CCSBT-OMMP/2606/09
(OMMP Agenda item 1)

Australia's National
Science Agency

Review of data inputs and preliminary work for the 2026 SBT stock assessment

Preece A, Eveson P, Hillary R
19 June 2026

CCSBT-OMMP/2606/09

Citation

Preece A, Eveson P, Hillary R (2026) Review of data inputs and preliminary work for the 2026 SBT stock assessment. CCSBT-OMMP/2606/09

Copyright

© Commonwealth Scientific and Industrial Research Organisation 2026. To the extent permitted by law, all rights are reserved and no part of this publication covered by copyright may be reproduced or copied in any form or by any means except with the written permission of CSIRO.

Important disclaimer

CSIRO advises that the information contained in this publication comprises general statements based on scientific research. The reader is advised and needs to be aware that such information may be incomplete or unable to be used in any specific situation. No reliance or actions must therefore be made on that information without seeking prior expert professional, scientific and technical advice. To the extent permitted by law, CSIRO (including its employees and consultants) excludes all liability to any person for any consequences, including but not limited to all losses, damages, costs, expenses and any other compensation, arising directly or indirectly from using this publication (in part or in whole) and any information or material contained in it.

CSIRO is committed to providing web accessible content wherever possible. If you are having difficulties with accessing this document, please contact csiro.au/contact.

Acknowledgement of Country

CSIRO acknowledges the Traditional Owners of the lands, seas and waters of the area that we live and work on across Australia and pays its respects to Elders past and present. CSIRO recognises that Aboriginal and Torres Strait Islander peoples have made, and will continue to make, extraordinary contributions to Australian life including in cultural, economic, and scientific domains.

Acknowledgements

This work was funded by AFMA and CSIRO.

Darcy Webber for assistance with model runs and the detective work required to get the models running this year.

CCSBT and members for data exchange.

Contents

Abstract ii

1 Introduction 1

2 Data inputs 1

3 Preliminary run of the reference set of models 2

4 Sensitivity tests 4

5 Preliminary fits to data sources 5

5.1 Abundance indices (CPUE and aerial survey) 7

5.2 Conventional tag data 9

5.3 Gene tagging data 10

5.4 Close-kin mark-recapture data 10

5.5 Size and age frequency data 13

5.6 Selectivity 16

6 Discussion 17

7 References 17

Abstract

In preparation for the 2026 full stock assessment, we have collated the data used in the new assessment models software. Three additional years of data have been included since the last assessment in 2023. This paper provides details on collation of the data inputs to the models and issues to consider at the OMMP, a preliminary run of the reference set of models used in 2023, and examination of fits to the data. There appears to be an issue with natural mortality in the model or code that will need to be resolved at OMMP.

1 Introduction

In preparation for the 2026 full stock assessment, we have collated the data used in the new assessment models software. Three additional years of data have been included since the last assessment in 2023 (Hillary et al., 2023). This paper provides details on collation of the data inputs to the models, preliminary examination of fits to the data, and notes issues that the OMMP and ESC may want to consider further.

2 Data inputs

The data inputs for the 2026 assessment are:

- Catch biomass by fishery (1952-2025), and age frequency (Indonesian, surface) or length frequency (longline fleets)
- Longline CPUE (fleet LL1) relative abundance index (1969–2025)
- Aerial survey juvenile relative biomass index (1993–2017)
- Convention tag-recapture data (release years 1990–1994, release ages 1–3)
- Gene tagging age 2 absolute abundance estimates (2016–2019, 2021-2024)
- CKMR Parent-Offspring Pairs (POPs) (juvenile birth years 2002–2020)
- CKMR Half-Sibling Pairs (HSPs) (older sibling birth years 2003–2020)
- Grid-type trolling index (GTI) (1996–2004, 2005–2014, 2016–2026)
- Estimates of the potential scale of non-member catches (2007-2025).

These are the same inputs as for the 2023 assessment, except for the following:

- the POP data has been partitioned into two groups; 1) adults for which the age is known (from otolith ageing) and, 2) those for which only length is available. Correspondingly, the likelihood for the POP data now accounts for uncertainty in age for comparisons where the adult only has a length measurement.

Data issues to consider:

- UAM: The estimates of unaccounted mortality from non-members, is from table 2 in Edwards and Hoyle (2026). The scenario used in the updated data files for the stock assessment is “Adj(JP)”. The Catch and Effort data underlying the models were revised for all available years, and therefore, estimates for all years have been updated through to 2023. For the last 2 years (2024 and 2025) the values for 2023 have been used.
- Gene-Tagging data: The most recent gene-tagging estimate, of absolute abundance of age 2 cohort in 2024, is very large and the CV of 0.3 is high (the CV is outside the precision that

the design study was aiming for). Few matches were found between the releases and harvest samples, but the number of releases in 2024 was low, and the increased number of samples from the harvest in 2025 were not enough to adjust for a larger cohort. To compensate for low release numbers in 2025, we have increased the number of samples collected at harvest this year.

- CPUE: The updated CPUE data "GAM22" were provided in paper CCSBT-OMMP/2606/06 (Itoh and Takehashi, 2026). The data were updated through to 2025.
- LL4 fishery proportions at length: As in previous years, the proportions at length have not been updated, even though some data have been provided (for small amounts of catch).
- Indonesian proportions at age: There is no updated data for the catch at age for the Indonesian fishery. The catch monitoring otolith sampling program was interrupted in recent years (since 2001/22, see Farley et al., 2025) and has only resumed recently (2024/25). Otoliths from the most recent year have not yet been aged. The age-length keys from previous years could be used with the newest length data to provide updated data for the assessment models.
- LL 1 proportion at length: Korea and New Zealand have not provided fully raised catch at length data, which may affect the proportions at length data for LL1. It may be easy to fix this issue and could be discussed further.
- CPUE selectivity: In 2025 the technical meeting agreed to include a new fishery that represents the selectivity of the Japanese CPUE data (this is fishery 7 in the new software). For this fishery 3 years of data were added to the data file. These are simply a copy of the previously held data (see lf_assesment.csv file), and this may need to be revisited before the full assessment is completed.

3 Preliminary run of the reference set of models

The assessment of SBT is based on a reference set of operating models (OMs) that encompass a range of plausible uncertainties. In our preliminary investigations here, we use the same reference set used in the 2023 stock assessment (Table 1). This set consists of 108 models resulting from all combinations of the following grid elements: four values of steepness (h), three values of natural mortality at age 0 (M_0), three values of mortality at age 10 (M_{10}), a single value of Omega (Ω) (implying a linear relationship between CPUE and LL1 exploitable biomass), a single age range used to standardize LL1 selectivity over time, a single CPUE series (GAM), and three values of psi (ψ) (power parameter for relative reproductive contribution by age).

From these 108 model results, 2000 runs are sampled to provide preliminary results for the reference set.

Table 1. Reference set grid used in preliminary investigations for the 2026 stock assessment. Sampling weight refers to how the grid of models is sampled to generate a distribution from 2000 parameter draws.

Parameter	Value	Cumul N	Prior	Sampling weight
H	0.55, 0.63, 0.72, 0.8	4	Uniform	Prior
M_0	0.4, 0.45, 0.5	12	Uniform	Posterior
M_{10}	0.065, 0.085, 0.105	36	Uniform	Posterior
Omega (Ω)	1	36	Uniform	Prior
CPUE	GAM	36	Uniform	Prior
CPUE age range	5-17	36	Uniform	Prior
Psi (ψ)	1.5, 1.75, 2.0	108	0.25, 0.5, 0.25	Prior

In addition to the range of uncertainties encapsulated in the reference set grid, a set of fixed parameters is used in the assessment. Here we use the same values used in the 2023 stock assessment, with the exception that the false negative probability for the close-kin mark-recapture half sibling pairs (CKMR HSP) data has been updated. Values for key fixed parameters are in Table 2.

