Attachment 8
(of the Report of the 25th Meeting of the Scientific Committee)

Specifications of the CCSBT Management Procedure

1. Introduction

The CCSBT adopted a Management Procedure (MP) to guide its global TAC setting process for southern bluefin tuna in 2011, known as the 'Bali Procedure'. The Bali Procedure has been used by the ESC to recommend the TAC for 2012-2020.

In 2019 the CCSBT adopted a new MP called the 'Cape Town Procedure' (CTP) which is described in this specification.

The CCSBT has been at the forefront of tuna RFMOs in development and implementation of Management Procedures as the basis for recommending changes in the level of fishing to meet the objectives of the Commission and its members (Hillary et al 2016). The impetus for this approach arose from a break-down in the institutional decision-making process arising from: a) high uncertainty in the status and productivity of the stock, b) conflicting views on the best approach to resolve this uncertainty, c) alternative methods for assessing the stock status, and d) lack of an agreed basis to determine the global TAC based on the scientific advice.

The issue of uncertainty in stock status and productivity was addressed by agreeing to develop a set of population dynamics models that encapsulated the range of plausible stock and fishery dynamics. This set of models are known as the CCSBT Operating Models (OMs). The SBT OMs have been modified and refined over the years to reflect the addition of data to existing datasets and new data streams (e.g. aerial survey (2009), close-kin (2013), gene-tagging (2019) and revision of assumptions as appropriate. The SBT OMs are used for i) periodic assessments of stock status, and ii) simulation testing of candidate Management Procedures.

The previously contentious issue of determining the global TAC, based on scientific advice and in a manner consistent with the Commission's objective, has been resolved via the development and testing of a wide variety of candidate Management Procedures and the selection and implementation of the "Bali Procedure" in 2011 (Anon. 2011, Hillary et al 2015, Hillary et al, 2016), and the "Cape Town Procedure" in 2019.

The role of stock assessment and the management procedure, for scientific advice to CCSBT, is distinct and is briefly explained below:

Assessment of stock status

The CCSBT Scientific Committee completes a "full stock assessment" every three years, as originally specified in the Meta-rules for the Bali Procedure. The stock assessment provides information on whether the stock is rebuilding, the projected timeframe to meet the objective of the rebuilding plan (i.e. 30% of TRO_0) and current stock size and fishing mortality relative to commonly used reference points. The stock assessment is **not** used to:

- Run the MP
- Recommend the TAC.

Running the MP for TAC advice

The Management Procedure is used to calculate the global TAC recommended by the ESC to the Commission for decision. The Cape Town Procedure uses **only** three monitoring series as inputs, the defined analyses and decision-rule to recommend the change in TAC. The MP is fully specified (as originally tested in the MSE process, 2019) and is not changed following selection by the Commission.

The running of the MP is independent of the SBT stock assessment. The MP is **not** used to:

- Estimate the spawning stock biomass
- Estimate if the rebuilding target has been met.

Technical details of the Cape Town Procedure, together with specifications of the monitoring data input to the MP, and the Metarule process that the Extended Commission has adopted for dealing with exceptional circumstances in the SBT fishery, are provided in the following sections of this document.

2. **Non-Technical description of the Cape Town Procedure**
3. **Specification of the population model and HCR used in the MP**
4. **Data analysis specification for the Gene-tagging abundance estimates used in the MP**
5. **Specification for the Close-Kin Mark-Recapture data used in the MP**
6. **Specification of Standardised CPUE for the MP**
7. **Metarule Process**

2. Non-Technical Summary of the Cape Town Procedure

The Cape Town Procedure (CTP) has 3 components based on the data inputs from the following monitoring programs: Gene-tagging, CPUE and Close-Kin Mark Recapture (CKMR). Gene-Tagging provides an index of recruitment (abundance of 2 year-olds), CPUE provides an index of abundance for the age-classes exploited by the Japanese longline fishery and CKMR provides two indices of spawning biomass (one from Parent-Offspring-Pairs and one from Half-Sibling-Pairs) as well as information on the total mortality on the spawning component of the population.

For the gene-tagging component, the input is the most recent 5-year weighted average of the abundance estimates, where the weighting is proportional to the number of matches in each year. For the 2020 TAC decision only 3 estimates are available (2016-2018). The TAC change variable for the gene-tagging component will be less than one if the recent average is below the fixed lower bound, or will be greater than one if the recent average is above the fixed upper bound. If the recent average is between the upper and lower bounds, then the TAC multiplier is equal to one. Missing data points have a weight of 0 in the calculation of the weighted average.

For the CPUE component, the TAC change variable is also calculated based on fixed upper and lower bounds. It uses the average of the 4 most recent years from the specified standardised CPUE time-series. If this average value is between the bounds, the contribution to the overall TAC change is zero. If this average is below the lower bound, then the TAC change variable is negative, and if above the upper bound, the TAC change variable is positive. As the current rebuilding target of 30% TRO0 is approached (approximated in the Close-Kin component), the MP is designed to become less reactive, i.e. the recommended TAC changes will be smaller, to minimise future fluctuations in TAC while maintaining the spawning stock close to the target level.

The Close-Kin Mark-Recapture (CKMR) Parent-Offspring-Pair and Half-Sibling-Pair data are used in a simple population dynamics model of abundance and total mortality of adults, which provides a trend in adult abundance. This trend is compared to a threshold growth rate required to rebuild the adult abundance to the target in 2035. If the trend in adult abundance is above the threshold growth rate then the TAC change variable will be positive, and if the trend is lower than the threshold growth rate, the TAC change variable will be negative. The threshold growth rate is not fixed in the CTP but is calculated in the population model. This TAC change variable also becomes less reactive as the target level of rebuilding of the stock is approached.

