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UPDATE ON CLOSE-KIN MARK-RECAPTURE MODELLING FOR SOUTH PACIFIC ALBACORE

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Update on close-kin mark-recapture modelling for South Pacific albacore

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Important disclaimer

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1 Executive summary

Tissue samples to inform a close-kin mark-recapture (CKMR) study for South Pacific albacore have been collected since 2023 under a sampling design first described in SC17-SA-IP-14 (Bravington et al., 2021) and re-examined in SC20-SA-IP-24 (Tremblay-Boyer et al., 2024). This Information Paper presents developments to the statistical design framework in preparation for the first iteration of the population estimation model planned for 2027. In particular, we present a comparison of the kin detected by the samples collected and analysed to date against the design's expectations.

Genotyping and kinship inference identified 28 half-sibling pairs (HSPs) and 4 parent-offspring pairs (POPs) out of the 24,253 samples analysed so far. Of these, 11 HSPs and 3 POPs were found within the 18,661 samples that met the assumptions of the original design model (i.e., excluding samples collected in the eastern Pacific, and only considering juvenile-juvenile comparisons for the HSPs). These observed kin aligned with the expected kin counts under one of the population scenarios used, indicating sampling levels and simplifying assumptions made by the design remain adequate.

In parallel, the design model assumed sample metadata would include epigenetic ages, but these are now unlikely to be available in the short to medium term. We confirmed juvenile ages could be reasonably assumed from assignment to a length mode based on the juvenile length distributions. For adults, we investigated the change in parameter uncertainty resulting from a modification to the POP probability calculation to include length-based age inference using a recent growth curve. While this decreased the expected precision relative to the initial design, the decrease was modest as long as independent age-composition samples from otoliths were also made available to the model. When absent, CVs on population parameters predicted from the length-based age inference approach were too high to be informative for management.

For the age composition, only a modest sample size is required to improve parameter precision (e.g., 250 samples per year). A further exploration of model settings showed that age samples would improve precision further if they were spread over multiple capture years rather than concentrated over the final year of the model.

With those considerations in mind, SC22 is invited to:

- Note the realised sampling progress for the South Pacific albacore CKMR and its alignment with the SC20 design;
- Note the change in precision with length-based age inference, and the importance of separate age-composition data in achieving useful CVs;
- Support otolith ageing for samples of $>$ 250 individuals per year, for multiple capture years, from at least one adult fishery;
- Support ongoing research on epigenetic ageing to improve the individual assignment to age.

2 Overview

The statistical design framework for South Pacific albacore (SPA) close-kin mark recapture (CKMR) has been fine-tuned over time and documented in successive Information Papers to

the Scientific Committee (Bravington et al., 2020, 2021; Tremblay-Boyer et al., 2024). Tremblay-Boyer et al. (2024; SC20-SA-IP-24) presented updated sampling targets ranging from 36,000 to 84,000 individuals over three years, depending on the population scenario used. Sample collection has been ongoing since 2023, first under the CSEPTA[1] project and now under the GCF[2] project (see also WCPFC Projects 100c and 100d). Tissue samples are being sequenced and analysed continuously to detect new kin pairs (parent-offspring pairs, POPs, and half-sibling pairs, HSPs). To date, 32 kin pairs have been found out of the 24,253 SPA individuals analysed to date (SPC and CSIRO, 2026).

The software initially developed for the statistical design is being adapted to generate an estimate of population abundance and other parameters from the samples collected between 2023 to 2026. This report documents ongoing updates to the software in preparation for the estimation model and examines how kin pairs observed to date match the statistical design's expectations under realised sampling levels. The aim is to confirm that the sampling strategy to date is consistent with the assumptions made in the statistical design, and explore avenues to improve the precision of parameter estimation where possible.

Four main changes were made to the statistical design framework outlined in SC20-SA-IP-24: (1) Multifan-CL predictions of catch-at-age from the 2024 stock assessment (Teears et al., 2024) are now used as input, (2) the assumed distribution of juvenile ages in the samples was updated to match that observed in juvenile samples so far, (3) uncertainty in adult age given length was incorporated in the calculation of POP probability, and (4) the statistical model is now implemented in RTMB (Kristensen, 2025). These changes are explored and validated here, and (2) to (4) are expected to be ported over to the estimation model for SPA. Other model components, including the population model structure, calculation of kin-pair probabilities, Fisher information construction, New Zealand sub-population proportion, and CV computation, all follow SC20-SA-IP-24 without modification.

One key assumption made by the initial design model was that there would be a small age-composition sample of 250 individuals available for each of the three years of the sampling programme. These samples were initially planned to be sourced from epigenetic ageing of the samples collected under the main sampling programme. As epigenetic ages are now unlikely to be available for the initial population model run in 2027, alternative avenues to generate these adult age-composition samples are now being explored. One such avenue is the ageing of otoliths of SPA present in the Pacific Marine Specimen Tissue Bank supplemented by additional samples to be collected in the next few months. We examine here the importance of this data input to the CKMR estimation process as well as explore different sampling strategies given expected model parameterisation.

