CCSBT-ESC/1409/BGD02
(previously CCSBT-ESC/1309/18)

MARINE AND ATMOSPHERIC RESEARCH/WEALTH FROM OCEANS
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Preliminary cost and precision estimates of sampling designs for gene-tagging for SBT

Ann Preece, Campbell Davies, Mark Bravington, Rich Hillary, Paige Eveson and Pete Grewe

CCSBT-ESC/1309/18

Prepared for the CCSBT Extended Scientific Committee for the 18th Meeting of the Scientific Committee 2-7 September 2013, Canberra, Australia

Acknowledgement

This work was funded by CSIRO and AFMA. Russ Bradford, Clive Stanley and Marinelle Basson provided background information used in this report.

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Abstract

The cost of DNA profiling for use in abundance estimation methods, such as close-kin approaches and genetic mark-recapture (e.g. gene-tagging), has been declining rapidly as new techniques and genetic markers are developed. This means that these methods are now feasible for regular monitoring and assessment of some commercially harvested stocks. In the case of SBT, the gene-tagging approach provides the potential to monitor the abundance and mortality of different components of the stock: juveniles and sub-adults. The advantages of the gene-tagging approach is that it provides quasi-fishery independent estimates for potential use in stock assessments, operating models and management procedures, that is not affected by the reporting rate problems that lead to the cessation of the CCSBT conventional tagging program in 2006. The successful completion of the close-kin abundance estimation project has demonstrated that it is practically feasible to process, manage and analyse the large samples and data sets associated with genetics-based approaches with a high standard of quality control. Preliminary cost estimates for obtaining abundance estimates with a specified level of precision (coefficient of variation) using different gene-tagging study designs indicate that it is now logistically feasible and likely to be cost-effective to implement for SBT. A summary of these preliminary analyses is provided for the CCSBT ESC to discuss potential collaborative research opportunities and explore the potential future use of gene tagging for monitoring different components of the SBT stock.

1 Introduction

The cost of DNA profiling for use in abundance estimation methods, such as close-kin (Bravington et al 2013a) and genetic mark-recapture methods (Davies et al 2008, Buckworth et al 2012, Dichmont et al 2012), has been declining rapidly as new techniques and genetic markers are developed. These cost reductions and technology developments mean that these methods are now cost-effective and feasible for regular monitoring and assessment of some commercially harvested stocks (Bravington et al 2012, Steele et al 2013).

In the case of SBT, gene-tagging and close-kin abundance estimation methods provide the potential to monitor the abundance and mortality of different components of the stock. The advantages of these methods are that they can provide data for use in stock assessments, operating models and management procedures that are quasi-fishery independent (for most potential outputs), and will not suffer from the reporting rate issues that lead to the cessation of the CCSBT conventional tagging program in 2006 (Anon. 2007, Davies et al 2007, Harley et al 2008; Davies et al 2008).

The Advisory Panel noted in 2000 (Att K, Anon. 2000) when considering the first CCSBT Scientific Research Program (SRP): "*Simulation studies have shown that the ability of depletion-type methods to correctly estimate abundance trends is particularly limited during population recovery (since catch is not a major factor explaining the increase). In other words, declining populations are estimated somewhat more accurately than increasing ones, particularly if there are questionable abundance indices and no absolute abundance estimates. Therefore, the panel feels that a tagging program similar in scope to that executed in the mid 1990s can provide important additional information on natural and fishing mortality rates to improve the ability to estimate changes in stock size. Such age-specific information on tag-recapture rates can be important since it is relatively independent from other abundance indices*."

Despite shared DNA profiling technology, gene-tagging and close-kin abundance estimation methods are quite different and need to be considered separately. The relevant links are: (i) the “technology infrastructure” (genetic markers and techniques), and; (ii) the fact that gene-tagging programs could provide the tissue samples from juveniles for use in a close-kin estimate of spawning biomass for no additional cost. This paper focuses on the potential for gene-tagging programs to provide estimates of absolute abundance and mortality of juvenile and sub-adult SBT. The potential benefits of a monitoring program that combines gene-tagging of juveniles and/or sub-adults and close-kin abundance estimation of spawners is something the ESC may wish to consider in future, but is not specifically addressed here.

