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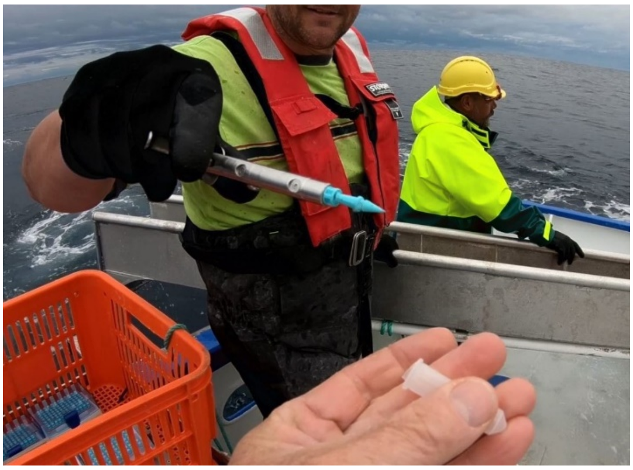
Southern Bluefin Tuna Gene-Tagging Program

The gene-tagging program is a new approach for monitoring absolute abundance of juvenile Southern Bluefin Tuna (SBT). It uses the unique genetic fingerprint of a fish to identify if a ‘tagged’ fish is recaptured. Gene-tagging resolves tag reporting rate issues in conventional tagging programs and is a fishery-independent alternative to catch-per-unit-effort indices.

The abundance estimates will be used in stock assessment models and is essential for a new management procedure to calculate the recommended global catch of SBT. The Commission for the Conservation of Southern Bluefin Tuna has funded an on-going gene-tagging program for recruitment monitoring of SBT.

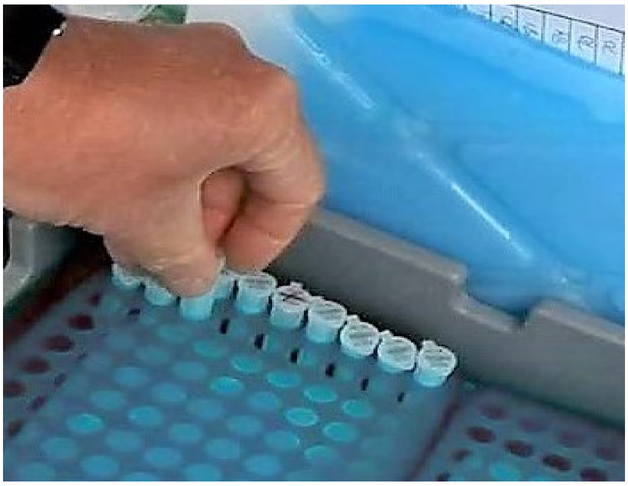
DNA identifies tagged & recaptured fish

- A small tissue sample is collected from fish (“tagging”) and the fish is released alive to mix with population. The unique genetic DNA fingerprint is the ‘tag’.
- A second set of samples is collected, 1 year later, during commercial harvesting of fish*.
- A multi-disciplinary team at CSIRO O&A developed tissue sampling tools and the set of genetic markers for reliable individual identification.



Key Advantages

- The data are fishery independent;
- No reporting rate issues; it is invisible, lasts forever, there is no tag shedding; and no tag rewards.



Pilot project verifies feasibility & logistics

The pilot program has demonstrated: high-throughput DNA extraction and cost-effective genotyping; and has delivered an estimate of abundance of juveniles.

- 20,000 fish tissue sampled each year
- First abundance estimate: 2.4 million 2 year old fish (similar to 2017 stock assessment models median estimate: 2.1 million)

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