List of the key focus questions for the panel regarding sardine, together with brief summaries of the documents provided

Following the development of a new stock structure hypothesis for South African sardine over the previous few years, a new model has been developed. Key questions relating to this model are:

i) The growth curve has been substantially modified over the past year to enable sardine which move from the West Coast to the South Coast to grow at the same rate as that of South Coast fish of the age corresponding to the length at the time of their movement to the South Coast. This requires the South Coast growth curve to be to the left of the West Coast growth curve, which is expected *a priori* (Sakamoto *et al*. 2020, van der Lingen *et al*. 2023). For this reason, the current 'base case' model estimates $L_{a=1}$, κ and t_0, but with the added constraint that L_∞ on the South Coast must be at least that of the West Coast. If $L_{a=1}$, L_∞ and t_0 are estimated then one must additionally constrain κ on the South Coast to be at least that of the West Coast. Is it acceptable to proceed with these additional constraints?

Note, in this context, that while S_0 estimates CTS west coast peak recruitment to correspond with peak spawning as indicated by GSI from fish sampled from commercial catches off the west coast, the peak recruitment estimated for the WTS off the south coast is later than that the peak spawning indicated by GSI from fish sampled from commercial catches off the south coast.

If the timing of WTS peak recruitment off the west coast is assumed to correspond with that of CTS off the west coast and not WTS off the south coast, the peak recruitment off the west and south coasts correspond more closely with peak spawning as indicated by GSI from fish sampled from commercial catches (e.g. S_{13}). The above constraint may, however, still be required in this case (S_{13*}).

ii) The current 'base case' model predicts substantially more biomass off the South Coast in 2020, in particular, than that estimated by the hydroacoustic survey. Substantial downweighting of the length frequency data in the likelihood indicates that there may be a conflict between fitting the model to the hydroacoustic survey data and the length frequency data. Alternatives such as dome shaped survey selectivity and less variability in the length-at-age have been considered, but have not helped in simultaneously fitting to the *average* survey length frequency data and the November survey estimate of South Coast biomass in 2020. What should be used for the 'base case' assessment model: i) the existing model with full weighting for the length frequency data; the model with the length frequency data substantially downweighted in some years; or iii) something else?

iii) The current 'base case' model estimates a non-negligible biomass of WTS off the west coast in many years in addition to that expected during the pulse of recruitment. Does this level of abundance contradict the meristic data?

iv) Is the proposal for extending the two-area, two-stock model to three-areas reasonable, and feasible given the available data on "mixing proportions"? Is the use of the probability of assignment of genetic data to stock as "mixing proportions" appropriate, together with the assumptions made to derive these proportions?

v) Does the panel have any recommendations with regards to generating future stock- and coast-specific recruitment in the MSE given the lack of clear stock recruitment relationships based on past estimates of spawner biomass and recruitment? Which of the following should serve as a base case, and which as robustness tests:

  a) A fit of the data for each stock/coast to a conventional parametric form, such as Beverton-Holt, Hockey-Stick or Ricker
  b) An empirical approach where future recruitment within each of a number of spawning biomass "bins" is drawn from historical estimates within those bins.
  c) Something else

vi) What is the panel's opinion about the new genomic analyses based on outliers identified using genome-environment association with all (strongly correlated) environmental variables available + Fst-based outliers, instead of the previous approach of using only consensus outliers between one environmental variable (temperature) and Fst-based outliers? Further, does the panel have suggestions about the following:

a) Calculation of migration rates based on outlier SNPs rather than neutral SNPs, given that the neutral dataset is not suitable to distinguish between stocks (CTS vs. WTS).

b) Alternatives to calculating effective population size (Ne) to convert migration rates into number of individuals. Ne can only be calculated using neutral data, but this will produce a single value (or, if calculated separately for each region, two values that are essentially based on two subsets of the same underlying neutral data). Would using census N be more meaningful in this case, given that separate values for CTS and WTS are available?

c) Is incorporating a selection coefficient into the fishery model necessary, given that only SNPs putatively under selection can be used to assess gene flow? Or does this complicate the model unnecessarily?

vii) Does the panel have suggestions for how to improve the planned work using whole-genome sequencing to address shortcomings of the present approach? This could relate to sampling and types of analyses, and incorporation of non-genetic evidence.

viii) Based on their experience in managing other fisheries, does the panel have suggestions for whether the management units of conservation should be stock-specific only or additionally coast-specific (over-and-above preserving each stock in its preferred habitat)? These management units of conservation will form the basis for risk statistics relating to MSE objectives associated with the target resource.