Table 2 Values for key fixed parameters used in preliminary investigations for the 2026 stock assessment.

Variable	Role	Value
φ^{tag}	Conventional tag overdispersion	1.82
φ^{gt}	Gene tagging overdispersion	1
q^{gt}	Gene tagging GAB fraction	1
q^{hsp}	CKMR HSP “catchability”	1
π^{η}	CKMR HSP false neg. probability	0.684
σ_r	Recruitment SD	0.6
ml_{50}	Length @ 50% maturity	150cm
ml_{95}	Length @ 95% maturity	180cm
ς_{max}	Max. age estimated Indo selectivity	25

4 Sensitivity tests

As part of the stock assessment for SBT, a set of sensitivity tests is specified for exploring additional uncertainties outside of the reference set of models. The tests used in the 2023 stock assessment are given in Table 3. These will need to be discussed at OMMP16 and the final set for inclusion in the 2026 stock assessment agreed upon.

Table 3 Sensitivity tests used in the 2023 stock assessment with priority ranking (H=high, M = medium, L = low)

Test name	Code	Conditioning and projection notes	Priority
UAMbycatch	UAMbycatch	Replace LL1 NCNM catches estimated using Japanese catch rates with estimates calculated using Taiwanese catch rates.	**H**
No UAM	noUAM	Remove NCNM catches from conditioning and projections.	**H**
LL1 Case 2 of MR	case2	LL1 overcatch based on Case 2 of the 2006 Market Report	**L**
CPUE_Drop5	Drop_5yrs	Eliminate the last 5 years of CPUE Series	**H**
Omega75	cpueom75	Power function for biomass-CPUE relationship with power = 0.75	**H**
Upq2008	Cpueupq	Estimate CPUE 2008 change in q for LL1 fleet	**H**
Q age range	cpue59	Age range for q equal to 5-9	**M**
LL1_sel	LL1_sel	Allow the terminal 3-years to be flexibly estimated to evaluate impact on year-class uncertainty and magnitude	**M**
Indo_sel	Indo_sel	Bi-modality in selectivity, more rigid (constrain amount of change) from 2013 on in Indonesian fishery	**H**
NoPOP&HSP	NoPOPHSP	Exclude both close-kin data (Parent-Offspring and Half-Sibling Pairs)	**H**
No HSP	NoHSP	Exclude half-sibling-pair close-kin data	**H**
GTI	Troll	Includes the grid-type trolling index as additional recruitment index. Increase CV of aerial survey to preclude aerial survey dominating the fit, given apparent conflicts in the data	**H**

5 Preliminary fits to data sources

The frequency of each of the grid elements in the sample of 2000 reference set models is shown in Figure 1 (note that only the elements with more than one value are included). Grid elements h and psi were sampled according to their priors, whereas M0 and M10 were sampled based on their posterior distributions (Table 1). The lowest value of M0 (0.4) was sampled most frequently and highest value of M10 (0.105) was sampled almost exclusively, which is a change from the 2023 assessment, where the middle value was the most frequent for both these parameters. Running the new models and software on the data sets used in the 2023 assessment leads to similar results, suggesting this is due to a change in the model, code or convergence, and not the updated data inputs. A test run of the ADMB code using an updated sbtdata2025.dat file and same grid run in 2023 showed sampling of a broader range of values for M0 and M10, which further indicates that it is something in the new model or software (see Figure 2). This needs to be investigated further.

We have used the best-fitting grid cell from this preliminary set of models to examine fits to the data (h = 0.63, M0 = 0.4, M10 = 0.105 and psi = 2). The fits to each of the data inputs based on this grid cell are shown in the subsections below. Since the set is preliminary and we have already detected some potential issues with sampling of the natural mortality grid parameters we have not commented in detail on fits to data. Where there appears to be some lack of fit, this may be resolved at the OMMP meeting.

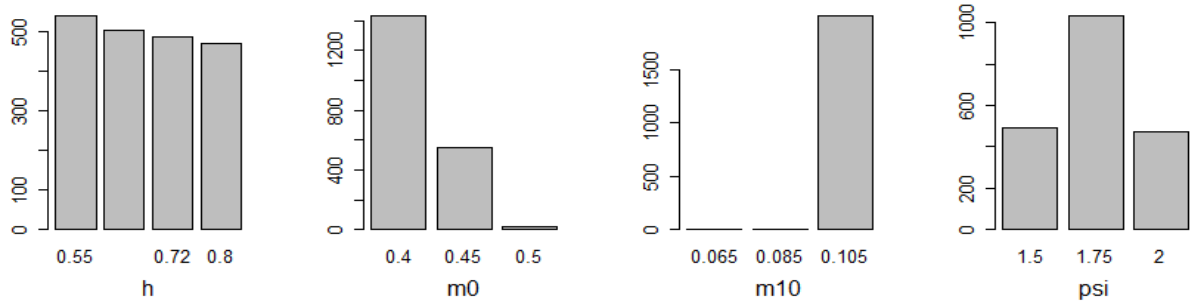


Figure 1. Frequency of grid elements h, M0, M10 and psi in this preliminary set of models.

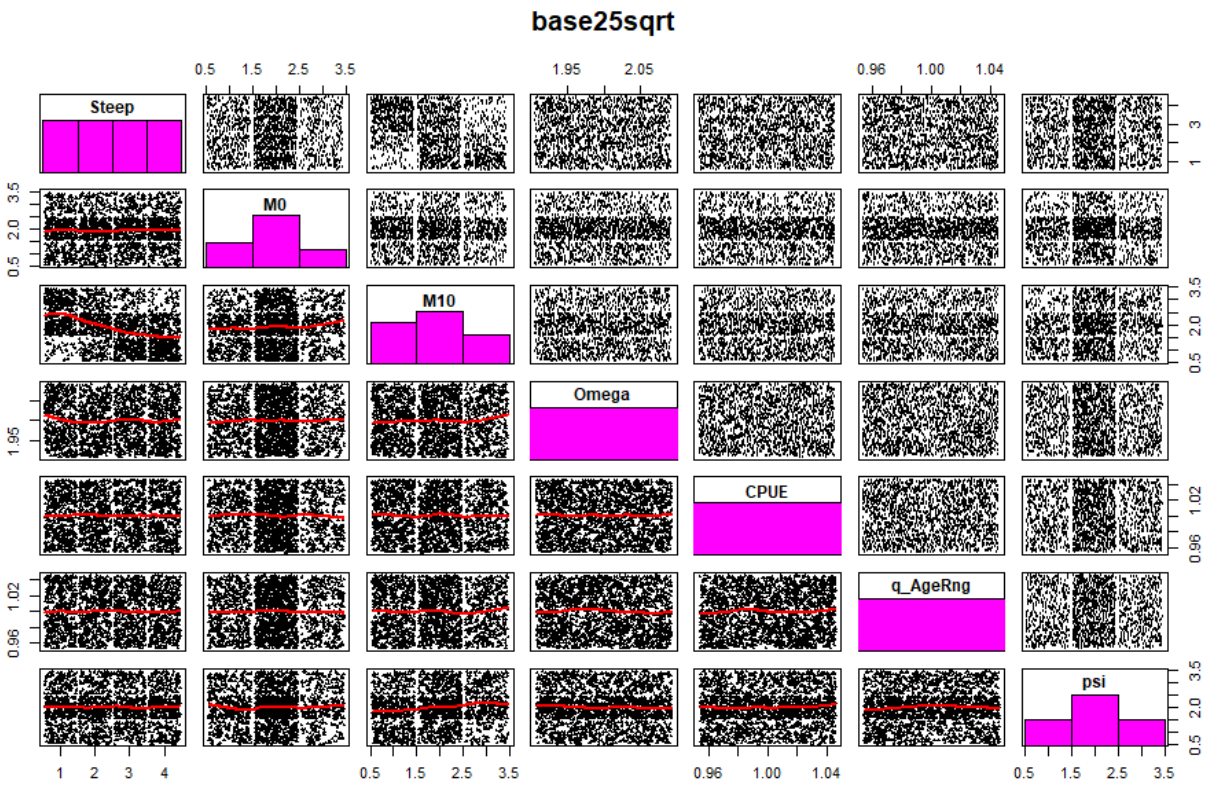


Figure 2. The level plot for the reference grid, using the ADMB software and an updated sbtdata2025.dat file.