In the gene-tagging approach, a fish is “tagged” by taking a tissue sample and subsequently “recaptured” by matching the tagged fish with itself via DNA profiling. Unambiguous matching of a fish with itself requires far fewer loci than matching parent-offspring pairs. Unit cost per sample for gene-tagging is, therefore, likely to be somewhat lower than for close-kin, though the required total sample sizes for gene-tagging need to be larger. Preliminary cost and feasibility estimates for a gene-tagging program for SBT have been done for a variety of sampling designs that the CCSBT ESC might want to consider. An absolute abundance estimate for a cohort is the minimum information that would be provided from such a project.

Extensions to this basic design potentially include multi-cohort, multi-year “releases”, similar to those used in the previous SRP conventional tagging program (Polacheck and Eveson 2007). This would deliver estimates of fishing and natural mortality, in addition to absolute abundance, for each cohort tagged. Either

of these designs could potentially be extended further by using a subset of the juvenile samples as inputs to a close-kin abundance estimate of the spawning component of the population.

Gene-tagging programs also have the potential to contribute to catch characterization, future management procedures and, if undertaken on a juvenile component of the SBT stock, could potentially provide a contingency for the scientific aerial survey, should that program fail to provide a relative abundance estimate for logistical reasons. Gene-tagging of older age classes (i.e. 4-10) could also be considered for its potential to provide a fishery-independent monitoring series as an alternative to CPUE in future models.

A range of simple examples and cost information are provided in this paper with the objectives of:

1. Supporting discussion in the ESC of potential use of the gene-tagging approach for monitoring various components of the SBT stock;
2. Scoping of potential collaborative efforts to further investigate potential design, logistic, capacity requirements and cost-benefits of the gene-tagging approach for SBT.

2 Differences between close-kin and gene-tagging programs

Gene-tagging and close-kin differ in the methods used for calculation of abundance estimates, the type of parameters that can be estimated and how genetic samples "tag" a fish. These differences are summarised briefly below for the purpose of clarifying the distinction between the two approaches.

Close-kin abundance estimation for SBT:

- Uses parent-offspring-pairs identified using genetic paternity testing to estimate absolute abundance of spawning stock
- Provides information on total mortality for the spawning stock and effective reproductive potential, in addition to the estimate of abundance of the spawning population.
- Samples adults (after capture) from the Indonesian fishery and juveniles (after capture) from the Australian surface fishery.

The initial close-kin project has produced quite a precise (15-20% CV) adult abundance estimate using a stand-alone assessment model (Bravington et al., 2013a), and the ESC is in the process of incorporating the data into the OM (Hillary et al 2012, 2013; Anon. 2013). Now that the necessary genetics processing, data management, quality control and analysis tools and a large SBT sample bank exists (including four years of samples not included in the completed project), the close-kin program could be continued (with lower annual sample sizes, and thus lower annual cost) to provide a fishery-independent time series of spawning stock abundance (Bravington et al., 2013b).

Gene-tagging methods:

- Use "tagging" and release of individuals, a subset of which are subsequently "recaptured" by identifying matches via DNA profiling.
- Provide estimates of absolute abundance by age and cohort and/or estimates of mortality (fishing, natural) depending on study design, via standard, well established, mark-recapture methods.

- Samples of tissue are taken from a fish and it's then released; this "tags" the fish. Recaptures are made by sampling a subset of the catch and matching DNA profiles with individuals that were "tagged".
- Tagging could be done on 4+ year old fish via releases from longline fisheries or on 1-3 year olds, as was the case for the CCSBT SRP conventional tagging program.
- Samples for recaptures could be taken i) on capture; ii) at processing, in the case of farming, or iii) at market.

The remainder of this paper focuses on further design considerations and likely costs and benefits of gene-tagging programs for monitoring SBT.

