

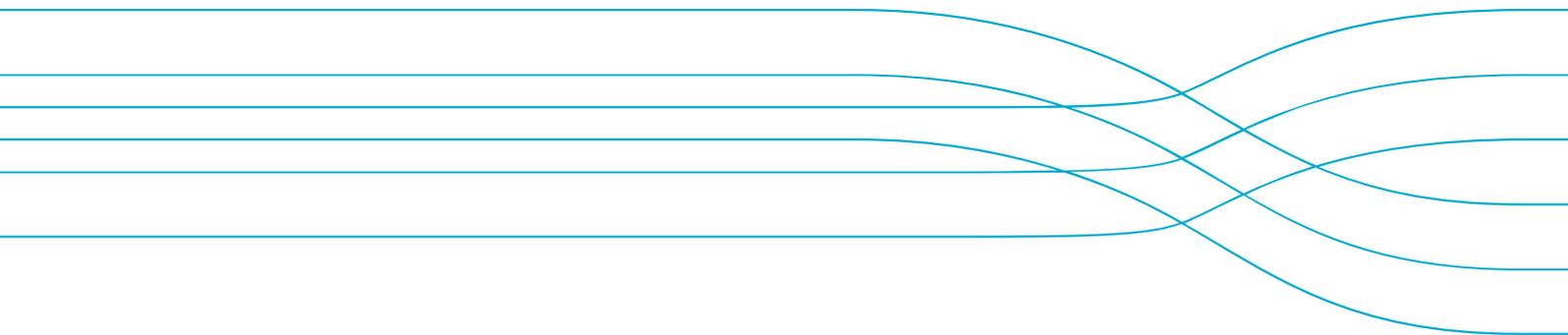


Gene-tagging 2017 work plan and research mortality allowance request

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CCSBT-ESC/1609/10

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Abstract

Gene-tagging has been proposed as an ongoing part of the CCSBT Scientific Research Program (Preece et al, 2015, 2014; Anon 2015, 2014). Annual tagging is proposed, to provide a time series of estimates of absolute abundance of juvenile SBT for use in the SBT operating model and future management procedures. A pilot gene-tagging project commenced in 2016 and will be completed in early 2018. A progress report on the pilot study, and the next steps in that study, is provided in CCSBT-ESC/1609/7 (Bradford et al, 2016).

The 2017 gene-tagging activities will involve tagging 5000 fish in February-March 2017 and collecting catch samples in 2018 during harvest. Tagging involves taking a small tissue sample from wild fish captured using pole and line fishing methods and releasing the fish alive.

The request for research mortality allowance (RMA) is for 3t to cover incidental mortalities during tagging in 2017. This is based on the RMA requests in 2016 for the pilot study (4t requested, <1t used) and RMA requests in the early 2000's for the CCSBT conventional tagging program conducted by CSIRO. A similar amount will be requested for the following years if the CCSBT continues ongoing monitoring of juvenile SBT via a gene-tagging program.

1 Introduction

Gene-tagging has been included as an ongoing part of the CCSBT Scientific Research Program (Preece et al, 2015, 2014; Anon 2015, 2014). Annual tagging is proposed to provide a time series of estimates of absolute abundance of juvenile SBT for use in the SBT operating models and future management procedures. A pilot gene-tagging project commenced in 2016 and will be completed in early 2018. A progress report and the next steps in that project are provided in CCSBT-ESC/1609/7 (Bradford et al, 2016).

Gene-tagging operates in a similar way to conventional tagging programs, however DNA profiles from genotyping tissue samples is used to match a tagged fish with itself upon recapture rather than a physical tag. This resolves the issue of non-reporting of tags, which led to the cessation of the CCSBT Scientific Research Tagging Program in 2007. A design study was completed in 2015 (Preece et al 2015). Fish are tagged by taking a small tissue sample from wild fish that are released alive. Catch sampling occurs at harvest after approximately 1 year at liberty to allow for mixing of the tagged and untagged fish.

