



The 2018 SBT gene- tagging program

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Contents

Acknowledgements.....	ii
1 Executive Summary.....	1
2 Introduction.....	1
3 Method.....	2
4 Results and discussion.....	2
5 Summary.....	3
References.....	4

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1 Executive Summary

The third full cycle of the CCSBT gene-tagging program has been completed to provide an estimate of absolute abundance of the age 2-cohort in 2018. The technique and protocols were described and fine-tuned in the design study in 2015, initial pilot study in 2016, and the tagging program in 2017.

The tagging component of the 2018 gene-tagging project was completed in March 2018, the collection of tissue samples during harvest was completed in August 2019, and DNA extraction and sequencing and estimation of abundance was completed in April 2020.

The analysis has identified 66 matches (recaptures) from 75.4 million comparisons. The estimate of abundance of age 2 fish in 2018 is 1,142,638 with coefficient of variation (CV) of 0.123. The data from each year of the gene-tagging program will be used in the stock assessment in 2020 and in the new Cape Town Management Procedure (Hillary et al., 2019).

2 Introduction

This report provides a brief summary of the 2018 gene-tagging program and the data provided to the CCSBT Scientific Data exchange in 2020. A more detailed milestone report containing preliminary results was provided to the CCSBT in January 2020 and distributed to the members.

This is the third full cycle of the CCSBT gene-tagging program, which provides an estimate of absolute abundance of the age 2-cohort in 2018. The technique and protocols were described and fine-tuned in the design study in 2015, initial pilot study in 2016 and tagging program in 2017 (Preece et al., 2015; 2019).

The tagging component of the 2018 gene-tagging project was completed in March 2018 (Preece and Bradford, 2018), the collection of tissue samples during harvest was completed in August 2019, and DNA extraction and sequencing and estimation of abundance was completed in April 2020.

The data from the gene-tagging program will be used in the stock assessment in 2020 and in the new Cape Town Management Procedure (Hillary et al., 2019).

3 Method

Gene-tagging SBT involves “tagging” fish by taking a very small tissue sample from a large number of 2-year-old SBT, releasing the fish alive, allowing 12 months for mixing with untagged SBT, and then taking tissue samples from the catch of 3-year-old fish at time of harvest. The two sets of tissue samples are genotyped and then compared in order to find the samples with matching DNA; 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 design study examined sample sizes, potential biases, costs and precision of estimates and integration of data in stock assessment and management procedure models (Preece et al., 2015).

The 2018 gene-tagging program followed the specifications for the pilot study as recommended in the design study. The design study recommended tagging and releasing 5000 fish and harvest sampling 10,000 fish.

The project involved the following steps:

1. Tag and release: Vessel charter and at-sea collection of tissue samples from age 2 fish in the Great Australian Bight during the summer of year 1 (2018). Nearly 8,200 fish were tagged (Preece and Bradford 2018).
2. Harvest sampling: Over 11,500 tissue samples were collected from age 3 fish in winter of year 2 (2019), during harvest of fish from farms that were caught by the Australian surface fishery.
3. DNA extraction and genotyping of tissue samples, using CSIRO-developed SNP markers. A small percentage of samples had poor quality or quantity of DNA and therefore were not successfully sequenced, although the success rate was very high (>96%).
4. Data analysis and calculation of an abundance estimate, and provision of results to the CCSBT scientific data exchange for use in stock assessment models in 2020 and the new management procedure. The genotype data were analysed to determine whether the same fish was in the tagged set and the harvest set (using the unique DNA fingerprint). This involved filtering the data to exclude fish with incomplete or poor genotype information (too few SNP markers with good sequencing results). Any fish outside the target release and harvest length ranges were also excluded. The length classes for age 2 and age 3 fish were reviewed in 2019, using information from otoliths and vertebrae direct ageing (Clear et al., 2019, Gunn et al., 2008).

4 Results and discussion

A fish was determined to have been recaptured if there was a fish with a matching set of markers in both the releases and harvest sample sets. The examination of 2018 releases against 2019

harvest samples is approximately 75.4 million comparisons. The analysis has identified 66 matches (recaptures). The estimate of abundance of age 2 fish in 2018 is 1,142,638 with coefficient of variation (CV) of 0.123

This abundance estimate is very similar to the 2017 estimate and is close to half of the estimate of age 2 fish in 2016 (Table 1) but is not as low as estimates for the age 2 cohorts from the years of very low recruitment in the stock assessment models (1999-2002) (Hillary et al, 2019).

The gene-tagging results from the 3 years which have been completed are presented in Table 1.

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.

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

The gene-tagging data used in the stock assessment models are the year of tag and release, age of fish at time of release, year of harvest sampling, the number of releases, number of harvest samples, and the number of matches. The gene-tagging data used in the Cape Town Procedure are year that estimate applies to, abundance estimate and number of matches.


5 Summary

The third implementation of the CCSBT gene-tagging program has successfully tagged over 8,000 fish and collected samples from over 11,500 fish during the harvest. DNA has been extracted from all suitable tissue samples. Quality control filtering of the sequencing data ensures only samples with good DNA (sequencing results of sufficient quality) are included in the analysis, and only fish in the specified length classes are included in the abundance estimation.

The 2018 program detected 66 matches in the tagging and harvest data sets and the abundance estimate is 1.14 million fish (C.V. 0.123). The completed data sets and final estimate was provided to the CCSBT scientific data exchange in May 2020. The 2016-2018 abundance estimates will be used in the 2020 stock assessment and in the new Cape Town Management Procedures for recommending the total global allowable catch for 2021-2023.

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