5.1 Abundance indices (CPUE and aerial survey)

CPUE fit: Observed and predicted fit to CPUE data and the one-step-ahead residuals (Figure 3 and Figure 4).

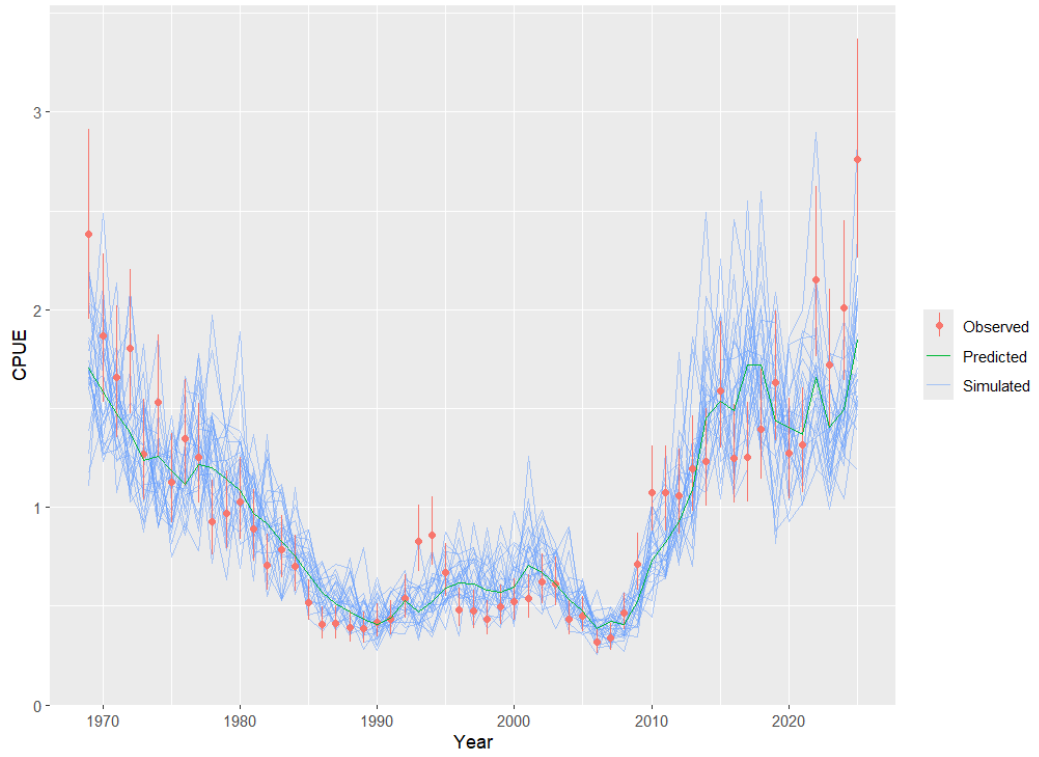


Figure 3. Fit to CPUE data for the best-fitting grid cell. The blue lines correspond to 25 simulated datasets based on estimated parameter values.

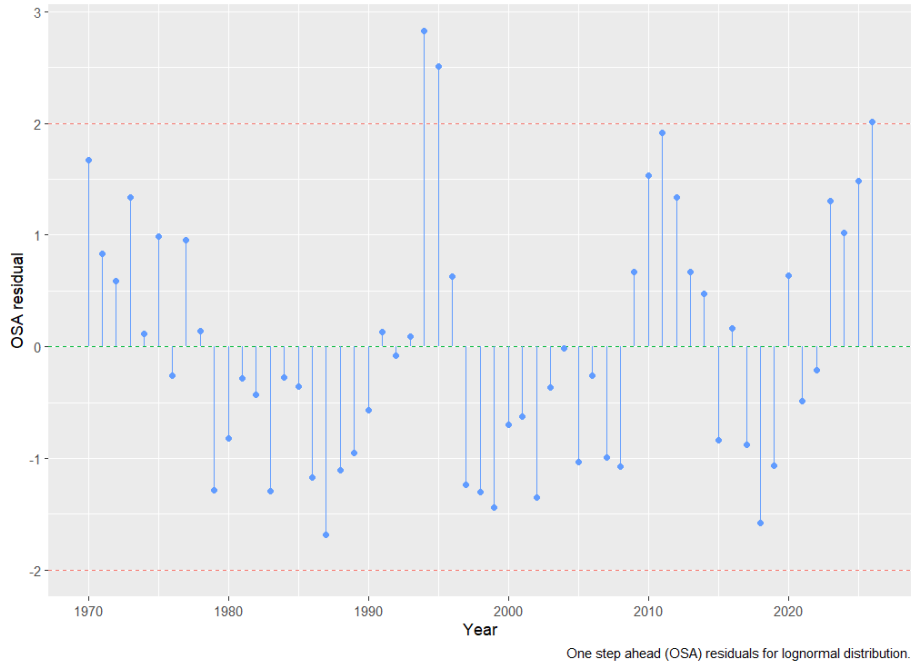


Figure 4. One-step-ahead (OSA) residuals for CPUE data, for the best-fitting grid cell.

Aerial survey fit observed and expected values (Figure 5).

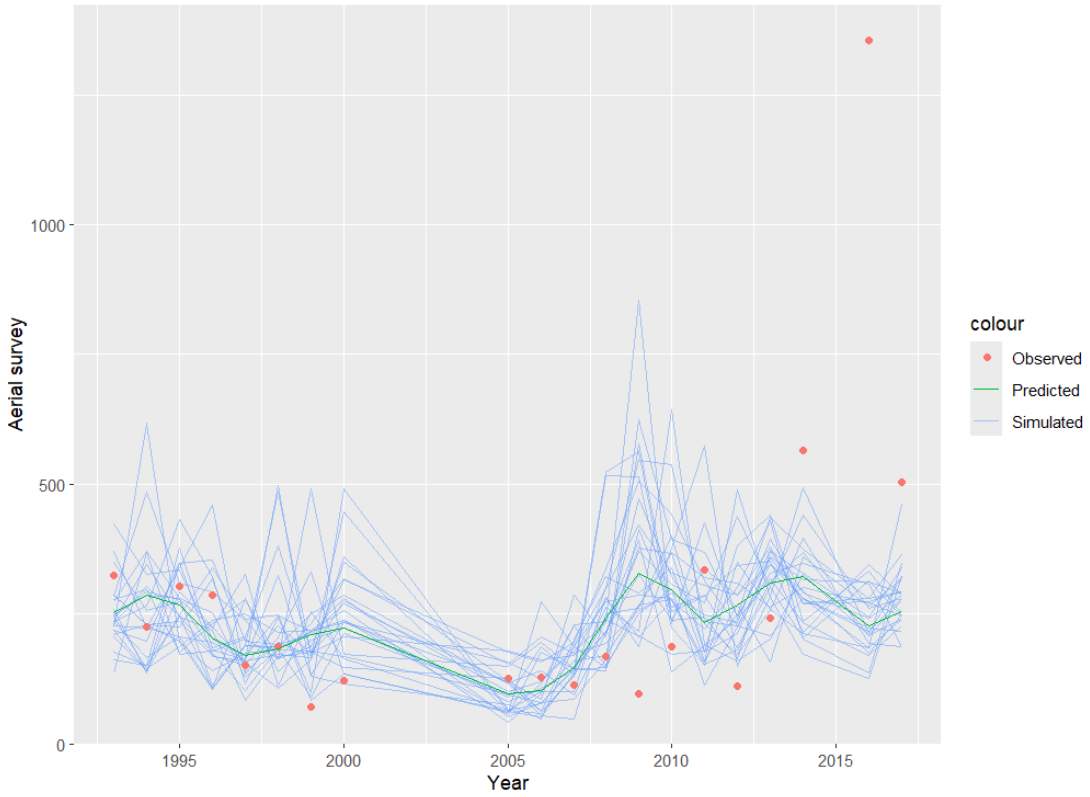


Figure 5. Fit to the aerial survey data for the best-fitting grid cell. The blue lines correspond to 25 simulated data sets based on the estimated parameter values.