ix) Does the panel have any comments on suitable reference points for harvesting small pelagic fish in an MSE (OMP) context? The lowest historical SSB (of each management unit of conservation) has previously been used as a limit reference point for South African sardine and anchovy in former MSEs, but recent extremely low levels of sardine, particularly off the west coast, may be too low to re-use this ‘rule’. How should plots of historical spawner biomass and recruitment be interpreted in this context? In terms of an acceptable level of risk for the target resource, one possibility for these small pelagic fish is that the risk under a Management Procedure should be at most 5% higher than that under a no catch scenario; which is an adjustment to the ICES rule to allow for the natural variability of small pelagic fish. Should this be evaluated for the reference operating model only, or over some integration of a reference set of operating models? Should the focus here be on fishing mortality rather than spawner biomass? Furthermore, the panel is additionally asked for comment on suitable reference points in an ecosystem context. For example, a performance statistic may relate to a target reference point of 75% of B_0 based off the Marine Stewardship Council assessment criteria, with an acceptable range about this target reference point, and how might dynamic B_0 considerations be taken into account in this context.

The documents provided are listed below. *A brief description of each document is provided in red italics.*

Primary papers

MARAM/IWS/2024/Sardine/P1: List of key focus questions for the panel regarding sardine, together with brief summaries of the documents provided.

MARAM/IWS/2024/Sardine/P2: de Moor CL. 2024. The assessment model for the revised sardine stock structure hypothesis.

The equations, parameter values and prior distributions for the revised stock assessment model for South African sardine. Values/priors correspond to S_0 of MARAM/IWS/2024/Sardine/P3.

MARAM/IWS/2024/Sardine/P3: de Moor CL. 2024. Results from fitting the sardine stock assessment model to data for alternative assumptions.

Results from fitting the model in MARAM/IWS/2024/Sardine/P2 to the data (MARAM/IWS/2024/Sardine/BG6) are shown with alternative assumptions chosen to correspond to Q(i), Q(ii) and Q(iii) above.

MARAM/IWS/2024/Sardine/P4: de Moor CL. 2024. A proposal to extend the two-area sardine model to three areas.

Following the 2023 Panel's recommendation that the three-area, three-stock model was overly complex given the available data, this document outlines how the two-area, two-stock model (MARAM/IWS/2024/Sardine/P2) could be extended to three-areas using 'mixing matrices' that would be estimated using observed "mixing proportions" (taken from probability of assignment given in MARAM/IWS/2024/Sardine/P5). This proposal relates to Q(iv) above.

MARAM/IWS/2024/Sardine/P5: Teske P. 2024. An example of how mixing proportions can potentially be determined based on genomic data from Teske *et al*. (2021)

This document describes the derivation of probabilities of assignment to the two stocks CTS and WTS to each of three-areas, using the data from MARAM/IWS/2024/Sardine/BG3. These probabilities might be used as stock mixing proportions if a three-area model is used (MARAM/IWS/2024/Sardine/P4). These data relate to Q(iv) above and can be compared with the approach of MARAM/IWS/2024/Sardine/P7 for Q(vi) above.

MARAM/IWS/2024/Sardine/P6: de Moor CL. 2024. Sardine stock-recruitment relationships and management units of conservation.

Some stock recruitment relationships are explored for potential use in projections. Possible 'units of conservation' are also listed, against which risk will be considered during the next OMP. This document relates to Q(v) and partially to Q(viii) above.

MARAM/IWS/2024/Sardine/P7: Teske P. 2024. Reanalysis of genomic data based on 2023 Panel recommendations.

This document shows new analyses using all six environmental variables (instead of SST only) to identify outlier SNPs (as well as outliers identified using two Fst-based methods) in response to a recommendation by the 2023 Panel. These initial results suggest the Southwest area is dominated by WTS and would result in different "stock mixing proportions" to those derived in MARAM/IWS/2024/Sardine/P5. These analyses relate to Q(vi) above.

MARAM/IWS/2024/Sardine/P8: Teske P. 2024. Description of planned whole-genomic sequencing.

This document describes a project which will hopefully begin during 2025 to further understanding of the population structure of South African sardine. This document relates to Q(vii) above.

MARAM/IWS/2024/Sardine/P9: de Moor CL. 2024. Initial projections with the sardine population dynamics model and no future catch

This document shows some initial projections under two methods of generating future recruitment to relate to Q(v) above.

MARAM/IWS/2024/Sardine/P10: de Moor CL. 2024. Further results from testing the South African sardine stock assessment model.

