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**Understanding connectivity of key tuna species in the Western Pacific and East Asia region
with the WCPFC Convention Area: results of Project 128**

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Prepared¹ by CSIRO, Indonesia, Philippines, Vietnam, and SPC

¹ The drafting team for this document were Brad Moore, Jessica Farley, Pierre Feutry, and Peter Grewe (CSIRO), Fayakun Satria and Lilis Sadiyah (Research Center for Fishery, National Research and Innovation Agency, Indonesia), Suzette Barcoma (National Fisheries Research and Development Institute, Philippines), Vu Duyen Hai (Directorate of Fisheries, Vietnam), and Giulia Anderson and Paul Hamer (SPC).

Understanding connectivity of key tuna species in the Western Pacific and East Asia region with the WCPFC Convention Area: results of Project 128

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Executive summary

The Western Pacific East Asia (WPEA) region supports valuable fisheries for skipjack tuna (*Katsuwonus pelamis*; SKJ) and yellowfin tuna (*Thunnus albacares*; YFT), providing a source of food and livelihood for millions of people in coastal communities in the region. Collectively, these fisheries account for over 30% of the total annual catch of tuna species and over 40% of the total YFT catch in Western and Central Pacific Fisheries Commission Convention Area (WCPFC-CA). While these fisheries are assumed to form part of a larger Western and Central Pacific Ocean (WCPO) stock for assessment and management purposes, evidence suggests there may be limited connectivity of SKJ and YFT between at least some areas of the WPEA region and the broader WCPO.

In recognition of the importance of understanding connectivity of key tuna species within the WPEA region, and between the WPEA region and broader WCPO, the WCPFC Secretariat contracted CSIRO to undertake a feasibility study (Project 128) to assess regional connectivity patterns of SKJ and YFT, with a particular emphasis on the WPEA region, and to develop a Terms of Reference (TOR) outlining the scope of work required to address this objective.

This paper presents the results of Project 128. The paper comprises three sections:

Section 1 provides a description of the project methodology, activities undertaken, and information reviewed and considered as part of Project 128, including current knowledge of SKJ and YFT connectivity in the WCPO, techniques to investigate connectivity, and information regarding the feasibility of sampling within the WPEA region to improve knowledge of connectivity of both species.

Section 2 comprises a draft TOR for a project designed to improve understanding of connectivity of SKJ and YFT within in the WPEA region, and between the WPEA region and the broader WCPFC-CA (i.e., the ‘full’ project). The draft TOR outlines a 4-year project using a modern genomic approach – Low Coverage Whole Genome Sequencing (LCWGS) – that could feasibly provide provisional results to inform the 2028 SKJ and 2029 YFT stock assessments, provided funding is sourced to allow activities to commence in Quarter 1 of 2026. Note that at this stage no funding is sought from WCPFC for this ‘full’ project.

In Section 3, a separate draft TOR is presented for a smaller project (‘Phase 1’ of the ‘full’ project detailed in Section 2) which would consist of a desktop study and preliminary genetic sequencing to inform the strategic direction of the ‘full’ project as well as refine cost estimates for the sample collection and processing components of the budget. This work would involve:

- (i) Modelling to assess the impact of different connectivity hypotheses on the results of the regional YFT (and potentially SKJ) stock assessment and subsequent management advice.

- (ii) An analysis of sample size requirements and feasibility of the LCWGS approach for assessing connectivity, including indicative costs, based on sequencing and analysis of existing samples.
- (iii) Refinement of the TOR for the ‘full’ project based on the findings of (i) and (ii) above.

We invite SC21 to:

- Note the activities undertaken as part of Project 128 outlined in Section 1.
- Review and provide feedback on the ‘full’ project design and draft TOR provided in Section 2.
- Support the draft TOR for the ‘full’ project provided in Section 2 as a scientifically sound and robust approach for assessing fine-scale connectivity for SKJ and YFT within the WPEA and WCPO regions using modern genetic tools.
- Consider prioritising the TOR provided in Section 3 when assessing new research projects for WCPFC funding in 2026.

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Introduction

The Western Pacific East Asia (WPEA) region, encompassing the waters of Indonesia, Philippines, and Vietnam, supports valuable fisheries for skipjack tuna (*Katsuwonus pelamis*; SKJ) and yellowfin tuna (*Thunnus albacares*; YFT), collectively taking over 30% of the annual catch of tuna species of the Western and Central Pacific Fisheries Commission Convention Area (WCPFC-CA), including 40% of the total YFT catch (McDonald 2021).

At present, SKJ and YFT in the WCPO are considered to represent single biological stocks for assessment and management purposes. However, there is evidence to suggest that SKJ and YFT in at least some areas of the WPEA region may exhibit more population structure than is currently assumed for management. Differences in genetic markers have been observed between YFT sampled from Indonesia's Archipelagic Waters (IAW) and the adjacent WCPO (Proctor et al. 2019), suggesting longer-term reproductive isolation, while biological differences have also been reported (Farley et al. 2018, Itano 2000). Tagging data, although mainly restricted to smaller fish and short times at liberty, indicate that most individuals are generally recaptured close to where they were tagged (Moore et al. 2020a).

In recognition of the importance of improving understanding of connectivity within the WPEA region, and between the WPEA region and broader WCPO, in 2025 the WCPFC Secretariat contracted the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia, to implement WCPFC Project 128: Understanding connectivity of the yellowfin and skipjack stocks in the Western Pacific and East Asia region with the WCPFC-CA. The objectives of Project 128 were to:

1. Undertake a feasibility study to understand the connectivity of key stocks (YFT and SKJ) across the region, with a particular focus on the western Pacific Ocean and East Asia region (Region 2 for YFT and Region 5 for SKJ) and the wider WCPFC-CA to reduce uncertainties in stock assessments and produce better CMMs.
2. Develop a Terms of Reference (TOR) and budget for SC21, considering the work necessary to answer this question.

This Working Paper is an output of Project 128. The paper is divided into three sections:

1. Section 1: A description of the project methodology, activities undertaken, and information reviewed and considered as part of Project 128, including a summary of current knowledge of SKJ and YFT connectivity in the WCPO and information regarding the feasibility of sampling within the WPEA region to collect the necessary material to improve knowledge of connectivity of both species.
2. Section 2: A draft TOR for a phased project designed to improve understanding of connectivity of key tuna species within the WPEA region, and between the WPEA region and the broader WCPFC-CA (i.e., the 'full' project).
3. Section 3: TOR for the Phase 1 work described in Section 2 above to undertake the necessary first steps to support further proposal development and external funding acquisition for the full project, including refinement of minimum sample size requirements and the resulting cost estimates involved with sample processing.

Section 1: Project 128 research methodology, activities undertaken, and information reviewed as part of WCPFC Project 128

In developing a draft TOR for a project to examine connectivity in the WPEA region and between the WPEA and WCPO regions, the research provider and proponents for Project 128 were tasked with considering: 1) current knowledge of connectivity/stock structure; 2) the relevant techniques to answer questions on stock structure/connectivity; 3) the samples needed to apply those techniques (including both sample numbers and optimal locations); and 4) the regional capacity to achieve required sampling levels. This section of the report details the activities undertaken and information reviewed during Project 128 and synthesises discussions among project staff regarding sampling design.

1.1. Technical workshop

A technical workshop with project partners was held on 1–2 May 2025, in Sydney, Australia. The workshop was attended by country representatives from each of the WPEA countries, the WPEA Sustainable Pacific Fisheries project (WPEA-SPF) Project Manager, and SPC and CSIRO project staff (Table 1).

Table 1. Participants at the 1–2 May 2025 technical workshop.

Participant	Organisation
Fayakun Satira	Research Center for Fishery, National Research and Innovation Agency (BRIN), Indonesia
Lilis Sadiyah	Research Center for Fishery, National Research and Innovation Agency (BRIN), Indonesia
Suzette Barcoma	National Fisheries Research and Development Institute (NFRDI), Philippines
Franciso Torres, Jr. (o)	National Fisheries Research and Development Institute (NFRDI), Philippines
Casiano Choresca, Jr. (o)	National Fisheries Research and Development Institute (NFRDI), Philippines
Luz Romena (o)	National Fisheries Research and Development Institute, (NFRDI), Philippines
Vu Duyen Hai	Directorate of Fisheries, Vietnam
Lars Olsen	WPEA-SPF Project Manager, WCPFC Secretariat
Giulia Anderson	Pacific Community (SPC), New Caledonia
Peter Grewe	CSIRO Environment, Australia
Pierre Feutry	CSIRO Environment, Australia
Brad Moore	CSIRO Environment, Australia

o = attended online

The technical workshop discussed and reviewed the following information:

1. Definitions of stock structure and connectivity relevant to pelagic fisheries management.
2. Techniques used to investigate connectivity (including emerging genomic approaches).