5.2 Conventional tag data

Conventional tagging fit: For the conventional tagging data of the 1990s we summarise fits to recaptures by release ages, aggregated across tagger groups (Figure 6).

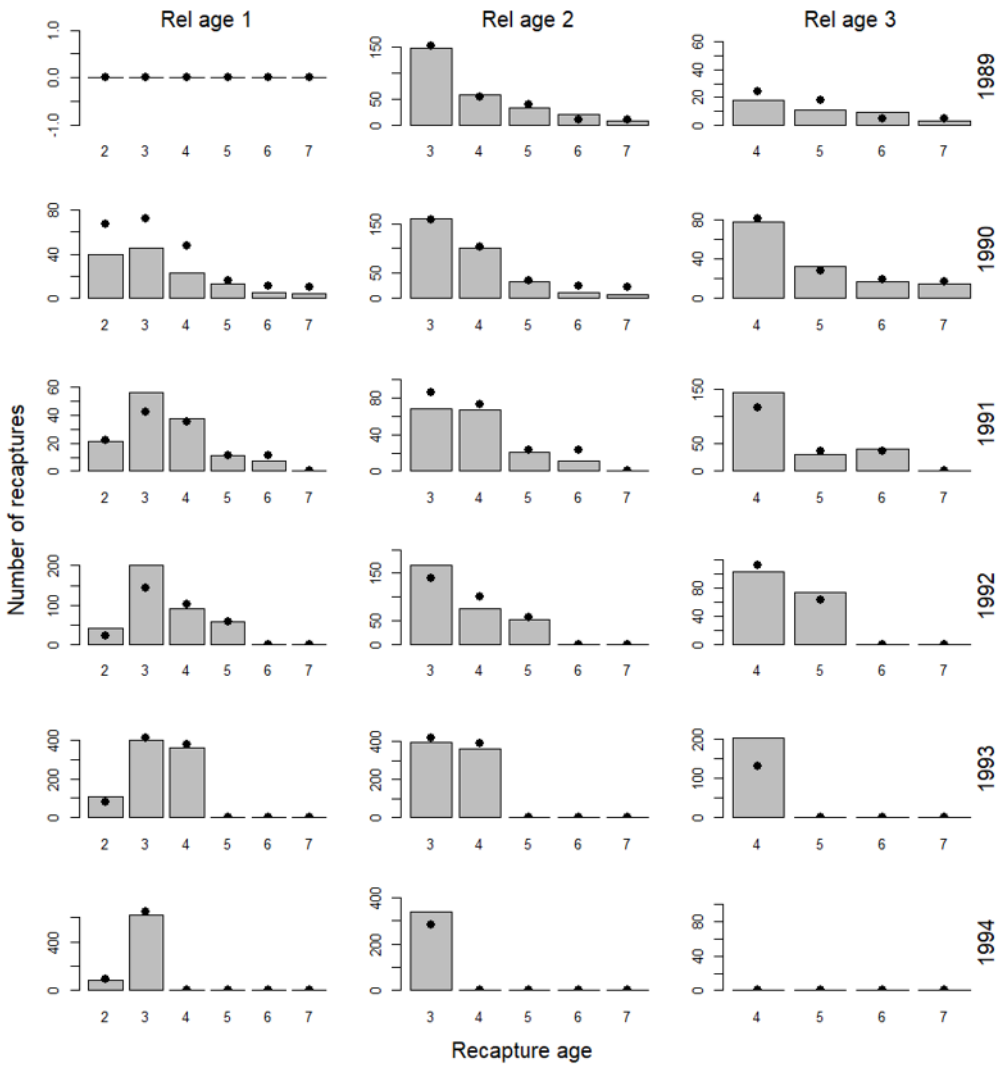


Figure 6. Fits to the number of recaptures in the conventional tagging data for the best-fitting grid cell. Recaptures are broken down by release cohort, release age and recapture age (aggregated over tagger groups). Rows correspond to release cohorts. Note that recaptures in the year of release are no longer being fitted.

5.3 Gene tagging data

Gene-tagging fit: fitting to the expected number of matches (inversely proportional to the absolute abundance of the age 2 fish in the population) (Figure 7).

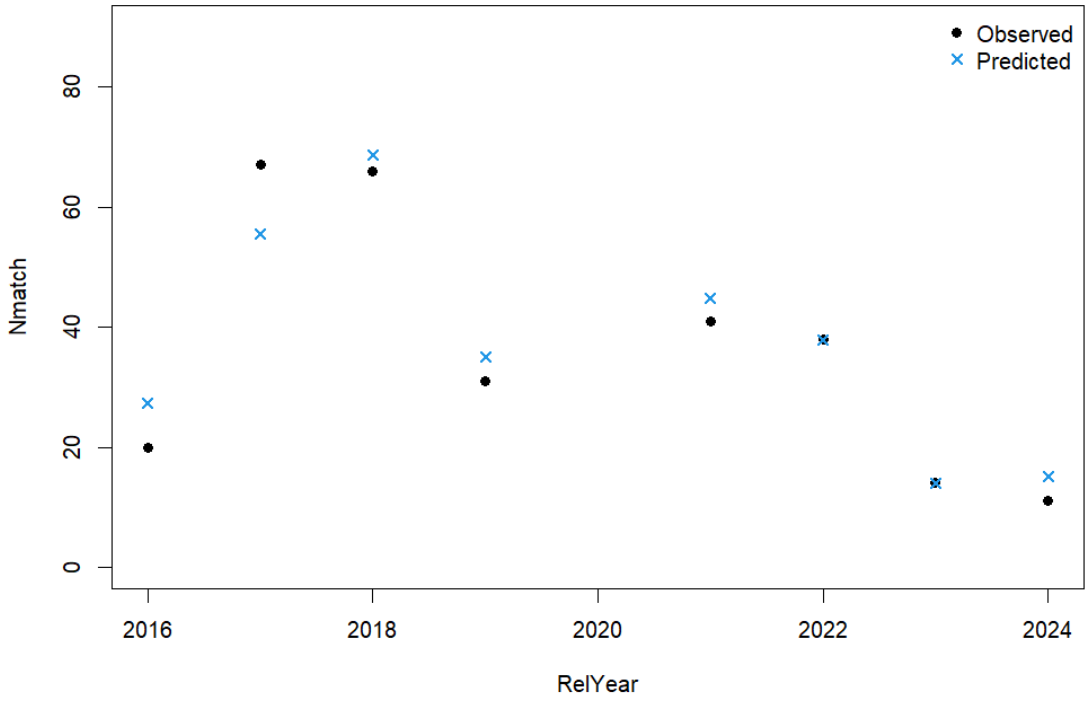


Figure 7. Fit to gene-tagging tagging data (number of matches by release year) for the best-fitting grid cell.

