



Notes on the close-kin analysis for 2020

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DNA extracts from the 2017/18 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. 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 2020 data exchange, using the same methods for genotype calling and kin-finding as last year. The total number of POPs to date is 89, and the total number of HSPs for which we have high confidence is 161, with a false negative rate estimated at 0.26 (i.e., by being cautious in our determination of HSPs, we expect to have underestimated the true number by 26%). More detailed results will be provided to the ESC.

As noted to the OMMP technical working group and ESC in past, as total sample sizes increase, there is greater potential for overlap between true HSPs and unrelated (or weakly-related) pairs. Thus, in order to keep the risk of false positives very low, we needed to increase the lower cut off on the “PLOD” statistic used for determining HSPs. This has resulted in fewer HSPs, and a higher false negative rate, than last year. In future, we aim to make use of a genome assembly for SBT to improve the separation and “reclaim” some of the HSPs currently being excluded; however, in the meantime, the number of HSPs is sufficiently large to provide reliable information for the MP.