These three components are combined to give a single multiplier of the current TAC (see technical section below). The final TAC recommendation is constrained to be within a maximum change of 3000t and minimum change of 100t.

3. Specification of the population model and HCR used in the MP

Specification of the population model and HCR used in the MP

Abstract

The Cape Town Procedure (MP) uses CPUE, gene tagging and CKMR (POP and HSP) data in three components of the Harvest Control Rule. For the CKMR component a simplified adult population model (abundance and total mortality) is fitted to the CKMR data. The log-linear trend in TRO is then used in the HCR. For the Gene-tagging and CPUE components of the HCR an upper and lower limit specifies a zone where no change is recommended to the TAC and above or below these limits there is a linearly increasing or decreasing change in TAC.

Adult population model

The adult population model is defined as follows:

$$
\begin{aligned}
N_{y_{\min},a_{\min}} &= \bar{R}\exp\left(\xi_{y_{\min}} - \sigma_R^2/2\right), \\
N_{y,a_{\min}} &= \bar{R}\exp\left(\epsilon_y - \sigma_R^2/2\right), \\
\epsilon_y &= \rho\epsilon_{y-1} + \sqrt{1-\rho^2}\xi_y, \\
\xi_y &\sim N(0,\sigma_R^2), \\
N_{y+1,a+1} &= N_{y,a}\exp\left(-Z_{y,a}\right) \qquad a \in (a_{\min}, a_{\max}), \\
N_{y+1,a_{\max}} &= N_{y,a_{\max}-1}\exp\left(-Z_{y,a_{\max}-1}\right) + N_{y,a_{\max}}\exp\left(-Z_{y,a_{\max}}\right), \\
Z_{y,a} &= Z_y \qquad a \leq 25, \\
Z_{y,a} &= Z_y + \frac{a-25}{a_{\max}-25}\left(Z_{a_{\max}} - Z_y\right) \qquad a \in [26, a_{\max}], \\
Z_y &= \frac{Z_{\max}e^{\chi_y} + Z_{\min}}{1+e^{\chi_y}}, \\
\chi_{\text{init}} &\sim N(\mu_{\chi_{\text{init}}}, \sigma^2_{\chi_{\text{init}}}), \\
\chi_{y+1} &= \chi_y + \zeta_y, \\
\zeta_y &\sim N(0,\sigma_\chi^2), \\
TRO_y &= \sum_a N_{y,a}\varphi_a
\end{aligned}
$$

The fixed parameters and settings of this model are given by the following table:

Parameter	Value
$a_{\min}$	6
$a_{\max}$	30
σ_r	0.25
ρ	0.5
σ_χ	0.15
$Z_{\min}$	0.05
$Z_{\max}$	0.4
$Z_{a_{\max}}$	0.5
$\mu_{\chi_{\text{init}}}$	-1.38
$\sigma_{\chi_{\text{init}}}$	0.2
q_{hsp}	1

The estimated parameters of this model are:

1. The mean adult recruitment, $\bar{R}$
2. The adult recruitment deviations, ϵ_y
3. The initial value, χ_{init}, that "starts" the random walk for Z_y (with an associated normal prior mean and SD)
4. The random walk deviations ζ_y

The likelihood for the POP data is similar to that used in the OM. The total reproductive output is calculated as follows:

$$TRO_y = \sum_{a=a_{\text{amin}}}^{a_{\max}} N_{y,a}\varphi_a$$

and consider a juvenile-adult pair $\{i, j\}$, where $z_i = \{c\}$ is the juvenile covariate and c is it's cohort (year of birth) and $z_j = \{y, a\}$ is the adult covariate and y and a are the year and age at sampling, respectively. The probability of that pair being a POP is given by

$$\mathbb{P}\left(K_{ij} = POP \,|\, z_i, z_j\right) = \mathbb{I}\left(c < y < c + a\right) \frac{2\varphi_{a-(y-c)}}{TRO_c}$$

This probability is used to create the binomial likelihood for the POP data. For the HSP data the comparison is of a juvenile-juvenile pair i and i', where the key covariates are their respective years of birth - or cohorts - c. The probability of finding an HSP is defined as follows:

$$\mathbb{P}\left(K_{ii'} = HSP \,|\, z_i, z_{i'}\right) = \frac{4\pi^{\eta} q_{\text{hsp}}}{TRO_{c_{\max}}} \left(\sum_a \gamma_{c_{\min},a} \left(\prod_{k=0}^{\delta-1} \exp\left(-Z_{c_{\min}+k,a+k}\right) \right) \varphi_{a+\delta} \right),$$

$$\begin{aligned}
\gamma_{y,a} &= \frac{N_{y,a}\varphi_a}{TRO_y}, \\
\{z_i, z_{i'}\} &= \{c_i, c_{i'}\}, \\
c_{\min} &= \min\{c_i, c_{i'}\}, \\
c_{\max} &= \max\{c_i, c_{i'}\}
\end{aligned}$$

and this probability forms the basis of the binomial likelihood for the HSP data.

