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SRP Proposal:

Estimating absolute abundance of juvenile SBT from gene-tagging: A pilot study

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Abstract

The 2013 Extended Scientific Committee (ESC) requested costed CCSBT Scientific Research Program (SRP) proposals for consideration at the 2014 ESC. A genetic mark recapture (gene-tagging) program to provide fishery independent abundance estimates of juveniles was classified as high priority. The pilot gene-tagging project proposed here would test the logistics and demonstrate the feasibility of gene-tagging to provide a fishery independent absolute abundance estimate, and demonstrate the integration of the data into the SBT operating model and potential for use as an input data series for a future management procedure. It is anticipated that gene-tagging could reduce the costs of monitoring juvenile recruitment in the fishery in comparison to the current scientific aerial survey. In the spirit of the SRP, this is a draft proposal for a collaborative project among members, for further development at the ESC. There are opportunities for contributions and capacity building in design, field, laboratory and analysis. In inter-sessional discussions, member scientists have indicated an interest in further collaboration on the project.

1 Introduction

The Extended Scientific Committee (ESC) in 2013 further discussed the CCSBT Scientific Research Program (SRP) for 2014-2018, and requested costed proposals for consideration at the 2014 ESC, to enable recommendations to be made to the Commission for future activities. A genetic mark recapture (gene-tagging) program to provide fishery independent abundance estimates of juveniles was classified as high priority. The pilot gene-tagging project proposed here would test the logistics and demonstrate the feasibility of gene-tagging to provide a fishery independent absolute abundance estimate, and demonstrate the integration of the data into the SBT operating model and potential for use as an input data series for a future management procedure. In addition, a pilot-study would provide a sound basis for establishing the costs of implementing a monitoring program using gene-tagging as a potential alternative to the current scientific aerial survey. It is anticipated that gene-tagging could reduce the costs of monitoring juvenile recruitment in the fishery in comparison to the current scientific aerial survey, and provide more precise information on recent recruitments (i.e. an absolute abundance estimate of year class strength compared with the aerial survey's relative abundance estimate over 3 age classes).

The objectives of the pilot gene-tagging study are:

Stage 1: A design study to refine the experimental design and, using simulated data, demonstrate methods for integration of the data into the SBT operating models as recommended in the ESC work plan for 2014, but was deferred until 2015 by the Commission

Stage 2: Field pilot study - tagging (wild capture, tissue sampling and release), recapture tissue sampling (landed fish), and genetic testing of tissue samples to identify genetic matches of individuals

Stage 3: Calculate abundance estimate, document incorporation of the abundance estimate into the stock assessment operating models, describe methods for potential inclusion in a future SBT management procedure and revised costing for alternative implementations of long term monitoring of recruitment.

In the spirit of the SRP, this is a proposal for a collaborative project among members. There are opportunities for contributions and capacity building in design, field, laboratory and analysis. In inter-sessional discussions on this project Dr Sung-Il Lee (Korea) and other members indicated their interest in collaborating further on this project proposal at the ESC.

A follow up project, not included in this proposal, would be to investigate whether the fish in the Great Australian Bight (GAB) are a sub-population of the larger SBT stock. Basson et al (2012) concluded that "*… the majority of juvenile SBT are likely to return to the GAB each summer, and that based on current evidence it is unlikely that a large proportion of juvenile SBT remain off South Africa over summer*". A follow up project could provide further evidence for this and would involve recapture (tissue) sampling the tagged cohort 2-3 years later – e.g. as 5 yr olds in the longline fisheries, to examine whether the absolute

abundance estimate is the same (indicating the original estimate is good and the GAB population is representative of the whole). If the abundance estimate was smaller, this would indicate that the tagged fish from the GAB are a sub-population of fish. Otolith micro-chemistry also has the potential to address this question (Clear et al 2014, CCSBT-ESC14/09/22).

2 Methods

Stage1: The design study would build on the cost, feasibility and precision estimates completed by Preece et al (2013), in which a broad suit of possible designs were canvassed, to define the target age class and timing and location of tagging, the sample sizes to tag and recapture for the required precision of the abundance estimates, the days at sea, equipment and personnel required. A simulated data set would be used to demonstrate the methods for incorporating the abundance estimate in the SBT operating model. A gene-tagging design study was included in the 2014 CCSBT ESC work plan but the CCSBT finance committee recommended that funding be deferred to 2015.

