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**REPORT ON PROJECT 100D: APPLICATION OF CKMR METHODS TO SP ALBACORE AND COST-
BENEFIT EVALUATION AND PRIORITIZATION OF CKMR TO WCPFC STOCKS
(TUNA, BILLFISH, SHARKS)**

WCPFC-SC22-2026-SA-WP11_Rev01
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Submitted by SPC¹ and CSIRO²

¹ Oceanic Fisheries Programme (OFP), Pacific Community, Noumea, New Caledonia

² The Commonwealth Scientific and Industrial Research Organisation, Australia

Executive Summary

SC21 established Project 100d to provide CKMR estimates for south Pacific albacore and to provide WCPFC with a cost-benefit evaluation of CKMR application for other WCPFC stocks (tuna, billfish, sharks) to guide future SC on when to apply CKMR, which species to apply it to, and approximate costs of application. The project is a continuance of project 100c (P100c) which established the foundations for the application of Close-Kin-Mark-Recapture to WCPFC stocks.

This working paper updates SC22 on progress over the past 12 months and is advised of the following:

- i) A cost-effective assay for epigenetic ageing for tuna remains a work in progress. CSIRO has initiated a new avenue of research, which if successful, would significantly improve the workflows and efficiency of large-scale applications of epigenetic ageing for CKMR.
- ii) A CKMR scoping study was completed for yellowfin tuna. The analyses indicate that 40,000 samples/yr collected over three years or 35,000 samples/yr collected over four years would be required to provide informative estimates of abundance and mortality from a stand-alone CKMR assessment model. Based on the progress with CKMR implementation study for south Pacific albacore, these samples sizes seem feasible from a logistics and workflow perspective.
- iii) Sample collection for south Pacific albacore is progressing with expectations of a first application of CKMR completed in 2027 to compliment the scheduled south Pacific albacore stock assessment. Note that additional otolith collection is required in 2026 for ageing purposes.
- iv) A desktop review has been completed to identify the current availability of information necessary to support CKMR applications to tuna, billfish and sharks. The review notes that addressing knowledge gaps in the life history for some of the billfish and sharks would facilitate CKMR application. These gaps are identified in the scientific committee's billfish research plan and shark research plan.

Recommendations

SC22 is invited to:

- note the progress on each activity;
- encourage the collections of south Pacific albacore otoliths for ageing to support CKMR analyses in 2027.

Background

Project 100c established the foundations for the application of Close-Kin-Mark-Recapture to WCPFC stocks demonstrating that the logistics of sample collection and identification of kin are feasible for applying CKMR to south Pacific albacore. SC21 established Project 100d to continue this work to provide the CKMR estimates to compliment the next south Pacific albacore stock assessment (scheduled for 2027). Following discussions at SC21, a second activity to provide WCPFC with a cost-benefit evaluation of CKMR application for WCPFC stocks (tuna, billfish, sharks) was requested to help guide future SC discussion on CKMR applications. Specifically, project 100d has the following scope of work.

Scope of Work

- i) CKMR application to south Pacific albacore
 - a. Collection of a further 50,000 tissue samples of south Pacific albacore to meet the 84,000 maximum estimated by Tembley-Boyer et al (2024).
 - b. Genotyping of up to 69,000 samples to identify the number of kin for CKMR estimation with a CV of 15% (*i.e.*, noting that 15,000 have already been genotyped by P100c).
 - c. Bioinformatics for the genotyped samples to identify kin and embedding them into a population dynamics model and estimate absolute adult abundance, mortality rates, and connectivity.

	2026		2027	
	Jan-Jun	Jul-Dec	Jan-Jun	Jul-Dec
Sample Collection				
Genotyping				
Bioinformatics				
CKMR estimates				

- ii) Desktop evaluation of future potential CKMR application to WCPFC stocks.
 - a. Draw on the global experience to provide WCPFC-SC with a guide on the approximate number of samples that need to be collected per WCPFC stock, the number of years of collection needed to obtain a first estimate, the logistical issues with collection, any genomic assay development needed, and expected costs to achieve the first estimate and then subsequent estimates.

	2026		2027	
	Jan-Jun	Jul-Dec	Jan-Jun	Jul-Dec
Desktop evaluation				

CKMR foundation activities undertaken since SC21

Epigenetic ageing

Epigenetic ageing has potential for direct, tissue-based age estimation, reducing reliance on otoliths. While progress has been made, developing high-throughput epigenetic methods

suitable for CKMR is still challenging. CSIRO is collaborating with Diversity Arrays Technology PTY (Canberra, AU) to develop a low-cost, targeted assay for scalability and routine application of epigenetic ageing in CKMR studies.

