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PROPOSED STANDARD OPERATING PROCEDURES FOR COLLECTING TISSUE SAMPLES FROM IOTC SPECIES FOR GENETIC RESEARCH

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Purpose, expectation and action intended (select one or more and include corresponding text)

Discussions (for information and open discussion):

The paper is to inform meeting participants of proposed standard operating procedures (SOPs) for collecting tissue samples for close-kin mark-recapture (CKMR studies), which have been developed from experience gained from existing sampling programs, including for southern bluefin tuna, and that these SOPs will be refined as experience is gained from wider sampling.

Feedback (to collect input and suggestions)

The paper is to request review and comments on proposed SOPs for collecting tissue samples from IOTC species for CKMR studies, using a spring-loaded biopsy (gene-tagging) tool fitted with single-use tips.

Recommendation (to ask the meeting to endorse a recommendation)

The paper is to seek endorsement on recommending the SOPs as a common standard for CKMR tissue sampling of IOTC species.

Abstract

This paper proposes standard operating procedures (SOPs) for collecting muscle tissue samples from IOTC species for close-kin mark-recapture (CKMR) studies. CKMR requires tens of thousands of samples with very low levels of DNA cross-contamination, processed through high-throughput laboratory workflows. The SOPs therefore describe sampling with a spring-loaded biopsy ('gene-tagging') tool fitted with single-use tips, which minimises the risk of cross-contamination between fish and produces small, uniform samples suited to high-throughput DNA extraction. The SOPs draw on documentation and experience from the southern bluefin tuna (SBT) gene-tagging program (2016-2026, 17,000 samples per year), the sampling protocol of the population structure of IOTC species and sharks of interest in the Indian Ocean (PSTBS-IO) project (Anon. 2018), and on the Pacific Community (SPC) biological sampling manual (Sanchez et al. 2023). The WPDCS is invited to review the proposed SOPs and consider their adoption as a common standard for CKMR tissue sampling under the developing IOTC biological sampling network.

Australia's National
Science Agency

Proposed standard operating procedures for collecting tissue samples from IOTC species for genetic research

IOTC Working Party on Data Collection and Statistics

Nov 2026

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Summary

This paper proposes standard operating procedures (SOPs) for collecting muscle tissue samples from IOTC species for close-kin mark-recapture (CKMR) studies. CKMR requires tens of thousands of samples with very low levels of DNA cross-contamination, processed through high-throughput laboratory workflows. The SOPs therefore describe sampling with a spring-loaded biopsy ('gene-tagging') tool fitted with single-use tips, which minimises the risk of cross-contamination between fish and produces small, uniform samples suited to high-throughput DNA extraction. The SOPs draw on documentation and experience from the southern bluefin tuna (SBT) gene-tagging program (2016-2026, 17,000 samples per year), the sampling protocol of the population structure of IOTC species and sharks of interest in the Indian Ocean (PSTBS-IO) project (Anon. 2018), and on the Pacific Community (SPC) biological sampling manual (Sanchez et al. 2023). The WPDCS is invited to review the proposed SOPs and consider their adoption as a common standard for CKMR tissue sampling under the developing IOTC biological sampling network.

Introduction

Genetic methods will increasingly be used to inform the assessment and management of IOTC species. Population genomics has been applied to the stock structure of tunas, billfish and sharks in the Indian Ocean (Davies et al. 2019, 2020), and close-kin mark-recapture (CKMR) is being developed for Indian Ocean yellowfin tuna (Hillary et al. 2022; Williams et al. 2023; Williams and Preece 2026). CKMR has also been used to estimate whale shark abundance in the region (Patterson et al. 2025) and a CKMR design study has been completed for shortfin mako shark (Patterson and Bessell-Browne 2025).

These research programs often depend on large numbers of tissue samples, collected across many fleets, ports and countries, that have low levels of DNA contamination, and are linked to accurate metadata (biological, spatial and temporal). These requirements are greatest for CKMR, which relies on accurately identifying close relatives from their genotypes, so cross-contamination even at low levels, can compromise the identification of kin pairs. The yellowfin tuna design study estimated that approximately 30,000 samples per year would be needed (Hillary et al. 2022). Inconsistent methods between sampling teams can also introduce artificial variation into the results (Anon. 2018).

Two projects, led by the IOTC Secretariat and the French National Centre for Scientific Research (CNRS), are currently evaluating the feasibility of tissue sampling for IOTC species and developing a biological sampling network across the Indian Ocean. A common set of SOPs would allow samples collected through this network to be combined and reduce duplication of effort. As noted in Williams and Preece (2026), this paper presents those SOPs for review by the WPDCS.

Different genetic applications have different sampling requirements. These SOPs are designed for CKMR and other large-scale studies that rely on high-throughput laboratory processing. Smaller studies, such as population structure and species identification, typically need fewer samples, and can be served by other methods, such as a biopsy punch or knife with the sample stored in preservative (Anon. 2018).

