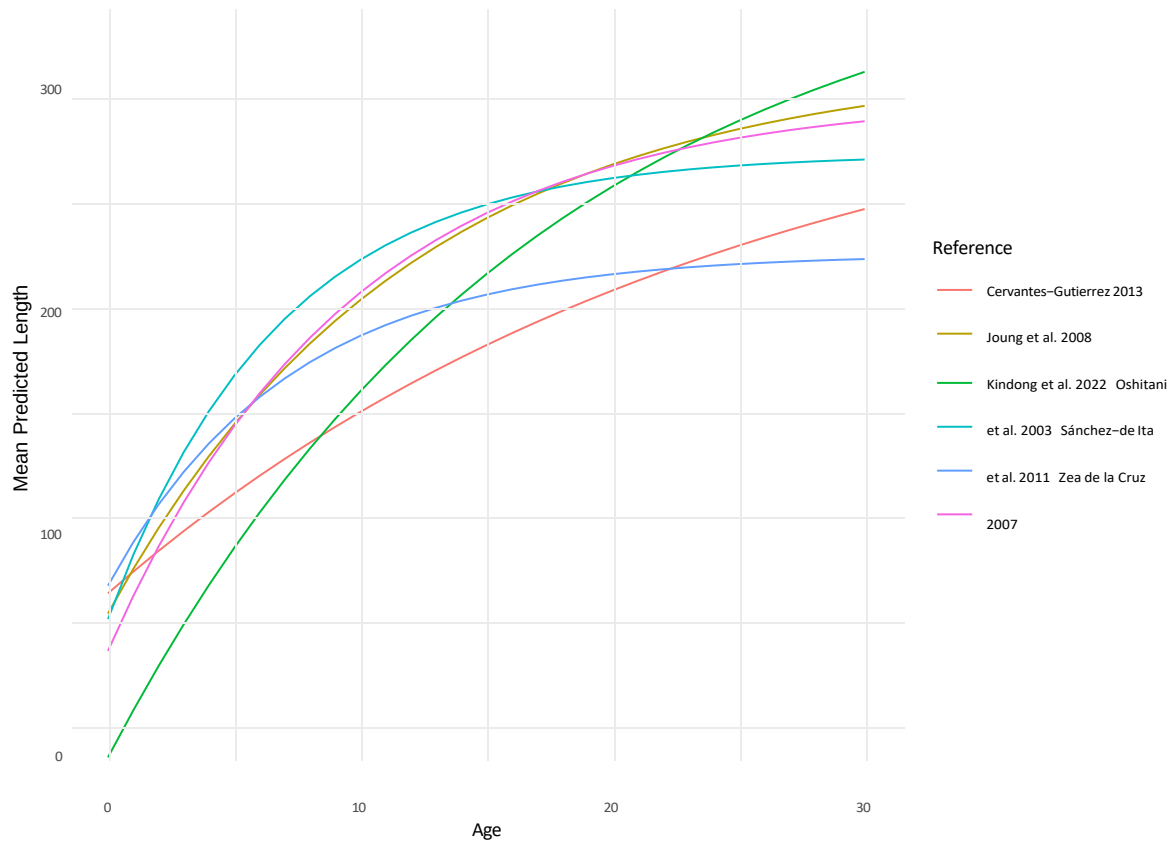


Figure 11: Range of silky shark growth curves reported by Talwar et al. (2025) from different studies in the EPO.

## Initial Sample Collection

Given the positive results from the simulation studies, a sampling protocol was developed for collecting silky shark tissue samples from artisanal fisheries in Mexico, Ecuador, and Peru, and collection of samples began. This initial sampling served three purposes. The first was to test and practice field sampling protocols to ensure that the volume of samples required for this project can be collected rigorously and safely. The second was to verify that the quality of DNA obtained through this sampling is sufficient for CKMR work. The third was, conditional on sufficient quality, to evaluate genetic stock structure in the region and begin to accumulate the number of samples required to develop the genetic tools needed to assign kinship between individual sampled sharks, the core basis of CKMR analyses.

As of December 2025, several hundred tissue samples had been collected. Most of these samples were collected in Ecuador, with the rate of sample collection increasing in Mexico and Peru. The initial protocol focused on the use of an automated tissue sampling tool developed by Biomark. The reason for this choice was to reduce the workload for fisheries observers who will be tasked with collecting these samples, particularly in the industrial fisheries. While these automated kits had some success on smaller sharks, they were found not to be suitable for use on larger sharks with thicker skin. Based on that result, an alternative sampling kit was developed based on materials that could be purchased within each country, and sampling with this new kit, along with the Biomark kits, has begun. Alternative sampling tools will continue to be explored to fit the needs of various fishery and observer contexts.