Previous work on southern bluefin tuna (SBT), undertaken in a separate but complimentary project, showed a clear age-associated signal but was constrained by low coverage and locus dropout. Further work is focusing on converting those results into a high coverage DArTag panel that can deliver more precise methylation estimates at a substantially lower per sample cost. The long-term goal is a single assay that works across several tuna species, not just SBT. A final marker panel of 2,640 CpG loci retained a strong age signal and is now ready for DArTag assay development across multiple *Thunnus* species. The next steps are to:

- Validate the test in SBT using more high confidence aged fish.
- Apply the same assay to albacore, bigeye, and yellowfin tuna.
- If needed, refine species specific markers (and associated assay) or run full methylome sequencing for each species to improve accuracy.

In the interim, SPC has initiated the collection of 300-500 otoliths from approximately four ports to provide a basis to estimate the fleet-specific age composition for albacore. Concurrently, and as part of Project 129, an alternative rapid ageing method will be developed utilising archived Albacore otoliths to develop an age prediction model that uses otolith biometrics and fish length within a multivariate analysis.

Swordfish (SWO) age estimation using otolith sections and the pursuit of validation using bomb radiocarbon (^{14}C) dating is nearing its conclusion. Twenty-seven ^{14}C measurements have been made on 24 Pacific SWO otoliths that were aged 1 – 21 years. In a parallel study of Atlantic SWO, 60 measurements of ^{14}C were made on SWO otoliths that were aged 1 – 15 years (Rosa et al. 2026). Results from Atlantic SWO indicated that the age reading of otoliths from this species can be difficult due to an irregular otolith shape and the fragile nature of the otolith material; however, there are a series of well-defined otolith sections from both the Atlantic and Pacific that appear to show growth zone structure that is reliable and supported by temporal alignment of the ^{14}C values. In terms of bomb-produced ^{14}C , both studies show clear indications of ^{14}C uptake variability in the earliest otolith growth period due to oceanographic patterns and early life history diving behaviour. As a result, no further SWO otoliths will be processed for core extractions and a synthesis paper on the results of the work for the Pacific and Atlantic is in progress. While the bomb ^{14}C results for SWO were limited, it is reasonable to assume that otolith growth zone structure, when well-defined, can be used to establish a reliable epigenetic clock for SWO age determination in lieu of otolith use for future population studies.

CKMR scoping study for yellowfin tuna

The scoping study for yellowfin tuna used population parameters and abundance estimates from the most recent WCPFC stock assessments for yellowfin tuna (Magnusson et al. 2023). The number of parent-offspring pairs (POPs) and half-sibling pairs (HSPs) expected to be found was estimated using the R package *microscoping* (Bravington 2024), under alternative scenarios of abundance, annual sample sizes, sample age distribution and sampling program lengths. Note that this does not consist of a comprehensive design study, but of a rough estimate of the number of kin that are expected to be detected under a range of sampling programs, given population size, age distribution, key life-history parameters and perfect mixing across the stock.

Uncertainty in population size was accounted for by repeating the sample size calculation for each model in the 2023 yellowfin tuna assessment structural uncertainty grid. The grid consists of 54 models varying assumptions about steepness, tag mixing and size and age data weightings, and each of these models is assumed to represent a slightly different population state. Numbers-at-age vectors for each grid model were constructed from the average age distribution over the last four assessment years. Life-history parameters were also the same as those in the 2023 stock assessment. Hence, the estimated sample numbers span population sizes and biological parameters that are consistent with this most recent stock assessment.

Programmes collecting between 30,000 to 45,000 annual samples for three, four and five consecutive years were assessed. Samples were evenly split across adults and juveniles, with juveniles defined as individuals of age < 1.5-year-old for simplicity. Two sampling scenarios of age distribution within the juvenile and the adult samples were investigated. In the first instance, “PMSTB”, the age distribution matched the fork lengths observed in yellowfin tuna muscle samples collected since 2023 and logged in the online version of the Pacific Marine Specimen Database (accessed July 1st 2026; <https://www.spc.int/ofp/PacificSpecimenBank/Search/SearchTool>). In the second instance, “MFCL”, the age distribution was set to match that predicted across all fisheries in the stock assessment model.