5.4 Close-kin mark-recapture data

As in previous assessments, for the POP fits we focus on higher aggregation levels than the base data is included at (juvenile cohort, adult capture year, adult age/length-at-capture). The first is the juvenile cohort level and in Figure 8a, we see that the data are well described by the model, with all points located within the 95% confidence interval. Figure 8b shows the fits to the POP data at the adult capture year level and all bar one data point are within the predictive interval. For the HSP data we compare an older and younger cohort and we have aggregated these data to the older cohort level – the fits are the number of detected HSPs found between the older cohort and the younger ones that were born after it (Figure 9). **Error! Reference source not found.** shows the summary of the HSP fits at this level and the trend is well captured and all bar one data point are contained within the predictive interval. The final summary is the overall number of POPs and HSPs shown in Figure 11 where both the overall median number of POPs and HSPs is underestimated in both cases, though the predictive intervals both clearly overlap with the observed numbers. It is likely that this under-estimation (not seen before to this degree) is driven by the M10 issue highlighted earlier, but this needs further exploration.

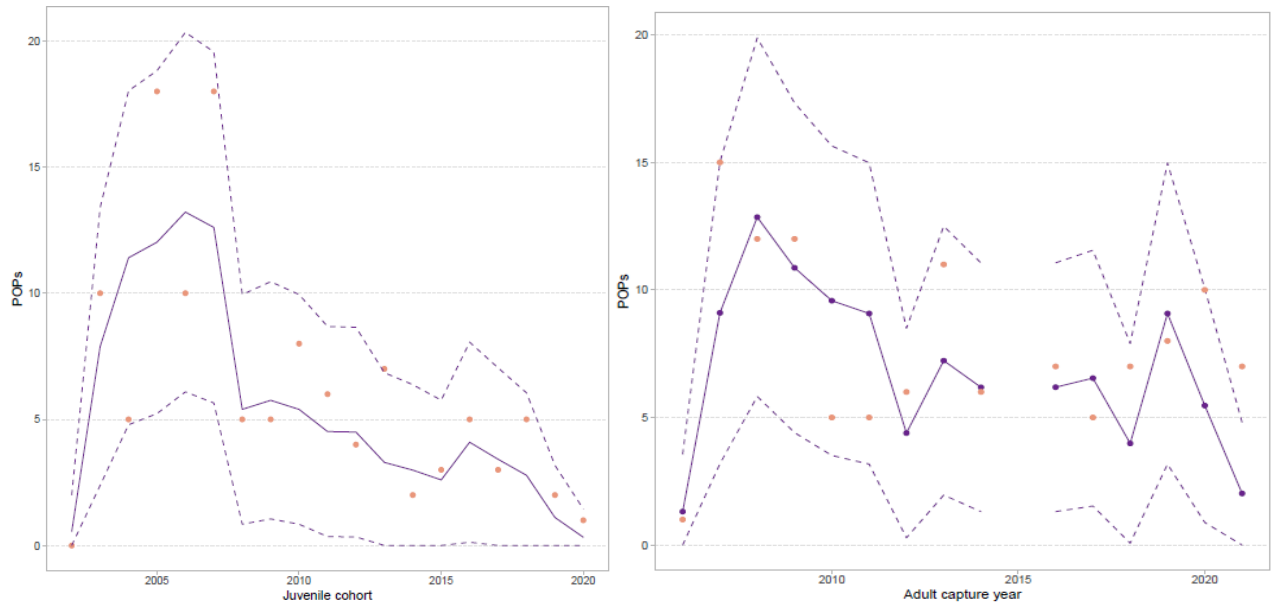


Figure 8a,b. POP fits, a) at juvenile cohort level, and b) at adult capture year level.

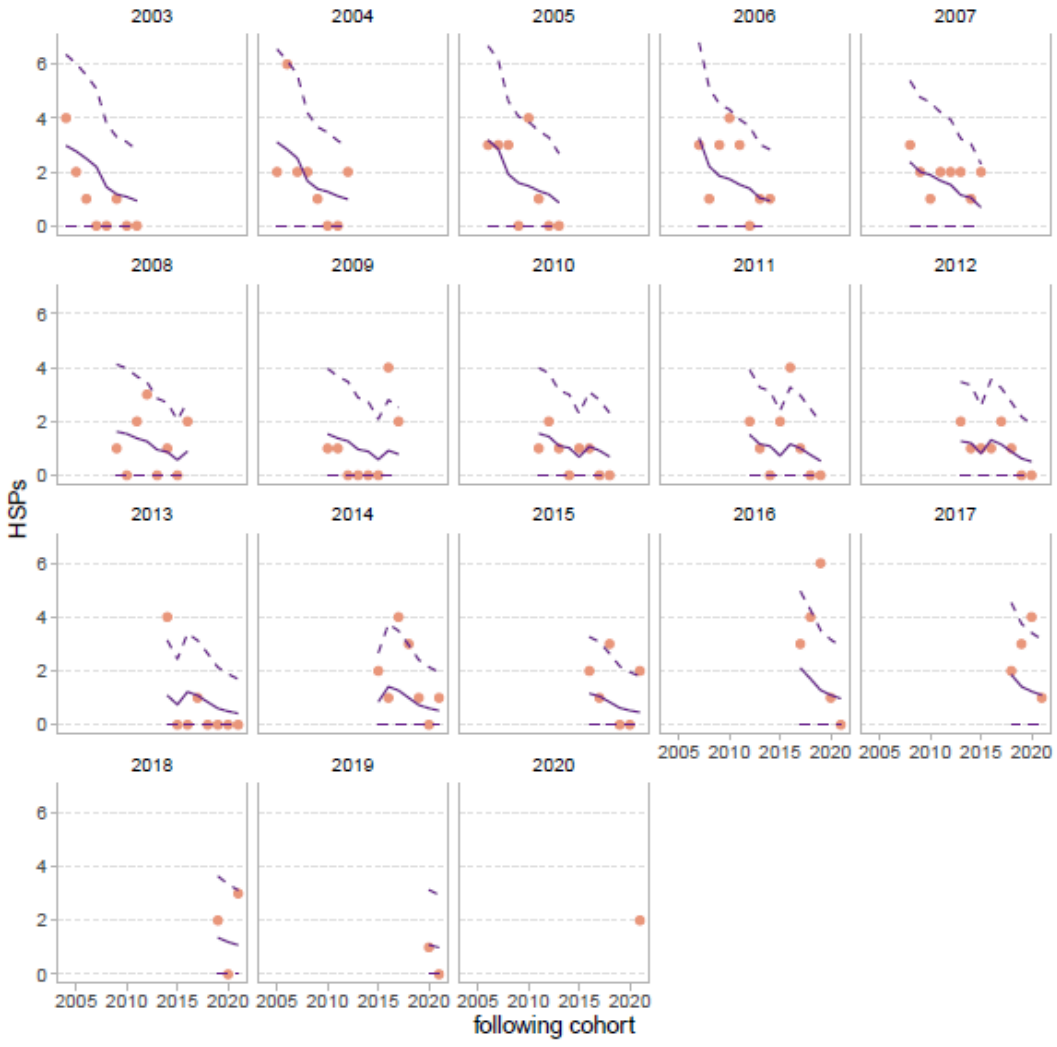


Figure 9. Fits of the number of detected HSPs found between the older cohort and the ones that were born after it.