3. National fisheries data (species, gears, locations, and sizes of fish caught), existing capacity to undertake sampling, and current port and observer sampling programs of the three WPEA countries.
4. Current knowledge of connectivity of SKJ and YFT in the region from genetic and non-genetic approaches.
5. What samples are already collected that could feasibly be analysed to provide insight into connectivity, without the need to embark on new sampling initiatives, at least initially.

The workshop then discussed knowledge gaps and key hypotheses regarding connectivity of SKJ and YFT that could be tested and mapped out a resulting draft sampling strategy. A summary of the information that was presented to the workshop, the key findings of the workshop, and the draft sampling strategy were then presented at the final day of the WPEA-SPF Stock Assessment and Harvest Strategy workshop, which was held from 5–9 May in Sydney, Australia (see [SC21-2025/RP-WPEA-01](#)). In drafting this document, follow-up discussions with project partners were held online.

1.2. Current knowledge of the connectivity of skipjack and yellowfin tuna between the WPEA region and the broader WCPO

This component reviews information on reproductive biology, spawning areas and larval distributions, growth, maturity, genetics, tagging data, otolith chemistry, parasites, and muscle stable isotopes, focusing primarily on the WPEA region and the broader WCPO. It provides a summary of current biological knowledge discussed at the May workshop and gleans from and builds upon information and literature summarised in recent reviews by Pecoraro et al. (2017)², Moore et al., (2020a, b), and Hamer et al. (2023).

Skipjack tuna

Spawning areas and larval distributions

Spawning in SKJ is considered to take place where sea surface temperatures (SSTs) generally exceed 24°C. This is thought to result in year-round spawning in tropical waters and seasonal spawning elsewhere. Predicted larval distributions from geostatistical modelling of Japanese larval survey data reported as Nishikawa et al. (1985) by Ijima and Jusup (2023) support the hypothesis of year-round spawning of SKJ in tropical waters, with larvae predicted to occur in a continuous band in the tropical WCPO, extending polewards seasonally (Figure 1).

² References for this section can be found in [Appendix 1](#).

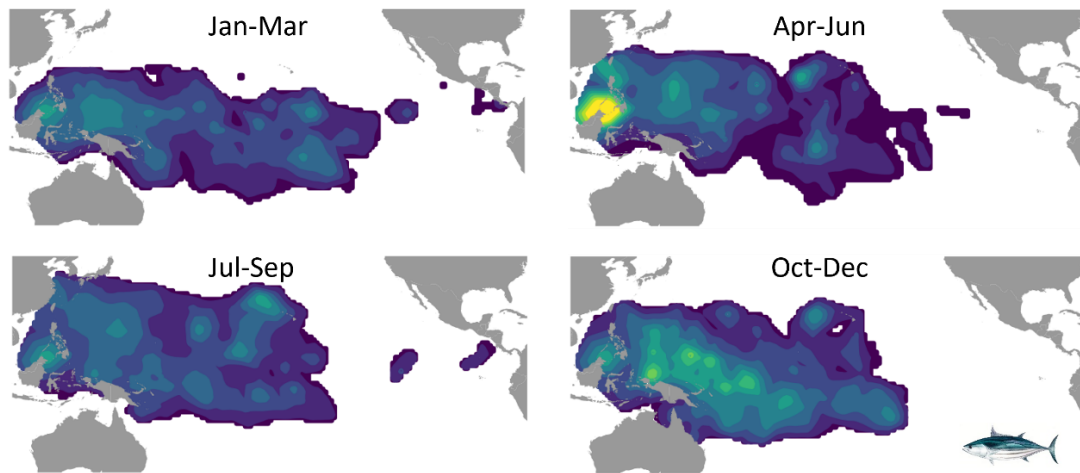


Figure 1. Seasonal densities of skipjack tuna larvae within the Pacific Ocean for the period 1960-1985 based on geostatistical modelling of the Nishikawa et al. (1985) data set by Ijima and Jusup (2023).

Growth

Ashida et al. (2018) report differences in growth rates of larval and juvenile SKJ collected in the Western Pacific Warm Pool and the North Pacific Tropical Gyre, suggesting that these fish had grown in different environments. In their meta-analysis of SKJ growth, Macdonald et al. (2022) noted the potential for SKJ growth to vary within the Pacific, evidenced in part by the large variation in published growth curves derived from different studies across the region, but highlighted the longstanding uncertainties in direct age estimation of SKJ from otoliths and other hard parts.

Maturity

Differences have been observed in SKJ length at 50% maturity, as well as batch fecundity and length of spawning season between tropical and temperate areas of the western Pacific Ocean (Ashida 2020), consistent with seasonal expansion of spawning grounds with increased SST.

Population genetics

Studies into SKJ population structure generally indicate some, albeit weak, structuring within the Pacific Ocean, with differences in blood groups observed between Hawaii and French Polynesia (Sprague and Holloway 1962), and in blood groups and isozymes between the far western Pacific (Japan, Northern Mariana Islands and Palau) and the central and eastern Pacific (including French Polynesia and Line Islands of Kiribati) (Fujino 1970). Based on allozymes, Sharp (1978) hypothesised that there were at least five units of SKJ in the Pacific Ocean, encompassing New Zealand, north-eastern Pacific, south-eastern Pacific, north-western Pacific, and Papua New Guinea (PNG) / Solomon Islands. From observed spatial clines in enzyme allele frequencies, Richardson (1983) proposed an Isolation by Distance (IBD) model for SKJ in the Pacific. In contrast, Ely et al. (2005) failed to detect any differentiation in mitochondrial DNA (mtDNA) and nucleotides between SKJ from Solomon Islands and the eastern Pacific Ocean (EPO).

Using next generation sequencing (NGS) and single nucleotide polymorphism (SNP) markers, Grewe et al. (2019) reported significant differentiation between SKJ sampled from the EPO

and the Indo-Pacific (Maldives, Bismarck and Coral Seas), but not within the Indo-Pacific. Further sampling and analysis, including of fish landed at Lampulo in the north-eastern Indian Ocean (IO), indicates limited connectivity of IO fish with those from the Bismarck and Coral Seas.

Tagging

A large number of SKJ have been tagged in the WCPO over many years, with approximately 140,000 releases of conventionally tagged SKJ conducted in the Skipjack Survey and Assessment Program (SSAP; 1977–1981), ~100,000 releases occurring in the Regional Tuna Tagging Programme (RTTP; 1991–1996), and ~300,000 releases of conventionally tagged SKJ occurring in the Pacific Tuna Tagging Programme (PTTP; 2006–present) (SPC-OFP 2025). A range of national initiatives have also been implemented (e.g. Japan has tagged approximately 160,000 SKJ between 1966 and 2021). Under the PTTP, dedicated tagging cruises took place in Indonesia and Philippines in 2008–2009. In recent years, focus has shifted towards the central and western equatorial Pacific.

There have been approximately ~58,500 recoveries of SKJ tagged under the PTTP to date (SPC-OFP 2025). In general, results from these tagging programs indicate that while some SKJ undertake long-distance movements, including from the WCPO to the EPO, most individuals are recaptured close to the vicinity in which they were tagged. Seasonal movements to higher latitudes with poleward flowing currents are also apparent (Blackburn and Serventy 1981, Fujino 1996, Kiyofuji et al. 2019).

Of those tag releases that have occurred in SKJ assessment region 5, i.e., the area covering the WPEA region, all recoveries have occurred between approximately 20°N and 10°S, and most recoveries have occurred in region 5 (Figure 2). Of note, no SKJ tagged in northern Indonesian waters have been reported as recaptured in the neighbouring Celebes or Sulu Seas. Where SKJ moved outside of region 5, most recaptures have occurred in the Bismarck Sea, and to a lesser degree the Solomon Sea, in assessment region 6, or northern PNG waters, High Seas Pocket 1 (HSP1), FSM, and Nauru, in assessment region 7 (Figure 2). Similarly, most SKJ recaptured in assessment region 5 were either originally tagged in the same region, or in assessment region 6 in the Bismarck and Solomon Seas (Figure 3). Notwithstanding caveats associated with time-at-liberty, the distribution of tag releases, the distribution and variability of fishing effort, and the point-to-point nature of the conventional tagging data, observations from these paired release-recovery data suggest some degree of regional fidelity of SKJ in the WCPO.