Stage2: The pilot gene-tagging program involves tagging fish by taking a small tissue sample from a wild caught fish at sea, and then releasing the fish. Current estimates are that around 5000 2-year-old fish should be tagged in the GAB requiring approximately 20 days of vessel charter. Tagging through taking a tissue sample is an "invisible" method of tagging; testing on SBT has shown that fish have completely healed within months (Bradford et al, in review). A sampling tool has been developed to maximise quality assurance and tracking of samples, and minimise handling (Bradford et al, in review). SBT are robust to capture and release from scientific tagging studies, and the tissue sampling is far less invasive than other tagging such as archival tags inserted into the body cavity. Tagged fish are left to mix with the untagged population over the following 12 months. Conventional and archival tagging studies (Polacheck et al, 2006; Basson et al, 2012) indicate there is a reasonably consistent and high level of mixing of juveniles throughout their range.

Recapture sampling occurs on landed fish. Processes have already been developed for tissue sampling as part of the SBT close-kin program (Bravington et al 2014). The approximate recapture sample size is 7,000 age 3 fish, which are available in large numbers in the Australian surface fishery. Samples may be taken at harvest time from the South Australian fish farms 12-18 months after tagging.

The tissue samples from tagging and recapture will be archived and processed. DNA extractions will use robotic protocols developed specifically for high throughput sample processing. Genetic analysis will be performed using a combination of existing microsatellite markers (Bravington et al 2014) and/or analysis of single nucleotide polymorphisms (SNPs, Grewe et. al, unpublished data) to determine the most efficient and cost-effective approach for accurate and repeatable DNA profiling.

Stage 3: The Petersen method will be used for estimating the absolute abundance of the age 2 fish in the year of tagging. The abundance estimate for a single year from the pilot study can be integrated directly into the current SBT operating models used for stock assessments and management strategy evaluation. The method would be similar to integration of other abundance estimates into the models, such as close-kin Parent-Offspring-Pair data (Hillary et al 2012). Documentation of the method and demonstration of the integration will be outputs from the project.

The incorporation of the gene-tagging data would provide the basis to evaluate and discuss the potential benefits and costs of including a time series of abundance estimates from this method in future stock assessments and/or management procedures, and the potential to replace the aerial survey data as the index of recruitment used in the MP. This would include evaluating whether a less frequent than annual index could be used, potentially reducing costs further if, for example, tagging only needed to occur every second or third year to provide a similar level of performance from a future MP. Completion of the pilot study in 2015 and 2016 would mean the results would be available for consideration by the ESC and Commission in time for the review of the MP scheduled for 2017.

3 Collaboration

Collaboration and member contributions are welcome in this project. In particular we welcome member assistance in the initial tagging work at sea in January/February, as well as the design and analysis phases. Twenty days at sea and 2 taggers are planned into this proposal. The 20 sea days could be broken up into several trips which would allow for other members to participate as taggers. CSIRO is willing to co-invest in this project.

4 Approximate Costs

STAGE	COMPONENTS	TIMING (BASED ON CCSBT CALENDAR YEAR FUNDING)	COSTS
Stage 1	Design study and demonstration of use of simulated data in OM, and discussion of use in potential future management procedures	Year 1	~$75,000
Stage 2	Pilot tagging (capture - tissue sample - release 5000 age 2 fish, 20 days at sea vessel charter, 2 taggers costs, set-up and equipment costs)	Year 2 (~January/February – 2 or more trips to share tagging work amongst participating members)	~$350,000
Stage 2	Recapture (tissue sampling landed fished age 3), set up genetic technologies, genetic analysis of tag and recapture tissue samples	Year 3 (~June-Sept)	~$400,000
Stage 3	Abundance estimation, integration of data into SBT OM, revise costs of potential future monitoring programs, project write up and finalization	Year 3 (Oct-Dec)	~$25,000
Total			**= ~$850,000**

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