For CKMR, the SOPs describe sampling with a spring-loaded biopsy tool, referred to here as the gene-tagging (GT) tool, fitted with single-use tips (Bradford et al. 2016). Compared with the knife- and scalpel-based methods used in earlier Indian Ocean sampling (Anon. 2018), this approach:

- substantially reduces a major source of cross-contamination, because each tip is used only once, and the tip pushes past potentially contaminated skin to collect a clean tissue sample
- collects a small, uniform sample (about the size of a grain of rice), and the tip with tissue is stored frozen in a tube and transferred directly into 96-well plate formats for high-throughput DNA extraction
- is fast to use, with minimal handling of the fish, which suits port sampling of large numbers of fish

- has been used to collect tens of thousands of samples each year in the SBT juvenile gene-tagging program 2016-2026 (Preece et al. 2015, 2026) and approximately 75,000 samples in the South Pacific albacore CKMR sampling from 2024 to 2026 (SPC and CSIRO 2026)

Scope and sources

The SOPs cover the collection, preservation, storage, labelling and shipment of muscle tissue samples for CKMR from key IOTC species, taken with the GT tool and tips during port sampling or by observers at sea. They may also suit other large-scale genetic studies that use the same high-throughput laboratory workflow.

The following are outside the scope of this paper:

- other biological samples, such as otoliths, gonads, vertebrae, spines, liver and stomachs, and the protocols for collecting them
- biopsy sampling of live fish before release, which requires specific permits and training
- sampling design, including target species, sizes, locations and sample sizes, which is set by each project

The SOPs draw extensively on three existing protocols (Table 1), which between them used a range of tissue sampling methods, including the GT tool and tip, biopsy punch, and knife or scalpel. These protocols have been adapted and combined for application in the IOTC context, and their contribution is gratefully acknowledged.

Table 1. Source protocols drawn on by these SOPs.

Source	Context	Tissue method	What these SOPs take from it
PSTBS-IO sampling protocol (Anon. 2018)	Port and observer sampling of 12 IOTC species, 2017–2018	Knife or scalpel, sample preserved in RNAlater-like buffer	Indian Ocean context, species identification, length codes, data fields and shipping requirements
SBT gene-tagging program (Preece et al. 2015, 2026)	Large-scale sampling of juvenile SBT (thousands per year)	GT tool and tip, sample frozen	High-throughput workflow and quality control, GT tool handling, care and sampling technique
SPC Biological Sampling Manual (Sanchez et al. 2023)	Observer and port sampling in the WCPO	GT tool and tip, or biopsy punch	GT tool and tip procedure, contamination precautions and labelling

Equipment

Each sampling team should assemble a kit before sampling begins (Table 2). Items marked as provided would be supplied by the coordinating laboratory to ensure consistency across the network.

Table 2. Equipment for tissue sampling with the GT tool and tips.

Item	Purpose	Notes
GT tool (handle), plus a spare	Taking the tissue sample	Provided; spring-loaded, never point a loaded tool at a person
Single-use tips, in tip boxes, plus a back-up box	Collecting the tissue	Provided; one tip per fish, never reused

Item	Purpose	Notes
Pre-labelled PCR-clean 1.5 ml or 2 ml tubes with hinged lids	Storing each sample	Provided; one per fish; no preservative. PCR-clean = certified free of DNA, nucleases and PCR inhibitors
Freezer boxes	Storing and shipping tubes	Provided
Pre-labelled PCR-clean 2 ml screw-cap cryovials, pre-filled with RNAlater or similar	Storing samples where freezing is not possible	Provided where needed; screw caps prevent the preservative leaking
Parafilm and scissors	Sealing cryovial lids before shipment	Only for screw-cap cryovials containing preservative. Not used for frozen samples in hinged-lid tubes
Gloves	Protecting samples from DNA and nucleases on the sampler's hands	Worn by the sampler; changed if torn or heavily soiled.
Bucket of soapy water and clean water	Washing gloved hands between fish	Replace when visibly dirty
Single-use wipes or paper towels	Drying gloved hands and wiping the tool handle	Use each wipe once
Spare labels and a permanent marker	Replacing damaged or unusable labels	Provided
Cool box with ice, or access to a freezer	Keeping samples cool after collection	4°C initially; -20°C or colder for storage
Measuring board, tape or callipers	Measuring fork length	Calibrated regularly
Data sheets on a clipboard, and pencils or waterproof pens	Recording data	Or an electronic template
Printed copy of these SOPs and a species identification guide	Reference during sampling	e.g. Appendix I of Anon. (2018)