Further results (following on from MARAM/IWS/2024/Sardine/P3) from fitting the model in MARAM/IWS/2024/Sardine/P2 to the data are shown with alternative assumptions chosen to correspond to Q(i) and Q(iii) above.

Background documents

MARAM/IWS/2024/Sardine/BG1: Coetzee JC and de Moor CL. 2024. A summary of the South African sardine fishery.

This is a summary document providing an overview of the sardine resource and fishery, and a brief description of the data available, together with past assessments and management of the fishery.

MARAM/IWS/2024/Sardine/BG2: de Moor CL and Teske P. 2024. Progress on recommendations from the 2023 review panel report.

This lists the recommendations from the 2023 international review panel, with responses to those recommendations.

MARAM/IWS/2024/Sardine/BG3: Teske PR, Emami-Khoyi A, Golla TR, Sandoval-Castillo J, Lamont T, Chiazzari B, McQuaid CD, Beheregaray LB, van der Lingen CD. 2021. The sardine run in southeastern Africa is a mass migration into an ecological trap.

This was presented as MARAM/IWS/2022/Sardine/P2 and MARAM/IWS/2023/Sardine/BG2. Genomic and transcriptomic data are used to identify two 'stocks': cool temperate (Atlantic Ocean) and warm temperate (Indian Ocean) sardine, with sardine participating in the Sardine Run off the east coast comprising primarily cool temperate sardine. This paper provided the primary foundation for the difference in stock structure described in MARAM/IWS/2024/Sardine/BG5 from the stock structure previously assumed. Note, in particular, Figure 3 with the majority of sardine found off the South coast having exclusively "warm temperate" ancestry, and very few individuals having some "admixed" ancestry (a mixture of cool and warm temperate ancestry). Given the high frequency of admixed sardine not only on the (south) west coast, but also in the Sardine Run (in which individuals from the "warm temperate" type that dominate the South coast do not participate), admixed sardine have been proposed by the SWG-PEL to behave as cool temperate sardine for modelling purposes – the preference being to model two population components rather than three.

MARAM/IWS/2024/Sardine/BG4: van der Lingen CD, de Moor CL and Coetzee JC. 2023. Available data for determining the occurrence and distribution of Cool Temperate and Warm Temperate Sardine components by life history stage.

This document was developed in direct response to the 2022 International Stock Assessment Review Panel's recommendation and compiles observed data on sardine from fisheries-dependent and fisheries-independent sources that may be useful in determining where the stocks are spatially during each month and by life stage, and for comparison with the behaviour of these components in the new Operating Model. Life stages / events considered are (i) eggs and larvae / spawning; (ii) pre-recruits; (iii) recruits and (iv) adults. Each stage is described separately. This was considered as MARAM/IWS/2023/Sardine/P2 at the 2023 workshop.

MARAM/IWS/2024/Sardine/BG5: de Moor CL, van der Lingen CD and Teske PR. 2023. A revised hypothesis for South African sardine stock structure.

The revised sardine stock structure hypothesis is conceptualised given, primarily, MARAM/IWS/2024/Sardine/BG4, including the genomic and transcriptomic research which has been the catalyst for a change in the stock structure hypothesis. The hypothesis consists of two primary components: (i) some fish of Atlantic Ocean origin (CTS) actively move eastward to take part in the Sardine Run on the East Coast; and (ii) some spawning products of Indian Ocean origin (WTS) are passively transported to the West Coast for a period of time before returning to the South Coast as adults. Those WTS which remain on the (South) West Coast as adults for a period of time before returning to the South Coast, are assumed to spawn there. It is assumed that spawning of CTS and WTS on the West Coast is not random, and that the components do not mix during spawning. This was considered as MARAM/IWS/2023/Sardine/P3 at the 2023 workshop.

MARAM/IWS/2024/Sardine/BG6: de Moor CL, Merkle D, Coetzee J and van der Lingen CD. 2024. The data used in the 2024 sardine assessment.

This document describes the data to which the sardine model is to be fit.

MARAM/IWS/2024/Sardine/BG7: Coetzee JC. 2024. The biomass-weighted proportion of South Coast-spawned sardine eggs that are simulated to be transported to the West Coast nursery area.

This document considers the proportion of eggs and larvae which arise from spawning on the South Coast and were estimated by two hydrodynamic particle-tracking individual based models to be transported to the West

Coast nursery area. The proportions moving (which differ by area) are weighted by the November survey biomass by stratum. A prior distribution of N(0.325,0.165^2*) is suggested from this work for the model estimated proportion of WTS recruits spawned off the South Coast which are passively transported to the West Coast (cf MARAM/IWS/2024/Sardine/P2).*