Harvest Control Rule

The general structure of the revised MP is as follows:

$$TAC_{y+1} = TAC_y \left(1 + \Delta_y^{\text{cpue}} + \Delta_y^{\text{ck}}\right) \times \Delta_y^{\text{gt}}, \tag{1}$$

Before detailing the functional form of the HCR we recap some useful variables:

- I_y^{ck}: moving average (of length τ^{ck}) of the estimated TRO from the MP population model (projected forward to the current year using the model to project forward for 4 years to avoid too much intertia in the signal when you need it)
- $\tilde{I}$: average estimated TRO from 2003 to 2014 (reference period w.r.t. relative rebuilding criterion)
- γ: proportional amount of TRO rebuilding we wish to achieve
- $\eta = I_y^{\text{ck}}/(\gamma\tilde{I}) - 1$: the variable at which passing from negative to positive indicates the point at which the TRO rebuilding has been achieved and the transition in the reactivity of the MP occurs (i.e. it goes from reactive to passive w.r.t. CPUE and CKMR signals *only*)

For the CPUE part of the HCR we used a density-dependent gain parameter:

$$k^{\text{cpue}}(\eta) = w_1^{\text{cpue}} \left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right) + w_2^{\text{cpue}} \left(1 + e^{-2\kappa\eta}\right)^{-1}$$

This is using the logistic function approximation to the Heaviside step function $H[\eta]$ ($H[\eta < 0] = 0$, $H[\eta \geq 0] = 1$). We set $\kappa = 20$ so the transition between the two gain parameters, given η, happens within $\pm 5\%$ of $\delta = 1$. The CPUE multiplier is then just defined as follows:

$$\Delta_y^{\text{cpue}} = k^{\text{cpue}}(\eta)\left(\delta_y^{\text{cpue}} - 1\right)$$

and δ_y^{cpue} is actually very similar in form to the gene tagging part of the HCR

$$\begin{aligned}
\delta_y^{\text{cpue}} &= \left(\frac{\bar{I}_{\text{cpue}}}{I_{\text{low}}}\right)^{\alpha_1} && \forall \bar{I}_{\text{cpue}} \leq I_{\text{low}}, \\
\delta_y^{\text{cpue}} &= 1 && \forall \bar{I}_{\text{cpue}} \in (I_{\text{low}}, I_{\text{high}}), \\
\delta_y^{\text{cpue}} &= \left(\frac{\bar{I}_{\text{cpue}}}{I_{\text{low}}}\right)^{\beta_1} && \forall \bar{I}_{\text{cpue}} \geq I_{\text{high}},
\end{aligned}$$

where $\bar{I}_{\text{cpue}}$ is the (4 year) moving average LL1 CPUE, $\bar{I}_{\text{low}}$ and $\bar{I}_{\text{high}}$ are upper and lower threshold CPUE values, and α_1 and β_1 allow for an asymmetric response above or below the threshold zone.

For the CKMR part of the HCR we try to ensure a minimum rate of increase in the TRO *beneath* the target level, and once it is achieved we would like to maintain the TRO at that level. To include this kind of behaviour in the HCR we also include some density-dependence in the log-linear growth rate at which the HCR moves from a TAC increase to a TAC decrease:

$$\begin{aligned}
\Delta_y^{\text{ck}} &= k^{\text{ck}}(\eta)\left(\lambda^{\text{ck}} - \tilde{\lambda}(\eta)\right), \\
k^{\text{ck}}(\eta) &= k_1^{\text{ck}}\left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right) + k_2^{\text{ck}}\left(1 + e^{-2\kappa\eta}\right)^{-1}, \\
\tilde{\lambda}(\eta) &= \lambda_{\min}\left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right)
\end{aligned}$$

The threshold level at which the log-linear trend, λ^{ck}, goes from supporting a TAC decrease to an increase essentially begins at $\lambda_{\min} > 0$ and, as the estimated TRO approaches the target level, rapidly decreases to zero (in a similar way to the CPUE trend term). This is to ensure that a minimum level of rebuilding is encouraged for **all** trajectories below the target, and where above the target the *status quo* is preferred.

To calculate the recent mean age 2 abundance from the gene tagging data consider a weighted moving average approach:

$$\bar{N}_{y,2} = \sum_{i=y-1-\tau^{\text{gt}}}^{y-2} \omega_i \widehat{N}_{i,2}$$

where ω_i is a weighting proportional to the number of matches used to produce the GT estimate $\widehat{N}_{i,2}$ (basically inverse variance weighting). The 2 year delay between having the estimate and what year it actually refers to is factored into the calculation. The multiplier for the GT part of the HCR is as follows:

$$
\begin{aligned}
\Delta_y^{\mathrm{gt}} &= \left(\frac{\bar{N}_{y,2}}{N_{\mathrm{low}}}\right)^{\alpha} \quad \text{if} \quad \bar{N}_{y,2} \leq N_{\mathrm{low}}, \\
\Delta_y^{\mathrm{gt}} &= 1 \qquad\qquad\quad \text{if} \quad \bar{N}_{y,2} \in (N_{\mathrm{low}}, N_{\mathrm{high}}), \\
\Delta_y^{\mathrm{gt}} &= \left(\frac{\bar{N}_{y,2}}{N_{\mathrm{high}}}\right)^{\beta} \quad \text{if} \quad \bar{N}_{y,2} \geq N_{\mathrm{high}}
\end{aligned}
$$

with N_{low} the limit level and N_{high} the upper level at where TAC increases are permitted. Table 2 details the parameter values for the HCR in the adqpted MP.

Parameter	Value
τ^{cpue}	4
w_1^{cpue}	0.9
w_2^{cpue}	0.005
I_{low}	0.45
I_{high}	1.42
α_1	1
β_1	1
τ^{gt}	5
N_{low}	1e+6
N_{high}	2.6e+6
α	1.5
β	0.25
τ^{ck}	3
k_1^{ck}	1.25
k_2^{ck}	0.05
γ	1.5
λ_{min}	0.001
κ	20

Table 2: *Fixed values of parameters of the HCR in the CTP.*

4. Data analysis specification for the Gene-tagging abundance estimates used in the MP

The CCSBT gene-tagging program provides an estimate of the absolute abundance of the age-2 cohort, in the year of tagging, and the number of matches (recaptures) detected for use in the Cape Town Procedure. The annual program which commenced in 2016 is described in the design study (Preece et al. 2015) and follows protocols for tagging and animal handling developed by CSIRO (Bradford et al. 2009).