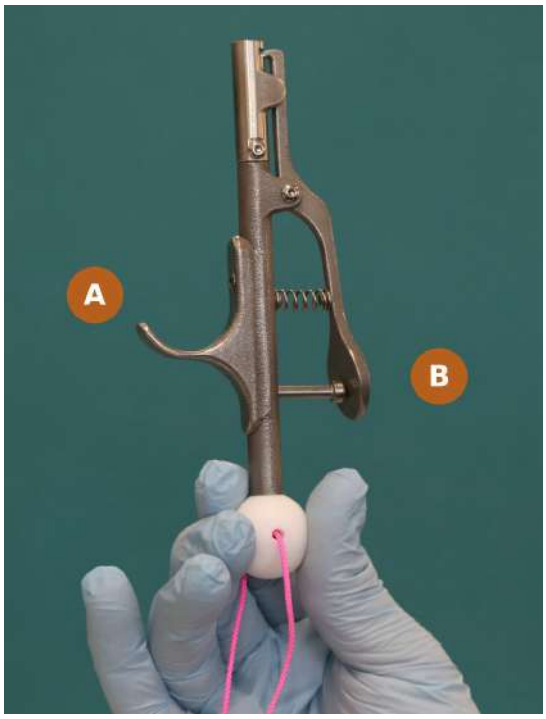


Figure 1. Gene-tagging (GT) tool handle: (A) trigger, pulled back with the index finger; (B) thumb lever, which releases the locking mechanism. Photo: CSIRO.

Preparation before sampling

Good preparation is the simplest way to avoid contamination and data errors.

- **Training.** All samplers should be trained before sampling begins, including species identification, use of the GT tool and tips, and data recording. Training builds confidence and capacity in the region and is central to collecting high-quality samples. Proficiency comes with practice, with multiple practice attempts required to develop a technique that consistently collects a good sample.
- **Access to fish.** Port samplers should arrange access with fishers, companies or port authorities in advance. Observers should inform the captain and company of the sampling before departure.
- **Freezer access.** Confirm access to a freezer at -20°C or colder before sampling begins. Freezing is the preferred way to store tip samples. Where it is not possible, tips must be stored in screw-cap cryovials pre-filled with preservative (see Preservation, storage and transport).
- **Work area.** Set up a work area close to the landing site, or alongside the processing line, with enough space, light, shade and access to clean water. A bench or table reduces handling of the fish.
- **Clean and dirty roles.** Where possible, two or three people should work together: a ‘scribe’ who remains clean and maintains the order of the tips and vials, a 'sampler' who has one clean hand for holding the GT tool, and the other hand for orienting the fish to be sampled, and preferably a 'fish handler' who sources fish to be measured and sampled, measures the fish, and removes the fish from the measuring station once sampling is complete.
- **Tubes and data sheet.** Tubes are pre-labelled with unique sample numbers (see Labelling and data recording). Lay them out in numerical order and use them in sequence, recording each number on the data sheet as each fish is sampled.
- **Tip boxes.** Keep tip boxes closed until needed. If tips are dislodged (e.g. a box is dropped), set the box aside and use the back-up. Re-seat the tips later in a clean setting while wearing sterile gloves and discard any tip that has touched another surface. Always wear laboratory gloves when loading tips into tip boxes. Once a box is full, place a rubber band around it so the lid cannot open accidentally. Clean empty boxes in hot water and dry them before reloading.
- **Fish condition.** Sample fish as soon as possible after capture or landing. Keep fish on ice or in a cool room until sampled. Do not sample a fish that cannot be reliably identified or measured.

Care of the GT tool

The GT tool should be cleaned and maintained regularly (CSIRO unpublished):

- **Daily cleanin**g. Clean the tools at the end of each day. Running water and a toothbrush are enough for the daily clean.
- **Sterilisation.** Sterilise the tools regularly, for example with bleach or ethanol, then rinse them well and allow them to air dry before the next use.

- **Maintenance.** Check the moving parts for wear and tear. A small amount of lubricant (e.g. silicone grease) can be used but keep it away from the end that holds the tip.
- **Storage.** Store the tools so that the tip end cannot be damaged. There is very little tolerance, and a dented end can cause tips to become wedged and difficult to release.

Sampling procedure

The steps below follow the GT tool and tip procedure in Sanchez et al. (2023), with the order of work adapted from Anon. (2018). Keeping to this order helps standardise sampling across teams and locations.

Before taking the sample

1. Confirm the species identification. Small yellowfin and bigeye tuna are easily confused, particularly once markings fade, so use several features and, if needed, internal characteristics (Figure 2; Appendix I of Anon. 2018). Where identification is uncertain, note this on the data sheet; species can be confirmed later from the tissue sample.
2. Assign the next pre-labelled tube to the fish and record its number on the data sheet with the species code.
3. Measure the fork length and record it with the length code (see Labelling and data recording).