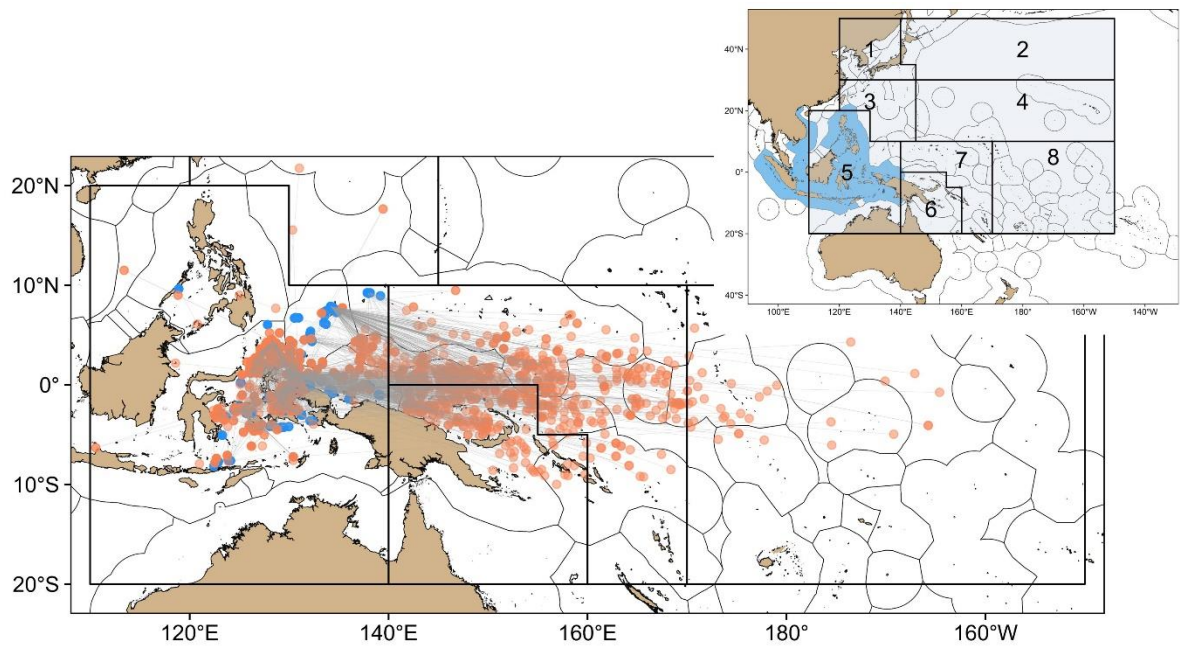


Figure 2. Locations of conventional tag releases (blue dots) and recaptures (orange dots) for SKJ tagged in assessment region 5. Records shown are for tagged individuals that were at liberty for at least 30 days. Shown in the inset map is the regional structure used in the 2022 WCPO SKJ stock assessment (Castillo Jordán et al. 2022).

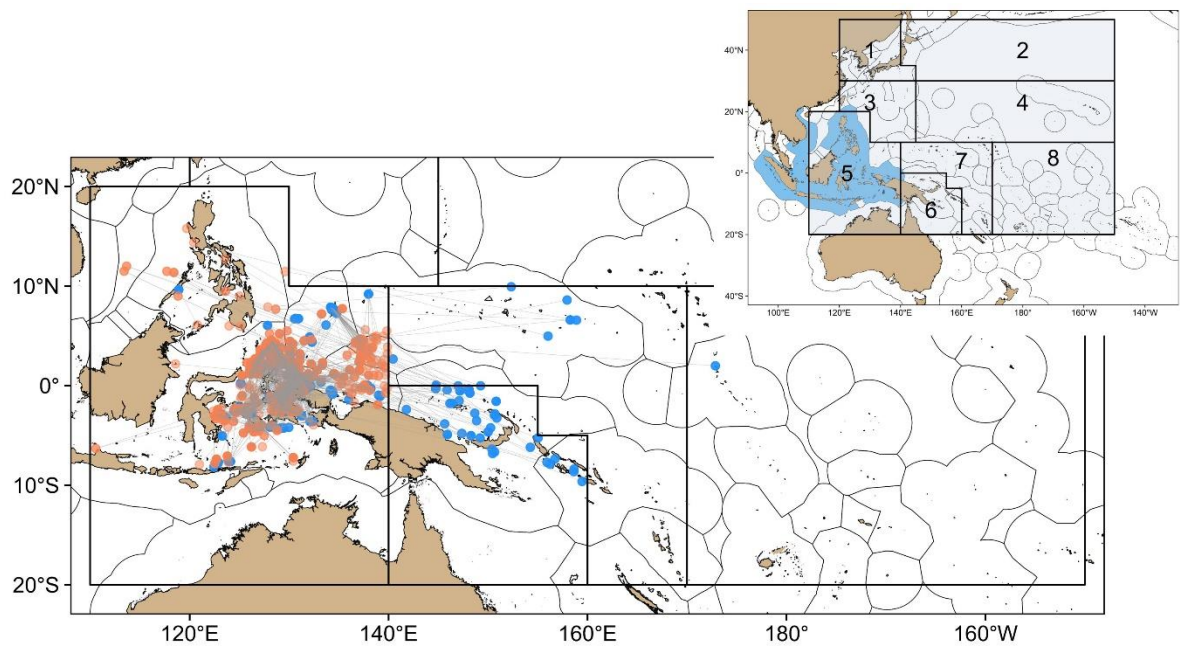


Figure 3. Locations of conventional tag releases (blue dots) and recaptures (orange dots) for SKJ recaptured in assessment region 5. Records shown are for tagged individuals that were at liberty for at least 30 days. Shown in the inset map is the regional structure used in 2022 WCPO SKJ stock assessment (Castillo Jordán et al. 2022).

Otolith chemistry

Otolith strontium: calcium ratios in SKJ sampled from the tropical western Pacific (Marshall Islands and Palau) and off the coast of Japan indicate similar movement patterns to that from tagging data, with most fish displaying regional residency in tropic waters, some displaying

seasonal cyclical movements between the tropics and temperate waters, and that SKJ in temperate regions have tropical origins (Arai et al. 2005).

Muscle stable isotopes

Based on $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ signatures, Chang et al. (2022) observed that SKJ off western Chinese Taipei had a slightly elevated trophic position compared to SKJ off eastern Chinese Taipei, suggesting these fish had not mixed, at least over the scale of their muscle nitrogen turnover rate (i.e., half-life = approximately 2–6 months). However, these results may have been confounded with size-related effects, with SKJ from eastern waters being significantly larger than those from the west.

Parasites

The only study to date that has used parasites as biological tags to inform SKJ movement found no evidence for the presence of more than one parasitological stock of SKJ in the Pacific (Lester et al. 1985).

Summary of SKJ connectivity

The information summarised above was used to develop a conceptual model of SKJ connectivity in the WPEA region and adjacent IO and WCPO waters (Figure 4). Genetic, biological, and tagging information to date suggest limited structure of SKJ within the WCPO, with connectivity between tropical and sub-tropical regions, as well as between tropical and temperate regions through poleward flowing currents (i.e., Kuroshio Current and East Australian Current). Population genetics suggests separation of fish from the eastern IO and those from the Bismarck and Corals Seas, however the relationships between fish from each of these areas and the WPEA region is unknown.