3 Methods

3.1 Catch inputs to the statistical design model

The CKMR design model uses recent catch-at-age (assumed constant) as one of its inputs when fitting the population model. SC20-SA-IP-24 generated this vector by allocating fishery catches to age classes based on catch-at-length records (as reported in the stock assessments' *.frq*

[1] Climate Science for Ensuring Pacific Tuna Access

[2] Green Climate Fund

files) and an age-at-length matrix generated from bootstrapping draws from the growth curve relationship (Farley et al., 2021). However, this approach did not account for the likely age structure of the population. In combination with the lack of length signal in the growth curve past age 6, this resulted in a disproportionately high number of catches allocated to older age classes, which the model struggled to reconcile with the numbers-at-age vector used as separate input.

Multifan-CL predicts the catch-at-age distribution as part of fitting the stock assessment model, so we are now using the predicted values as the input catch-at-age instead since they account for the likely age structure of the population. The 2024 stock assessment diagnostic case was extracted from the catch-at-age from the *ests.rep* file, which was generated by rerunning the fitted stock assessment for a single iteration with 'parest' flags 188 and 190 set to 1. Catch-at-age was averaged over the last three years of the assessment period (i.e., 2020 to 2022) to create a 'representative' and recent catch-at-age as input to all population scenarios. Note that this change does not impact the estimation model, as catch-at-age will be estimated separately as part of the fitting procedure.

3.2 Age distribution of juveniles

The initial version of the CKMR design model made a 'best-guess' assumption for the age distribution of the juvenile samples (i.e., individuals aged 3 years or less). With more than 16,000 juvenile samples now collected, we can update this assumption based on lengths recorded so far. Juvenile records were filtered to retain individuals for which an upper jaw to fork length (UFL) measurement had been collected (about two-thirds of records). Of note, the length measurement collected for the remainder of the juveniles is the second finlet to fork length. Project 127a is currently building a conversion key between this measurement and UFL, which will be used to expand the pool of juvenile UFL measurements when it becomes available.

An initial exploration of the distribution of the resulting 10,708 UFL measurements showed three distinct modes with minimal overlap. Based on the Farley et al. (2021) growth curve, these length modes correspond to ages 1, 2 and 3 and their presence has been well discussed in previous SPA stock assessments (e.g., see Tremblay-Boyer et al. 2018). We fitted a Gaussian mixture (with variable variance) using the R package *mclust* (Scrucca et al., 2023) to assign individuals to each of the annual age classes. This approach will result in some individuals being allocated to the wrong age given the overlap in the predicted distribution, but as the mis-allocations will occur in both directions (e.g., some age 1s will be classified as age 2s, and vice versa), the impact on overall juvenile proportions-at-age is unlikely to be large.

3.3 Tracking analysis

We examined the number of kin pairs detected so far to see whether it tracked with the statistical design's expectations given actual sampling levels (henceforth, the 'tracking analysis'). SPA tissue samples genotyped to date were surveyed to confirm they passed genotyping and kinship identification control (c.f. the *kinference* R software, Bravington et al. 2026), and had key metadata fields available (capture date, sampling location, length recorded). Individuals were classified as juvenile or adult based on UFL (threshold of 80 cm) as well as fishery-of-origin (e.g., New Zealand troll and US fleet samples were all classified as juveniles).

For the design comparison, the sample dataset was subsetted to match the original design's expected distribution of sampling locations, i.e., adult samples coming from across all longitudes

of the WCPFC-CA and juveniles available exclusively from New Zealand. As such, 'eastern' juveniles (i.e., those fished by the US fleet) were not included in the analysis.

Secondly, year-and-age-specific sample size arrays were built from the observed New Zealand juvenile and adult samples across the WCPFC and used as inputs to the Fisher Information calculation underpinning the statistical design (the 'realised sampling' arrays), replacing the even annual targets used in the original design (e.g., for the 2024 population scenario, 84,000 samples over three years, evenly split between adults and juveniles).

Observed kin pairs (HSPs and POPs) were tabulated by location and stage. Comparisons were restricted to WCPFC adults and New Zealand juveniles, and only juvenile-juvenile HSPs were included, consistent with the definition of kin probabilities in the design model. The resulting number of observed HSPs and POPs were compared against the corresponding predicted distribution by kin type under each of the three population scenarios (i.e., corresponding to the 2018, 2021 and 2024 stock assessments; SC20-SA-IP-24). The predicted distributions were generated from a Poisson density distribution with μ set to the expected number of HSPs and POPs and sampling levels set to the 'realised sampling' arrays as defined above.

3.4 Length-based age inference

An estimate of the age of samples is required to compute the probability of observing the different types of kin pairs. For instance, POP probabilities are based on quantities dependent on the offspring birth year as well as the age of the parent when the offspring was born. The CKMR design from SC17-SA-IP-14 (Bravington et al., 2021) assumed adults would be aged via epigenetic methods. However, adults sampled to date only have length as a proxy for age, and it is unlikely epigenetic ages will be available for the initial population model estimate in 2027.

As an alternative to a direct age estimate, we modified POP probabilities to be length-based, informed by the sex-specific von Bertalanffy (VB) growth curves published in Farley et al. (2021). Since juveniles can be assigned to their age class based on length with reasonable certainty (see above), only the parent component of the POP probability was modified to account for length-based age, and HSP probabilities were left as is (since the design currently only accounts for juvenile-juvenile HSPs). We include these updated length-based POP probabilities in the design model and report below on its impact on the expected precision of key population metrics relative to those estimated in the original design for which adult age was assumed known. The quantitative framework is described in Appendix A.