Figure 2. Small yellowfin (YFT, top) and bigeye (BET, bottom) tuna of about 35–38 cm FL in fresh condition. Distinguishing features: (1) larger eye in BET; (2) longer pectoral fin in BET, reaching the second dorsal fin; (3) closely spaced vertical lines alternating with rows of dots in YFT, and broader, irregular lines in BET; (4) deeper, more rounded body in BET; (5) longer head in BET; (6) more pronounced notch in the caudal fork of YFT. Photo modified from Itano (2004), reproduced from Anon. (2018).

Loading a tip

Hold the GT tool in whatever way is most comfortable and consistently collects a good sample. Many samplers start with a pistol grip, with the thumb on the thumb lever and the index finger on the trigger, but other grips can give more control and reduce the risk of accidentally releasing the tip.

1. Pull back the trigger with your index finger (Figure 1A).
2. With the trigger held, push down the thumb lever to release the lock (Figure 1B).
3. Push the handle straight down onto a tip in the tip box, then release the thumb lever to lock the tip in place.
4. Pull the handle straight up so the tip does not catch, and check there is no gap between the tip and the handle (Figure 3). Also check that the tooth on the depressor arm is engaged behind the lip of the tip (Figure 4).

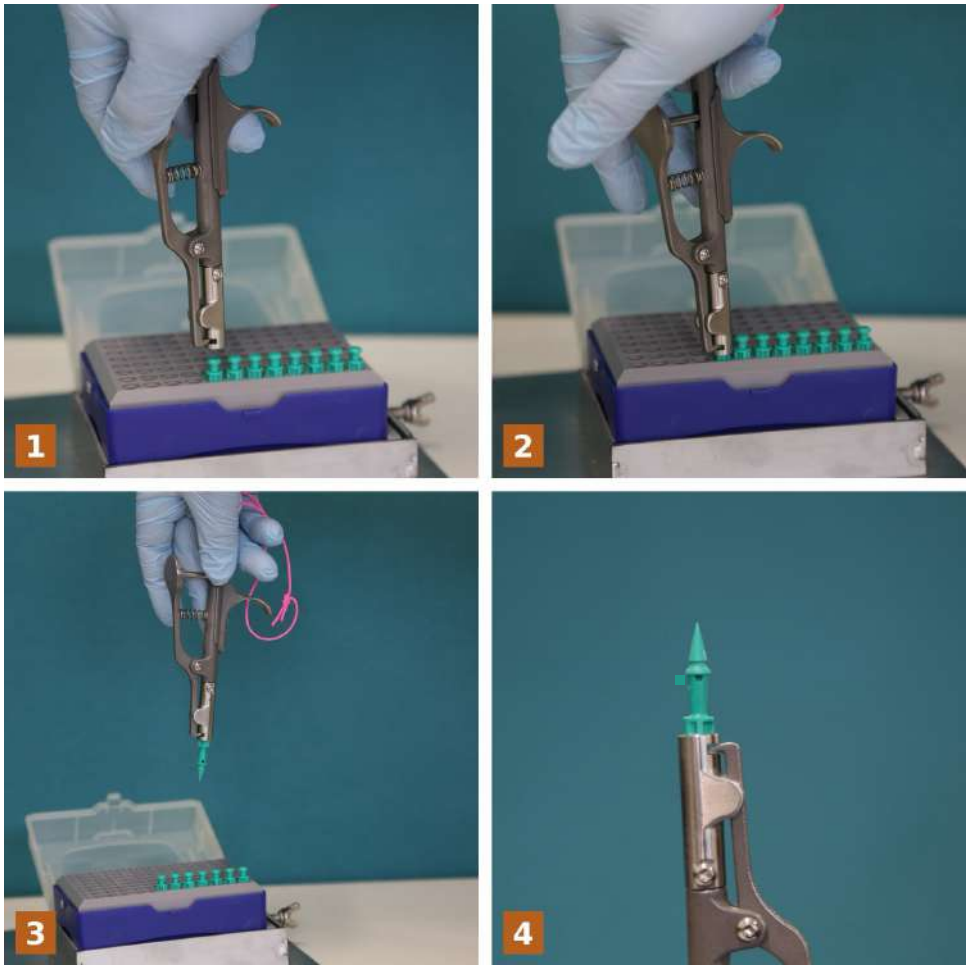


Figure 3. Loading a tip onto the GT tool: (1) position the handle directly above a tip in the tip box; (2) push the handle straight down onto the tip; (3) pull the handle straight up so the tip does not catch; (4) check the tip is fully seated with no gap. Photos: CSIRO.