Gene-tagging SBT involves "tagging" fish by taking a very small tissue sample (Bradford et al. 2015) from a large number of 2-year-old SBT and releasing the fish alive. A physical tag is not used. A year later, a second set of tissue samples is collected from the catch of 3-year-old fish at time of harvest, allowing time for the tagged fish to mix with untagged SBT throughout the population (Polacheck et al. 2006; Basson et al. 2012). The two sets of tissue samples are genotyped and then compared in order to find the samples with matching DNA (using the unique DNA fingerprint); a match indicates that a tagged and released fish was recaptured. The abundance estimate is calculated from the number of samples in the release and harvest sets and the number of matches found.

The genotype analysis involves filtering the data to exclude fish with incomplete or poor genotype information (too few SNP markers with good sequencing results). To be included, the sample must have at least 30 of the 59 markers with a genotype call with a total count of at least 20 (Preece et al. 2019). Any fish outside the target release and harvest length ranges are also excluded. The length range for 2-year-old fish is 75-85 cm FL, and for 3-year-old fish is 98-109 cm FL. These length ranges are regularly reviewed (Preece et al. 2019; Clear et al. 2019).

The process takes about 2 years from initial collection of tissue samples ('tagging') through to calculation of the abundance estimate.

An estimate of cohort abundance at the time of tagging (N) is given by:

(1) $N = T * S/R$

where T is the number of fish in the cohort that were tagged, R is the number of tagged fish "recaptured" in the harvest sample i.e. the number of 'matches', and S is the harvest sample size. Eq. (1) is often referred to as the Petersen (or Lincoln-Petersen) estimator of abundance (e.g. Seber 1982). Assuming a Poisson recapture process, the coefficient of variation (CV) of the abundance estimate can be approximated by:

(2) $CV = \mathrm{sqrt}(N/(T*S))$
$= \mathrm{sqrt}(1/R)$

Only the abundance estimates and number of matches each year are used in the Cape Town Procedure (Table 1, unshaded columns). These data are submitted annually as part of the CCSBT data exchange. The data in Table 1 are the gene-tagging results for the 3 years (2016-2018) available for use in the MP in 2020.

Table 1. The results of the gene-tagging programs 2016-2018 which provide the absolute abundance estimate for the age-2 cohort in the year of tagging. The unshaded columns indicate the data used in the Cape Town Procedure.

YEAR	COHORT AGE	N RELEASES	N HARVEST	N MATCHES	ABUNDANCE ESTIMATE (MILLIONS)	CV
2016	2	2952	15389	20	2.27	0.224
2017	2	6480	11932	67	1.15	0.122
2018	2	6295	11980	66	1.14	0.123

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5. Specification for the Close-Kin Mark-Recapture data used in the MP

Close-Kin Mark Recapture (CKMR) uses modern genetics to identify close relatives (parent-offspring-pairs (POPs) and half-sibling-pairs (HSPs)) amongst large sample sizes of fish, in order to estimate adult abundance and make demographic inferences about the adult stock (Bravington et al. 2016). As part of the CKMR program for SBT, genetic samples have been collected annually since 2006 from adults on the Indonesian spawning grounds and from juveniles (3-year-olds) in the Great Australian Bight (Davies et al. 2018). Each year, updated numbers of POPs and HSPs, along with the numbers of comparisons made in identifying these kin pairs, are provided to the CCSBT data exchange. In the Cape Town Procedure, these data get used in a population dynamics model to provide an index of abundance of reproductive adults (or total reproductive output, TRO), which is then used to modify the TAC (Hillary et al., 2019).

In Indonesia, tissue samples are collected from adult SBT of all sizes at the Benoa Fishing Port each spawning season during processing of catches from the longline fishery. In Australia, tissue samples are collected from juvenile SBT each June-July at the tuna processors during harvest in Port Lincoln; samples are obtained from fish ranging from 98 to 109 cm fork length to ensure 3-year-olds are being sampled. In both sampling locations, sample collection is spread as evenly as practical throughout the harvest season.

DNA is extracted from the tissue samples selected for genotyping. Archived plates of extracted DNA are shipped to Diversity Arrays Technology (DArT) in Canberra for genotype sequencing, referred to as "DArTcap", and when completed, the sequencing data are provided to CSIRO Hobart. These data are used to call the genotype (i.e., to infer the pair of alleles present) for each fish and locus in the data set using sophisticated algorithms developed at CSIRO specifically for DArTcap sequencing data. The genotyping error rate is also estimated for each locus (of which ~1500 are used in kin-finding), which is important in the identification of HSPs. A series of quality control (QC) steps are applied to the genotyped data to remove fish with unreliable genotype calls and provide a final data set for kin-finding. Note that the QC steps have evolved (and may continue to) over the course of the program, so the exact sample sizes used in kin-finding can change; Table 1 gives the sample sizes used in the 2020 analysis.

POPs are identified across all genotyped adult-juvenile pairs using a modified Mendelian-exclusion statistic referred to as the Weighted-PSeudo-EXclusion (WPSEX) statistic (see Appendix B of Bravington et al. 2017). The numbers of POPs obtained from the 2020 analysis, broken down by juvenile birth year and adult capture year, are given in Table 2 (note this includes POPs that were identified using microsatellites prior to the genotyping method changing in 2015 to DArTcap sequencing; see Bravington et al. 2015, 2017).