3 Gene-tagging design and data generated

3.1 Calculation of absolute abundance for a single cohort

The simplest and lowest cost design for a gene-tagging program is for estimation of the absolute abundance of a tagged cohort. Field operations would involve capturing, measuring length (to determine if the fish is in the target age class), taking a tissue sample, and releasing thousands of fish. This provides a "tagged" cohort of the target age-class. Sampling for recaptures is done by taking a tissue sample from a randomly selected sample of fish following capture by the fishery. This sample is examined for matches with "tagged" fish via DNA profiling of the release and recapture tissue samples. Recapture sampling can be done on board a vessel, at farm harvest or at market. A distinction between the design of gene-tagging and conventional tagging studies is that for conventional tagging studies the entire catch is (in theory, but not always in practice due to non-reporting) examined for recaptures, whereas for gene-tagging studies a fixed sample size of the catch is examined.

At its simplest the calculation of abundance is:

$$N = T * S/R \qquad (2.1)$$

where, N is the estimated abundance of the cohort, T is the number of fish in that cohort that were tagged, R is the number of tagged fish "recaptured" in the recapture sample, and S is the recapture sample size.

As an example, a simple implementation of this sort of program might involve a single release year ($T_{a,y}$, where a is age and y is year) followed by recapture sampling in the following year ($R_{a+1,y+1}$) to allow for mixing. A logical extension would be to develop a time series of abundance estimates of cohorts through successive release and recapture events. This need not be an annual series. For example, releases and recapture exercises could be done every second year to obtain a biennial abundance series for each cohort, if this was shown to be more cost-effective.

An important consideration when using this form of cohort abundance estimation is that it is not necessary to account for mortality of "tagged" individuals (natural or fishing) between tagging and re-sampling as the total mortality of the tagged and untagged populations will be equal if the population is well mixed. Assume that the rate of total mortality is Z. In the following year the number of tags in the cohort is $T' = T * \exp(-Z)$; the number of animals in the cohort is $N' = N * \exp(-Z)$. The probability of getting a tagged fish

from the cohort is T'/N' = T/N as the mortality rate (*Z*) of the tagged and un-tagged population is the same, assuming the population is well mixed. From a random re-sample of the population of size S, the expected number of recaptures is R = (T/N) * S; simple rearrangement gives Eq. (2.1) in terms of the cohort size estimator.

The relationship between the tagged fish and the whole population depends on two things: (i) that they are suitably mixed into the population (so the T/N probability above is valid) and (ii) that the sample scanned for gene tags, S, is a random sample from the population. Examination of mixing in previous SBT tagging projects has concluded that there is reasonably good mixing of juveniles throughout their range (Basson et al 2012, Polacheck et al 2006), although there is less known about the older age classes. In contrast to conventional tagging where the whole catch is scanned for tags, in gene tagging a recapture sub-sample can be taken in ways that maximise the likelihood of a random sample. Mixing and stock structure hypotheses could also be examined in extensions to a gene-tagging project.

Costs of collecting tissue samples can differ for releases and recaptures and where the samples are collected. However for a given unit cost of sample collection, we can calculate the optimal sample sizes for tagging and recapture to obtain a target CV on the estimate of abundance. A simplified calculation of the CV of the abundance estimate, assuming a Poisson recapture process, is:

$$CV = \mathrm{Sqrt}(N/(T*S)). \qquad (2.2)$$

The key point from Eq. (2.2) is that the precision of the abundance estimate scales (i.e. goes up) with population size (N) for a given level of tagging (T) and re-sampling (S). The cost estimates and CVs provided in the examples below (Table 1) are conditional on the current estimates of cohort size from the operating model. If cohort sizes are larger, the sample sizes will be too low for the target CV, and the opposite occurs for smaller cohorts. However, because the scaling is square-root proportional to N, an underestimation of cohort size (N) of a factor of 3 (for example) results in an underestimate of the total sample size (T+S) by a factor of only 1.73 (assuming T=S).

Also, for a given population size, the CV is inverse square root proportional to the product of the initial tag numbers and re-sample sizes. If sample sizes are increased there is an inversely proportional decrease in the CV (i.e. doubling the sample size halves the CV). This is the same effect seen in the close-kin method, which is not applicable in conventional tagging methods where only the initial tag numbers (and not the numbers of fish re-sampled) can be controlled by the researcher.