3.5 Influence of age-composition data

The original design expected that a small sample of age-composition data would be available for each year of the sampling programme. Scenarios of age-composition data availability were further explored to inform the strategy for otolith collection and ageing to generate these samples. The impact of the age-composition data on the predicted CV of key population metrics was assessed by testing scenarios where no age-composition data were available against alternatives where 250 and 500 samples were available for each of the three years of the sampling programme. The predicted CVs should otoliths only be available for the final year of the sampling programme were also tested for sample sizes of 250, 500 and 750.

Unless otherwise specified, all projections were conducted under the '2024 stock assessment' population scenario, assuming an optimal sampling design of 84,000 individuals over three years, evenly split across adults and juveniles (c.f. Tremblay-Boyer et al. 2024).

4 Results

The effect of ongoing updates to software and data inputs were examined to confirm they did not have a large impact on the original design's predictions (Figure B1). The switch to the Multifan-CL-generated catch-at-age vector improved expected CV for key population metrics by a few percentage points, but other updates to the software had minimal impact on predicted quantities. The distribution of juvenile ages in the samples to date differed substantially from the initial expectation (0.3, 0.5 and 0.2 vs. 0.6, 0.3 and 0.1 for ages 1, 2 and 3, respectively; Figure B2) but updating these values had negligible impact on expected CVs from the estimation model (Figure B1).

Genotyping results and metadata for 24,253 SPA tissue samples were available for the design tracking analysis. Of these samples, 24,244 were deemed useable for analysis based on their metadata (see also SPC and CSIRO 2026 for further discussions of genotyping and kinship identification quality control). After cleaning, the dataset comprised 7,800 adults (32% of the total) distributed across the longline fisheries, and 16,444 juveniles dominated by the New Zealand troll fishery. An additional 9,750 predominantly adult samples were submitted for genotyping in June 2026, but largely from the 2025 sampling year. These samples are expected to improve the adult proportion toward the design's 50:50 target, but we were unable to include them in this analysis due to timing. In addition, as eastern juveniles were not considered in the original design, we do not report on the implications of the approximate 5,583 eastern juvenile samples in the design tracking comparison. In total, therefore, 18,861 samples were tabled for the design tracking analysis.

Of the 28 HSPs and 4 POPs detected across all samples, 11 juvenile-juvenile HSPs were from the New Zealand EEZ, 5 from the central-eastern Pacific, and 12 were *non*-juvenile-juvenile pairs (Table 1). One of the POPs is a match between an adult and a juvenile from the central-eastern area (see also Figure S1 in SPC and CSIRO 2026).

Table 1: **Summary of number of HSPs and POPs detected by inferred sampling location and life stage.** I_1 and I_2 refer to individual 1 and 2 of the pair.

Locations (I_1-I_2)	Stage I_1	Stage I_2	N_{HSPs}
New Zealand - New Zealand	juvenile	juvenile	11
South central-eastern Pacific - South central-eastern Pacific	juvenile	juvenile	5
New Zealand - Solomon Islands	juvenile	adult	4
Fiji - New Caledonia	adult	adult	2
New Zealand - Tonga	juvenile	adult	2
Fiji - New Zealand	adult	juvenile	1
Fiji - Solomon Islands	adult	adult	1
New Caledonia - New Zealand	adult	juvenile	1
New Caledonia - Tonga	adult	adult	1
			N_{POPs}
New Zealand - New Caledonia	juvenile	adult	1
New Zealand - Solomon Islands	juvenile	adult	1
Solomon Islands - Fiji	adult	adult	1
South central-eastern Pacific - Samoa	juvenile	adult	1

4.1 Stock assessment scenario comparison

The tracking analysis compares the number of kin pairs detected from the realised sampling programme against the expected counts predicted by the design model under the three stock assessment scenarios. The three population scenarios were carried forward from the SC20-SA-IP-24 design update, i.e., the 2018 stock assessment (Tremblay-Boyer et al., 2018), which assumed the stock was contained within the WCPFC convention area; the 2021 stock assessment (Castillo-Jordán et al., 2021), which extended the stock to the eastern Pacific and was the lowest predicted numbers-at-age (noting only the WCPFC-CA component was used for the design); and the 2024 stock assessment (Teears et al., 2024), which also assumed a Pacific-wide stock but also revised natural mortality assumptions leading to the highest numbers-at-age across all scenarios. The distribution of expected kin detections from each of those population scenarios under sampling numbers to date was compared against the number of observed HSPs and POPs.

The observed kin totals detected from the genotyped samples and consistent with the original design were 11 HSPs and 3 POPs. These aligned best with the mode of the HSP and POP distributions from the 2024 stock assessment scenario (Figure 1). The expected numbers of kin from the 2024 scenario were 4 POPs and 10 HSPs. The observed counts lay in the tails of the kin-number distribution for the other two stock-assessment scenarios; both expected that a higher number of kin pairs should have been detected given current sampling levels. Results for subsequent analyses are presented under the 2024 stock assessment population scenario given it is the most consistent with the observed data.