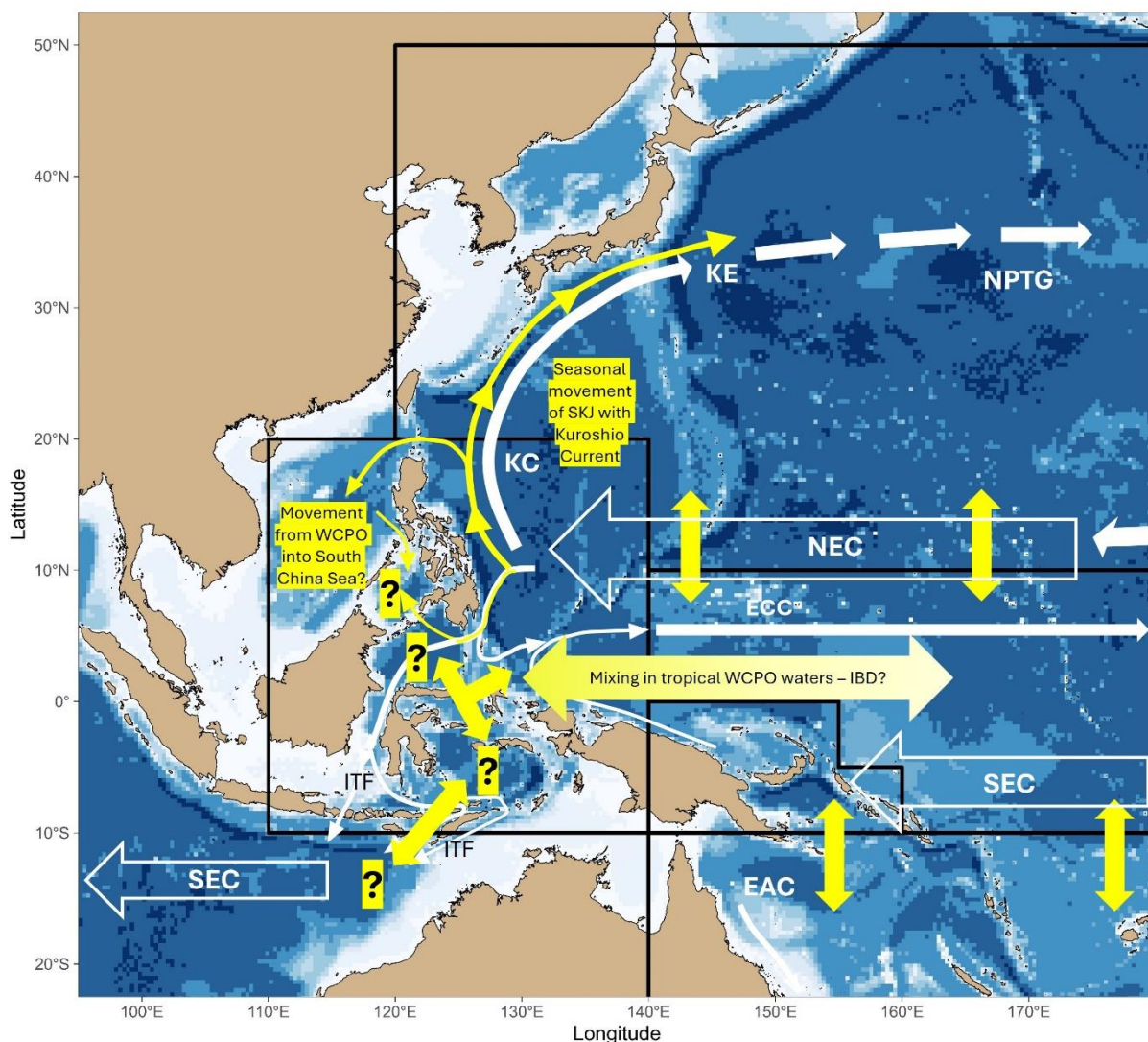


Figure 4. Conceptual model of SKJ population connectivity in the WPEA region and western Pacific Ocean. Potential fish movement/connectivity is shown with yellow arrows. Key knowledge gaps are indicated with question marks. Also shown are the major currents in the region (white arrows), bathymetry (darker blue = deeper areas), and the regional structure used in the 2022 SKJ stock assessment (Castillo Jordán et al. 2022). IBD = Isolation by Distance. EAC = East Australian Current, ECC = Equatorial Counter Current, ITF = Indonesian Through Flow, KC = Kuroshio Current, KE = Kuroshio Extension, NEC = North Equatorial Current, NPTG = North Pacific Tropical Gyre, SEC = South Equatorial Current.

Yellowfin tuna

Spawning areas and larval distributions

Information from reproductive studies and larval sampling of YFT show a broad continuous spawning region across tropical waters of the WCPO. Spawning occurs all year in the tropics, and seasonally in the sub-tropics when SSTs exceed 24°C. Seasonal spawning has been observed in the Coral Sea in October-March, while seasonal spawning peaks also appear to occur around Philippines, despite SST being consistently above 24°C. Geostatistical modelling of Japanese larval survey data by Ijima and Jusup (2023) estimate higher larval densities in a

broad region of the western Pacific from Philippines south to PNG and Solomon Islands across all seasons, with lower densities occurring throughout the entire equatorial region of the WCPO (Figure 5).

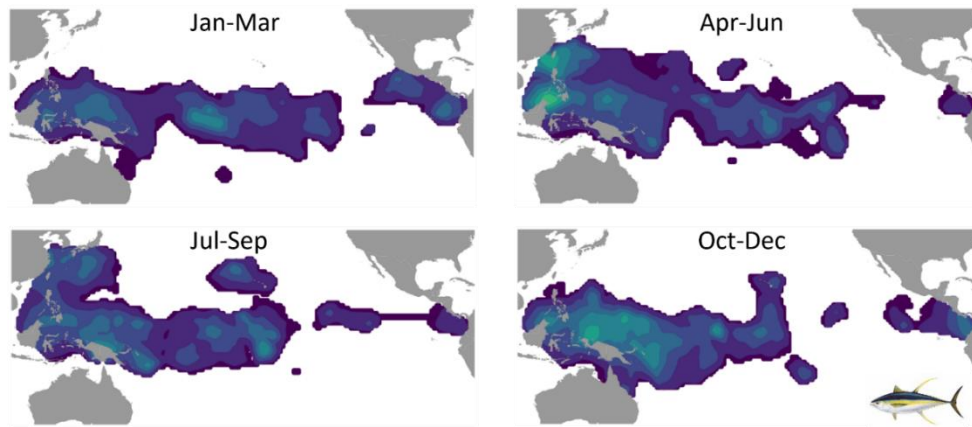


Figure 5. Seasonal densities of yellowfin tuna larvae within the Pacific Ocean for the period 1960–1985 based on geostatistical modelling of the Nishikawa data set by Ijima and Jusup (2023).

Growth

Geographic variation in YFT growth has been observed between the WCPO and Hawaii. However, it is unclear whether these differences reflect spatial structuring or result from methodological differences in otolith preparation and ageing among studies or differences in sample numbers between areas and across different parts of the growth curve (Farley et al. 2018, Hamer et al. 2023). Growth estimates from length modes within MULTIFAN-CL models suggest slower growth of YFT in Indonesia and Philippines compared to the broader WCPO (Hoyle et al. 2009).

Maturity

Geographic differences in the length at which 50% of female YFT mature (L_{50}) have also been observed in the WCPO, with female YFT in Indonesia and Philippines maturing at smaller lengths (95% confidence intervals around L_{50} estimates ranging from 96.5 to 99.5 cm fork length (FL)) than those in equatorial western Pacific (107.2–108.5 cm FL), and Hawaii (110.1–114.6 cm FL) (Itano 2000).

Population genetics

Early genetic studies of YFT in the WCPO did not detect any significant population structure, likely due to the sensitivity of the markers used. For example, Fujino and Kang (1968) found no difference in transferrin markers among samples from Hawaii and Kiribati (Line Islands), or between these locations and the EPO. Scoles and Graves (1993) found no difference in mtDNA markers between YFT sampled from Australia, PNG, Hawaii, Mexico, or Ecuador.

Recent genetic studies have yielded contrasting results. Using microsatellite markers, Appleyard et al. (2001) found no evidence of population structure among YFT from Indonesia, Coral Sea, Solomon Islands, and east Australia, but “small but significant” differentiation between Philippines and Fiji. Also using microsatellites, Aguila et al. (2015) suggested

population structure in YFT between Philippines (pooling samples from West Philippines Sea, Sulu Sea, East Philippines Sea, and Celebes Sea) and the Bismarck Sea, PNG. Based on SNPs, Grewe et al. (2015) observed evidence for population structuring among YFT from the EPO, Tokelau, and the Coral Sea, concluding that YFT from these locations represent reproductively isolated units. No difference was found in SNPs of YFT from Australia, Fiji, and Marshall Islands (Evans et al. 2019).

In a recent study funded by the Australian Centre for International Agricultural Research (ACIAR, project FIS/2009/059), Proctor et al. (2019) used SNPs, as well as otolith chemistry and parasites (see below) to examine connectivity of YFT (and BET) among the Indonesian Archipelago and adjacent waters. They sampled young-of-the-year (YOY) fish (approximately 25–50 cm FL) from 11 ports in both 2013 and 2014: 9 locations across the Indonesian archipelago and 2 ‘outlier’ locations: Maldives and Solomon Islands. The Indonesian sampling ports were Padang (West Sumatra), Palabuhanratu (West Java), Prigi (southern East Java), Kendari (SE Sulawesi), Gorontalo (North Sulawesi), Bitung (North Sulawesi), Ambon (Maluku), Sorong (West Papua), and Jayapura (Papua) (Figure 6). The outcomes of the genetic analyses suggested at least 2 or 3 genetic groupings for both species, with separation of YFT between IAW and both the eastern IO and the WCPO.