3.2 Multiple-year recapture sampling

If the tagged cohort as described above is sampled for recaptures at capture/harvest/or market in a year sometime after the initial recapture sample year (giving R*a,y* and R*a+x, y+x*), and possibly in other areas/fisheries, this would provide additional information including mortality and mixing, and information on whether the tagged component is representative of the whole stock. The additional samples would also improve the precision of the absolute abundance estimate for the cohort.

3.3 Multiple-year and multi-cohort tagging and re-sampling

If multiple cohorts are tagged over a number of successive years and re-sampled over several years, then the gene-tagging program will closely resemble the previous CCSBT SRP tagging program (e.g. Eveson and Polacheck 2007, Anon. 2001) and will provide data on natural and fishing mortality, mixing, potentially

some spatial information (depending on where samples and recaptures take place), and improved precision in the estimates of the abundance of each cohort over successive recapture exercises. Catch-at-age (CAA) information is required for estimation of natural mortality and fishing mortality in the case of gene-tagging studies because the proportion of the catch sampled for "recaptures" needs to be known/estimated. Hence, these data and the resulting estimates are not strictly fishery independent and uncertainties in the CAA data can affect precision and bias of the mortality estimates (Polacheck and Eveson, 2007; Polacheck et al, 2006).

4 Sampling design considerations

4.1 By whom

Tagging and re-sampling could be done via a variety of means including: as a dedicated, collaborative gene-tagging program; as add-on duties in an observer program; as an additional component of an existing research project; or in combinations of these. In a dedicated CCSBT coordinated project, the time at sea and labour involved in taking the tissue samples could be undertaken by a variety of members and is an opportunity for scientists to work collaboratively together and build capacity across all members. Similarly in the case of observer programs all members could potentially contribute. There may be some capacity to add gene-tagging to existing research projects or monitoring programs. Tagging and release could also be considered for vigorous and healthy looking discards from commercial operations by observers, to ensure quality control of the health of the fish released. A potential disadvantage of this option would be that the mortality rate for the discards would need to be evaluated by concurrent dedicated tagging, and regularly re-evaluated, to assess the extent to which the abundance estimates may be biased by differential mortality of fish released from commercial operations (versus dedicated tagging exercises).

4.2 Where

Tagging of large numbers of fish in Western Australia (WA) and South Australia (SA) has been demonstrated as feasible in past conventional and electronic tagging programs. In addition, tagging could potentially be undertaken in the longline fisheries, as has been demonstrated in archival tagging projects (Basson et al 2012, Sakai and Itoh 2012 and earlier papers).

Recapture sampling at harvest, or possibly at market, could occur in any of the fisheries that take sufficient catches of the cohort being studied.

Abundance estimates from conventional tagging of only one component of a fishery has been previously been examined by Polacheck et al (2004) using the 1990s tag data on juveniles in the Great Australian Bight (GAB). Their study concluded that abundance estimates/trends could be estimated because there was evidence of "reasonably consistent and high levels of mixing" with the complete population of juvenile fish.

4.3 Which Ages

All age classes could in principle be targeted in a gene-tagging program. In practice, however, the relevant constraints include: ability to access and tag sufficient number of individuals and the larger cohort sizes associated with younger age classes. Experience to date has shown that it is generally easier and lower cost to access and tag large numbers of 1-3 year olds. The trade-off is that the generally higher abundance of

these younger cohorts means that larger numbers of releases are required to achieve the desired level of precision in the abundance estimate, relative to older age classes.

Some of the uncertainties around the mortality rates and movement of 1 yr olds located off WA (Polacheck and Eveson 2007) could be addressed through a gene-tagging program, with recapture sampling in multiple years post tagging (and not necessarily concurrent years). However, tagging other age classes that do not appear to have the same levels of uncertainty would provide much the same information for use in an OM or MP, for less risk and in a shorter timeframe. Trade-offs between costs and risks will depend on the sampling design and whether tagging could be undertaken as part of existing research projects to reduce costs.

Tagging of age 2 and 3 year old fish has been demonstrated to be feasible in previous conventional tagging studies, and would provide information on the juvenile component of the stocks.