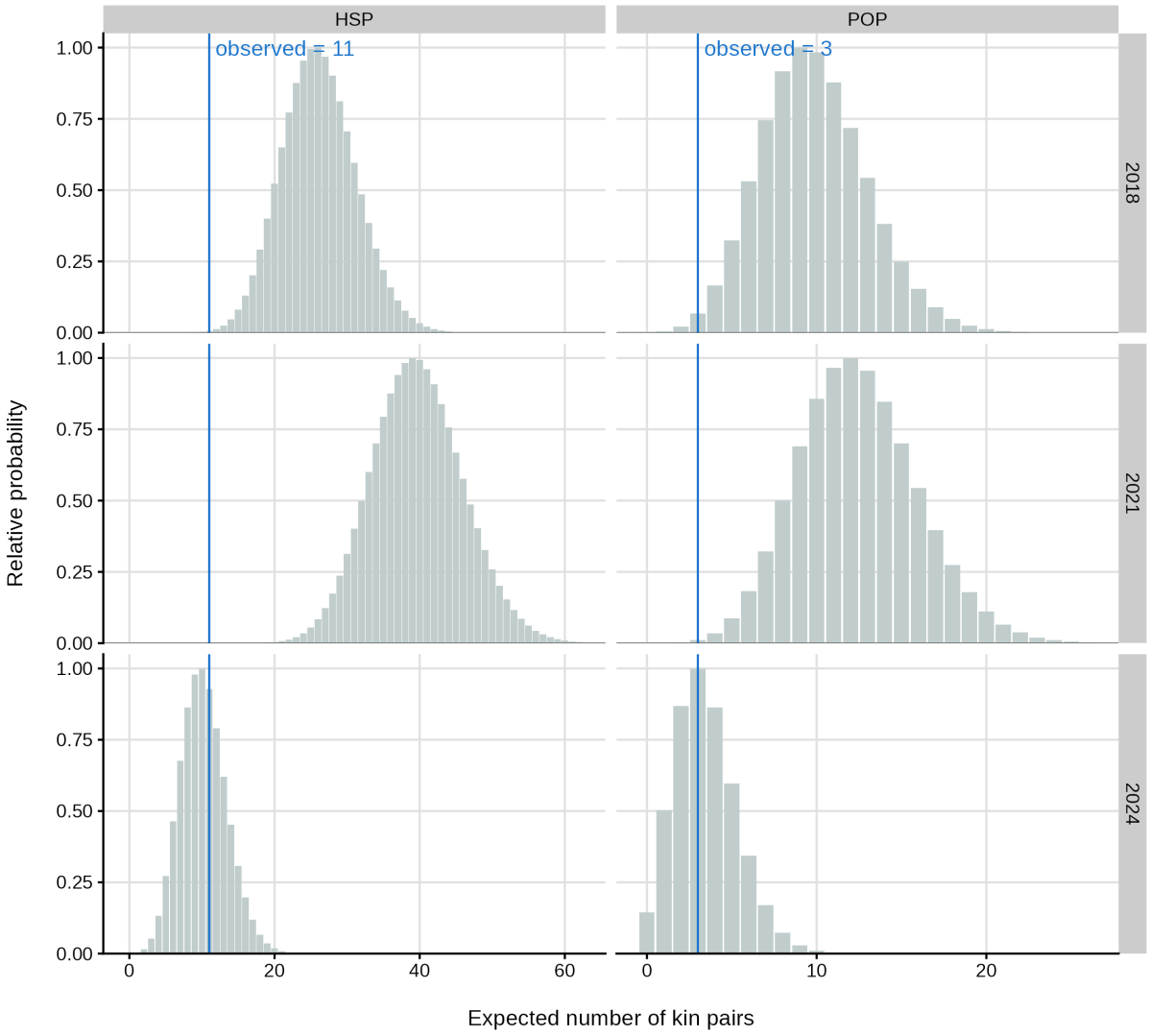

Figure 1: Observed kin number versus expected kin detection of HSPs and POPs (in columns) under the three stock assessment population scenarios (in rows). Grey histograms are Poisson distributions with the expected number of kin detected as the rate parameter, generated from the design with the observed sample numbers. Vertical blue lines show the observed number of kin. Observed kin number follow the spatial and kinship scope of the original design.

4.2 Uncertainty change with length-based age inference

An important development reported here is the inclusion of length-based ageing as opposed to assuming known ages in the statistical design model. We compared the effect of using length-based ageing on CVs expected from the population model for key population metrics under the optimal sampling design for the 2024 populations scenario (i.e., 84,000 individuals over three years; Figure 2). The effects of a low-sampling scenario (50% of samples) was also examined. We see an expected increase in uncertainty for key model parameters, with total reproductive output (TRO) estimates the worst affected. The effect on adult biomass and natural mortality is more modest, noting these simulations assume that an age-composition sample of 250 individuals per year is also available (this assumption is explored in the next section). However, when sampling occurs at low levels, the expected CV in the adult biomass estimate increases by almost two-fold.