HSPs are identified among all genotyped juvenile pairs using a pseudo-log-odds-ratio (PLOD) statistic, which measures the relative probability of a pair of fish having their observed genotypes if they are HSPs compared to if they are unrelated (see Appendix C of Bravington et al. 2017). Unlike the WPSEX statistic for identifying POPs, the

PLOD statistic does not give a clear separation between HSPs and unrelated/less-related fish (see Figures 3 and 4 of Farley et al. 2019). Thus, the theoretical means and approximate variances of the PLOD distributions for HSPs and unrelated/less-related pairs are used to determine a lower cut-off PLOD value that minimises the number of false positive HSPs whilst still maintaining a large enough number of HSPs for the estimate to have good precision. An inevitable consequence of ensuring that false positives are rare is that a reasonable number of false negatives will be present; the false-negative rate is estimated using the expected PLOD distribution for HSPs, and is allowed for in modelling (Bravington et al. 2017). Note that the division between PLOD values for HSPs and more related fish (i.e., full-sibling-pairs) is clear. The numbers of high-confidence HSPs identified from the 2020 analysis, broken down by birth years of siblings, are given in Table 3.

Table 1. Number of fish available for kin-finding analyses in 2020 after quality control checks. For the adults, samples were collected from Indonesia in the fishing season ending in the year shown (i.e., samples collected over the 2005/06 fishing season are referred to as year 2006).

Year	Adults	Juveniles
2006	0	1317
2007	0	1325
2008	0	1356
2009	0	1347
2010	972	1315
2011	958	963
2012	536	876
2013	959	903
2014	922	899
2015	0	953
2016	951	854
2017	971	948
2018	700	777
Total	6969	13,833

Table 2. Number of POPs identified in the 2020 analysis (including those identified using microsatellites; see Bravington et al. 2016) broken down by juvenile birth year (rows) and adult capture year (columns). Note: The exact number of POPs identified, and the total number of comparisons made, may vary between each year's analysis, as the entire updated data set is quality controlled and re-analysed.

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2016	2017	2018
2002	0	0	0	0	0	NA	NA	NA	NA	NA	NA	NA
2003	0	5	1	2	0	0	0	1	0	1	0	0
2004	0	2	0	0	3	0	0	0	0	0	0	0
2005	1	4	5	4	1	0	0	1	2	0	0	0
2006	NA	4	3	2	0	0	0	0	0	0	0	0
2007	NA	NA	3	4	1	3	2	0	2	0	1	0
2008	NA	NA	NA	NA	0	1	1	1	0	0	0	2
2009	NA	NA	NA	NA	0	1	1	1	0	0	0	0
2010	NA	NA	NA	NA	0	0	1	4	0	2	0	0
2011	NA	NA	NA	NA	0	0	1	2	1	2	0	0
2012	NA	NA	NA	NA	0	0	0	1	1	0	0	1
2013	NA	NA	NA	NA	0	0	0	0	0	1	1	3
2014	NA	NA	NA	NA	0	0	0	0	0	0	1	0
2015	NA	NA	NA	NA	0	0	0	0	0	1	0	0

Table 3. Number of HSPs identified in the 2020 analysis broken down by birth year of younger sibling (rows) and older sibling (columns). Note: The exact number of HSPs identified, and the total number of comparisons made, may vary between each year's analysis, as the entire updated data set is quality controlled and re-analysed.

	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
2003	2	4	2	1	0	0	1	0	0	2	0	2	1
2004		6	3	6	2	2	1	0	0	2	0	0	0
2005			5	3	3	3	0	5	1	1	0	2	0
2006				8	4	1	3	5	3	0	1	1	1
2007					3	3	2	2	2	2	2	1	2
2008						5	1	1	2	3	0	1	0
2009							1	2	1	0	0	0	0
2010								2	1	2	1	0	1
2011									3	2	1	0	3
2012										3	2	1	1
2013											2	4	1
2014												2	2
2015													4

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6. Specification of Standardised CPUE for the MP

Data to be used

The CPUE dataset to be used in the MP is based on the longline catch and effort data of Japanese, Australian (Real-Time Monitoring Program in the 1990s) and New Zealand (NZ) charter vessels at the shot-by shot resolution. Southern bluefin tuna (SBT) aged 4 years or older are used in the CPUE dataset. In the most recent year of the dataset, CPUE (number of SBT individuals per 1000 hooks) is calculated from Japanese data available at the time which are mainly from RTMP. From this dataset, a set of core vessels are selected which meet certain conditions. These conditions are: CCSBT statistical areas (Area) 4-9, Month 4-9, x (top rank of SBT catch in a year) = 52, and y (number of years in the top ranks) = 3.

The dataset each year is further adjusted by:

- Deleting records from operations south of 50^0S;
- Combining operations of Area 5 into Area 4 and that of Area 6 into Area 7; and
- Deleting operations with extremely high CPUE values (>120).

The shot-by-shot data are then aggregated into 5x5 degree cells by month before standardization. Aggregated data cells with little effort (<10,000 hooks) are deleted.

CPUE standardization

Unweighted CPUE

The aggregated CPUE dataset is standardized using the following Generalised Linear Model (GLM) [1] :

$$log(CPUE+const) = Intercept + Year + Month + Area + Lat5 + BET\_CPUE + YFT\_CPUE + (Month*Area) + (Year*Lat5) + (Year*Area) + Error \quad (1)$$

where

Area	is the CCSBT statistical area
Lat5	is the latitude in 5 degree
BET_CPUE	is the bigeye tuna CPUE
YFT_CPUE	is the yellowfin tuna CPUE
const	is the constant as 0.2 derived as 10% of the mean nominal CPUE in Nishida and Tsuji (1998)

Area weights

To obtain the area weighted CPUE indices described below, the area of SBT distribution was calculated based on a 1x1 degree square resolution. The area was calculated in the form of an area index such that an area size of 1x1 degree square along the equator was defined as 1, and the area size for other 1x1 degree squares of different latitudes was determined as the proportion of the square area along the

[1] Currently, there is no specification of the procedure to be followed for the GLMs here and below that have fixed interaction effects if in a future year one of the associated cells is empty of data.

equator. The area index for the Constant Square (CS)[2] was simply a union of fished 1x1 degree squares through all years (1969-present) and was calculated for each quarter, month, statistical area, and latitude (5 degree) combination. The area index for the Variable Square (VS) was the sum of fished 1x1 degree square areas and was calculated for each year, quarter, month, statistical area, and latitude combination. For VS, a square counts as fished only for the month in which fishing occurred. More details of the area index calculation are described in Nishida (1996).