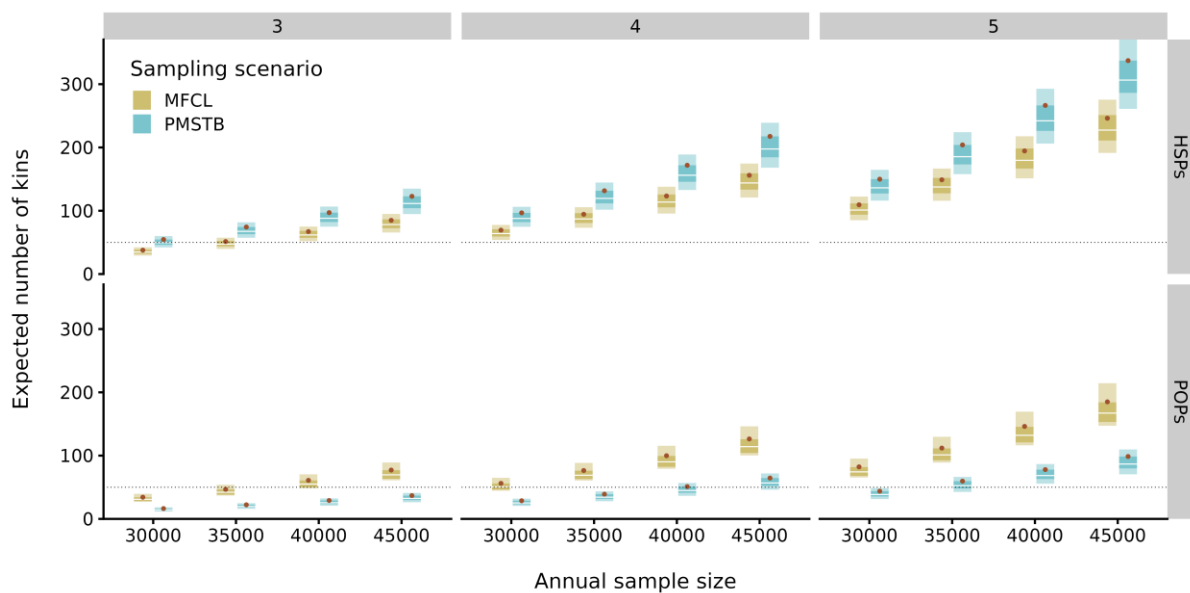


Figure 1 Distribution of expected kin (half-sibling-pairs, HSPs, top panel; parent-offspring pairs, POPs, bottom panel) by sampling scenario (annual sample size (x-axis) and sample age distribution, coloured bars) for three, four and five years sampling programmes. The coloured bars show the 10-90th quantile interval (pale bar), the inter-quartile interval (darker bar), and the median (white line) across the 54 models in the structural uncertainty grid. The coloured dot represents the prediction for the “diagnostic” model as defined in Magnusson et al. (2023).

Results summarised over the 2023 structural uncertainty grid indicate that sampling of 40,000 individuals annually over three years, or 35,000 individuals annually over four years, are expected to yield sufficient number of kin (i.e., at least 50 pairs each of half-siblings and parent-offsprings; Figure 1) over most population state scenarios included in the most recent stock assessment. Importantly, the sampling-at-age strategy is influential in the likely number of kin identified: sampling-at-age matching the catch-at-age distribution across all fisheries was more likely to result in enough POPs in the three to four years range than sampling following the age distribution currently available in the PMSB. This appears to be because samples logged in the

PMSB to date focus on younger adults, while the stock assessment estimated catch-at-age predicts that older individuals should be present in the longline catch (Figure 2).

Importantly, these sampling scenarios are based on the assumption that an acceptable level of precision (<15% CV) would be achieved should at least 100 kin of the required type be found. The approach does not directly predict the expected CV for population metrics of interest. A comprehensive design study, such as the one for South Pacific albacore (Tremblay-Boyer et al. 2024), would ideally represent biology, population, stock structure and fisheries dynamics more realistically, and also be able to provide more a comprehensive assessment of sampling levels required for estimates of population metrics required to provide a useful degree of precision. However, the completion of the scoping exercise over all models of the structural uncertainty grid from the most recent stock assessment gives some confidence that the estimated sample size is a reasonable starting point for considering the feasibility and approximate cost of an application to of CKMR to yellowfin tuna in the WCPO. Given the progress made with the South Pacific albacore feasibility study and lessons learnt from that process, these sample sizes seem logistically manageable by the sampling program established, although there will be the need to access samples from at sea sampling by observers in some areas/age classes (see following item).