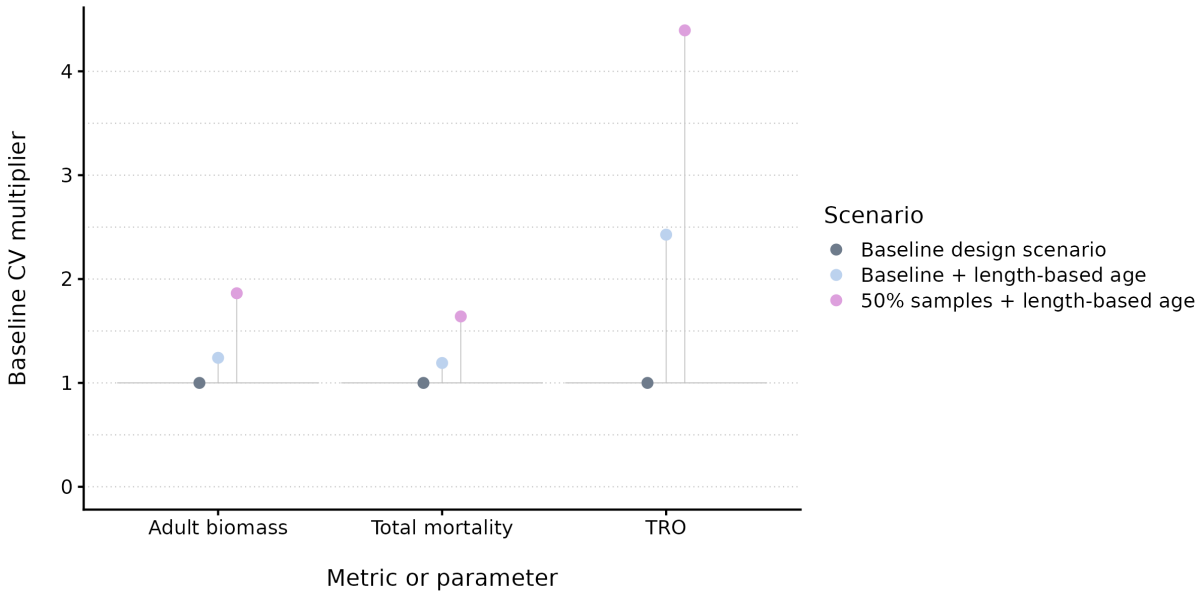

Figure 2: Relative change in expected CVs for key population metrics resulting from the shift to length-based age inference in the statistical design model for SPA CKMR under the 2024 stock assessment scenario. A horizonal line is included for context at the baseline design scenario using known age, optimal sampling numbers and an age-composition data input of 250 individuals for each year of the sampling programme.

4.3 Uncertainty change without adult age composition

The CKMR design framework proposed in SC17-SA-IP-14 (Bravington et al., 2021) remarked that both individual ageing (otolith or epigenetic) and the adult age composition are important for CKMR. This is because the kinship probabilities are a fecundity-weighted sum across the numbers at age, which informs TRO. CKMR data can attribute reproductive output to age classes but large numbers of POPs and HSPs are required, as the information comes from seeing the same age classes consistently across many sampling years. This CKMR informed attribution is further aided by accurate age data. The adult age composition also assists CKMR in resolving

total mortality. When age is uncertain, having an independent data source for the adult age composition can assist with resolving the attribution of TRO to age classes.

We looked at the effect of running the 2024 stock assessment scenario using length-based ageing with and without adult age composition information of 250 and 500 individuals in each sampling year, and also tested additional scenarios where an age-composition sample was only available for the final year (Figure 3). Under length-based ageing, CVs increase by a large amount if no age-composition samples are included, with the largest increase for total mortality (near doubling). Increases are much more modest when samples of at least 250 per year are provided, and precision is improved when samples are provided for multiple years (e.g., CVs are better for 250 samples over three years than 750 samples over the final year). This supports the need for otolith ageing of $>$ 250 samples from sampling years within at least one adult fishery.