Area weighted CPUE

With the estimated parameters obtained from the CPUE standardization above (1), the Constant Square (CS) and Variable Square (VS) CPUE abundance indices are computed by the following equations:

$$CS_{4+,y} = \sum_m \sum_a \sum_l (AI_{CS})_{(yy\text{-}present)} [\exp(Intercept + Year + Month + Area + Lat5 + BET\_CPUE + YFT\_CPUE + (Month*Area) + (Year*Lat5) + (Year*Area) + \sigma^2/2) - 0.2] \quad (2)$$

$$VS_{4+,y} = \sum_m \sum_a \sum_l (AI_{VS})_{ymal} [\exp(Intercept + Year + Month + Area + Lat5 + BET\_CPUE + YFT\_CPUE + (Month*Area) + (Year*Lat5) + (Year*Area) + \sigma^2/2) - 0.2] \quad (3)$$

where

$CS_{4+,y}$	is the CS abundance index for age 4+ and *y*-th year,
$VS_{4+,y}$	is the VS abundance index for age 4+ and *y*-th year,
$(AI_{CS})_{(yy\text{-}present)}$	is the area index of the CS model for the period *yy*-present (*yy*=1969 or 1986 depending on the period of standardization,
$(AI_{VS})_{ymal}$	is the area index of the VS model for *y*-th year, *m*-th month, *a*-th SBT statistical area, and *l*-th latitude,
σ	is the mean square error in the GLM analyses.

The w0.5 and w0.8 (B-ratio and geostat proxies) CPUE abundance indices are then calculated using the following equation (Anonymous 2001a):

$$I_{y,a} = wCS_{y,a} + (1-w)VS_{y,a} \qquad \text{where } w = 0.5 \text{ or } 0.8 \quad (4)$$

The final CPUE input series is the arithmetic average of the w0.5 and w0.8 series.

Data calibration

The estimated CPUE value in the most recent year, which is mainly derived from RTMP data, is corrected using the average of the "Logbook based CPUE / RTMP based CPUE" ratio for the most recent three years of logbook data.

The area weighted CPUE series between 1986 and the most recent year are then calibrated to the historical CPUE series between 1969 and 2008 using the following GLM (equation 5), described in Nishida and Tsuji (1998) for 5x5 degree cells by

[2] For explanation of Constant Square and Variable Square CPUE interpretations, see Anonymous (2001b).

month data for all vessels (i.e. both core and other vessels) in Areas 4-9 and Months 4-9:

$$log(CPUE+const) = Intercept + Year + Quarter + Month + Area + Lat5 + (Quarter*Area) + (Year*Quarter) + (Year*Area) + Error \quad (5)$$

where

const is 10% of the mean nominal CPUE.

CPUE series for monitoring

Two additional CPUE series will be used for monitoring purposes of the status of the stock and MP implementation. These include:

(1) Same procedure as specified above, but at the shot-by-shot level rather than the aggregated 5x5 level.
(2) Same procedure as specified above, but using the simpler GLM given by:

$$log(CPUE+0.2) = Intercept + Year + Month + Area + Lat5 + (Month*Area) + Error \quad (6)$$

Historical CPUE Series used as input to the Management Procedure

The CPUE series used in the MP is the average of the base CPUE series (w0.5 and w0.8) and is adjusted in the years 1989 -2005 for the case 1 LL over-catch. The overcatch correction is based on the same assumptions used in the base-case operating model used for MP testing, namely: (i) that 25% of the unreported catch was attributed to the LL1 reported effort and (ii) that the LL overcatch was distributed amongst LL1 subfleets, areas and months in proportion to the nominal catch, except for the Australian joint venture and New Zealand charter fleets (called Option A in Attachment 4 of OMMP 2009 meeting report). In 2009, the extent of LL1 overcatch corresponding to the Case 1 market estimates provided by Lou and Hidaka for 1985-2005 (with unreported catch in 2005 set equal to unreported catch in 2004) were re-estimated using a new equation for the lag from catch to market (documented in Attachment 4 of the OMMP2009 meeting report).

The resulting catch and CPUE multipliers are provided in Table 2. The CPUE multipliers are not exactly 0.25 because a small proportion of the CPUE catch (from the Australian joint venture and New Zealand charter fleets) is not affected by the overcatch. The historical CPUE series to be used as input of the MP is calculated using the following equation:

$$CPUE = (w0.5 + w0.8)/2 * (1+(Catch\_multiplier-1)*CPUE\_multiplier)$$

Table 2. Year, CPUE multipliers and Catch multipliers for the Case 1 LL CPUE adjustment.