Tagging of 4 year olds in the GAB may be feasible and recapturing throughout the fishery as 5 year olds or older would provide new information on natural mortality and a time-series of abundance estimates that would provide alternative information to the CPUE inputs to the OM and MP. It should be noted that if sufficient numbers of fish were tagged as juveniles, then these fish are tagged for life, and various parameters could be estimated at much later stages in their lives if re-sampled then.

Tagging of older age classes from longliners would provide important new information on abundance, fishing and natural mortality rates, mixing and spatial structure for those age classes for which we currently rely on relative abundance time-series and catch at size information with high uncertainties.

5 Costs

The main costs associated with a gene-tagging program are: the development and validation of a suitable set of markers, the genetic testing of the tissue samples, the initial costs of taking the samples, the costs of collecting the recapture samples, calculation of abundance indices and other outputs, and administration.

The numbers of loci required for DNA matching a fish with itself is far fewer than the more complex paternity tests required for the close-kin method. In the case of SBT the costs of marker development have already been met via the close-kin project. The costs of DNA profiling for a gene-tagging program have dropped significantly to approximately AUD$10[1]. In addition the costs estimates provided here allow an additional ~AUD$5 for the initial step of DNA extraction from the sample.

The details of other costs depend on the sampling design. Some can be estimated from previous programs. For instance, to tag 5000 2 yr old fish in the GAB would require approximately 20 days of vessel charter, tagger labour, and relatively small equipment and consumable costs. Recapture sampling costs should only involve the cost of taking a small tissue sample at the same time a fish is being measured to meet CDS requirements, plus transport of samples to the genetics facility for processing. The cost of analysis of the data is likely to be similar to the costs of providing other abundance indices for the CCSBT. Administration of a gene-tagging program would have some components that are similar to previous tagging projects (e.g. for running the initial tagging component of the work), but there would be significant savings in the

[1] These costs estimates are based on experience with the close-kin project where the majority of the processing was done at CSIRO. If a long-term gene tagging program were established for SBT it is reasonable to expect these per unit costs would decrease as the genetic processing could be done at more cost-effective facilities, provided the required quality assurance and quality control protocols were in place.

recapture component as there is a large saving from not having to pay for, or administer, tag return rewards. In addition, there are substantial "savings", relative to the previous conventional tagging programs as the number of releases and recaptures required to achieve the same CV as conventional tagging are lower, as there is no need to allow for tag loss, reporting rate and tag seeding.

5.1 Example cost estimates for some options for a gene-tagging project for SBT

Using the approximate cost information above, we have provided two hypothetical scenarios for a gene-tagging program, to assist the ESC discussion of the potential merits of the approach:

1) tag 1 year olds in WA and recapture as 2 year olds at harvest in Pt Lincoln in the following year, and;
2) tag 2 year olds in SA and recapture as 3 year olds at harvest in Pt Lincoln in the following year.

These two examples are the easiest to do, as they closely resemble the previous SRP tagging program in terms of logistic costs. The primary result would be an estimate of the absolute abundance of the tagged cohort.

Sample sizes were calculated for the minimum number of fish required to be tagged and resampled to achieve a CV close to the target of 0.25 for the minimum cost. Note that tagging fish costs more than sampling for recaptures.

The following input data were used:

1) Estimates of abundance of 1 and 2 yr olds from the most recent years of the 2012 OM grid with close-kin data included (baseCKmk5sqrt, Hillary et al, 2012). The costing scenarios are presented based on the median estimate of the numbers (N) of age 2 fish (approximately 2 million) and the maximum (2.2 million). For the numbers of age 1 fish, the median of the recent estimates is 2.9 million and max is 3.3 million.
2) Processing costs of $15 per sample.
3) Vessel charter and labour costs. We looked at 2 alternatives: costs per day, or a fixed number of days for tagging. These costs were estimated from the costs of the CCSBT SRP tagging program that aimed to tag 8-10,000 fish in 40 days at sea in SA (= 200 tags/day on average). Assuming charter and labour costs have increased since 2006, we calculated that each release could now cost ~$65/tag. If there was good weather, or good tagging conditions (~250 tags/day on average), or if tagging occurred in WA where traditionally a smaller and cheaper vessel has been used, each release could cost ~$50/tag. We also examined the sample sizes and costs of fixing the days at sea to 20 days (and 250 tags/day).
4) Administration, analysis and fixed costs have been included at $150,000.
5) Target CV = 0.25, which is equivalent to the CV for the scientific aerial survey. We also examined the effect on the CV of under estimating the population size (details not included here), and there was little impact on the CV for the values examined (see the explanation of the relationship between population size and CV at eqn 2.1).
6) Over-dispersion: We examined the potential impact on costs and sample sizes of an over-dispersion factor, as is used in the OM for the conventional tagging data (Anon 2009). Results for over-dispersion of 2.35 (consistent with the current value in the OM) and 1 (no over-dispersion), are provided as the two extremes. We would expect 2.35 to be higher than would be realised by a gene-tagging program (as discussed below).