Figure 12 provides an illustration of the kinds of information now being collected by the field teams. In addition to basic sample information such as size and sex, they have also often been able to obtain metadata such as capture location. This information highlights that sampling only a few ports in Ecuador can provide samples that originated from across a wide range of the eastern EPO fishing ground.

In addition to serving as the basis for initial kinship panel development, the initial round of tissue samples supported by IATTC CKMRfeas will be analyzed by a team of collaborators at Nova Southeastern University to refine the current understanding of population structure of silky sharks in the EPO, including validation or refinement of the potential three-stock hypothesis highlighted by Talwar et al. (2025). These results will help refine future sample collection strategies and model structure.

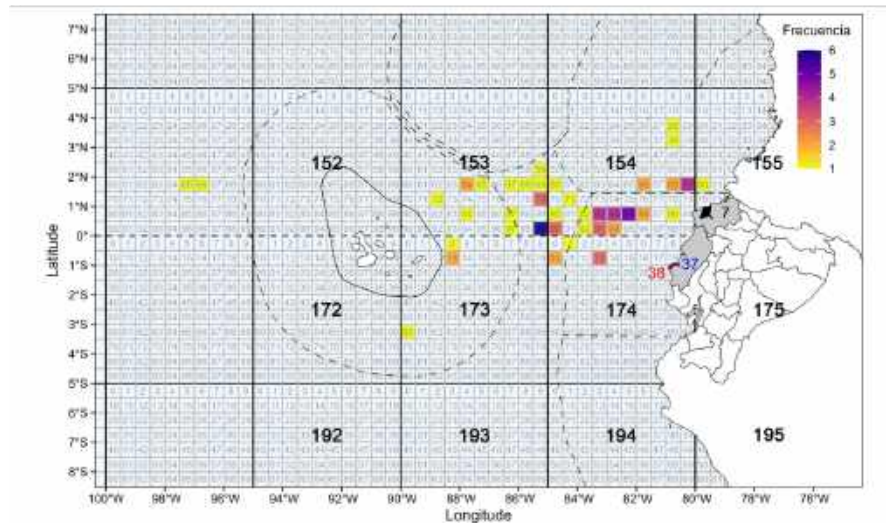


Figure 12: Self-reported capture locations of silky sharks sampled at ports in Ecuador.

## Tissue Quality Evaluation

Export permits under the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) are pending; once they arrive, the tissue samples will be shipped to the project partners, who will evaluate the quality of DNA that can be extracted from them. The number of samples (roughly 40) needed for DNA quality evaluation is already available from both Ecuador and Mexico, and the minimum sample number should be reached soon in Peru as the core period of silky shark catches in the region begins.

## CITES Permits

Silky sharks are listed on Appendix II of CITES. Consequently, an export permit must be obtained from each country with vessels that will be relied on for silky shark samples in order to have the samples shipped to the USA for processing. This permit is granted by the country-specific Management Authority once the Scientific Authority of the State makes a 'non-detriment finding' (NDF) advising that export will not be detrimental to the survival of the species. Similarly, if a vessel flies the flag of a country different from the one where the catch is landed, the flag State will require an export permit and legal acquisition finding prior to landing. Acquisition of the necessary permits is presently in progress but must be completed prior to export of any silky shark tissue samples.

The project's regional fishery coordinator is currently managing the process of obtaining the required CITES permits to ship from each of the sampling countries (Mexico, Ecuador, and Peru) to the USA. The permits required in each country are expected shortly, but the process of obtaining CITES permits in each country has been complex. Once obtained, these permits should cover the initial stages of the project, but obtaining and maintaining CITES permits is a clear challenge that will need to be managed over the course of a successful silky shark CKMR project.

## Key Findings and Recommendations

Completion of IATTC CKMRfeas has provided a number of key lessons for the establishment of a full-scale CKMR assessment of silky sharks in the EPO. These lessons are synthesized below.

The first consideration in any CKMR study is whether the number of tissue samples required to obtain sufficiently high-quality results is logistically and financially feasible to collect. While back-of-the-envelope sample size requirements were developed in earlier phases of this study, they were refined here. The results suggest that 3,000 samples per year over three years (9,000 total) may be a reasonable floor if population sizes are on the order of 1 to 2 million individual silky sharks and MAPE values in absolute adult abundance below 50% are desired. If the population size is on the order of 10 million or more, closer to 10,000 samples per year for three years (30,000 samples total) may be required to achieve similar MAPE values in absolute adult abundance according to the simulation model. In addition, given the likely impacts of aging error and other uncertainties not yet accounted for in the model, erring on the side of larger sample sizes is recommended for the initial study.