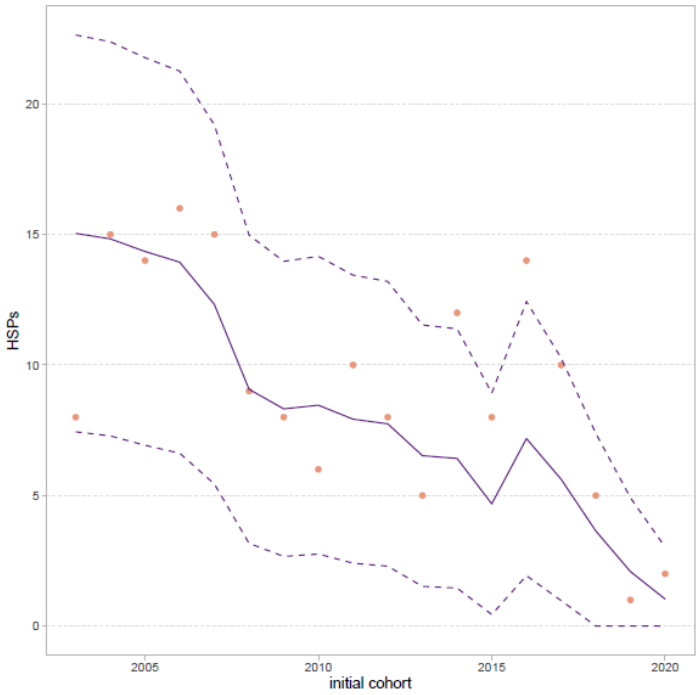


Figure 10. Summary of fit to the HSP data.

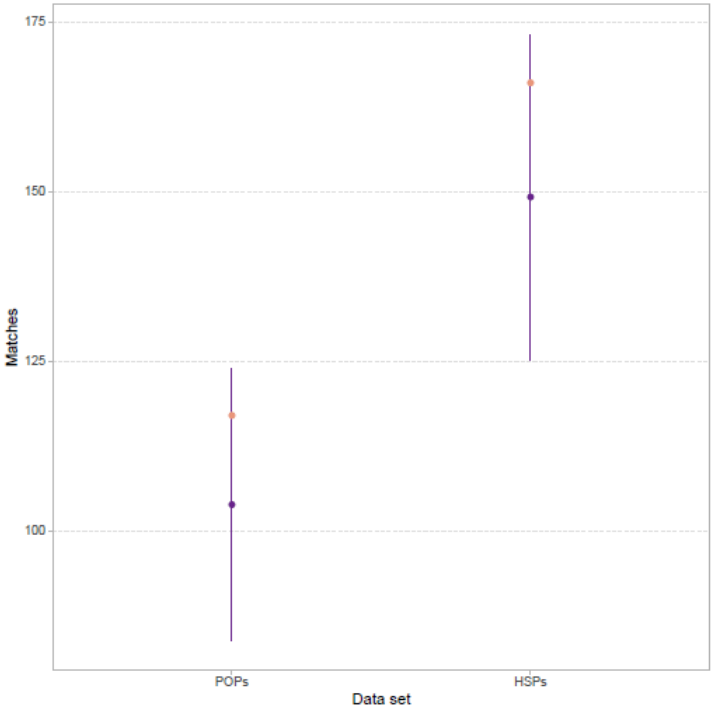


Figure 11. The median number of POPs and HSPs observed and predicted.

5.5 Size and age frequency data

Fits to the size frequency data (Figure 12 to Figure 16)