This document outlines the work plan for 2017 and includes the research mortality allowance (RMA) request to cover any incidental mortalities associated with tagging fish.

2 Long-term monitoring of juvenile abundance via an annual gene-tagging program

For on-going monitoring of abundance of juvenile SBT, the gene-tagging work program involves: 1) tagging and release of age 2 wild caught fish in Feb-March each year, and 2) catch sampling of age 3 fish in the following year, at time of harvest from the Australian surface fishery. The required sample sizes estimated from the design study are 5000 age 2 fish (tagged at sea) and 10,000 age 3 fish (tissue sample taken at harvest to identify recaptures). These sample sizes were based on the 2014 stock assessment estimates of the numbers of age 2 fish in recent cohorts. The cost of tagging fish is more expensive relative to catch sampling, because of the costs of vessel and crew charter. If more samples can be collected during tagging, then fewer fish need to be sampled at the time of harvest. In both cases, more samples will be collected and processed, if possible and funds allow, to meet and/or improve the precision of the estimates.

Tagging involves taking a small tissue sample, using a purpose designed tool developed by CSIRO to quickly collect high-quality tissue samples that are uncontaminated (Bradford et al., 2015). A target size class is defined to maximise the possibility that fish are likely to be age 2. Otoliths and other biological samples are collected from any incidental mortalities that occur during tagging operations. The length, date, latitude, longitude, tagger and sample number are recorded. Tissue samples are stored in labelled tubes, and the DNA is extracted in the laboratory (DNA digestion). A robot is used to extract a prescribed quantity of DNA sample for genotyping. Databases will store

and link all the collected data. Quality control methods have been developed for all stages of the tissue handling, data collection and pre-analysis processes.

Protocols for tagging and fish handling have been developed and are based on the work in 2001 for the CCSBT 2001-2006 conventional tagging program (CSIRO 2015). Fish that are not in excellent condition are not tagged. Mortalities occurred in the 2016 pilot program, but the total number was small (47 fish, estimated to be less than 1t in total weight). Fish handling time for gene-tagging is shorter than for conventional tagging or archival tagging and less invasive – gene-tagged fish are returned to the water very quickly.

The catch sampling will be done in the commercial processing plants at the time of harvest for the surface fishery, therefore no RMA is required for this part of the project. The catch sampling year for the 2017 tagged fish will be 2018.

Member scientist who are interested in assisting with the at sea tagging work are welcome to contact us to discuss the requirements. The potential for additional participation will largely be determined by available space aboard the chartered vessel and resourcing requirements.

3 RMA request for 2017

Project: Estimating absolute abundance of juvenile SBT from gene-tagging 2017

Principal Investigator: Ann Preece, CSIRO. **RMA timeframe:** Dec 2016- Dec 2017

Research Mortality Allowance Request for 2017 (tonnes)

The request is for 3t of RMA for 2017. This is based on the RMA requests in the early 2000's for the CCSBT conventional tagging program conducted by CSIRO. Four tonnes was requested for the pilot study, and less than 1 t was used. A similar amount would be requested for the following years if the CCSBT continues ongoing monitoring of juvenile SBT via a gene-tagging program. Note, that this RMA request is to cover any incidental mortality associated with taking a tissue sample from wild fish and releasing them alive.

Project aims and benefits

Annual tagging to provide estimates of absolute abundance of juvenile SBT for use in the SBT operating model and future management procedures is proposed. The CCSBT is currently planning to conduct gene-tagging in 2017 & 2018.

The gene-tagging design study (Preece et al, 2015) recommended that approximately 5000 fish be tagged, by taking a small tissue sample and releasing the fish alive at sea. If more fish are encountered in the right size class, additional samples will be collected, up to 10,000 fish. Recapture tissue samples will be taken from fish at time of harvest in 2018.

Previous Related Projects

RMA was requested for the 2016 pilot gene-tagging project funded by the CCSBT and CSIRO. This work is similar to conventional tagging projects in the Great Australian Bight, which were last undertaken 2001-2006.

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