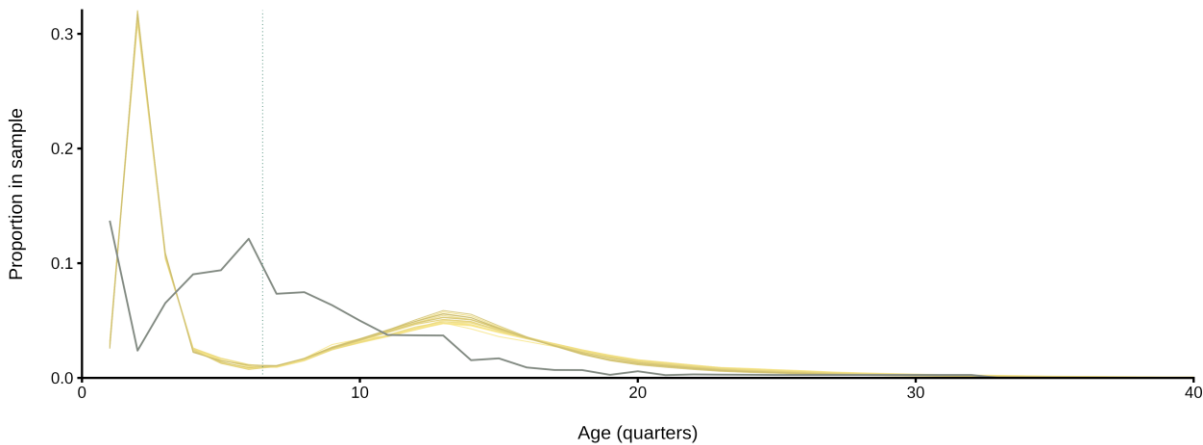


Figure 2 Comparison of the sampling-at-age distributions assumed under the PMSTB sampling scenario (dark green line) and the MFCL sampling scenario (yellow lines, all models of the structural uncertainty grid). Ages are in quarter and follow the 2023 stock assessment definition (Magnusson et al. (2023)).

Develop capacity within WCPFC to implement CKMR

Between 1 July 2025 and 30 June 2026, SPC-OFP staff have led 6 training events that included CKMR sampling. These events included induction of new samplers and refresher/upskilling courses for existing samplers. In total, these events were attended by 80 port samplers, fisheries observers, government and industry staff from 6 countries (Table 1). Since 2023, a total of 241 participants from 17 countries have been trained. Table 2 provides a by-country breakdown of trained staff.

Table 1 Summary of training events for 1 July 2025-30 June 2026

Trainings	Dates	Participants trained
CKMR training in American Samoa	July 2025	3
Refresher training on biological sampling routine Marshall Islands	August 2025	5

CKMR follow up training in PNG	October 2025	33
CKMR training in Palau	February 2026	18
CKMR Training in Solomon Islands	February 2026	9
CKMR, finlet to fork length ratio and biological sampling routine in FSM	April 2026	12
Grand Total		80

Table 2 Summary of trained samplers in participating countries

Country	Participants trained	
	July 2025-June 2026	Total
American Samoa	3	3
Cook Islands	0	1
Federated States of Micronesia	12	41
Fiji	0	20
French Polynesia	0	2
Kiribati	0	12
Marshall Islands	5	22
Nauru	0	2
New Caledonia	0	2
New Zealand	0	3
Palau	18	18
Papua New Guinea	33	67
Samoa	0	3
Solomon Islands	9	28
Tonga	0	13
Tuvalu	0	2
Vanuatu	0	2
Grand Total	80	241

P100d Activities

Sample collection

As of 1 July 2026, roughly 29,000 south Pacific albacore samples were collected between 1 July 2025 and 30 June 2026, for a project total of over 75,500 since 2024 (see Table 3 for a precise breakdown). The past year's sampling volume tracks positively with the updated modelled sampling requirements from SC20 (36,000-84,000 tissue samples over three years; Tremblay-Boyer et al. 2024). However, the distribution of samples over space, time, and age classes is not as even as desired, with implications for distribution of kin pairs across the study region (see Annex 1). Issues that have led to sampling gaps include administrative challenges (e.g. sampling equipment held up in customs), infrastructure limitations (e.g. freezer storage space), technological errors (e.g. uploading data from sampling tablets to database), and uncontrollable circumstance (e.g. poor fishery performance). Port-specific plans were reviewed in April-June 2026 to ensure consistent or improved sampling through December 2026.