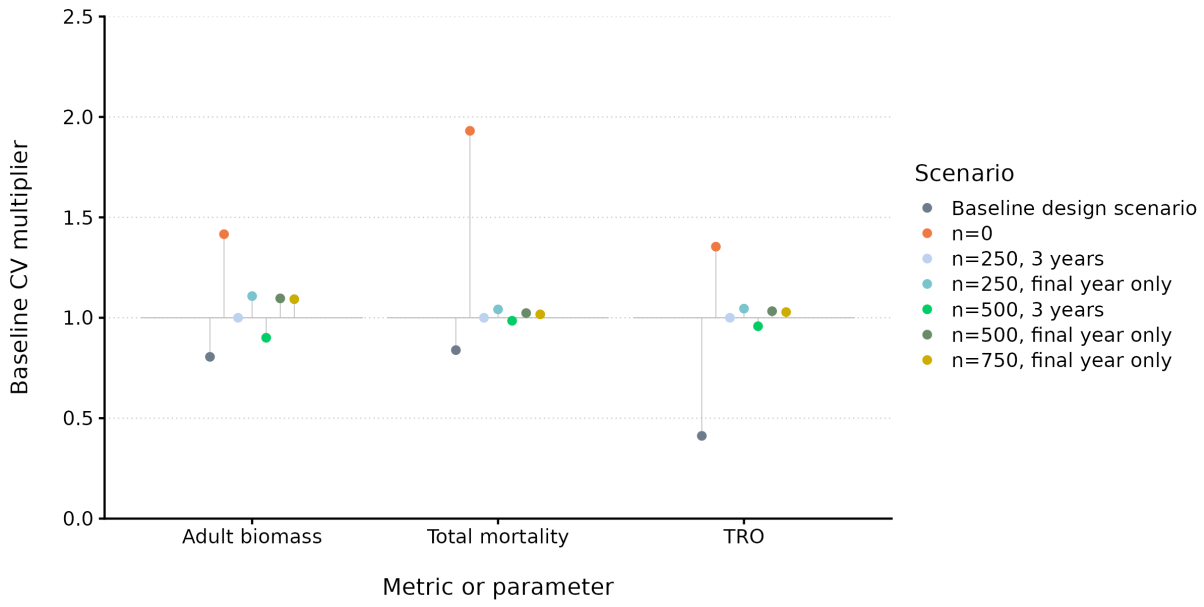

Figure 3: Relative change in expected CVs for key population metrics resulting from different scenarios of adult age composition availability. A horizontal line is included for context for a design scenario using length-based age, optimal sampling numbers and an age-composition data input of 250 individuals for each year of the sampling programme i.e., scenario n = 250, 3 years, light blue point. The relative CV under the original design where age is assumed known ('baseline'; dark grey point) is included for further context.

5 Discussion

This paper documents ongoing explorations to the modelling approach used to inform the SPA CKMR statistical design model. Even though the initial sampling programme is set to conclude this year (2026), examining and modifying the design is helpful as it can spotlight issues ahead of time and further inform the strategy for the population estimation model. It also allows for a performance assessment of the sampling strategy to date.

A key source of uncertainty in the initial design model was the true population abundance. Population abundance is an important uncertainty behind each CKMR implementation as CKMR is

usually undertaken because of unresolved uncertainty about population size, but true population size also dictates the number of samples required under an optimal sampling programme. To account for this uncertainty, the statistical design predicted the number of kin that should be detected as a function of population abundance under three scenarios matching the most recent stock assessments for SPA. From this early comparison of observed kin pairs against design expectations, the kin detected appear most consistent with the 2024 stock assessment: the observed counts for the western stratum, 11 HSPs and 3 POPs, fell comfortably within the expected distributions under realised levels of sampling for this scenario, while falling in the tails of the distributions for the 2018 and 2021 scenarios. Given the small number of kin pairs available at this stage, this comparison does not exclude the other population scenarios, but it does indicate that the emerging data are most consistent with the larger population implied by the 2024 stock assessment.

The number of kin detected to date is too low to result in a precise estimate of population numbers according to the design (c.f. target CV of 15%). Still, this result supports the recommendation of ongoing sampling and genotyping of SPA for CKMR under the current strategy, as assumptions about population abundance made in the design model appear to have been reasonable under at least one of the population scenarios. Any further detection of kin will improve the CVs that can be achieved by the estimation model.

We investigated the change in parameter uncertainty expected due to the lack of epigenetic age information, as it was assumed available under the first iterations of the design. This impacts the estimation model as adult ages, required to compute the probability of detecting POPs, now have to be deduced from lengths. As such, the calculation for the POP probability was updated here to include length-based age inference. The analysis showed that the use of length-based information for age decreases the precision relative to the known age expectation of the initial design. However, we also showed that the decrease in precision is modest as long as independent age-composition samples are available. When age-composition samples were absent, we observed CVs from the length-based age inference approach that were much too high to be informative.

Investment in otolith ageing of a small subset of longline fleet catch in a single location (or two or more geographically distant locations) would substantially improve the information content of the data, particularly when resolving the adult age structure independently of kin pair signals. We also showed that parameter precision was improved when samples were provided for multiple years. This supports the need for otolith ageing of $>$ 250 samples from sampling years within at least one adult fishery, and inventory of existing otolith samples to see if historical samples would be available for ageing.

One interesting point regarding the adult age composition is that the limited length signal in the growth curve past 6 years old actually assists in population age composition estimation. That is because adults older than 6 or 7 years will be of similar lengths, and thus any gear selectivity on length is unlikely to impact the age composition of older adults. As such, we should be drawing an unbiased set from the adult age composition in the adult fishery, which will aid in otolith selection as well as the interpretation of the resulting age composition signal.

Another potential source of uncertainty is population structure. We note that 14 out of the 28 kin pairs detected to date from the tracking analysis were not included in order to match assumptions made in the original design model. Model extensions are planned so that the estimation model can incorporate those additional kin pairs. This should also improve expected CVs given

sampling to date. Planned modifications fall under two main categories. First, additional kin probabilities will be included to account for adult-juvenile and adult-adult HSPs. Second, the spatial configuration will be modified so that additional pools of juveniles (e.g., those sampled east of the New Zealand EEZ) can be accounted for. We saw little evidence of cross-stratum kin pairs with HSPs dominated by within New Zealand and South of French Polynesia pairs. Adult-juveniles HSPs were all within western and western-central adult areas, and/or included New Zealand juveniles. POPs showed a similar east-west divide. This suggests that models with a different spatial structure to that assumed in the design will need to be explored.

