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Inputs to the Cape Town Procedure for 2025

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Abstract

This paper outlines the key features of both the data inputs to the Cape Town Procedure (gene tagging, Japanese longline CPUE, CKMR POPs and HSPs), and the model-derived quantities from the adult population model that is fitted to the CKMR data. We do not cover Exceptional Circumstances (EC) issues in this paper; those are addressed at the Extended Scientific Committee (ESC). We now have 7 years of gene tagging data (2016–2023 minus 2020) and the 2023 estimate is the highest, but also the most uncertain, in the series. The most recent standardised CPUE point from the Japanese longline fleet is also an increase and is the highest value of the whole series (1969–2024). The CKMR data now cover the years 2002–2020 in terms of information on adult population dynamics. The fits to the updated CKMR data are both acceptably within predicted confidence intervals, and the estimated trend in Total Reproductive Output (TRO) is continuing to increase, consistent with a recovering adult stock. Overall, the data and model-derived inputs to the Cape Town Procedure are all positive, and the fits of the adult population model (contained within the CTP) to the CKMR data all look fine. We do not foresee any immediate issues with respect to running the CTP on the basis of the data and model-derived inputs.

1 Background

This paper details the key data and model-estimated inputs to the Cape Town Procedure (CTP) [1] which is to be run in 2025 to set the global TAC for the 2027–2029 period.

2 Data inputs

There are four data inputs in the CTP:

1. **Gene tagging**: the MP uses the abundance estimate and the number of matches associated with that estimate to generate a weighted recent average abundance of age 2 fish
2. **Japanese LL CPUE**: the agreed Japanese long-line CPUE series
3. **CKMR POPs**: the updated parent-offspring pairs
4. **CKMR HSPs**: the updated half-sibling pairs

2.1 Gene tagging

We now have seven years of gene tagging 2 year old abundance estimates for the years 2016–2023 (minus 2020). Table 2.1 details the estimates and the number of recaptures associated with the estimate as these are the inputs to the MP. The most recent estimated (age 2 abundance in 2023) is the highest estimate of the series, but also the most uncertain (lowest number of matches).

2.2 Japanese long-line CPUE

The CPUE used in the CTP is now the revised GAM-based single CPUE series that has been developed. Figure 2.1 shows the CPUE index used as an input to the CTP, as well as the key MP-related values that drive the CPUE part of the HCR in the CTP. The series runs from 1969 to 2024 and the most recent point is the highest of the series.

Year	Estimate	Recaptures
2016	2.27e+6	20
2017	1.15e+6	67
2018	1.14e+6	66
2019	1.52e+6	31
2020	-	-
2021	1.67e+6	41
2022	1.97e+6	38
2023	2.62e+6	14

Table 2.1: *Gene tagging abundance estimates and associated recaptures, both used as inputs to the MP.*

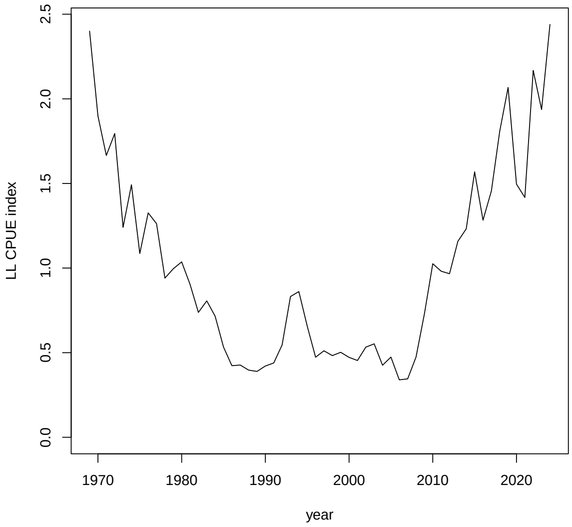

Figure 2.1: *CPUE index used as input to the 2025 MP.*

2.3 CKMR POPs & HSPs

The juvenile cohorts covered by the CKMR POP and HSP data are now 2002–2020 - these are in effect the years for which we have direct information on the abundance, overall mortality and age-structure of the adult population. In terms of POPs there are now 119 POPs from 197 million comparisons. The overall detection rate has stabilised over the last few years. In terms of HSPs there are 157 true HSPs, from 130 million juvenile comparisons, above the false-positive threshold PLOD value, which currently implies a false-negative retention probability (key MP input) of 0.682.

We provide the key data fitting summaries and adult population dynamic variables from the model fitted to the CKMR POPs and HSPs in the CTP. Figure 2.2 details the POP fitting summaries; Figure 2.3 the HSP fitting summaries; and Figure 2.4 the TRO and mean adult total mortality summaries. To make the POP fits easier to visualise (there are almost 4,000 rows in the POP data frame) we aggregate the data and predictions to (a) the juvenile cohort level in Figure 2.2 on the left, and (b) the adult capture age in Figure 2.2 on the right. Overall, all bar one of the observations are contained within the predicted 95% interval (and the one point is *just* outside the interval). The HSP data are less sparse than the POPs so we plot the fits to the data (a) at the input level (juvenile cohorts of the comparison groups) in Figure 2.3 on the left; and (b) aggregated to the oldest cohort of the comparisons groups in Figure 2.3 on the right. Almost all of the HSP observations (104 of the 108) are contained within the predicted confidence intervals at the data input level, and at the initial cohort aggregated level all the data points are contained within the predicted confidence interval.