Table 3 Summary of SP albacore samples collected and uploaded to Tufman2 through 30 June 2026, as queried on 1 July 2026. Note that samples are organised by port of sampling, but some samples come from surrounding EEZs (e.g. Samoa, where fish originated from the Cook Islands EEZ).

Port	Pre-July 2025	July 2025-June 2026	Total
Fiji	6258	769	7027
French Polynesia	5319	2533	7852
New Caledonia	4752	5228	9980
New Zealand	10113	7105	17218
Samoa/Cook Islands	245	204	449
Solomon Islands	6264	8703	14967
South of French Polynesia	6618	1597	8215
Tonga	1882	3065	4947
Total	41451	29204	70655

Genotyping and Bioinformatics

Development of genetic sequencing and data processing pipelines was reported to SC21 (CSIRO and SPC-OFPb, 2025; SPC-OFP and CSIRO, 2025). A further analysis of kin found to date in the context of the design study and assumptions therein are described in Lloyd-Jones et al. (2026).

Evaluation of CKMR to WCPFC stocks (tuna, billfish, sharks)

Ideally CKMR applications include detection of at least two types of genetic kinship relationships: Parent-Offspring-Pairs (the sampled individuals are identified as parent and its offspring, POPs) and Half Sibling Pairs (the two juveniles sampled share a parent; HSPs). POPs provide the most direct estimate of absolute adult abundance at the time the offspring were spawned (i.e. for an offspring sampled at age a in year t , the corresponding POP probability references adult abundance in year $t - a$). Therefore, POPs reflect the estimated adult abundance in the year the juvenile was spawned. Estimates can be disaggregated into sex-specific abundances if parentage assignment distinguishes maternity from paternity. The rate at which older vs younger adults appear as parents in POP can be used to estimate relative reproductive contribution/potential by length and/or age. Detection of cross-cohort HSPs allows for the estimation of adult survival. Two individuals from different cohorts sharing a parent require that parent to have survived between the two birth years. The rate at which cross-cohort HSPs decrease as the number of years separating the cohorts increases directly informs parent survival and mortality rates. Detection of juvenile HSPs informs adult survival rates during the recent inter-cohort years, while adult HSPs informs adult survival rates further in the past. The rate of within-cohort HSPs (siblings born in the same year) can estimate how many parents contributed to that cohort. Comparing within-cohort HSP rates across years can estimate recruitment variability and changes in effective spawner abundance between years. Elevated within-cohort HSP rates relative to expectations from POP-derived abundance estimates signal potential bias in expected reproductive success assumed in the CKMR model and/or underestimation of the variance in individual reproductive success.

The extent of potential applications in WCPFC has already extended from south Pacific albacore, Pacific bigeye, yellowfin tuna and south-west Pacific swordfish (all identified during P100c) to south-west Pacific striped marlin, north Pacific mako with other candidate billfish and

sharks. Project 130, a joint bycatch assessment workshop for billfish and sharks has been tasked with reviewing and identifying potential candidate stocks for CKMR. The following section provides a summary of the general design principals that need to be considered when evaluating whether CKMR is likely to be feasible, and/or cost-effective, for particular stocks.

Design Options and constraints

In practice, there are three main factors that can limit the application of CKMR to a given stock. First, larger populations require large sample sizes to identify sufficient kin to estimate parameters of interest with the desired precision. In some cases, the scale of the sample sizes required might not be feasible due to costs and/or sampling logistics. Second, for some species, individuals are only available for sampling many years after they were born. In that case, the CKMR-based estimate of abundance might be too far in the past to be useful to management. Finally, uncertainty in life-history parameters, especially age estimation, fecundity-at-age and population structure, can complicate the application of CKMR. CKMR might still be possible (and has been done successfully for species in that category) but careful consideration of the available information and sampling logistics are required.

A CKMR design ideally includes both adults and juveniles to maximise the inference from CKMR. The power of the combined design is that different kin types (POPs and HSPs) provide statistically independent estimates of abundance of adults as well as total mortality and relative reproductive contribution. These parameters are central to estimating the status and the productivity of the population. This form of design (POPs + HSPs) is particularly important in the case of applications to teleosts due to the non-linear relationship between fecundity and length/age. However, other types of designs are also possible and effective, especially for species where fecundity does not vary substantially with age, as is the case for some shark species. The foundational information that needs to be considered for any CKMR application are outlined in Table 4.