Recommendations

SC22 is invited to:

- Note the realised sampling progress for the South Pacific albacore CKMR and its alignment with the SC20 design;
- Note the change in precision with length-based age inference, and the importance of separate age-composition data in achieving useful CVs;
- Support otolith ageing for samples of $>$ 250 individuals per year, for multiple capture years, from at least one adult fishery;
- Support ongoing research on epigenetic ageing to improve the individual assignment to age.

AI declaration

Generative AI tool Claude was used to assist with software development. The authors reviewed and verified all AI-assisted output. The methodology, model implementation, and scientific conclusions are the responsibility of the authors.

6 Acknowledgements

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References

Bravington, M., Farley, J., Hampton, J., and Nicol, S. (2020). Preliminary analyses for a Close Kin Mark Recapture feasibility study in WCPO. Information paper WCPFC-SC16-2020/SA-IP-15 to the Sixteenth Regular Session of the Scientific Committee of the Western Central Pacific Fisheries Commission, virtual meeting, 12–19 August 2020.

Bravington, M., Nicol, S., Anderson, G., Farley, J., Hampton, J., Castillo-Jordán, C., and Macdonald, J. (2021). South Pacific Albacore Close-Kin Mark-Recapture: update on design (Project 100b). Information Paper WCPFC-SC17-2021/SA-IP-14 to the Seventeenth Regular Session of the Scientific Committee of the Western Central Pacific Fisheries Commission, virtual meeting, 11–19 August 2021.

Bravington, M. V., Baylis, S. M., Eveson, J. P., and Feutry, P. (2026). Kinference: Pairwise kinship detection for close-kin mark-recapture. *bioRxiv*, pages 2026–05.

Castillo-Jordán, C., Hampton, J., Ducharme-Barth, N., Xu, H., Vidal, T., Williams, P., Scott, F., Pilling, G., and Hamer, P. (2021). Stock assessment of South Pacific albacore tuna. Working Paper WCPFC-SC17-2021/SA-WP-02 to the Seventeenth Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, virtual meeting, 11–19 August 2021.

Farley, J., Krusic-Golub, K., and Eveson, P. (2021). Updating age and growth parameters for South Pacific albacore (Project 106). Information Paper WCPFC-SC17-2021/SA-IP-10 to the Seventeenth Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, virtual meeting, 11–19 August 2021.

Kristensen, K. (2025). *RTMB: 'R' Bindings for 'TMB'*. R package version 1.7.

Scrucca, L., Fraley, C., Murphy, T. B., and Raftery, A. E. (2023). *Model-Based Clustering, Classification, and Density Estimation Using mclust in R*. Chapman and Hall/CRC.

SPC and CSIRO (2026). Report on Project 100d: Application of CKMR methods to SP albacore and cost-benefit evaluation and prioritisation of CKMR to WCPFC stocks (tuna, billfish, sharks). Working Paper WCPFC-SC22-2026/SA-WP-11 to the Twenty-Second Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, Apia, Samoa, 11–19 August 2026.

Teears, T., Castillo-Jordán, C., Davies, N., Day, J., Hampton, J., Magnusson, A., Peatman, T., Pilling, G., Xu, H., Vidal, T., Williams, P., and Hamer, P. (2024). Stock assessment of South Pacific albacore tuna. Working paper WCPFC-SC20-2024/SA-WP-02 to the Twentieth Regular Session of the Scientific Committee of Western and Central Pacific Fisheries Commission, Manila, Philippines, 14–21 August 2024.

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 WCPFC-SC20-2024/SA-IP-24 to the Twentieth Regular Session of the Scientific Committee of the Western and Central Pacific Commission, Manila, Philippines, 14–21 August 2024.

Tremblay-Boyer, L., Hampton, J., McKechnie, S., and Pilling, G. (2018). Stock assessment of South Pacific albacore tuna. Working Paper WCPFC-SC14-2018/SA-WP-05 to the Fourteenth Regular Session of the Scientific Committee of the Western and Central Pacific Commission, Busan, Republic of Korea, 8–16 August 2018.

A Length-based age inference

The equations governing the probability of detecting a POP were modified to rely on the length of the adult instead of its observed age. To do so, we built a conditional probability matrix for A_{len}, which is the length-inferred age (point estimate from the Farley et al. 2021 growth curve; $\mu_s(a)$) for each true age A_{true} given animal sex s. For each true age $A_{true} = a$, we simulated 10,000 lengths from $N(\mu_s(a), \sigma_s)$ using sex-specific VB parameters. For each simulated length, we back-calculated the posterior mode of age using

$$\hat{a}_i^{\text{mode}} = \arg\max_{a \in \mathcal{A}} P(a \mid L_i, s_i),$$

$$P(A_{true} \mid L = l, s) = \frac{P(L = l \mid A_{true} = a, s)\, \pi_s(a)}{\sum_{a' \in \mathcal{A}} P(L = l \mid a', s)\, \pi_s(a'),} \tag{A.1}$$

where $\pi_s(a)$ is the probability of encountering an individual of age a in the population.

