WCPFC SC21
Nuku'Alofa, Tonga
13-21 August 2025

Pacific Community
Communauté du Pacifique

APPLICATION OF CLOSE-KIN-MARK-RECAPTURE METHODS (PROJECT 100C)

WCPFC-SC21-2025/SA-WP-09

WCPFC-SC21-2025/SA-WP-10

WCPFC-SC21-2025/SA-WP-14

SPC-OFP & CSIRO

FOUNDATIONAL RESEARCH - CKMR APPLICATION.

Species	Scoping Study	Pop Gen	Sex Assay	Kin Assay	Ageing
SP Alb	Scoping (~30,000) Design (36,000-84,000)	🟩	🟩	🟩	Epigenetic clock Otolith Shape
BET	Scoping (60,000-100,000)	🟨	🟩	🟨	Epigenetic clock Otolith Shape
SWO	Scoping (~10,000)				Radiocarbon dating

AGEING.

- Epigenetic Ageing
  - A high-throughput platform in collaboration with Diversity Arrays Technology (DArT), Australia is under development.
  - Revision of the assay of Mayne et al 2020 to increase its robustness is being evaluated
    - Consider this to be a more cost effective approach than developing a specific assay for each species.
  - Epigenetic age calibration of Pacific tunas will be undertaken after assay revision and once the technology is transferred to DArT.
- Longevity
  - 13 measurements of 14C have been made on 10 SWO aged 3-12 years by Fish Ageing Services. A follow up set of 50 SWO otoliths is currently being processed.

ASSAY DEVELOPMENT: QUALITY CONTROL & KIN IDENTIFICATION.

- Sample Quality Control Procedures and Assay has been developed for high throughput application to provide DNA quality assurance
  - Contamination
  - Degradation
- Kin Identification Assay developed for SP Alb
  - Adaptable for the other tuna species
- Population Genetics
  - High throughput method using DArTseq
- Sex
  - Marker has been developed and successfully evaluated for WCPFC tuna stocks

STANDARD OPERATING PROCEDURES

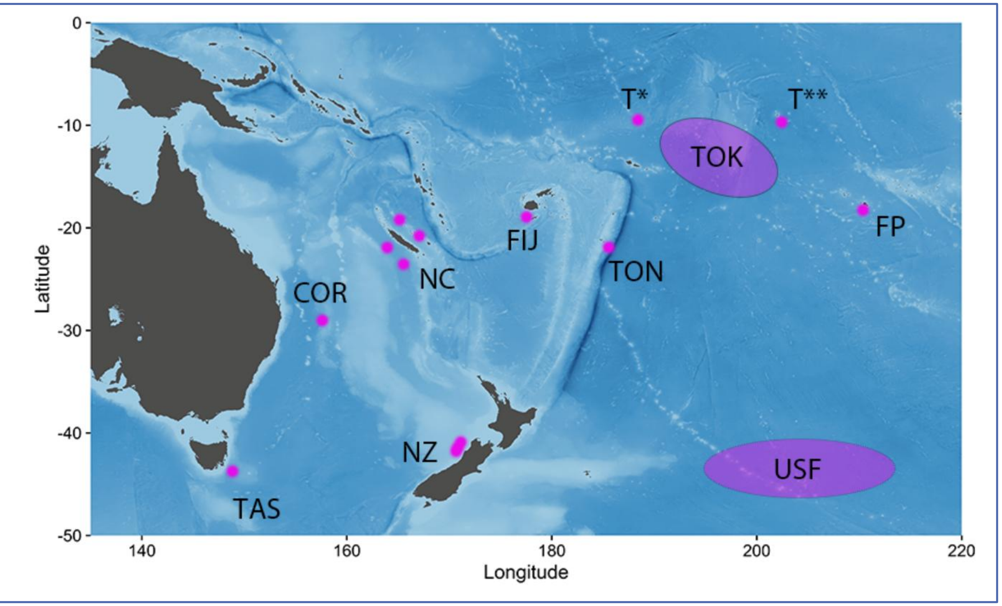
- SOP have been developed and tested over the last 2 years
- 161 samplers trained (port and observer) in applying the SOP to July 2025
- 35,990 tissue samples collected to July 2025
- ~15,000 of these samples have been sequenced and screened for data quality
- Less than 4% of sequenced samples were rejected from analysis due to quality issues, including DNA degradation, cross contamination or species misidentification.