Table 4. Information needs and design principals for CKMR application

Biological & Life History	
<i>Known or estimable reproductive biology</i>	Spawning season, age at maturity, fecundity-at-age, and sex ratios must be reasonably well characterised
<i>Stable population demographics</i>	CKMR theory generally assumes stability over the sampling window; trends in adult populations complicate abundance estimation and generally require longer-time series
<i>Identifiable kin relationships</i>	The target species must have sufficiently distinct genetic signatures to reliably detect parent–offspring pairs (POPs) and/or half-sibling pairs (HSPs)
<i>Well-characterised population structure</i>	Population structure must be accounted for in the design and sampling
<i>Longevity</i>	Longer-lived species with overlapping generations are better suited, as they offer more opportunity to detect kin pairs across cohorts.
Sampling	

<i>Sufficient sample size</i>	The number of expected kin pairs drives sample size (exact numbers depend on population size and kin type targeted). The required sample size depends on the objectives of the study and the precision required for the priority parameters of interest. This and the practicality and cost of collecting the required distribution and number of samples are the primary consideration in assessing the feasibility of CKMR for an application. In principle, the more kin pairs detected, the greater the statistical power available to the CKMR model to estimate population quantities with required precision.
<i>Representative spatial coverage</i>	Generally, sample collections should be spatially representative of the population to avoid bias. The practicality of sampling should be considered during the design phase.
<i>Temporal spread</i>	Sample collections ideally span multiple years to capture parent–offspring and half-sibling relationships across cohorts and allow estimation of adult survival/mortality
<i>Age or length data</i>	Accurate ageing (otoliths, length-at-age keys, epigenetic age) is important, for determining the birth year of kin and, therefore, identifying individuals to be included in <u>legitimate</u> kin comparisons.
<i>Known or estimable sampling fractions</i>	Ideally the proportion of the population sampled in each stratum (age, sex, area, year) can be quantified. This should be considered during the design phase.
Genetics	
<i>High-resolution genotyping</i>	Sufficient markers to assign kin relationships with very high probability
<i>Low genotyping error rate</i>	Errors inflate false positives and negatives; quality filtering thresholds must be established
<i>Tissue sample quality</i>	Adequate DNA yield and quality from the tissue type used

Key practical considerations for assessing CKMR feasibility by candidate species in the WCPFC include access to samples by age (e.g., availability of port-sampling or potential for collection by observers; whether the catch is frozen, etc.), required sample sizes, jurisdictional coordination across fishing countries and/or other RFMOs when stock span more than one area of competency, and availability and quality of life-history information. For shark species covered by non-retention CMMs, non-lethal avenues for tissue collection may need to be considered.

Using the information on the design considerations we triaged the potential applications of CKMR for the potential candidate species (Table 5). CKMR application for five species, south Pacific albacore, yellowfin tuna, bigeye tuna, southwest Pacific swordfish and southwest Pacific striped marlin appears feasible based on currently available information. The CKMR scoping studies undertaken during project 100c for south Pacific albacore, yellowfin tuna, bigeye tuna, and southwest Pacific swordfish also conclude that CKMR application was feasible. The design phase for southwest Pacific swordfish and southwest Pacific striped marlin will need to account for juveniles only constituting a small fraction of the size classes retained by longline fisheries in the WCPFC jurisdiction. The design phase for bigeye tuna should also consider IATTC sampling participation given the likely cross-jurisdictional nature of the stock.

Improving the foundational knowledge and/or resolving logistic constraints would facilitate application for the other species considered. The magnitude of the skipjack population would require an extremely large budget for sequencing and analyses. Moreover, the sampling would be largely restricted to onboard observers (as nearly all fish are frozen upon capture) and significant work would need to be undertaken to assess the feasibility of observers collecting the quantity of samples required given their other onboard duties. The CMMs for oceanic whitetip and silky sharks would prevent sampling of sufficient numbers of these. Gaps in the life-history also need to be resolved (see shark research plan). Similar issues are present for other sharks and billfish. Addressing these knowledge gaps (as identified in the Shark Research Plan and Billfish Research Plan) will facilitate CKMR application. Sampling for these species will likely also present logistical challenges given the low longline observer coverage and the incidental nature of their catch (i.e., low probability of observers onboard - see results from SC Sampling Plans for these species) and the localised unloadings of these species for domestic markets that do not regularly have port sampling undertaken.