Under a uniform prior $\pi_s(a) = 1/|\mathcal{A}|$, the prior cancels and the posterior reduces to the normalised likelihood,

$$P(A_{true} \mid L = l, s) = \frac{\phi(L;\, \mu_s(a),\, \sigma_s)}{\sum_{a' \in \mathcal{A}} \phi(L;\, \mu_s(a'),\, \sigma_s)} \tag{A.2}$$

where μ_s and σ_s are the point-estimate and standard deviation of length at age a from the sex-specific growth curve.

We then tabulated the frequency in each $A_{len} = a_l$ bin and normalised columns so each $A_{true} = a$ column sums to 1.

Ageing error can now be accounted for from length based inference in the POP probability calculation in the following way:

$$P(A_{true} = a | A_{len} = a_l) = \frac{P(A_{len} = a_l | A_{true} = a) \cdot N_{s,Y_{ad},a}}{\sum_{a'} P(A_{len} = a_l | a') \cdot N_{s,Y_{ad},a'}}. \tag{A.3}$$

Here, $P(A_{len}|A_{true})$ is the ageing error matrix and $N_{s,Y_{ad},a'}$ represents population abundance for each of the years where adults were sampled (i.e., the prior), informed by the model values at iteration i of the estimation. The final probability is the sum over all possible true ages, weighted by this posterior:

$$P(\text{POP}|A_{len}) = \sum_a P(\text{POP}|A_{true} = a) \times P(A_{true} = a|A_{len} = a_l). \tag{A.4}$$

B Additional results

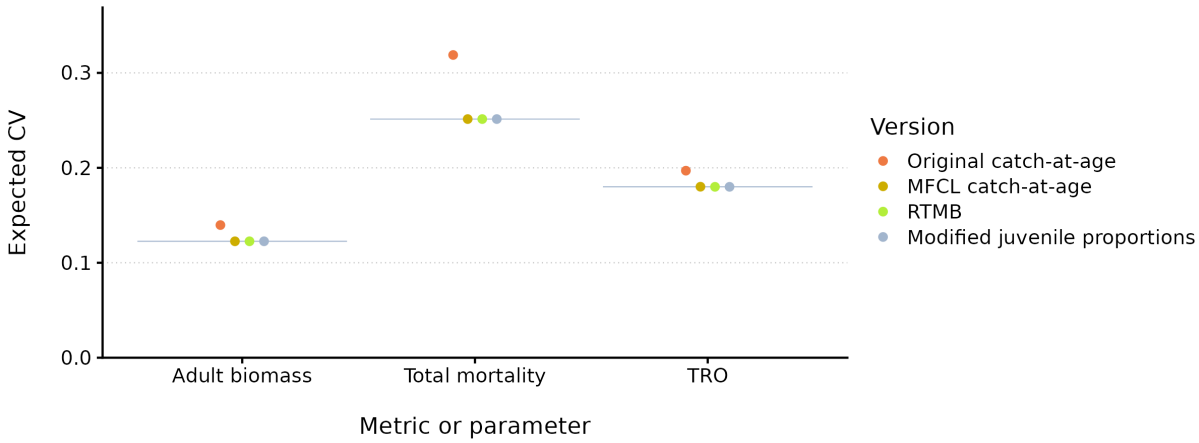

Figure B1: Expected CVs resulting from cumulative updates (coloured dots, from left to right) to data inputs, assumptions or software underpinning the statistical design. The CVs expected from the estimation model are shown for three key population metrics: adult biomass, total mortality and total reproductive output.

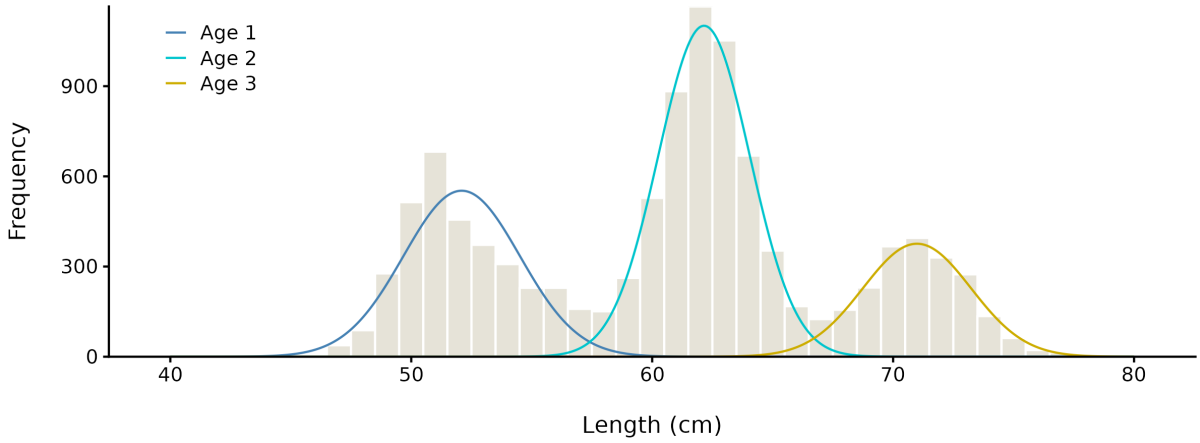

Figure B2: Distribution of recorded juvenile lengths with predictions from a three-component Gaussian mixture model overlaid. Each mode is assumed to belong to a different age class based on its position on the growth curve (coloured lines).

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