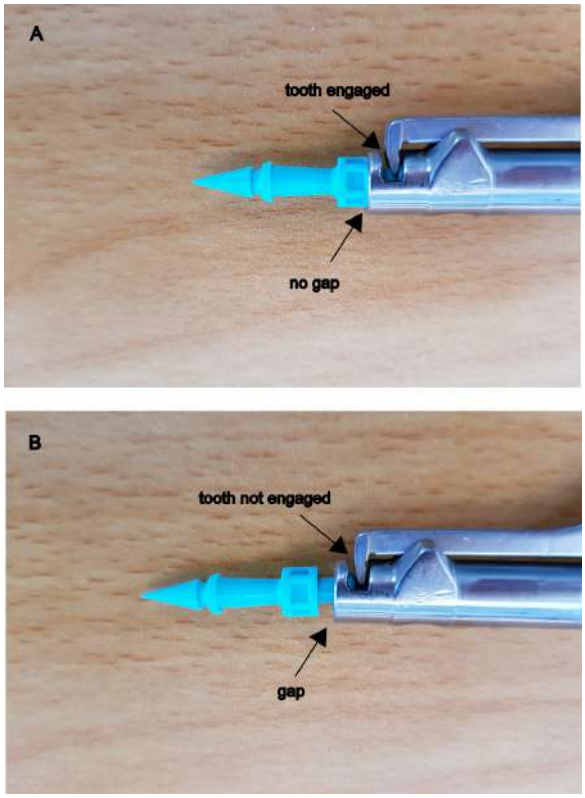


Figure 4. (A) A correctly loaded tip: no gap between the handle and the tip, and the tooth on the thumb lever engaged behind the lip of the tip. (B) A tip that has not been loaded correctly (gap exaggerated). Photos: CSIRO.

Taking the sample

1. Choose a sampling site with firm muscle at least 2 cm thick, usually near the dorsal fin or towards the tail. Avoid the area around the anus, any site with visible blood, and any site that would damage the fish for later processing. Record the sampling site on the data sheet.
2. Do not take the sample through slime or blood. If a clean spot cannot be found, wipe the site with a clean wipe or, preferably, rinse it with clean water first. Do not touch the site with your hands.
3. Push the tip into the muscle at a slight angle, so it passes through the muscle bands rather than between them (Figure 5), until it is embedded almost to the handle. Frozen fish need much more force than fresh or chilled fish and may need a different grip.
4. Give the handle a quick, small twist to break the tissue free, then pull it straight out. For some fish, a slight scooping motion as you pull out helps to collect the tissue.
5. Check that the hole in the tip is filled with tissue. If there is no tissue, or very little, load a new tip and take another sample from a different spot, not the same hole. With practice, a second attempt is rarely needed.

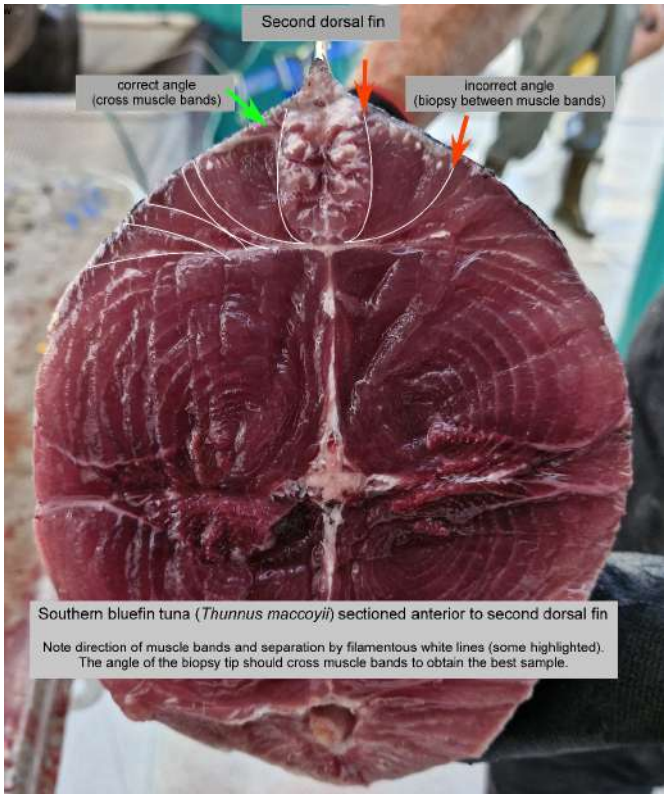


Figure 5. Cross-section of a southern bluefin tuna cut in front of the second dorsal fin, showing the muscle bands separated by fine white lines. The tip should be angled to pass through the muscle bands (correct angle) rather than between them (incorrect angle). Photo: CSIRO.

Transferring the sample

This process requires two people, the clean scribe (two clean hands) and the sampler (one clean hand holding the GT tool).

1. The scribe, with a clean gloved hand, opens the tube and presents the open tube to the sampler. Do not touch the inside of the tube or lid.
2. The sampler places the tip partly into the tube, then pull the trigger and push down the thumb lever to release the tip into the tube (Figure 6).
3. The scribe closes the lid immediately and check the tube number matches the data sheet.
4. The scribe places the tube on ice or in a cool box, out of direct sunlight, until it can be frozen.