Table 5 Summary of sampling and life-history characteristics of candidate species considered for potential CKMR application

	Sampling				Biology/Life History				
	Expected sample size	Adult	Juvenile	Sampling Practical	Ageing	Repr. biol	Pop str.	Genome	CKMR Application
South Pacific Albacore	Medium	LL	Troll	Port	Validated	Established	Established	Available	Sampling can be undertaken in a few ports of unloading
Pacific Bigeye	Medium	LL	PS	Port, Observer	Validated	Established	Established	Available	Port and observer sampling - likely require EPO samples
Yellowfin	Medium	LL	PS	Port, Observer	Validated	Established	Established	Available	Port sampling supplemented by observer
Skipjack	Large	PS	PS	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Sampling by observers as fish frozen in PS prior to unloading. Sample size likely to be very large, with commensurate cost
South west Pacific swordfish	Small	LL	LL, PS	Port, Observer	Additional investment	Established	Additional investment	Additional investment	Port sampling
South west Pacific striped marlin	Small	LL	LL	Port, Observer	Additional investment	Established	Additional investment	Additional investment	Port sampling
NP Blue Shark	Medium	LL	LL	Port, Observer	Additional investment	Additional investment	Additional investment	Additional investment	Detailed analyses of unloading to ascertain true feasibility (ie can sampling be largely port based)
Oceanic Whitetip	Small	LL, PS	LL, PS	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Observer sampling dependent –CMM likely restrict sampling opportunity
Silky Shark	Small	LL, PS	LL, PS	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Observer sampling dependent –CMM likely restrict sampling opportunity
Blue Marlin	Small	LL	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Sampling will need high participation by domestic observer and local unloading operations
Black Marlin	Small	LL	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Sampling will need high participation by domestic observer and local unloading operations
Shortbill spearfish	Small	LL, PS	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Sampling will need high participation by domestic observer and local unloading operations
Sailfish	Small	LL	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Sampling will need high participation by domestic observer and local unloading operations
SWP Shortfin Mako	Small	LL	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Detailed analyses of unloading to ascertain true feasibility (ie can sampling be largely port based)
NWP Shortfin Mako	Small	LL	LL	Observer	Additional investment	Additional investment	Additional investment	Additional investment	Detailed analyses of unloading to ascertain true feasibility (ie can sampling be largely port based)

Declaration of generative AI and AI-assisted technologies in the SC paper preparation process.

Generative AI tool Claude was used to assist with software development, and for occasional grammatical review of the text in this document. The authors reviewed and verified all AI-assisted output. The methodology, model implementation, and the scientific conclusions are the responsibility of the authors.

References

Bravington MV (2024). microscoping: Preliminary feasibility for CKMR. R package version 1.0.71, <https://github.com/markbravington/microscoping>.

CSIRO and SPC-OFP. (2025a) Population genetics and connectivity of albacore tuna in the Western and Central Pacific Ocean to inform sampling design and marker development for close-kin mark-recapture (CKMR). Working Paper to the Twenty-First Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, WCPFC-SC21-2025/SA-WP-10. Nuku'alofa, Tonga, 13-21 August 2025. <https://meetings.wcpfc.int/node/26685>

CSIRO and SPC-OFP. (2025b) Close-Kin Mark-Recapture of South Pacific Albacore: a proof of concept for application in WCPFC tuna and associated species. Working paper to the Twenty First Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, WCPFC-SC21-2025/SA-WP-09. Tonga, 13-21 August 2025. <https://meetings.wcpfc.int/node/26756>

Lloyd-Jones, Luke, Tremblay-Boyer, Laura (2026). Updates on statistical modelling towards an application of CKMR for South Pacific albacore. Information paper to the Twenty-second Regular Session of the Western and Central Pacific Fisheries Commission Scientific Committee, WCPFC-SC22-2026/SA-IP25. Apia, Samoa, August 11-19 2026.