One of the advances that has made CKMR viable for larger populations is the dramatic decrease in the cost of processing each sample and identifying kinship pairs. The exact costs can vary depending on the degree of investment made in genomics tools needed for kinship analysis. Using RADseq technologies, subsequent costs per sample could be as high as \$40. Using amplicon sequencing incurs more up-front costs, but can bring per-sample costs down to below \$10 (Meek and Larson 2019). For that reason, the plan is to develop an amplicon panel to serve as the basis for long-term CKMR assessment of silky sharks in the EPO, with an estimated up-front cost of roughly \$200,000, but providing substantial long-term savings given the large number of tissue samples that will need to be processed over the span of the project.

Assuming a cost of roughly \$10 per sample after amplicon panel development would imply direct kinship assignment costs of roughly \$90,000 for 3,000 samples per year

(9,000 total), or \$300,000 for 10,000 samples per year (30,000 total). However, there are clearly many other costs that need to be factored into the full expense of processing these samples (sampling technicians, sampling equipment, shipping costs, etc.). As a baseline, if the full cost of each sample is assumed to be three times its kinship cost, so \$30 per sample, that would bring the total cost up to \$270,000 for 9,000 samples over three years or \$900,000 for 30,000 samples over three years. These approximations can be incorporated into the sample size calculations to provide an estimated sample collection cost that may be needed to achieve a target MAPE value for a range of different attributes of the population under different assumptions of the total population size (Figure 13), with the understanding that these are rough approximations at this point.

This is not the full estimated cost for a CKMR assessment of silky sharks in the EPO. Additional costs will be the initial development of the amplicon panel needed to assign kinships, support for model development and contractor time beyond sampling technicians, travel, workshops, conferences, publications, and potentially expanded projects such as development of epigenetic aging methods. However, the steps taken here provide an estimate of the core costs of the program, the collection and processing of tissue samples.

While the *internal* tests used to provide these cost estimates are useful, they depend on the assumption that the silky shark population structure and biology used in the estimation model are in fact correct. While this will never truly be the case, it is a useful starting point for analyses. The individual-based model (*ibm*) tests present an alternative approach that allowed model performance to be tested when the model generating the kinship data and the CKMR assessment model were not based on exactly the same set of assumptions. Specifically, these tests included scenarios such as spatially defined sub-stock structure with imperfect mixing and imperfect skip reproduction. While the full set of diagnostics produced for the *internal* simulation tests is available, for the sake of brevity only the visual assessment shown in Figure 10 was presented. These results demonstrate that the models may still be able to provide accurate estimates of adult population size even if faced with these types of issues. The *ibm* tests will continue to be refined as understanding of silky shark population dynamics in the EPO evolves.

One of the key benefits of CKMR is the potential ability to generate absolute abundance estimates, along with other relevant parameters, based only on sampling a relatively small proportion of the population. However, that does not mean that other sources of data are without value. The results presented here show that augmenting tissue samples with estimates of the recent volumes of catches, even uncertain estimates, can reduce error in a wide range of parameters, including absolute abundance but most notably for parameters that are highly useful for management such as fishing mortality rates or depletion levels. These results emphasize the value of maintaining efforts to