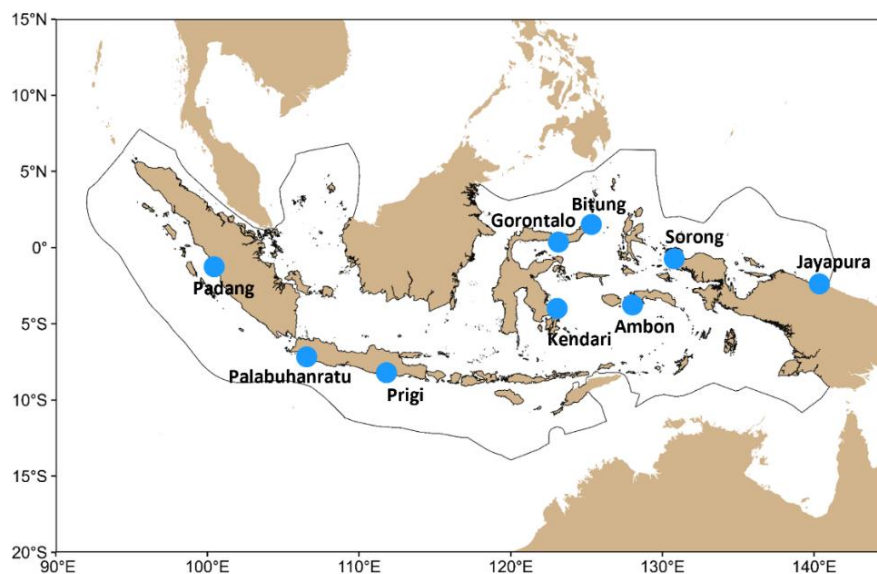


Figure 6. The nine Indonesian ports where sampling of yellowfin and bigeye tuna took place under the ACIAR project FIS/2009/059 by Proctor et al (2019). Also sampled during that project were the Maldives in the Indian Ocean and Noro in Solomon Islands.

Tagging data

Approximately 120,000 releases of tagged YFT have occurred during the PTPP, with a further ~50,000 releases occurring collectively during the earlier SSAP and RTPP (SPC-OFP 2025). A range of national initiatives have also been implemented.

There have been approximately 19,500 recoveries of fish tagged under the PTPP to date (SPC-OFP 2025). Of those releases that have occurred in YFT assessment region 2, i.e., the area covering the WPEA region, most recoveries have occurred in the same region (Figure 7). Of

note, no fish tagged in northern Indonesian waters have been reported as recaptured in the neighbouring Philippines. Where YFT moved outside of region 2, most recaptures have occurred in the western Bismarck Sea, in assessment region 3, or northern PNG waters, in assessment region 4 (Figure 7). Similarly, most YFT recaptured in assessment region 5 were either originally tagged in the same region, or in assessment region 3 (Figure 8). Notwithstanding caveats associated with time-at-liberty, the distribution of tag releases, the distribution and variability of fishing effort, the point-to-point location information yielded by conventional tagging data, and the overall small size of YFT tagged, these observations suggest some degree of regional fidelity of YFT.

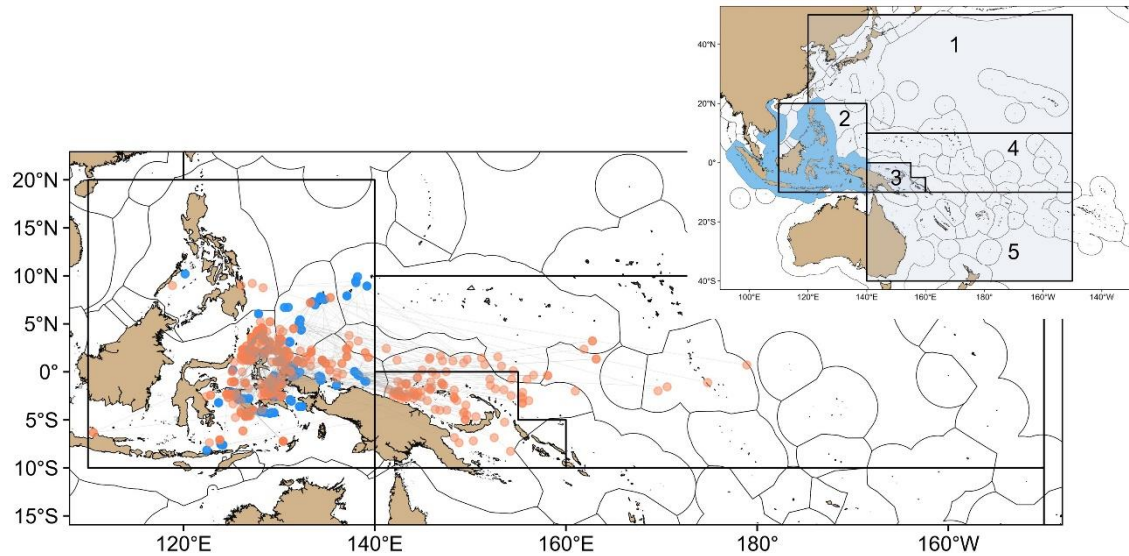


Figure 7. Locations of conventional tag releases (blue dots) and recaptures (orange dots) for YFT tagged in assessment region 2. Records shown are for tagged individuals that were at liberty for at least 30 days. Shown in the inset map is the regional structure used in the 2023 YFT stock assessment (Magnusson et al. 2023).

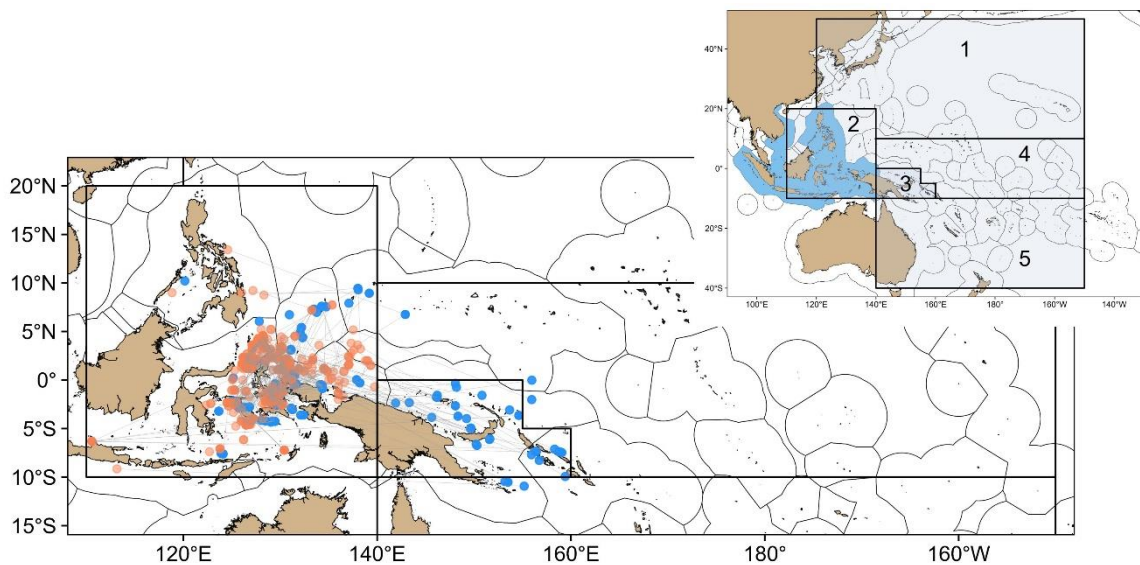


Figure 8. Locations of conventional tag releases (blue dots) and recaptures (orange dots) for YFT recaptured in assessment region 2. Records shown are for tagged individuals that were at liberty for at least 30 days. Shown in the inset map is the regional structure used in the 2023 YFT stock assessment (Magnusson et al. 2023).

A summary of tagging data for YFT (and BET) tagged during Japanese tagging programs was provided by Matsumoto and Satoh (2017). Of those YFT tagged around Nansei Islands, in Japan's EEZ between Japan and Taiwan, several fish moved south into the waters of Philippines and Indonesia, including into the West Philippines/South China Sea, the Celebes Sea, and Pacific Ocean waters east of Philippines and north of West Papua. No YFT tagged in Japan were reported as being recaptured within IAW. Several fish tagged around Nansei islands also moved eastwards with the Kuroshio Extension, potentially linking with populations in the eastern part of the WCPO/Hawaii through the North Pacific Tropical Gyre.

A number of electronic tag deployments of YFT have also occurred in recent years. In the western Pacific, most releases have occurred in the Bismarck and Solomon Seas. Movement paths typically indicate that most tagged fish remain close to regions in which they were tagged (Figure 9).