Macdonald, J., Anderson, G., Krusic-Golub, K., Prioul, F., Cueurapuru, C., Hosken, M., Barthelemy, V., Raoulx, T., Grewe, P., Nicol, S., and Panapa, A. (2024) Spatial Structure and Regional Connectivity of South Pacific Albacore Tuna in the WCPO and EPO. Information paper to the Twentieth Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, WCPFC-SC20/SA-IP-04. Manila, Philippines, 14-21 August 2024. <https://meetings.wcpfc.int/node/23127>

Magnusson, A. Day, J., Teeares, T., Hampton, J., Davies, N., Castillo Jordán, C., Peatman, T., Scott, R., Scutt Phillips, J., McKechnie, S., Scott, F., Yao, N., Natadra, R., Pilling, G., Williams, P. and Hamer, P. (2023) Stock assessment of yellowfin tuna in the western and central Pacific Ocean: 2023. Technical report WCPFC-SC19-2023/SA-WP-04 to the 19th Regular session of the WCPFC Scientific Committee, Koror, Palau 16–24 August 2023. <https://meetings.wcpfc.int/node/19352>

Rosa D, Stewart N, Gioacchini G, Borrego-Santos R, Andrews AH, Krusic-Golub K, Carneval O, Macias D, Hanke A, Gillespie K, Coelho R. 2026. FINAL REPORT FOR PHASE SEVEN OF THE ICCAT SHORT-TERM CONTRACT FOR CONTINUATION OF THE SWORDFISH GROWTH, REPRODUCTION AND GENETICS STUDIES: BIOLOGICAL SAMPLES COLLECTION AND ANALYSIS. Col. Vol. Sci. Pap. ICCAT, 83(2), SCRS/2026/041: 1–58

SPC-OFP and CSIRO. (2024) Progress Towards a Close-Kin-Mark-Recapture Application to South Pacific Albacore (Project 100c). Information paper to the Twentieth Regular Session of the

Scientific Committee of the Western and Central Pacific Fisheries Commission, WCPFC-SC20-2024/SA-WP-09. Manila, Philippines. 14-21 August 2024.

<https://meetings.wcpfc.int/node/23123>

SPC-OFP and CSIRO. (2025) Progress Towards a Close-Kin-Mark-Recapture Application to South Pacific Albacore (Project 100c). Information paper to the Twenty-First Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, WCPFC-SC21-2025/SA-WP-09. Nuku'alofa, Tonga. 13-21 August 2025.

<https://meetings.wcpfc.int/node/26684>

Tremblay-Boyer, L., Bravington, M., and Davies, C. (2024) Updated design models informing the sampling strategy for a close-kin mark-recapture application to South Pacific albacore.

Information paper to the Twentieth Regular Session of the Scientific Committee of the Western and Central Pacific Commission, WCPFC-SC20-2024/SA-IP-24. Manila, Philippines, 14-21 August 2024. <https://meetings.wcpfc.int/node/23132>

Annex 1: Kin Finding results

Of 24,266 samples that have been analysed to date, 28 half-sibling pairs and 4 parent-offspring pairs have been identified. See Tables S1a and S1b for their distribution, also visualised in Figure S1. The uneven concentration of kin pairs in western EEZs is likely driven by the higher sampling effort in that subregion, which is then reflected in the sequencing effort (see Table S2). Further inferences should not be made until the full set of samples have been analysed.

Table S1a Distribution of parent-offspring pairs. Samples are organised alphabetically by parent's EEZ.

Parent's EEZ	Offspring's EEZ	N
Fiji	Solomon Islands	1
New Caledonia	New Zealand	1
Samoa	South of French Polynesia	1
Solomon Islands	New Zealand	1

Table S1b Distribution of half-sibling pairs. Siblings and sibling pairs are reported alphabetically.

Sibling 1's EEZ	Sibling 2's EEZ	N
Fiji	New Caledonia	2
Fiji	New Zealand	1
Fiji	Solomon Islands	1
New Caledonia	New Zealand	1
New Caledonia	Tonga	1
New Zealand	New Zealand	11
New Zealand	Solomon Islands	4
New Zealand	Tonga	2
South of French Polynesia	South of French Polynesia	5

Table S2 Number of individuals implicated in kin pairs per EEZ relative to the number of samples included in the current analysis, and the total samples collected.

EEZ	Kin	Samples analysed	Samples collected
Fiji	5	2024	7027
French Polynesia	0	1131	7852
New Caledonia	5	2311	9980
New Zealand	32	10780	17218
Samoa/Cook Islands	1	15	449
Solomon Islands	7	1650	14967
South of French Polynesia	11	5583	8215
Tonga	3	666	4947

Figure S1 Visual distribution of kin pairs at the EEZ level. Kin pairs from different EEZs are connected with lines, while kin pairs from the same EEZ are marked with a circle. The number of kin pairs shared between/within EEZs is indicated by the weight of the line.

