CCSBT-OMMP/1906/07
(OMMP Agenda item 2.2)

OCEANS AND ATMOSPHERE
www.csiro.au

Notes on the close-kin analysis for 2019

J Paige Eveson, Mark Bravington

Report to the Commission for the Conservation of Southern Bluefin Tuna Operating Model and Management Procedure technical working group, Seattle, June 2019.

Notes on the close-kin analysis for 2019

DNA extracts from the 2016/17 muscle tissue samples from adults sampled on the spawning grounds and juveniles sampled in Port Lincoln were processed by DArT and the genotype data sent to CSIRO in early 2019. These data were used to update the close-kin analysis and provide updated numbers of parent-offspring pairs (POPs) and half-sibling pairs (HSPs) for the CCSBT 2019 data exchange. The total number of POPs to date is 82, and the total number of HSPs for which we have high confidence is 167, with a false negative rate estimated at 0.16 (i.e., by being cautious in our determination of HSPs, we expect to have underestimated the true number by 16%). More detailed results will be provided to the ESC.

Although the total number of POPs is substantial, we note that there are rather few corresponding to recent juvenile cohorts (only 5 where the juvenile was born in 2012-2014). Thus there is not much direct information about adult stock size in those recent years. As the adult stock continues to rebuild, there will be even fewer "POPs per cohort per comparison" in future. Consequently, it may be necessary to increase annual sample sizes somewhat, in order to maintain robust and up-to-date information on adult stock size. The MP-testing process is a way to explore what sample sizes might be appropriate in future.

Some improvements were made this year to the procedures used for genotype calling and kin-finding. None of these changes affect interpretation of the results, or how the data gets used in the operating model or in a management procedure. However, for completeness, we summarize the changes below.

Genotype calling: We noted last year in CCSBT-ESC/1809/08 that "the DArTcap data added to the analysis this year was not entirely consistent with the previous data (e.g., the sequence counts for some loci were significantly higher or lower on average than before). […] As a consequence, some modification to the genotype-calling process was required (which is being investigated further)." The DArTcap data for 2016/17 had the same issue. After further investigation, we concluded that the differences in loci performance were largely at a plate level (each plate of 96 samples sent to DArT gets processed in the exact same manner). As such, we applied a plate-level standardization to the sequence count data from all years before calling the genotypes. This ensured that, for a given loci, the average count across all samples on a plate was the same for every plate, which greatly improved the consistency and accuracy of the genotype calls.

HSP-finding: Based on detailed intersessional investigation of our half-sibling data, we made substantial improvements to our kin-finding processes, to ensure that false-positive kin pairs do not become a problem. This was necessary because with larger total sample sizes, there is greater potential for overlap between true HSPs and unrelated (or weakly-related) pairs. This required significant research effort, but with continued work to optimize the information we get out of the data, we do not anticipate any need to change the underlying DartCap genotyping method in the foreseeable future.