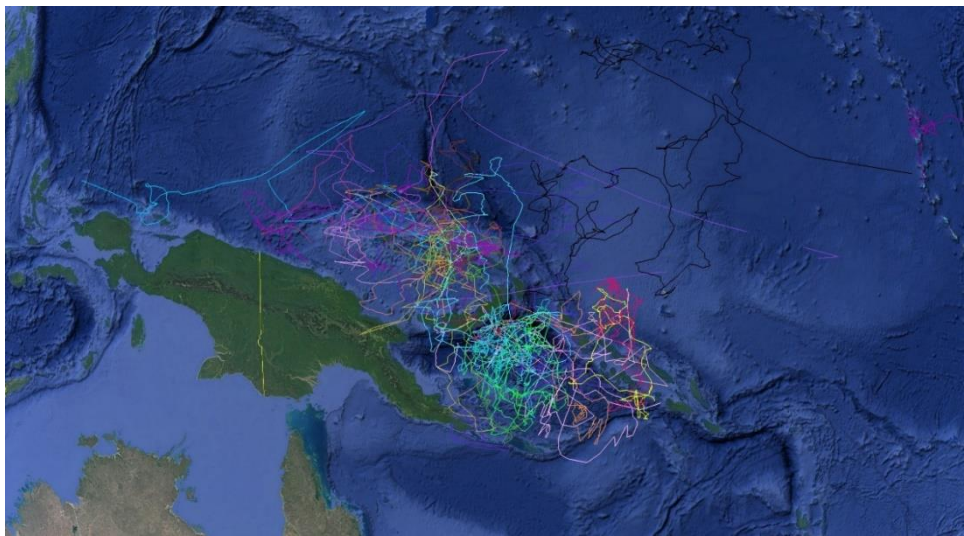


Figure 9. Tracks of electronically tagged YFT in the western Pacific. Data are from the Pacific Tuna Tagging Portal managed by SPC.

Otolith chemistry

Several studies have investigated patterns in otolith chemistry to examine movement and connectivity of YFT in the WCPO. Wells et al. (2012) found that YOY YFT collected from Hawaii, Kiribati's Line Islands, Republic of the Marshall Islands (RMI), Philippines, and Solomon Islands had distinct $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ isotopic signatures in their otolith cores. The authors then examined sub-adults (age-1) collected from Hawaii to investigate nursery-specific contribution rates. Most sub-adult YFT in the Hawaiian fishery had otolith core chemistries representative of nursery areas within Hawaii, with a small number having core chemistries indicating that they had originated from equatorial nurseries outside Hawaii.

Using trace elements as well as $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ isotopes, Rooker et al. (2016) reanalysed the same otoliths examined by Wells et al. (2012), along with additional samples from subadult YFT from RMI. Results suggested that none of the sampled subadult YFT in RMI or Hawaiian waters were derived from Indonesia/Philippines, but rather that almost all individuals were derived from local spawning.

As part of ACIAR project FIS/2009/059, Proctor et al. (2019) examined stable isotopes of carbon ($C^{13}:C^{12}$) and oxygen ($O^{18}:O^{16}$) in whole otoliths, as well as elemental concentrations at point locations using laser ablation inductively coupled plasma mass spectrometry (LA-ICPMS), in YOY YFT collected from Maldives, Indonesia, and Solomon Islands (Figure 6). These approaches showed distinct patterns in chemistry of otoliths sampled from these areas, leading Proctor et al. (2019) to conclude that there was little mixing of juvenile YFT among areas, including between IAW and the WCPO.

Satoh et al. (2023) investigated mixing rates of YFT between Japan and areas of the western Pacific Ocean using $\delta^{13}C$ and $\delta^{18}O$ isotopes in whole otoliths of small juveniles (mean: 5.8 cm standard length (SL)) and in otolith cores of large juveniles (mean 32.4 cm SL). Observed patterns suggested that most large juveniles captured around Japan have tropical origins, and that immigration from the equatorial western Pacific spawning areas, likely via the North Equatorial Current and the Kuroshio Current, was most important for juvenile recruitment around Japan.

Parasites

Information on parasites as biological tags of YFT movement appears to be limited to the study by Moore et al. (2019), conducted under ACIAR project FIS/2009/059 (Proctor et al. 2019). Differences in individual parasite abundance and prevalence, as well as parasite species assemblages, of juvenile YFT collected from Indonesia, Maldives, and Solomon Islands, suggest a lack of mixing of these young fish among areas, including limited movement from IAW to the eastern IO or WCPO (Moore et al. 2019).

Muscle stable isotopes

Studies investigating variability in muscle stable isotope ratios suggest limited movement of YFT in the WCPO. Spatial trends in muscle $\delta^{15}N$ values have been observed, suggesting short-term restricted movement of individuals and high regional residency at least over the lifetime of these signals (Houssard et al. 2017). Enriched size-standardised mercury (Hg) concentrations in muscle of YFT at southern latitudes (south of $15^{\circ}S$) relative to the equator have also been reported (Houssard et al. 2019), indicating constrained latitudinal movement.

Summary of YFT connectivity

The information summarised above was used to develop a conceptual model of YFT connectivity across the WPEA region and adjacent IO and WCPO waters (Figure 10). From available genetic, tagging, and biological information, there appears to be limited connectivity between YFT in IAW and the adjacent WCPO and IO. However, the relationships of YFT in IAW and those in the nearby Celebes Sea, Sulu Sea, or South China/West Philippines Seas are unclear. In the WCPO, YFT off the coast of West Papua, off the eastern coast of Philippines, and in HSP1, appear to be part of a larger WCPO stock, as evidenced by genetics (Proctor et al. 2019) and tagging data.

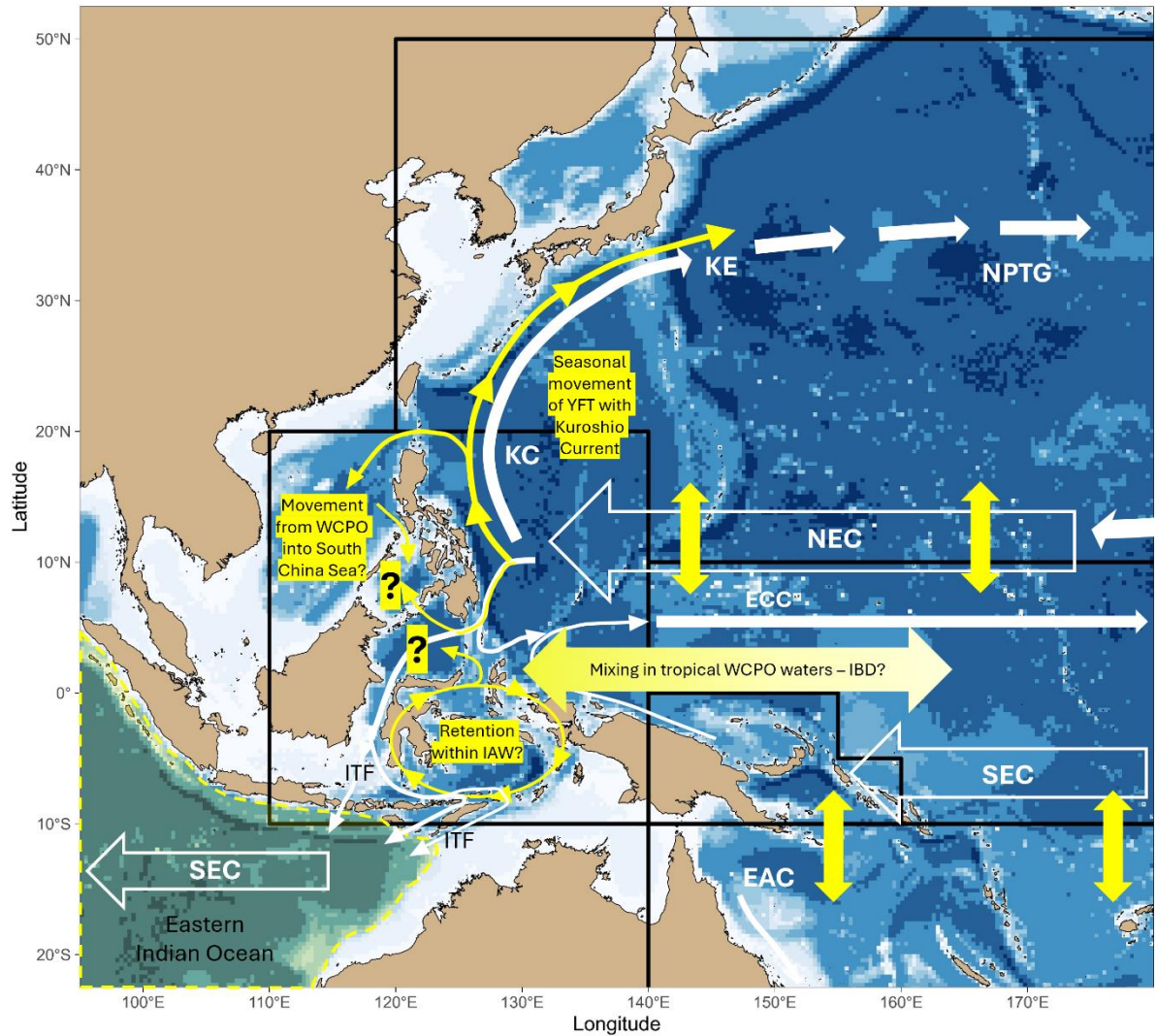


Figure 10. Conceptual model of YFT population connectivity in the western Pacific Ocean. Potential fish movement/connectivity is shown with yellow arrows. Key knowledge gaps are indicated with question marks. Also shown are the major currents in the region (white arrows), bathymetry (darker blue = deeper areas) and the regional structure used in the 2023 YFT stock assessment (Magnusson et al. 2023). IBD = Isolation by Distance. EAC = East Australian Current, ECC = Equatorial Counter Current, IAW = Indonesia's Archipelagic Waters. ITF = Indonesian Through Flow, KC = Kuroshio Current, KE = Kuroshio Extension, NEC = North Equatorial Current, NPTG = North Pacific Tropical Gyre, SEC = South Equatorial Current.

