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Update on the SBT gene-tagging recruitment monitoring program 2026

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1 Abstract

The CCSBT Southern Bluefin Tuna (SBT) gene-tagging program provides an estimate of the absolute abundance of the age-2 cohort, for use in the Cape Town Procedure and stock assessment models. The program has been running since 2016. Since the last Extended Scientific Committee (ESC) the project has completed genotyping of the 2024 releases and 2025 harvest samples to provide an estimate of age-2 abundance in 2024 for use in this year's stock assessment. We have also completed another year of tagging and harvest sampling that will provide abundance data in future.

From the 38.8 million comparisons of genotypes from 3,522 age-2 fish tagged and released in 2024 and 11,011 age-3 fish sampled during harvest in 2025, only 11 matches were detected. The estimate of abundance is 3.53 million fish, which is the highest abundance estimate in the series. Correspondingly, the precision of the estimate is reduced, with CV of 0.3. The OMMP review of the data for the stock assessment agreed that this higher CV is not a concern and is expected with higher abundance (given unchanged sample sizes). The next abundance estimate will be available in 2027, from tagging completed in 2025 and harvest sampling completed in 2026.

We are seeking 1t of Research Mortality Allowance (RMA) in 2027 for low numbers of mortalities that occur during fishing and tagging, if the gene-tagging program proceeds. We used 0.345t of the 2025 RMA, and 0.198t in 2026.

2 Introduction

The gene-tagging program provides an annual estimate of absolute abundance of juvenile Southern Bluefin Tuna (SBT). These estimates of abundance are used in the Cape Town Procedure (Anon., 2020) to provide a management recommendation on the global Total Allowable Catch (TAC), in the annual review of indicators, and in the assessment of stock status (e.g., Hillary et al., 2023 and CCSBT-ESC/2608/20).

The gene-tagging program was designed in 2015 (see design study, Preece et al., 2015) to provide an abundance estimate for the Cape Town Procedure which provides TAC advice to the Commission. The gene-tagging data provides an early warning of low recruitment if it occurs. This makes the Cape Town Procedure robust to climate change impacts that affect recruitment success (Anon., 2025).

3 Method

Gene-tagging SBT involves “tagging” fish by taking a very small muscle 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 muscle tissue samples from the catch of 3-year-old fish at time of harvest. The tissue samples from tagging and harvesting are processed to extract DNA which is then genotyped, and the genotypes from the two sets of samples are compared to detect samples with matching DNA. A match indicates that a tagged and released fish has been recaptured. The estimate of abundance is calculated from the number of samples in the release and harvest sets and the number of matches found.

The gene-tagging program follows the specifications for the pilot study as recommended in the design study (Preece et al., 2015). The design study examined sample sizes, potential sources of bias, costs and precision of estimates and integration of data in stock assessment and management procedure models. Twenty days at sea was considered the minimum viable period to achieve the desired samples size, allowing for bad weather and poor fishing days, based on previous experience with conventional SBT tagging projects. The design study recommended tagging and releasing 5,000 fish and harvest sampling 10,000 fish. Budget constraints have led to reduced days at sea in the last 2 field work seasons. Additional samples have been collected during the harvest in 2026 to compensate for low release numbers in 2025.

4 The estimate of abundance of age-2 cohort in 2024

4.1 Tagging in 2024

Weather conditions during the 2024 field work were challenging. Strong winds throughout the season resulted in extensive upwelling conditions and cooler water temperatures, especially around the areas traditionally targeted by gene tagging. Over 3,700 SBT were tagged in the size range of 70–85 cm FL. This is below the sample size target of 5,000 fish. The tagged fish are released alive, to mix with the untagged population. Tissue samples (tagging) are only taken from fish in excellent condition.

4.2 Harvest sampling in 2025

In 2025, tissue samples were collected from over 13,000 age-3 fish as they were processed during the harvest from the purse seine fishery farms in Port Lincoln, South Australia (June-July). This is over the 10,000 fish target level of sampling. Tissue is collected through the skin using the gene-tag tool (Bradford et al., 2015) and loaded into individually labelled vials. Additional data were recorded (e.g., date, collector, sample number).

The harvest sampling is designed to select fish at random from across the different farms and processing factories, and throughout the full harvest period. A wider range of length classes were sampled to cover changes in length at age observed over recent years.