Results – potential costs and CVs for hypothetical gene-tagging scenarios

Table 1. Approximate costs ('1000 AUD$) for hypothetical gene-tagging scenarios. Costs are for the sample sizes in Table 2. Scenarios cover: different cohort sizes for 2 ages (estimate of numbers (N) from the 2012 OM, median or maximum value from the grid), over-dispersion is included or not included, and 3 methods for calculating the days at sea required for tagging ($65/tag, $50/tag or fixed 20days at sea to do all the tagging).

	COSTS (AUD$ x 1000)					
	Over-dispersion factor included			Over-dispersion factor not included		
Assumed cohort size (N)	$65/tag	$50/tag	20 days	$65/tag	$50/tag	20 days
Median N age 2	750	680	710	540	510	580
Maximum N age 2	760	710	725	560	520	590
Median N age 1	870	800	800	620	570	620
Maximum N age 1	920	840	860	650	600	650

Table 2. Sample sizes for the initial tagging, and for the recapture sampling for the scenarios in Table 1. Sample sizes have been calculated to give an abundance estimate with CV = 0.25, for the minimum approximate costs. Scenarios cover: different cohort sizes for 2 ages (estimate of numbers (N) from the 2012 OM, median or maximum value from the grid), over-dispersion is included or not included, and 3 methods for calculating the days at sea required for tagging ($65/tag, $50/tag or fixed 20days at sea to do all the tagging).

	Sample sizes: Tag(n), Re-sample (n)					
	Over-dispersion factor included			Over-dispersion factor not included		
Assumed cohort size (N)	$65/tag	$50/tag	20d sea	$65/tag	$50/tag	20d sea
Median N age 2	3700, 20000	4000, 18000	5000, 15000	2500, 13000	3000, 12000	5000, 6500
Maximum N age 2	3700, 21000	4500, 18000	5000, 16000	2500, 14000	3000, 12000	5000, 7000
Median N age 1	4500, 24000	5000, 22000	5000, 21000	3500, 13000	3000, 15000	5000, 9000
Maximum N age 1	4800, 26000	5500, 22000	5000, 24000	3500, 15000	3500, 15000	5000, 11000

Discussion

The preliminary cost/tag options provided here are based on minimising costs through decreasing the initial tagging sample size. However this reduces the number of days at sea to low numbers which may not allow for bad weather, travel to fishing grounds and days spent finding fish. In reviewing the numbers of

conventional tags released in previous programs, it is clear that on good days when fish have been found, large numbers can be tagged, but that there are also days when none are tagged. This means that the fixed 20 days of sea time with the aim of gene-tagging around 5000 fish may be a more realistic method for calculating the field costs associated with particular designs. The lowest cost of the scenarios explored is to tag 2 yr old fish. These costs would most likely be distributed over 2 years, with tagging in year one and analysis in year two, to allow for sufficient mixing.

Consideration of the over-dispersion factor significantly increases costs. There are sampling design considerations that could be used to minimize the potential for over-dispersion and, hence, reduce the cost below that provided here. The over-dispersion value used here and in the OM is based on the fit to the conventional tagging data in the 1990s. It should be considered an overestimate in the case of gene-tagging designs because it includes uncertainties associated with estimating reporting rates, and conventional tagging issues such as tag loss and tags being missed at processing. These issues would not apply in a gene-tagging program. With a one year gap between tagging and recapture, we could assume that the population of tagged fish was well mixed (Polacheck et al 2004).