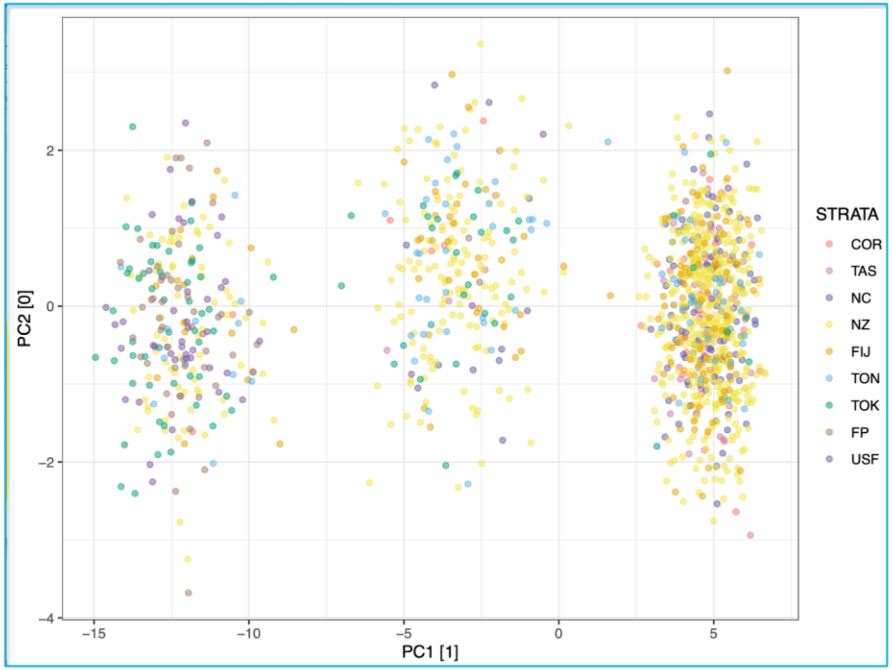
KIN IDENTIFICATION (SA-WP-14)

- Among the 15,000 samples sequenced, kin-finding analyses identified 3 parent-offspring pairs and 12 half-sibling pairs.
- The addition of more samples will produce disproportionately more opportunities to identify a close relative.
    - No refinement to the number of samples collected as recommended in Tremblay-Boyer-et al.,(2024) is expected to be required.
    - Recommend to target the upper 84,000 samples as not all need to be sequenced if adequate numbers of kin are identified for a CKMR estimator before all samples are processed.

POPULATION GENETICS (SA-WP-10)

- 1867 SP ALB sequenced (DArTseq) to evaluate population structure.
- 3 Genetic Groups identified
- Spatial distribution of samples suggest mixed fishery