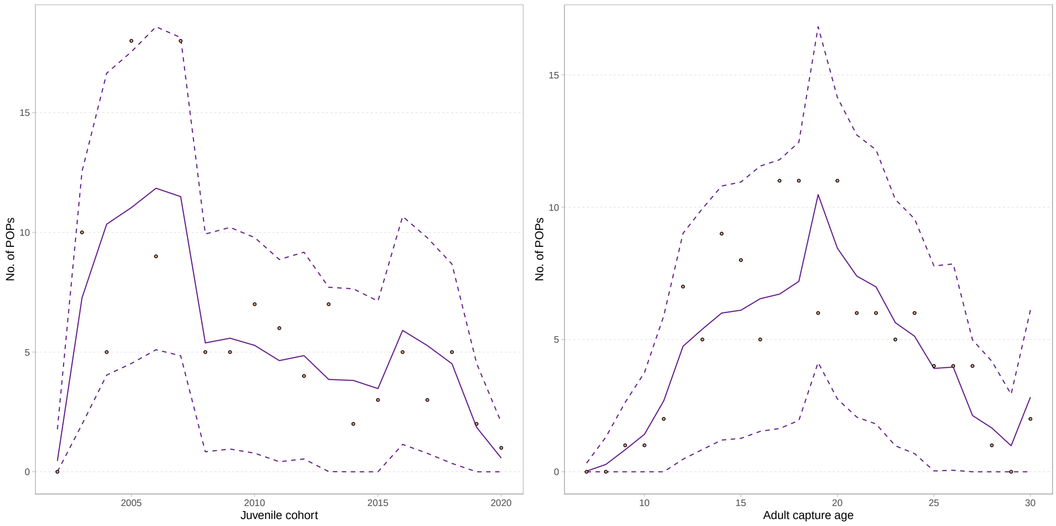

Figure 2.2: *Fits to the CKMR POP data at the juvenile cohort (left) and adult capture age (right) aggregation levels. Dot points are observations, median and approximate 95%iles are the full and dotted lines, respectively.*

3 Discussion

This paper detailed the structure of the Cape Town Procedure, the four data sets used as inputs (gene tagging, Japanese long-line CPUE, CKMR POP and HSP data). Additionally, we show fits to the POP and HSP data CKMR driven model-estimated adult population dynamic variables actually used in the CTP. The Exceptional Circumstances (EC) issues is not addressed in this paper and will be covered in separate papers for the Extended Scientific Committee. In summary, the updated data inputs to the CTP for the 2025 run are positive, and the adult population model fitted to the CKMR data also displays continuing positive recovery trends and fits acceptably to these data. At this stage there are no clear issues relating to the running of the CTP in 2025.

4 Acknowledgements

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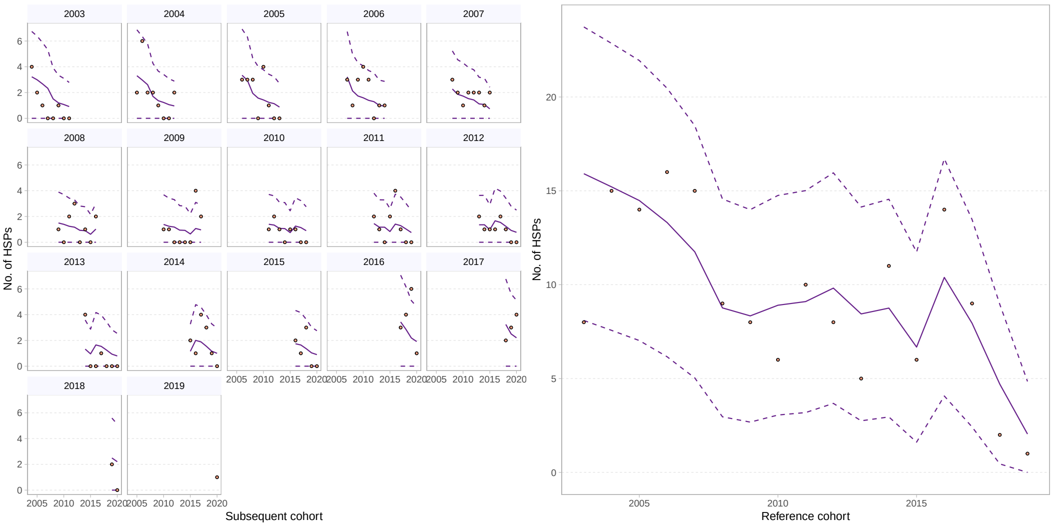

Figure 2.3: *Fits to the CKMR HSP data at the base (left) and initial cohort (right) aggregation levels. Dot points are observations, median and approximate 95%iles are the full and dotted lines, respectively.*

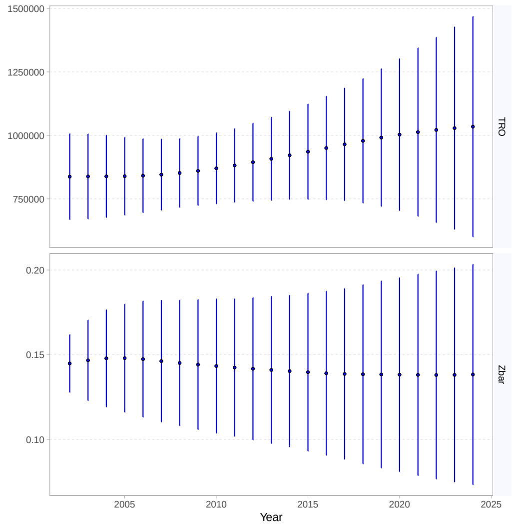

Figure 2.4: *Absolute TRO (top) and mean adult total mortality (bottom) median (dots) and approximate 95%ile (whiskers) for the CKMR-driven population model in the CTP.*

References

[1] Anonymous (2019) Report of the 24th meeting of the Extended Scientific Committee. Cape Town, South Africa.

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