1.3. Review and selection of techniques for assessing connectivity

A range of techniques available for assessing connectivity of fish populations were reviewed during the technical workshop. Broadly, these were summarised as genetic or non-genetic approaches. These techniques operate over different time scales and provide different perspectives of connectivity. For example, depending on the approach used, genetic/genomic approaches can provide direct information on gene flow (movement of genes via spawning) over 1–2 to multiple generations, while conventional and electronic tagging, otolith chemistry and parasites provide indirect information on gene flow and can provide information on

movements over the course of days to years. In reviewing candidate techniques, the workshop considered their sensitivity (i.e. the power to detect structure should it exist), the time scale of the signal detected (e.g. whether it provides information over the last few months or years experienced by a fish, the fish's lifetime, or over generations), cost, and sampling efficiency (see Table 2).

The SNP genotyping approach (DArT-seq™) used by Grewe et al. (2015) to explore population structure of YFT in the Pacific Ocean and by Proctor et al. (2019) to examine connectivity of YFT and BET in ACIAR Project FIS/2009/059 was given initial consideration. However, the workshop concluded that newer approaches with increased sensitivity could have better success at identifying structure should it exist.

Close Kin Mark Recapture (CKMR) was also considered. CKMR takes advantage of modern genotyping methods to identify close relatives (e.g. parent-offspring, half-brother-sister) among large collections of tissue samples (i.e. biopsies). The number of kin-pairs found, and the way they are distributed in space and time, can provide direct information on the degree to which fish in different geographic localities are connected genetically (Hillary et al. 2018). A key disadvantage of CKMR, in the context of the current study, is that the number of samples to be collected, and their spread across adult and juvenile cohorts, needs to be sufficient to give statistically clear results (i.e. to contain enough kin-pairs). Given the large population sizes estimated for both SKJ and YFT in the region, the workshop considered that lower cost approaches with smaller sample size requirements be explored first.

Low Coverage Whole Genome Sequencing (LCWGS) was selected by the workshop as the preferred candidate technique for answering the question at hand. LCWGS is a cost-effective approach that allows population-scale screening of the entire genome while retaining individual information at a comparable cost to DArT-seq™. Costs are kept low by sequencing the genomes at low depth. Compared to common genome complexity reduction sequencing approaches such as the SNP genotyping approach used by Grewe et al. (2015), LCWGS increases uncertainty at each genetic variant, but that uncertainty is largely compensated by screening orders of magnitude more genetic variants.

The emerging genomic approaches of identity by descent track length, Distant Kin Mark Recapture (DKMR), and epigenetics were also considered. However, the workshop concluded that each of these approaches still require substantial research and development before they could be applied to Pacific tuna. While epigenetics has been used to investigate population structure of marine fish (e.g., Liu et al. 2025), the timescales at which the epigenetic markers vary over are not yet fully understood. For example, it is currently unclear whether the epigenetic markers operate over a short term (such as a response to a marine heatwave) or over generations. While DKMR (a similar approach to CKMR, but one in which distant kin such as aunts, uncles, cousins etc are identified in addition to full or half siblings) requires lower sample sizes than CKMR, the approach still requires substantially more samples than LCWGS, and therefore was not selected for the current study. However, this does not rule out using these techniques on collected material in future.

Consideration was given to including otolith chemistry and parasites. These techniques use chemical and parasite markers as naturally occurring tags to provide information on the past histories of fish, including whether they have lived under differing environmental conditions, from which population structure is then inferred. In the context of the current project, however, both techniques would necessitate purchasing fish for dissection, significantly increasing project costs. While examining body tissues for parasites is considered a cost-effective approach in that it requires little specialist equipment (Lester and Moore 2014), the costs associated with freight and storage of frozen samples (gills and viscera) were deemed prohibitive. Using isotopic signatures in muscle tissue (e.g., $\delta^{13}\text{C}$, Houssard et al. 2017) as an indicator of connectivity was also considered but ruled out due to the lack of direct information on gene flow and the relatively rapid turnover times of isotopic signatures in muscle tissue (2–6 months) (Table 2).

Consideration was also given to undertaking large-scale tagging in Indonesia, Philippines, Vietnam, and adjacent areas of the WCPO, including the deployment of conventional and electronic tags. Ultimately, the workshop concluded the costs associated with achieving sufficient numbers of tag deployments in the region and ensuring adequate reporting of captured tagged fish were too high. Available evidence suggested it would also be difficult to secure an appropriate vessel or vessels from which to tag fish, and that an adequate supply of baitfish might be difficult to source in some areas. The alternative of using genomics is considered a cost-effective approach to addressing the same questions, with the added benefits of providing capacity development to Indonesian, Philippines, and Vietnam scientists in an advancing fisheries research area. This does not diminish the importance of pursuing tagging activities in the region in the future, should funding and logistics allow.

Table 2. Summary of potential approaches to assessing connectivity considered under this work. Green highlight = genetic approaches, blue shading = non-genetic approaches. R & D – Research & Development.

Technique	Power to detect structure	R & D needed?	Sample size needed	Cost	What does it measure?	Time scale	Storage required	Comment
DArT-seq™	Decent	No	50–100 per sample ¹	Moderate	Subset of genomic variation	Evolutionary scale	Frozen at -20°C or colder or stored in preservation buffer	Safe, within cost range, but emerging approaches likely to have better success at identifying structure should it exist.
Close kin mark recapture (CKMR)	Pretty good	A little	Probably > 100,000, but needs design study to inform	Very high	Spatial and temporal distribution of kin	1–2 generations	Frozen at -20°C or colder or stored in preservation buffer	Sample size requirements probably too high to be useful for question being addressed.
Low coverage WGS (LCWGS)	Better than DArT	A little	30–50 per sample?	Moderate	Most genomic variation	Evolutionary scale	Frozen at -20°C or colder or stored in preservation buffer	Most likely pathway to find novel results within reasonable budget.
Identity by descent track length	Good	Lots	Slightly less than CKMR	High	Spatial and temporal distribution of kin	A few generations	Frozen at -20°C or colder or stored in preservation buffer	Technology still a couple years away, but samples processed for LCWGS could be used at a later date.
Distant kin mark recapture	Good	Lots	Slightly less than CKMR	High	Spatial and temporal distribution of kin	A few generations	Frozen at -20°C or colder or stored in preservation buffer	Technology still a couple years away, but samples collected for LCWGS could be used at a later date.
Epigenetics	Good	Lots	Low for initial discovery, high for application	Moderate	Variation of DNA molecule modifiers	?	Frozen at -20°C or colder or stored in preservation buffer	Technology not ready but has potential.
Otolith chemistry	Modest	No	Around 50 per sample	Moderate	Individuals	Days-lifetime	In vials, shelf stable	No information on gene flow

Parasites	Modest	No	Around 50 per sample	Low	Individuals	Days-lifetime	Frozen	No information on gene flow
Muscle isotopes	Modest	No	Around 50 per sample	Low	Individuals	2–6 months	Frozen at -20°C	No information on gene flow
Conventional tagging	Modest	No	100s–1000s per sample	High	Individuals	Days-years	None	Need to tag a lot of individuals at specific locations; tag return location related to locations of fishing effort; probably too costly and limited to be useful
Electronic tagging	Good	No	100s per sample	High	Individuals	Days-years	None	Need to tag lots of individuals at specific locations; can't tag larvae/small young-of-year individuals; probably too costly and limited to be useful

¹ Here a sample is a distinct sampling unit e.g. young-of-year individuals in Year X from Location Y.