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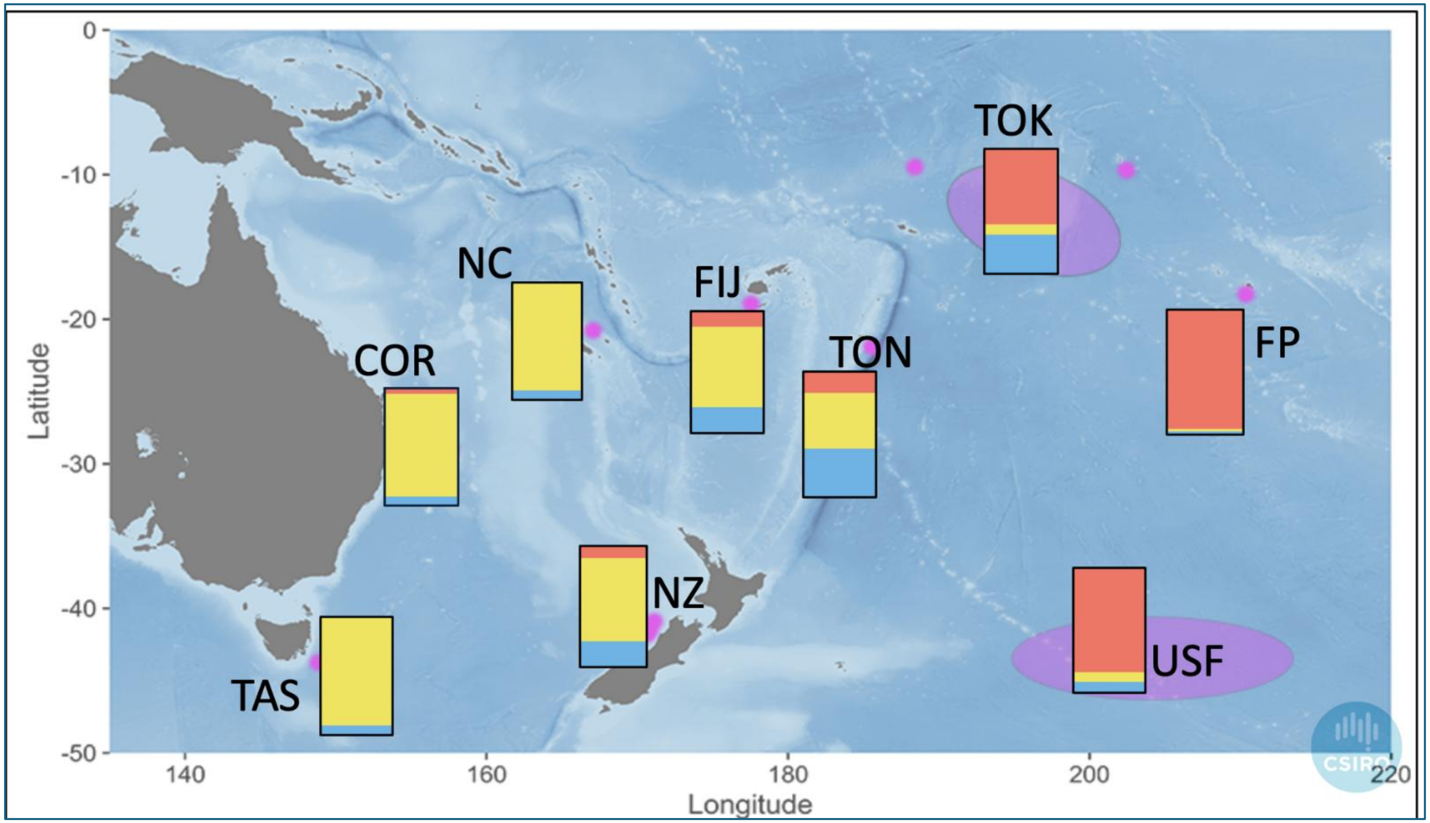

Sample Location	Group 1	Group 2	Group 3
COR	0.04	0.85	0.11
TAS	0	0.90	0.10
NC	0	0.92	0.08
NZ	0.11	0.68	0.21
FIJ	0.12	0.65	0.23
TON	0.17	0.43	0.40
TOK	0.61	0.08	0.31
FP	0.94	0.02	0.04
USF	0.82	0.08	0.10

INTERPRETING THE POPULATION GENETICS

- We are not able to differentiate the mechanism that separates the 3 genetic groups (spatial or temporal disaggregation).
- Additional sampling of spawning adults (spatially and temporally) would clarify this mechanism.
- The analyses does not include samples east of French Polynesia at this stage
  - Collaborations with SOU have been established for collection of samples from the SE Pacific.
  - There may be further genetic groups
- The SP ALB CKMR Assay can be updated to include genetic group assignment

KEY RECOMMENDATIONS

- Note the need for sampling of spawning adults of SP Alb in the WCPO to clarify how best to integrate this information into the SP Alb assessment.
- Sampling east of French Polynesia remains a priority to clarify SP Alb genetic structure.
- The mixed distribution of the non-spawning adult populations means that fishing mortalities estimates will need to be disaggregated to ensure no group is below reference points or target reference points set conservatively.

KEY RECOMMENDATIONS

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- Note there are no logistical constraints to implementing CKMR for SP Alb.
    - The SOP are highly effective and the sampling infrastructure allows for ~50,000 samples to be collected per year.
- The kin identification assay is effective for SP-Alb and can be modified to include genetic group assignment.
- The preliminary results suggest that the 36,000-84,000 samples recommended by SC20 for a CKMR estimator does not need adjustment.
- The cost of the first CKMR estimator for SP-Alb is USD1.6M
    - ~73% of this cost is available through co-funding by other non-WCPFC projects at SPC
    - This costs would be substantially less for subsequent estimators as fewer new kin pairs would be required (~25-50% reduction in cost)