X. 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) $CV = \text{sqrt}(N/(T*S)) = \text{sqrt}(1/R)$

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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