6 Potential benefits

These simple examples and preliminary cost estimates show that it may be feasible to obtain an absolute abundance estimate from gene-tagging programs for comparable, or lower, cost than the current "relative" abundance estimate provided by the scientific aerial survey. For example, a project that tags 2 year olds in SA and recaptures these by sampling the surface fishery in the GAB as 3 years olds the following year is estimated at ~AUD$580,000 over 2 years. The output would be an estimate of absolute abundance for the 2 year olds in the year sampled. This absolute abundance estimate could be used in the current OM in a similar way to the relative abundance estimate from the scientific aerial survey. As an absolute estimate of abundance for a single cohort (rather than a relative index of 3 years classes) it would potentially provide greater information on stock size estimates, in a similar manner to the addition of the 1990s tagging and close-kin data.

Contingency data series

If developed as a time-series of abundance estimates, the gene-tagging estimates could be used as complementary or contingency data series for existing abundance indices used in the OM and in future MPs. In the case of the OM the incorporation of any future gene-tagging data would be relatively straightforward. In the case of the MP this would require some refinement. However, the stage-structured nature of the mini-assessment in the MP (i.e. recruitment+ relative biomass, Anon 2012, attachment 7) means that the essential form of MP would stay the same, but the input data series for the indices of recruitment and/or relative biomass would change depending on which component of the stock the gene tagging data series was available for.

Collaboration and capacity building

The nature of the field operations and multiple potential age classes and release areas means that a gene-tagging program provides considerable scope for participation and collaboration among members. There would be potential for collaboration and participation of research personnel and national observers from multiple members. It also offers opportunities to build the research and monitoring capacity across CCSBT members and improve understanding and confidence in the method and results. The design of any future

program should consider the potential to “piggy back” on other CCSBT national research projects or observer programs.

Gene tagging in combination with close-kin

An additional potential benefit, if the design includes collection of samples from juveniles at harvest in Port Lincoln, is that a subset of these samples could be used for estimating the spawning biomass using close-kin abundance estimation. This would require data for more loci than processed for gene-tagging, but it could be done using the same samples. This would potentially provide a time series of estimates of abundance for the adult component of the stock. These synergies between the two approaches would potentially result in additional cost savings – not just from an operational cost perspective, but there is also the potential that the combined information provided by the two independent sources of abundance data for different components of the stock would reduce uncertainty in the assessment more than either data source on its own.

Only a small set of scenarios, with potential costs and issues for current population sizes, have been examined here. There are a range of logistic issues, design and technical details that would needed to be included in an evaluation to provide a comprehensive cost-benefit analysis. However, the preliminary costings presented do indicate, relative to earlier exercises (e.g. Davies et al 2008), that the costs have reduced substantially and the potential use of gene-tagging as a monitoring approach for different components of the SBT stock is worth this more detailed discussion and consideration by the ESC.

7 Future work suggestions:

The ESC could consider the merits of a collaborative gene-tagging program in the context of future monitoring and assessment requirements for the fishery. This would require detailed consideration of design, field logistics, genetics processing, data management, funding models and implementation. As a basis for discussion by the ESC, initial steps might include:

1) A collaborative gene-tagging design exercise to examine, in detail, potential sampling options, refine cost and sample size estimates, refine alternative designs, and approaches for how the data may be included in the OM.
2) Based on the ESC considerations of the outcomes of 1 above and securing required funding, conduct a pilot gene-tagging project to trial field operations and provide a single abundance estimate and additional data to refine the design and field operations of future programs.
3) Consideration of the frequency of release events and recapture sampling for a time series of abundance estimates, improved precision, and information on mortality and harvest rates, and implementation of such a program. The CCSBT OM could be used to evaluate different designs and identify the most cost-effective options.

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CONTACT US

t 1300 363 400
+61 3 9545 2176
e enquiries@csiro.au
w www.csiro.au

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CSIRO Marine and Atmospheric Research
Ann Preece
t +61 3 6232 5222
e ann.preece@csiro.au
w www.csiro.au/wfo