The tip stays in the tube with the tissue.

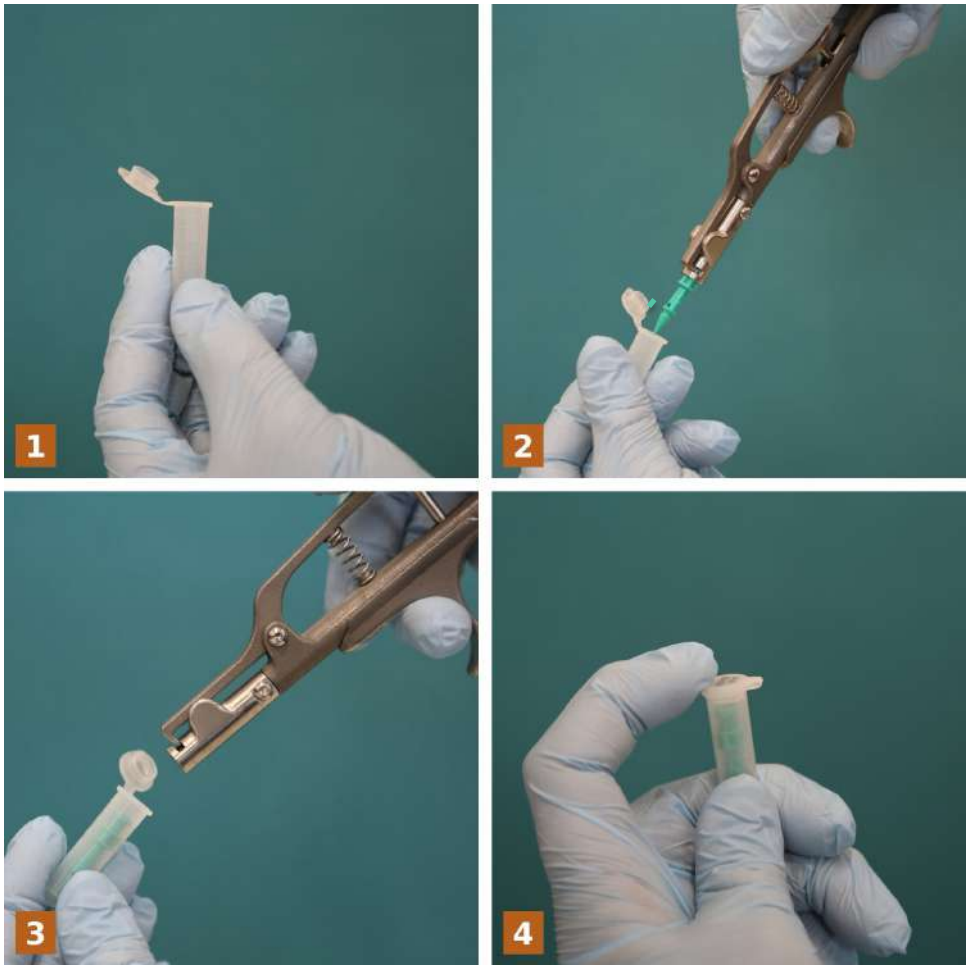


Figure 6. Transferring the tip to the tube: (1) open the tube with a clean gloved hand, without touching the inside of the tube or lid; (2) place the tip partly into the tube and release it; (3) withdraw the tool, leaving the tip and tissue in the tube; (4) close the lid immediately. Photos: CSIRO.

Contamination control

Preventing cross-contamination between samples is the highest priority, because DNA from one fish carried into another fish's sample can prevent reliable genotyping and kinship analysis (Anon. 2018). The GT tool and tips remove the main contamination risk, but contamination can still come from hands, tubes and tips. Samplers should follow these rules for every fish:

- Wear gloves when handling the tool, tips, tubes or vials. Gloves protect samples from DNA and nucleases on skin, as well as from fish tissue.
- Keep gloved hands clean and dry, with no blood or slime. Wash gloved hands in soapy water for 5–10 seconds between handling a fish and handling sampling equipment, and dry them on a clean wipe, never a reusable cloth. Change gloves if they tear or become heavily soiled.
- Never touch the tip with anything except the GT tool.
- Never touch the inside of a tube or lid with anything except the tip.
- Open tip boxes and tubes only immediately before use, and close them straight away.
- Protect tips and tubes from splashes.
- Use each tip only once. Discard any tip that falls out or touches another surface.

- Regularly check the end of the tool handle for any material stuck to it and wipe it off with a clean wipe.
- Use each wipe only once.
- Use the 'clean and dirty' division of roles where two people are available.

Practical risks to watch for: do not re-use a tip after a failed attempt on a different fish, handle tubes with bloody gloves, or leave tubes open on the bench while handling the next fish.