4.3 DNA extraction and sequencing

DNA was extracted from over 16,000 tissue samples using a modified high-throughput protocol (Preece et al., 2025). The protocol enables efficient digestion of tissue collected with the gene-tag tool and rapid automated DNA purification using a liquid handling system.

Quality control (QC) was performed on 25% of samples from each plate to assess DNA extraction performance, including DNA concentration, purity, integrity, and plate-to-plate consistency. QC samples were selected from three representative columns distributed across each plate to capture spatial variation and provide an overall assessment of extraction quality. QC sample preparation was automated using a liquid handling system, improving reproducibility and minimizing manual handling error.

The extracted DNA samples were sequenced using specific SNP markers developed by CSIRO. A series of QC steps were applied to the genotyped data to exclude fish with poor genotypes, or where there was evidence of contamination.

4.4 2024 age-2 abundance estimate

In recent years there has been an apparent decrease in the size of fish available during tagging relative to the target size range, so additional samples have been collected from smaller sized fish.

For the 2024 age-2 cohort an adjustment to the size range did not seem necessary, so only fish in the original target range have been used in the final analysis: 75–85cm (inclusive) for releases and 98–109cm (inclusive) for harvest samples.

After excluding fish that did not pass QC and that were outside the target length ranges, 3,522 release samples and 11,011 harvest samples remained for analysis. From these samples, 11 matches were found (from ~38.8 million comparisons), giving an abundance estimate of 3.53 million age-2 fish in 2024 (CV = 0.302).

5 Data collection for 2025 and 2026 abundance estimates

In 2025, during the reduced program of 12 days of sea field work time, over 3,600 fish were tagged in the size range of 70–85 cm FL. This is below the sample size target of 5,000 fish. The 2026 harvest sampling of the 3-yr olds has recently been completed with over 17,000 fish sampled. These samples will be processed and sequenced to provide an abundance estimate of the 2025 age 2 cohort, for the data exchange in 2027.

Tagging in 2026 has successfully been completed in March 2026 and is described in Appendix 1 field trip notes. Harvest samples will need to be collected in 2027 to detect these tagged fish, and provide an abundance estimate of the 2026 age 2 cohort in 2028.

6 RMA request for 2027

We are seeking 1t of Research Mortality Allowance in 2027 for low numbers of mortalities that occur during fishing and tagging, if the gene-tagging program proceeds. We used 0.345t of the 2025 RMA, and 0.198t in 2026.

7 Summary of gene-tagging results 2016–2026

The gene-tagging program provides the estimates of absolute abundance of the age-2 cohort in the year of tagging. The gene-tagging program's (2016–2026) sample collection and abundance estimates are provided in Table 1. The gene-tagging data are used in 2026 in the assessment of stock status.

Table 1 Genetic tagging programs sample collection 2016–2026. Estimates of the absolute abundance for the age-2 cohort in the year of tagging are available where the full cycle of tagging, harvest sampling, genotyping and analysis has been completed. For completed gene tagging cycles (tagging years 2016 to 2024), the numbers of release and harvest samples are the numbers used in the analysis after quality control checks; for the incomplete gene tagging cycles (i.e. tagging years 2025 and 2026), these are the numbers collected.

YEAR OF TAGGING (Y)	AGE AT TAGGING	N RELEASES	N HARVEST (IN Y+1)	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
2019	2	4242	11109	31	1.52	0.180
2020	Interrupted by Covid-19				-	-
2021	2	6401	10742	41	1.68	0.162
2022	2	5084	14714	38	1.97	0.162
2023	2	2759	13297	14	2.62	0.267
2024	2	3522	11011	11	3.53	0.302
2025	2	3680	17000	-	Available 2027	-
2026	2	3066	-	-	Available 2028	-

8 Summary

The 2024 estimate of age-2 abundance from the gene-tagging program have been delivered this year and these data will be used in the 2026 stock assessment.

The 2025 estimate of abundance is on track with tagging and harvest tissue samples collected. These will be processed to extract DNA, which will then be genotyped. We expect that the 2025 abundance estimate will be available on time for the 2027 data exchange.

In the 2026 field program, 3066 fish were tagged and released.

Appendix A CCSBT-CSIRO Southern Bluefin Tuna Gene Tagging – March 2026

A.1 Trip report

Report on Gene Tagging Operations for 2026 Field Work.