	CPUE multiplier	Catch multiplier
Year	S=0.25-A	Case 1
1983	0.25	1
1984	0.25	1
1985	0.25	1
1986	0.25	1
1987	0.25	1
1988	0.25	1
1989	0.244	1.28
1990	0.249	1.8
1991	0.25	1.53
1992	0.275	1.24
1993	0.273	1.62
1994	0.266	2.66
1995	0.247	2.14
1996	0.25	2.2
1997	0.246	2.6
1998	0.247	1.82
1999	0.248	1.77
2000	0.247	2.13
2001	0.248	2.16
2002	0.249	2.13
2003	0.249	1.92
2004	0.248	1.75
2005	0.249	1.69
2006	0	1

Reference

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7. Metarules for the Cape Town Procedure

Preamble

Metarules can be thought of as a set of conventions for the implementation of the Management Procedure (MP). This includes "rules" which prespecify how to proceed in the event that exceptional circumstances arise when application of the total allowable catch (TAC) generated by the MP is considered to be highly risky or highly inappropriate. Metarules are not a mechanism for making small adjustments, or 'tinkering' with the TAC from the MP. It is difficult to provide very specific definitions of, and be sure of including all possible, exceptional circumstances. Instead, a process for determining whether exceptional circumstances exist and whether the implication(s) arising from them is sufficiently severe to warrant revising the TAC advice from the MP is described below. The need for invoking exceptional circumstances provisions should only be evaluated at the ESC based on information presented and reviewed at the ESC.

All examples given in this document are meant to be illustrative and are not meant as complete or exhaustive lists.

Process to determine whether exceptional circumstances exist

Every year the ESC will:

- Review stock and fishery indicators, and any other relevant data or information on the stock and fishery; and
- Consider and examine whether the inputs to the MP are affected
- Consider if the population dynamics are potentially substantially different from those for which the MP was tested (as defined by the 2019 Reference set of operating models, OMs)
- Consider if the fishery or fishing operations have changed substantially
- Consider if recent catches and other removals have been greater than the MP's recommended TACs

On the basis of this review, determine whether there is evidence for exceptional circumstances.

Examples of what might constitute an exceptional circumstance include, but are not limited to:

- A gene-tagging juvenile abundance estimate outside the range (95% probability intervals for projections)[3] for which the MP was tested (i.e. the 2019 reference set of OMs);
- A CPUE result outside the range for which the MP was tested;

[3] The "range" refers to 95% probability intervals for projections for the index in question made using the reference set ("grid") of the OMs during the testing of the MP (i.e. 2019 OMs).

- Substantial improvements in knowledge, or new knowledge, concerning the dynamics of the population which would have an appreciable effect on the operating models used to test the existing MP; and
- Missing input data for the MP[4], resulting in an inability to calculate a TAC from the MP (i.e. consistent with the manner in which it was tested).

Every three years (not coinciding with years when a new TAC is calculated from the MP) the ESC will:

- Conduct an in-depth stock assessment; and
- On the basis of the assessment, indicators and any other relevant information, determine whether there is evidence for exceptional circumstances (an example of exceptional circumstances would be if the stock assessment was substantially outside the range of simulated stock trajectories considered in MP evaluations, calculated under the reference set of operating models).

Every six years (not coinciding with years when a new TAC is calculated from the MP) the ESC will:

- Review the performance of the MP; and
- On the basis of the review determine whether the MP is on track to meet the rebuilding objective or a new MP is required.

If the ESC concludes that there is no or insufficient evidence for exceptional circumstances, the ESC will:

- Report to the Extended Commission that exceptional circumstances do not exist.

If the ESC has agreed that exceptional circumstances exist, the ESC will:

- Follow the "Process for Action".

Process for Action

Having determined that there is evidence of exceptional circumstances, the ESC will in the same year:

- Consider the severity of the exceptional circumstances (for example, how severely "out of bounds" is the CPUE) and, where possible, examine its potential impacts on the performance of the MP;
- Follow the Guidelines for Action if TAC change is considered necessary (see below);
- Formulate advice on the action required (for example, there may be occasions when the severity and impacts of the 'exceptional circumstances' are deemed to be low, so that the advice is not for an immediate change in TAC, but rather

[4] Missing years of gene-tagging data have zero weight in calculation of 5-year weighted average.

a trigger for a review of the MP or collection of ancillary data to be reviewed at the next ESC); and

- Report to the Extended Commission that exceptional circumstances exist and provide advice on the action to take.

Guidelines for Action

If there is a risk associated with TAC being too high, then consider TAC changes where:

a) The MP-derived TAC should be an upper bound;
b) Action should be at least an x% change to the TAC, depending on severity.

If there are risks associated with TAC being too low, then consider TAC changes where:

a) The MP-derived TAC could be a minimum;
b) Action should be at least an x% change to the TAC, depending on severity.

An urgent updated assessment and review of indicators will take place, with projections from that assessment providing the basis to select the value of the x% referred to above.

The Extended Commission will:

- Consider the advice from the ESC; and
- Decide on the action to take.