Preservation, storage and transport

The tissue sample is very small, so it must be cooled and frozen quickly to prevent DNA degradation.

Preservation

Freezing is the preferred method of preservation for tip samples, because frozen tissue is easier to remove from the tip in the laboratory and suits high-throughput DNA extraction. Where freezing is not possible, tip samples can be preserved in RNAlater or another suitable preservative. These samples must be stored in screw-cap cryovials pre-filled with preservative, rather than hinged-lid tubes, to prevent the preservative leaking.

Storage

- During sampling, keep tubes on ice or below 4°C, out of direct sunlight.
- At the end of each session, place tubes in numerical order in a labelled 96-well rack freezer box (Figure 7) and record the range of sample numbers on the lid.
- Each rack must contain 92 field samples; leave wells G12 and H12 empty and include two additional blank control tubes (positions designated by the laboratory) for internal quality control (Figure 7).
- Store boxes in a freezer at -20°C or colder. Keep boxes in the freezer at all times except when loading samples or moving them.
- If using a preservative, keep tip samples below 4°C for at least the first 24 hours. After that they can be held at room temperature for transport, and should be stored at 4–8°C or frozen as soon as possible.
- If sampling at sea, label the boxes clearly and tell the crew, so they are not discarded.



Figure 7. Tip tubes stored in order in a fully loaded 96-well rack after sampling, each with a unique label on the lid. Vials with a red X are the 4 blank control vials. Photo: CSIRO.

Packaging and shipment

- Do not seal hinged-lid tubes with parafilm. Frozen samples do not need it, and removing it greatly slows high-throughput processing in the laboratory.
- Wrap the lids of screw-cap cryovials containing preservative with a strip of parafilm about 1 cm wide to prevent leaks.
- Ship frozen samples in a pre-cooled cool box packed with frozen ice blocks, with the lid taped shut. Do not open the box until the samples can be transferred to a freezer at the destination.
- Send copies of the data sheets with the samples, and scan them to the coordinating laboratory before shipment.
- Confirm the shipment date with the receiving laboratory and avoid delivery on weekends or public holidays where possible. Record and report any transport delay, leakage, thawing or other issues.
- Receiving laboratory should record any issues with the shipment, such as defrosted samples, so that these can be rectified for future shipments.
- Contact the receiving laboratory before shipping to confirm the import permit and documentation requirements. Samples from species listed under CITES, such as scalloped hammerhead, require both the sending and receiving organisations to be registered for exchange of CITES specimens.

Labelling and data recording

A genetic sample is only useful if it can be linked to accurate data on the fish it came from. Errors in recording the sample number can make a sample unusable, and erroneous data can be worse than no data (Anon. 2018).

Unique identifiers

- Each tube or vial is pre-labelled with a unique sample number, using labels that withstand freezing (and preservative, where used). The labelling format will vary between projects.
- Each fish is identified by the number on its tube or vial. Where other samples are taken from the same fish (e.g. otoliths) by another program, all samples and records should carry the same number.
- Use tubes or vials in numerical order. If a pre-labelled one cannot be used, write the number clearly on a spare label in permanent marker and note this on the data sheet.
- Check the sample numbers against the data sheet at the end of each session, while errors can still be corrected.

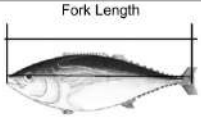
Minimum data fields

The fields in Table 3 combine the PSTBS-IO data sheet (Anon. 2018) and the SPC port and observer forms (Sanchez et al. 2023). Fields marked as required are needed for every genetic sample; recommended fields should be recorded wherever possible.

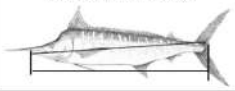
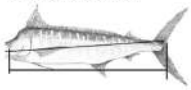
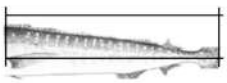
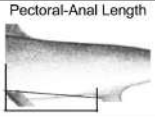
Table 3. Minimum data fields for each tissue sample.

Field	Level	Notes
Sample number (fish ID)	Required	Unique number on the pre-labelled tube or vial
Species code	Required	FAO three-letter code
Sampling date	Required	dd/mmm/yyyy
Sampling start and finish times	Required	Time sampling began and time samples were placed in the freezer (or, for preserved samples, in the cool box), to show how long samples were held before freezing
Sampling location	Required	Port name, or latitude and longitude at sea
Length and length code	Required	Fork length to the nearest cm; IOTC length codes (e.g. FL, LJFL, OFL) where FL is not possible (Figure 8)
Sampler name	Required	Full name
Gear	Required	e.g. LL, PS, GN, PL, HL
Fishing area	Required	Latitude and longitude range of sets, or best available area for artisanal fleets
Preservation	Required	Frozen, or the preservative used (e.g. RNAlater)
Catch or landing date	Recommended	Date of capture, or first and last successful set
Vessel name and trip dates	Recommended	As on the fishing licence
Muscle site	Recommended	e.g. D (near dorsal fin), T (tail)
Fish state	Recommended	Fresh, frozen, slightly defrosted, defrosted
Sex and maturity stage	Recommended	Only where gonads are examined by another program
Comments	Recommended	Failed attempts, replacement labels, damaged fish