The field team departed Port Lincoln, South Australia, on the evening of the 18th March and transited directly to the Shelf area ~50 nautical miles (nM) Southwest of Linguanea Island. Fishing activities extended from sunrise to sunset on all active fishing days of the 12 days of charter. There were two days when the weather was not suitable for the poling and tagging of SBT. The field team returned to Port Lincoln on the evening of the 30th of March 2026.

A total of 5,005 SBT were polled; 3,066 of those were in the target size range of 73–85 cm FL (Figure A1). Only fish in excellent condition were tagged. The key tagging locations and numbers tagged are provided in Table A1. A further 14 SBT were caught on the troll lines. Of all SBT caught (pole or troll), 22 were killed as a result of injury sustained during fishing operations. Biological samples (muscle, vertebrae, heart, otoliths) were collected from each mortality. Length and weight were recorded for all mortalities and troll caught SBT (Figure A2), estimated total weight of mortalities was 198 kg (Table A2).

Table A1. Summary of southern bluefin tuna gene tagged in the 2026 field season.

Area	Approx. Latitude	Approx. Longitude	Number Tagged
Shelf edge south of Rocky Island	-35.49	134.77	175
Nuyts Reefs	-32.22	131.9	2072
Rocky Islands	-34.8	134.7	819

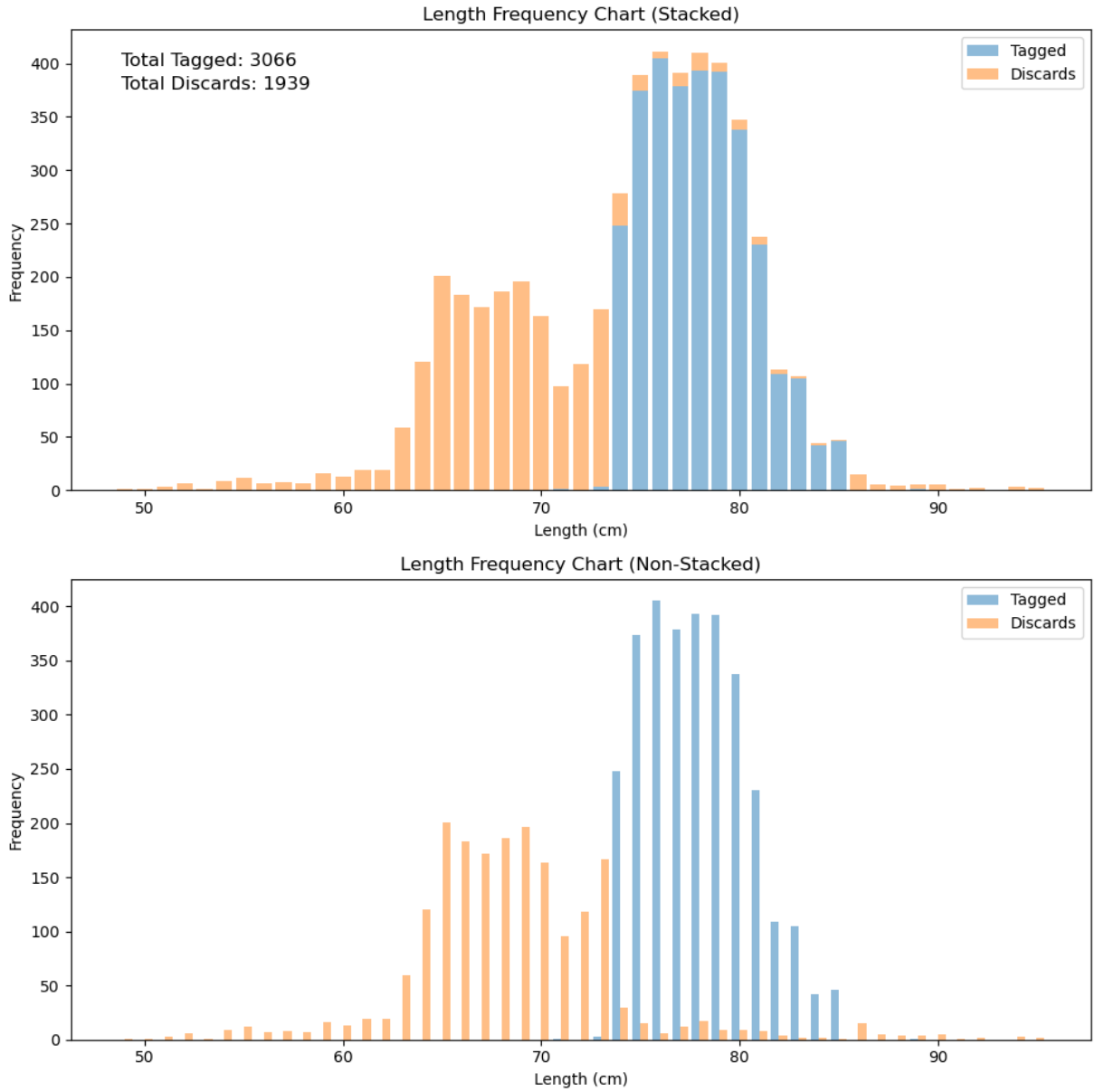


Figure A1. Length frequency histogram of polled southern bluefin tuna during the 2026 gene tagging field operations.

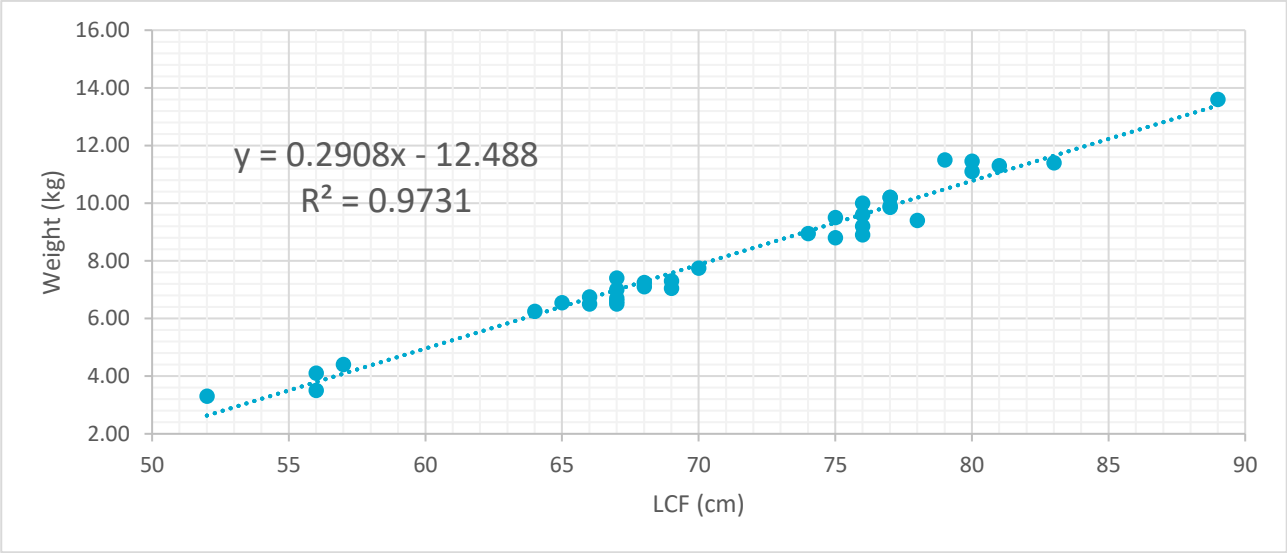


Figure A2. Weight-length relationship of southern bluefin tuna sampled during gene-tagging field operations in 2026

Table A2 - Length and weight data for all southern bluefin tuna mortalities collected during the SBT gene tagging field work in March 2026.

Date	Mort No	Length (cm)	Weight (kg)
19/03/2026	1	76	8.90
19/03/2026	2	76	10.00
21/03/2026	3	67	6.50
21/03/2026	4	68	7.10
21/03/2026	5	69	7.30
21/03/2026	6	81	11.30
21/03/2026	7	83	11.40
21/03/2026	8	78	9.40
22/03/2026	9	52	3.30
22/03/2026	10	80	11.10
22/03/2026	11	77	9.90
23/03/2026	12	75	8.80
23/03/2026	13	70	7.75
23/03/2026	14	67	7.00
23/03/2026	15	66	6.75
23/03/2026	16	68	7.25
23/03/2026	17	77	9.85
28/03/2026	18	89	13.60
28/03/2026	19	77	10.20
28/03/2026	20	77	10.20
28/03/2026	21	80	11.45
28/03/2026	22	74	8.95

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