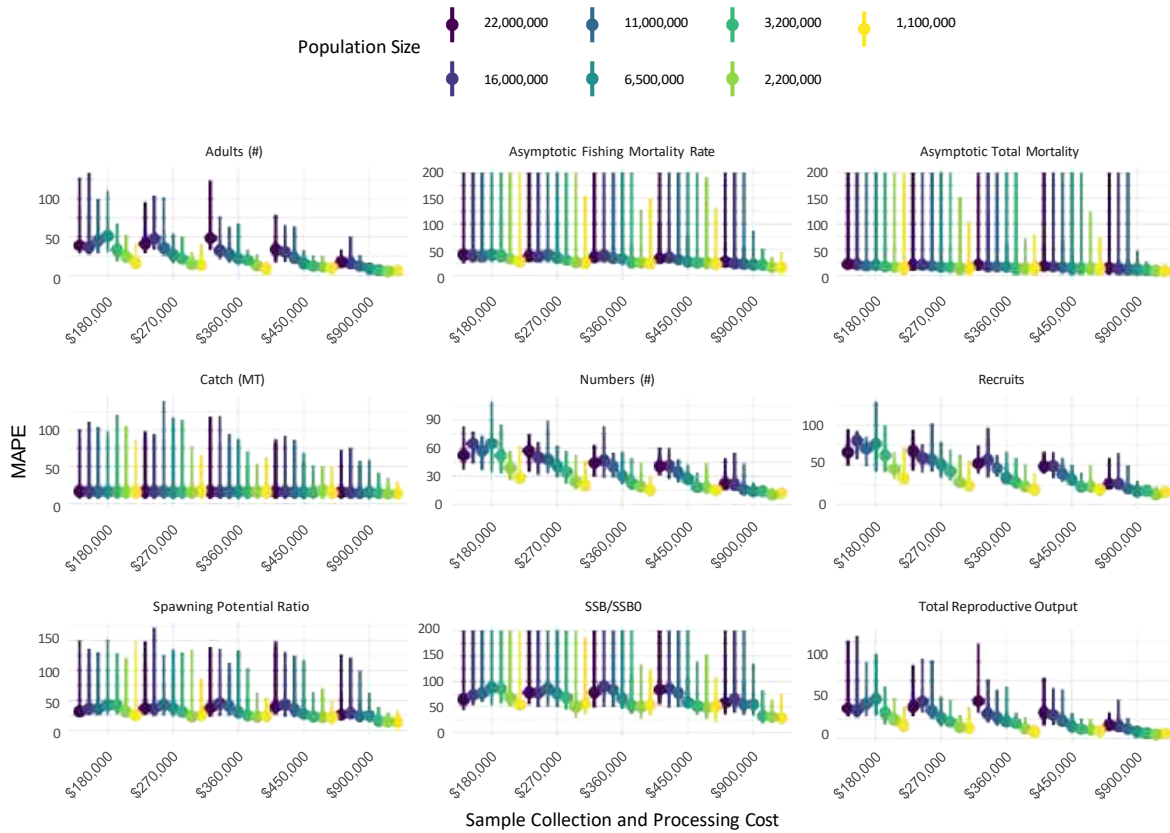


Figure 13: Distribution of MAPE as a function of roughly estimated total sampling costs (assuming \$30 per sample) over three years (x-axis) and recent population size (color).

collect additional sources of data such as catches and length composition that can be incorporated into eventual CKMR assessments.

The literature review conducted in Talwar et al. (2025) and the experience of the field teams highlight that investment in a better understanding of length and age dynamics of silky sharks in the EPO will likely be needed. Specifically, strategies will need to be developed for accurately converting various forms of landed sharks (e.g., processed trunks) into ages. Growth studies of silky sharks in the region should also be revisited, as demonstrated by the high across-study variability shown in Talwar et al. (2025). An alternative would be to develop epigenetic aging protocols (Newediuk et al. 2025) for silky sharks that would allow sample ages to be estimated directly from the tissue samples themselves. While long-term this may be the best option, it will likely take several years of research and development, and potential advances in associated genetics techniques, to rely on this method.

Based on this pilot study, the specific sampling tools for use in different contexts are still being refined. The Biomark kits are highly efficient, but have not been durable enough for prolonged use in the field. The skin on larger sharks is often too tough for the sampling technicians to easily punch through, requiring high levels of force which quickly result in the applicator tool breaking down. The field teams have been able to procure the materials needed to construct kits manually in each country, which has been slower but more reliable. When time is not a limiting factor, these manually constructed kits may be a viable option. However, tissue sampling has yet to be tested during commercial purse-seining operations, when speed and efficiency may be more critical. Ongoing tests will be needed to determine optimal tools for collecting the volume of samples required under these conditions.

Lastly, this pilot study has emphasized the critical importance of having a highly skilled field team with deep knowledge of local fishery dynamics and governance. The project's field coordinators have been able to navigate the complex tasks of finding suitable and safe sampling sites, building relationships with local authorities, obtaining permits, and collecting high-quality samples and metadata. Their work has demonstrated that the IATTC team is capable of collecting high-quality tissue samples at scale from artisanal fisheries from Mexico to Peru that will enable a full-scale CKMR assessment of silky sharks in the EPO. In addition, the expertise of the field staff has been instrumental in facilitating the CITES permit process. While this phase of the study has focused on silky sharks, the methods and knowledge gained through this study will greatly facilitate expansion of CKMR programs at the IATTC to hammerhead sharks and other relevant species at a later date.

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