Tunas:

Type	Description	Code
Fork Length 	Projected straight distance from the tip of the upper jaw to the shortest caudal ray (fork).	FL
Pre-dorsal Length 	Straight distance from the tip of the upper jaw to the insertion of the first dorsal spine.	LD1

Billfish:

Type	Description	Code
Lower jaw-Fork Length 	Projected straight distance from the tip of the lower jaw to the shortest caudal ray (fork).	LJFL
Orbital-Fork Length 	Projected straight distance from the centre of the eye to the shortest caudal ray (fork).	OFL
Pectoral-Fork Length 	Projected straight distance between the most anterior insertion of the pectoral fin and the fork of the tail.	PFL
Pectoral-Dorsal Length 	Projected straight distance between the most anterior insertion of the pectoral fin and the most anterior insertion of the second dorsal fin.	PDL
Pectoral-Anal Length 	Projected straight distance between the most anterior insertion of the pectoral fin to the most posterior rim of the anal sphincter.	PAL

Sharks:

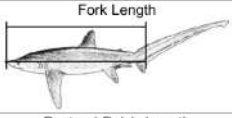
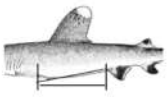
Type	Description	Code
Fork Length 	Projected straight distance from the tip of the snout to the fork of the tail.	FL
Pectoral-Pelvic Length 	Projected straight distance between the most posterior insertion of the pectoral fin to the most anterior insertion of the pelvic fin.	PPS
Interdorsal Space 	Projected straight distance between the most posterior insertion of the first dorsal fin to the most anterior insert ion of the second dorsal fin (if any).	IDS
Pectoral-Anterior Margin 	Projected straight distance between the tip and the base of the anterior margin of the pectoral fin (shark fins).	P1A

Figure 8. IOTC length measurement options and codes for tunas, billfish and sharks, in order of preference. Where fork length (or lower jaw-fork length for billfish) cannot be measured, the next measurement in the list is used and its code recorded. Reproduced from Anon. (2018), based on IOTC conventions.

Data should be recorded on a standard data sheet or entered directly into a standard electronic template, and submitted with the samples, so that sample and data records can be checked against each other on arrival.

Quality assurance

Quality assurance should check that sampling meets these SOPs in practice, and pick up problems early, before large numbers of samples are affected.

- **Training records.** Keep a record of who has been trained and when. New samplers should be supervised for their first sessions, and refresher training provided when procedures change.
- **Data checks.** On arrival, the receiving laboratory checks every sample against the data sheet for missing, duplicate or mismatched numbers, and implausible lengths or species codes.
- **Contamination screening.** Before a new sampling site or team contributes samples at scale, a subsample (e.g. 100 samples) should be genotyped and screened for cross-contamination, for example using individual heterozygosity. Results should be reported back to the sampling team.
- **Ongoing monitoring.** Contamination rates, DNA quality and data errors should be tracked by site and team, so that retraining can be targeted where needed.
- **Feedback.** Samplers should record and report any problems, such as dislodged tips, thawed samples or lost data sheets, on the data sheet or to the coordinator.

Discussion and recommendations

A common set of tissue sampling SOPs for CKMR would allow samples collected across the Indian Ocean to be combined in a single analysis and reduce the risk of artificial differences between sampling teams. The GT tool and tips are well suited to this role, because they combine low contamination risk, fast sampling and samples ready for high-throughput DNA extraction. These are the main requirements for large-scale programs such as CKMR.

The SOPs are deliberately limited to CKMR tissue sampling. Smaller genetic studies, such as population structure and species identification, have different requirements and are better served by larger tissue samples collected with a biopsy punch and stored in preservative. The SOPs are also designed to sit alongside protocols for other biological samples, such as otoliths and gonads, so that a single fish can be sampled for several purposes with one shared identification number.

Adoption across the network will depend on practical issues that the SOPs do not resolve, including:

- the supply and cost of GT tools, tips and pre-labelled tubes, and who coordinates their distribution
- access to freezers at sampling sites, which determines whether tip samples can be frozen or need to be stored in preservative
- arrangements for storing samples and data, and for agreeing their access and use

The WPDCS is invited to:

1. review the proposed SOPs and provide feedback
2. consider recommending the SOPs as a common standard for CKMR tissue sampling of IOTC species, including through the biological sampling network being developed by the IOTC Secretariat and CNRS
3. note that the SOPs will be refined as experience is gained from wider sampling

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