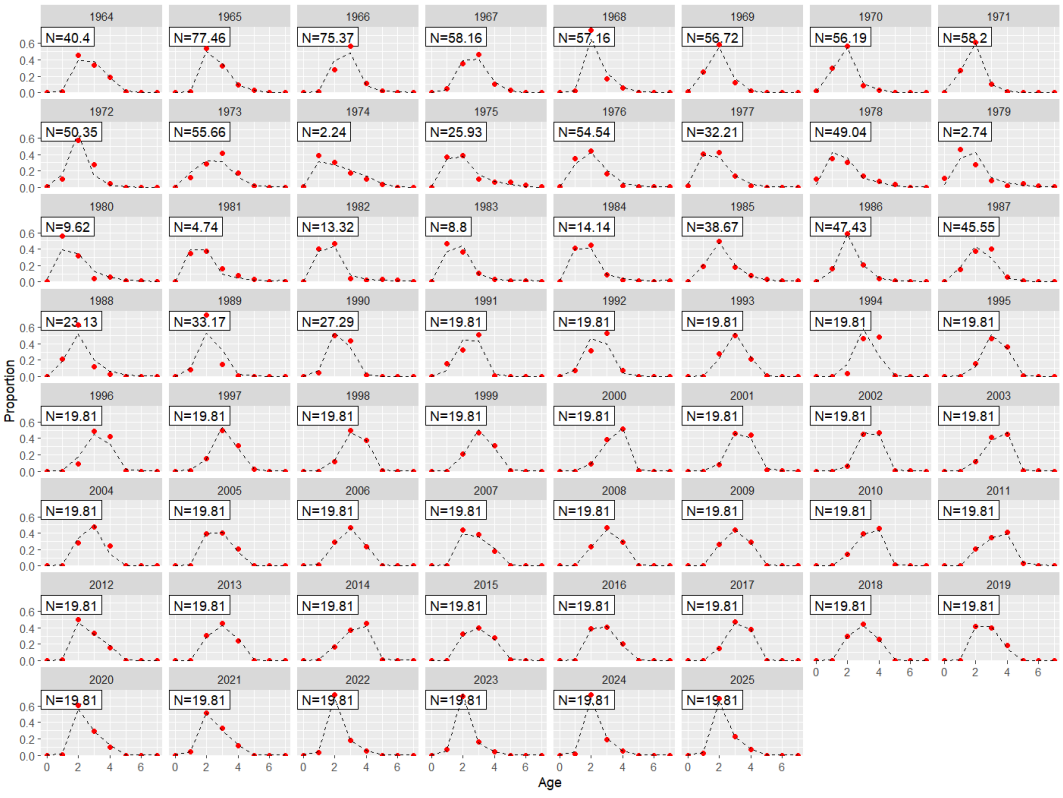


Figure 12 Australian age-frequency fit

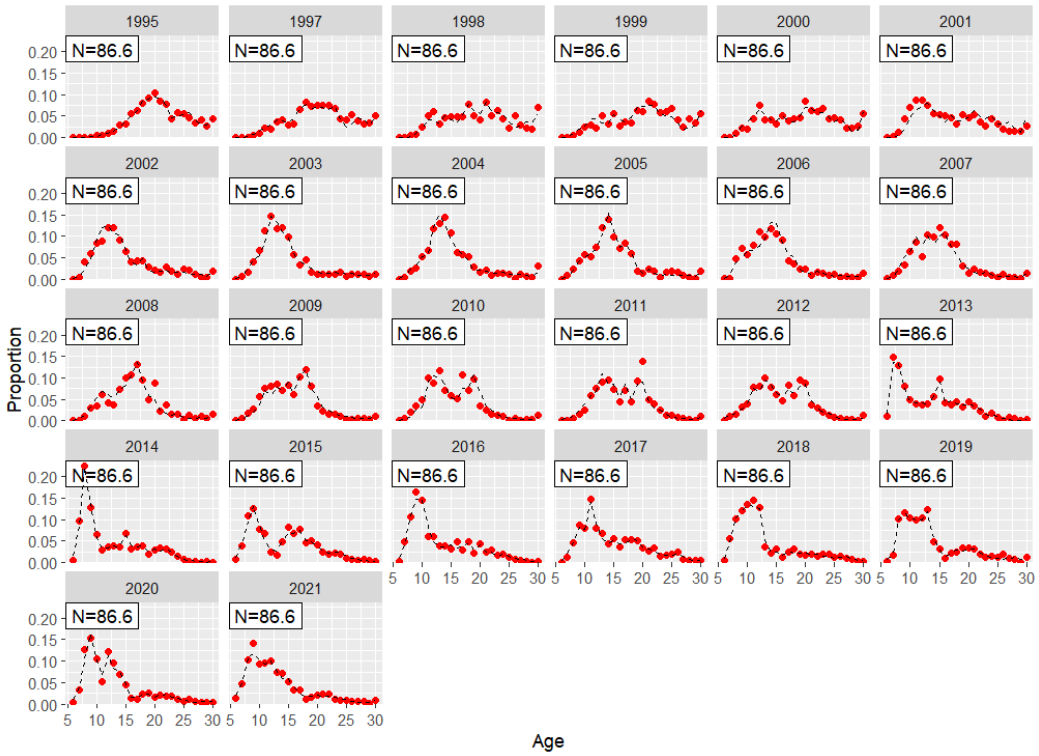


Figure 13 Indonesian age-frequency fit

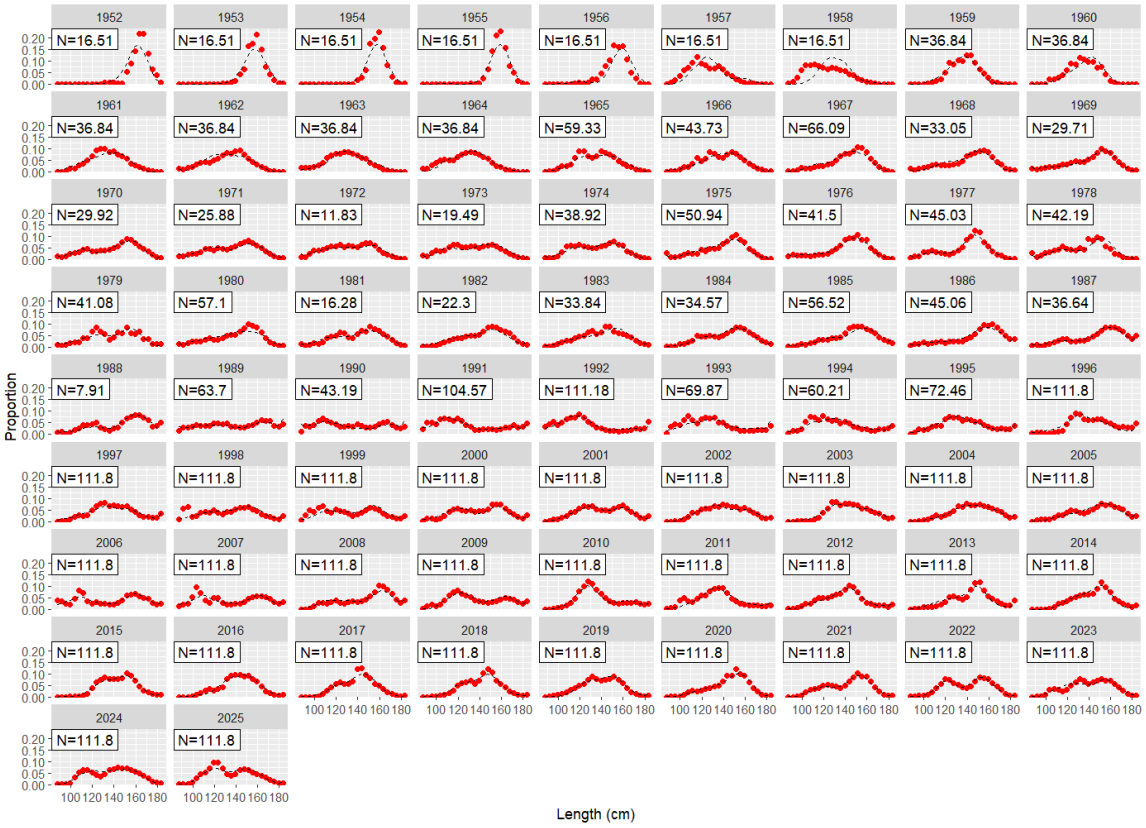


Figure 14 LL1 length-frequency fit

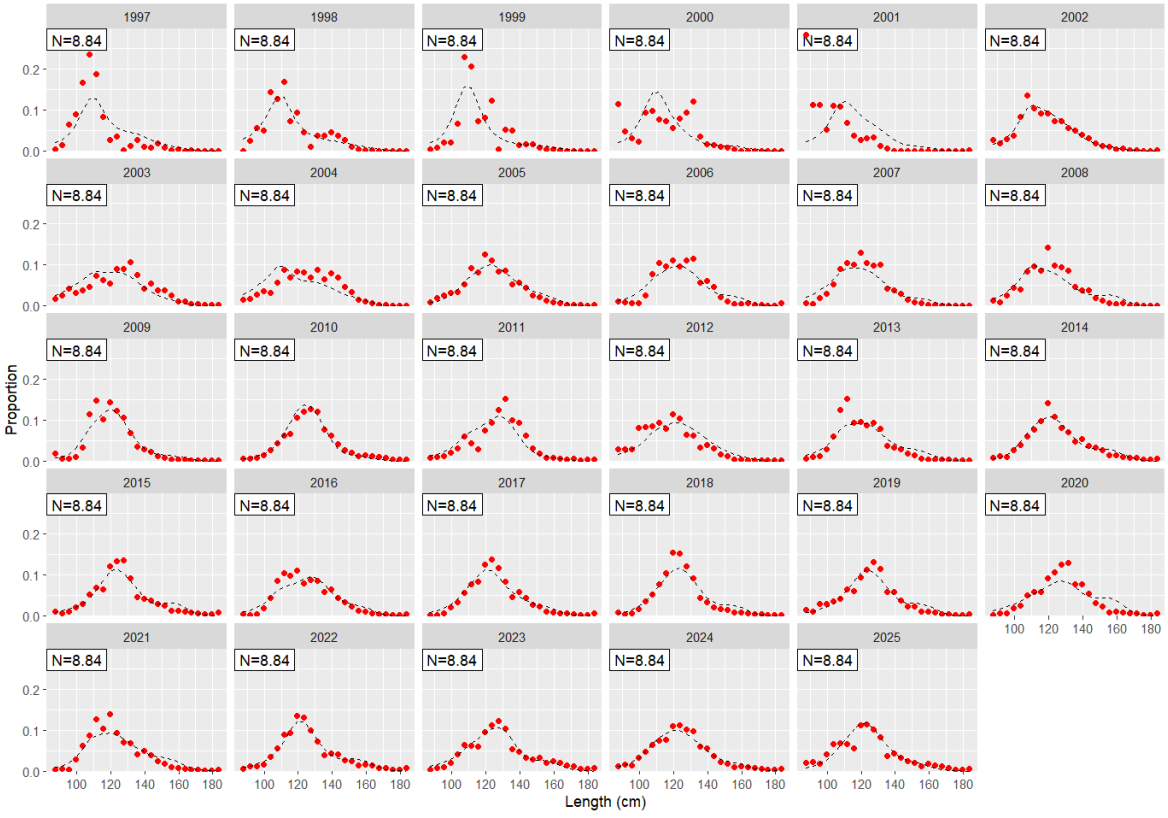


Figure 15 LL2 length-frequency fit

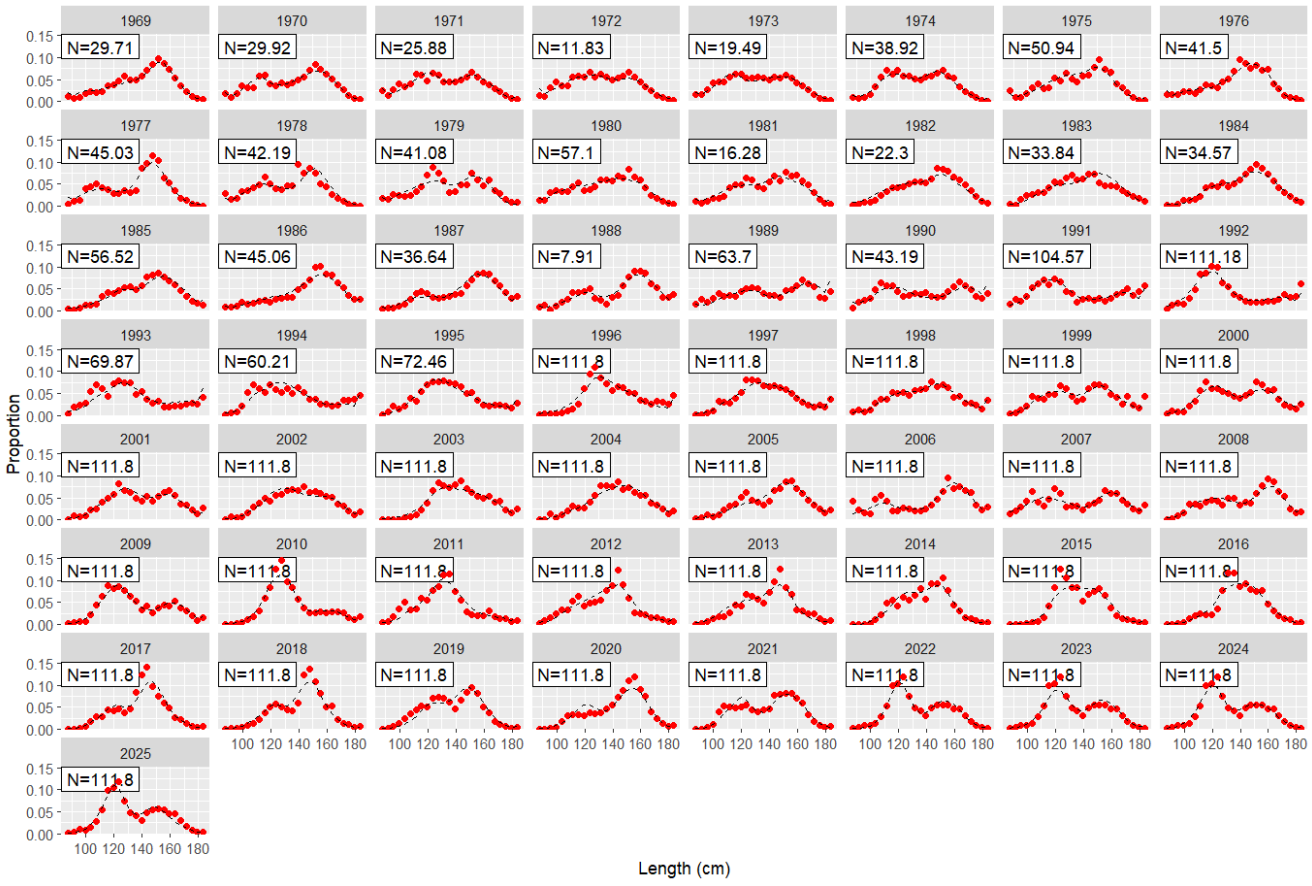


Figure 16 Japanese LL CPUE length-frequency fit

5.6 Selectivity

Summary of the selectivity for each fishery (Figure 17).

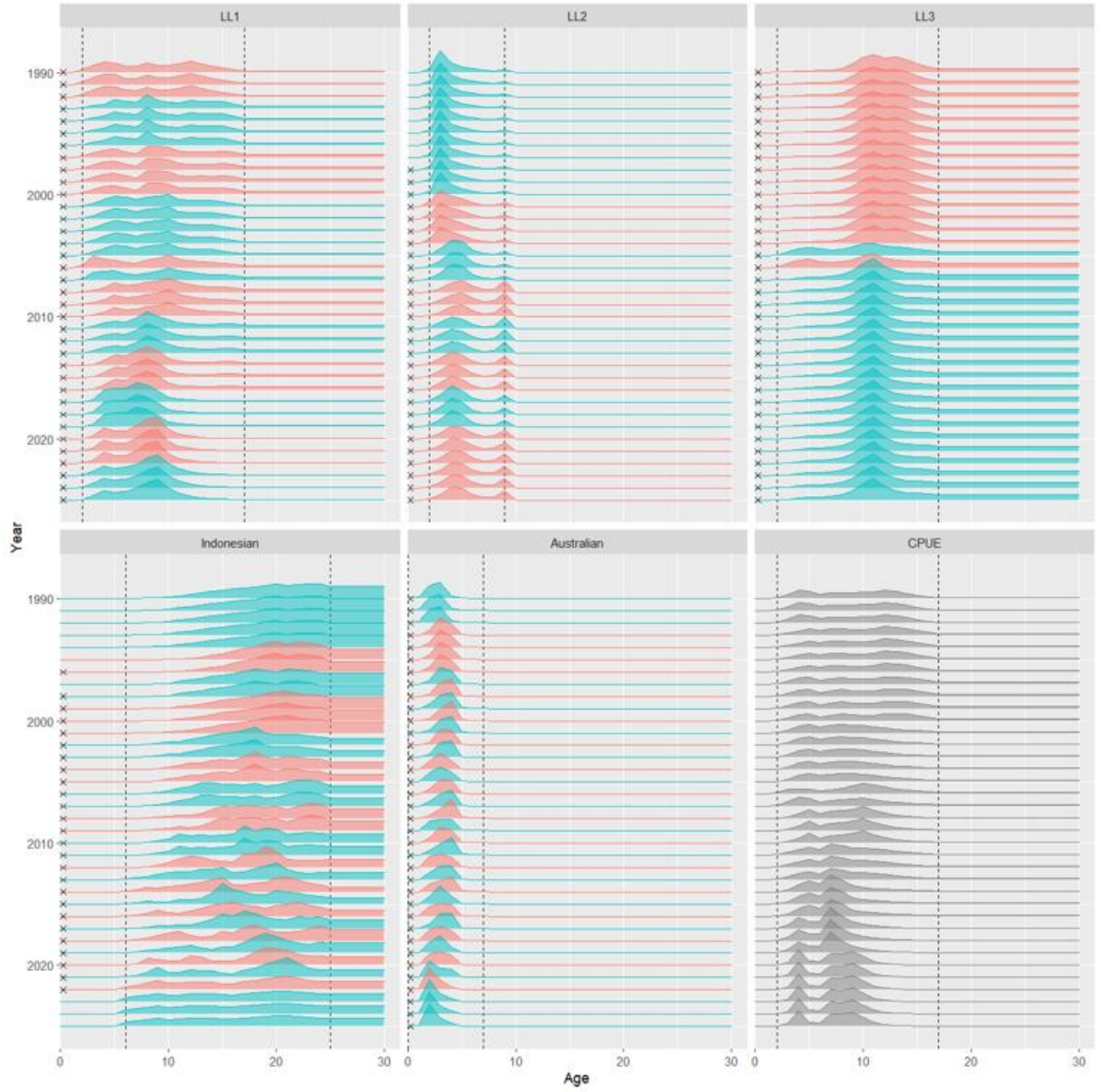


Figure 17 Selectivities (just showing 1990-2025)

6 Discussion

Preliminary model runs have identified some coding issues that have been resolved and issues with the natural mortality that still need to be resolved.

Fits to the data are very preliminary, but in general there don't appear to be major issues in relation to new data included since the last assessment.

Issues with data collation are noted and some of these items may need updating following discussion at OMMP.

7 References

Farley J, Eveson P, Gunasekera R. (2015) Update on the SBT close-kin tissue sampling, processing and kin-finding 2025. CCSBT-ESC/2508/08

Hillary RM, Preece AL, Takahashi N, Davies CR and Itoh T. (2023) The southern bluefin tuna stock assessment in 2023. CCSBT-ESC/2308/16

Itoh T, Takahashi N. (2026) Update of CPUE abundance index using GAM for southern bluefin tuna in CCSBT (GAM22) up to the 2025 data. CCSBT-OMMP/2606/06

CSIRO is Australia's national science agency, delivering solutions for a productive, sustainable and secure future.

CSIRO. Improving the life of every Australian.

Contact us

1300 363 400
+61 3 9545 2176
csiro.au/contact
csiro.au

For further information

E**nvironment** Research Unit
Ann Preece, Paige Eveson, Rich Hillary
+61 3 6232 5222
Ann.preece@csiro.au
www.csiro.au