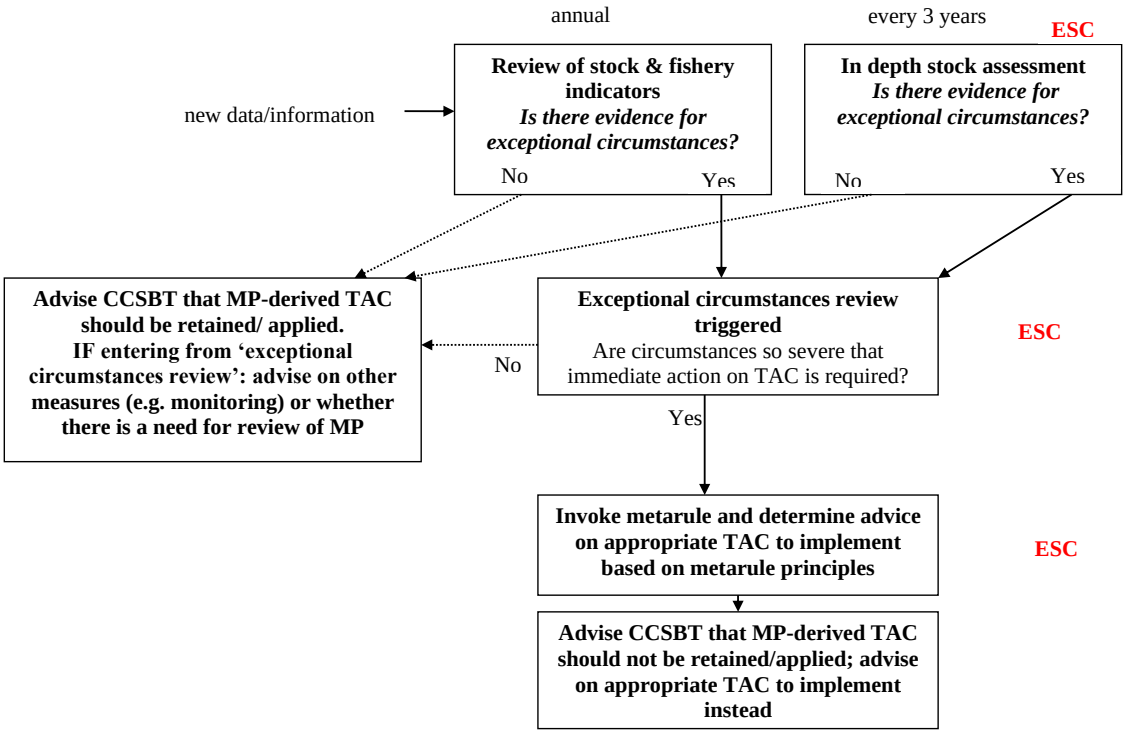
Examples of meta-rules implementation

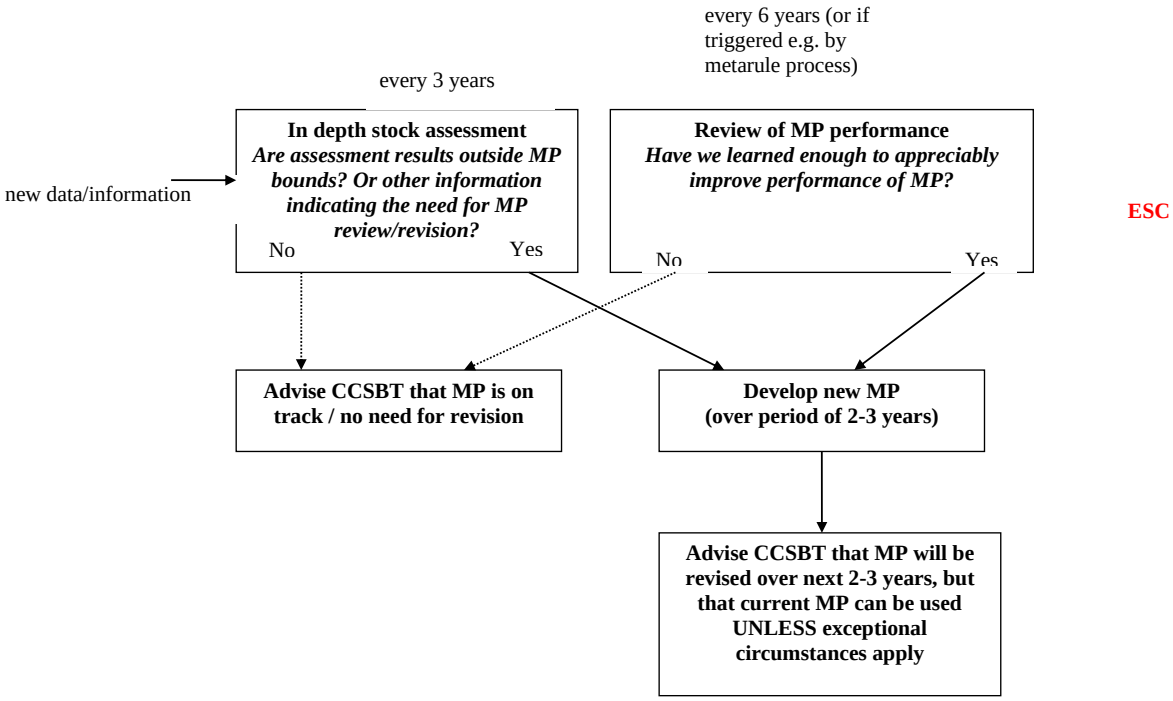
In 2012 a very low aerial survey data point in the timeseries was identified as on the border of the range of projections used for testing the Bali Procedure (NB this index is not used in the Cape Town Procedure). The ESC considered the data, analysis and additional information available on recruitment. Given that the Bali Procedure was shown to be robust to low recruitment scenarios, the ESC recommended to the Commission that there should be no action on TAC in that year, but that further analysis of environmental and fishery data should be considered at the next ESC.

In other years, exceptional circumstances (both negative and positive) have been identified but the ESC has not recommended action to alter the Bali Procedure derived TAC. Rather, the ESC has recommended gathering of additional information (e.g., implement gene tagging after suspension of the aerial survey) or alternative actions in the meta-rules process (e.g. development of a new MP), and the Commission has adopted these recommendations.

Meta-rules Flow Chart

Figure 1: Flowchart for Metarules process




every 6 years (or if triggered e.g. by metarule process)
every 3 years
In depth stock assessment
Are assessment results outside MP bounds? Or other information indicating the need for MP review/revision?
No
Yes
Review of MP performance
Have we learned enough to appreciably improve performance of MP?
No
Yes
new data/information
ESC
Advise CCSBT that MP is on track / no need for revision
Develop new MP (over period of 2-3 years)
Advise CCSBT that MP will be revised over next 2-3 years, but that current MP can be used UNLESS exceptional circumstances apply