1.4. Feasibility of undertaking large-scale biological sampling in the WPEA region

Indonesia

Indonesia supports a large tuna fishery, with approximately 512,000 t taken from the WCPFC-CA in 2023 (MMAF 2024). The main fishing gears used are handline, purse seine, pole-and-line, and longline. Pole and line, surface handline, and purse seine typically catch small (< 50 cm FL) tuna within IAW and the Indonesian EEZ. A large-fish handline fishery operates in the northern archipelagic waters, primarily within FMA 715. This fishery targets large YFT (100–150 cm FL) and mostly lands catches at Bitung in North Sulawesi.

Length, weight, and species compositional data are collected at almost all the major tuna landings areas in Indonesia. Indonesia has been the focus of past and current biological sampling efforts. As discussed in Section 1.2 above, biological sampling for otoliths, viscera, and muscle tissue was undertaken at nine Indonesian ports under ACIAR project FIS/2009/059 (Proctor et al. 2019; see Figure 6). All sampling was conducted under a standardised sampling protocol developed in the project that was well adhered to by port sampling teams. Collected muscle samples were of high quality for genetic analysis, showing little DNA contamination or degradation. Sampling personnel are available at these ports although refresher training in genetic sampling would be required.

Under ACIAR project FIS/2016/116, approximately 30 muscle samples of SKJ, YFT, and BET have been collected from Palabuhanratu, Kendari and Bitung (Figure 6). These samples are currently stored frozen in-country.

Philippines

Tuna fisheries in Philippines can be categorised into two components; the municipal fleet, which operates using artisanal gears within municipal waters (within 15 km of the shore) in Philippines EEZ, and a commercial fleet, which includes purse seine and large-fish handline fisheries that operates in Philippines EEZ (vessels > 3 GT are required to fish outside of municipal waters), as well as in international waters (including HSP1) and the EEZ's of other WCPFC Member countries (e.g. PNG). The total catch of SKJ and YFT by Philippines in the WCPO in 2024 was approximately 115,355 mt and 79,865 mt, respectively (Philippines 2025).

Most of the catch by commercial vessels, including that from the large-fish handline fishery and the HSP1 fishery, is landed as fresh/ice chilled product at General Santos City (Philippines 2025). Landings by the municipal fleet, which typically target small SKJ and YFT (20–30 cm) are made throughout the country. Most of the municipal catch is landed as “wet” fish (i.e. fresh).

No biological sampling is currently being conducted for tuna at landing sites, but length, weight, and species compositional data are collected at almost all the major tuna landings areas through the National Stock Assessment Program (NSAP). SPC has provided training in biological sampling, including collection of otoliths and gonads to Philippines sampling personnel (including port samplers and fishery observers from Bureau of Fisheries and Aquatic Resources (BFAR) and Soccsargen Federation of Fishing and Allied Industries, Inc. (SFFAIL) in General Santos City in January 2020 and December 2022, but not in genetic sampling

protocols. Sampling personnel at General Santos and other ports would therefore need training in genetic sampling protocols before commencing with tissue sample collection.

Vietnam

The Vietnamese tuna fleet operates out of 20 ports across 12 coastal provinces. All fishing for tuna takes place within Vietnam's EEZ. Approximately 150,000 t of tuna were caught in 2023, with most catches taken by purse seine (102,414 t), gillnet (27,028 t) and handline/longline (21,346 t) (Vietnam Department of Fisheries 2024). SKJ is the main species caught, comprising approximately 50% of the total tuna catch in 2023, with YFT comprising 17%. BET are a minor component of the catch, representing around 1% of the total tuna catch (Vietnam Department of Fisheries 2024). Most SKJ and YFT are landed in Binh Dinh, Phu Yen, Quang Ngai, and Khanh Hoa provinces in central Vietnam. Vũng Tàu and Thanh Hoa in the southern and northern regions, respectively, are also important locations for tuna landings (Vietnam Department of Fisheries 2024).

No biological sampling is currently being conducted for tuna at these ports or by observers, but length, weight, and species compositional data are collected. Sampling personnel will need training in sampling protocols before commencing with tissue sampling. There has been some previous sampling of YFT eggs throughout the Vietnam EEZ. These samples are stored in ethanol at the Research Institute for Marine Fisheries (RIMF); however, the DNA quality of these samples is unknown.

1.5. Sampling strategies

In deriving a sampling strategy, the workshop discussed the key elements of sampling: what (i.e., what life history stages) to sample, where (i.e., what locations) to sample, and when (i.e., how many times to sample each location, and what time of year) to sample.

Regarding what to sample, it was concluded that targeted sampling of spawning adults and larvae would be the best approach to assessing connectivity. However, broadscale sampling of adults and larvae is likely to be very costly, and successful sampling would take a considerable amount of searching time. It was concluded that sampling YOY, as small as possible, could serve as a suitable proxy for sampling spawning adults and larvae, as it was assumed that they would have had insufficient time to move far from their original hatching locations. Thus, if there was genetic structure, be it from individuals not moving far throughout all life history stages, or from adults returning to their spawning areas of origin, this structure would be evident in the YOY samples (see Scenario A in Figure 11). If, on the other hand, there was considerable movement and mixing of adults during spawning, it would be expected that there would be limited genetic structure evident in the YOY samples (see Scenario B in Figure 11). Sampling as small as possible YOY would also help to minimise the potential for sampling the same group of fish at different locations. Under either scenario, it was recommended that spawning adults and larvae be sampled on an ad-hoc basis where possible, but in at least three locations where YOY fish are sampled, to help confirm patterns observed in the YOY and validate the hypothesis that YOY fish remain close to their location of hatching.

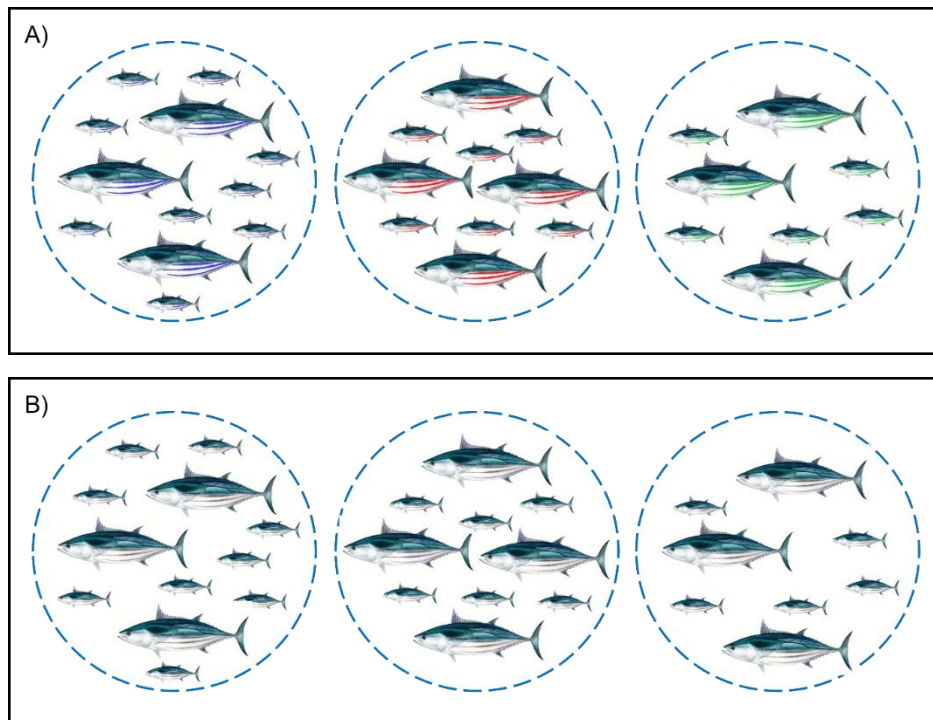


Figure 11. Hypothetical example of different connectivity scenarios for SKJ among locations (dashed circles) with a managed area (black rectangle). In Scenario A, there has been sufficient reproductive isolation of spawning adults to generate local adaptation in all life history stages, manifested as different colour belly stripes. In Scenario B, there has been sufficient interbreeding among locations to prevent local adaptation, with all individuals exhibiting the same colour belly stripes.

Considerable discussion was held during and after the workshop on where sampling should be conducted. Consideration of locations was informed by the review of current knowledge and conceptual models of SKJ and YFT movement and connectivity presented in Section 1.2, the sampling strategies developed under WCPFC Projects 177 and 118, the Individual-based Kinesis, Advection and Movement of Ocean ANimAls model (IKAMOANA: Scutt Phillips et al. 2018), oceanographic considerations, and logistical considerations presented in Section 1.4 (e.g., are there port samplers working at this location already? Are enough appropriately sized fish available to sample at this location?). Considering all available information, the workshop recommended a few key priority areas for sampling (with justifications in parentheses):

- 2–3 locations within Indonesia’s archipelagic waters (locations sampled under ACIAR project FIS/2009/059 were considered the best option, as they had been successfully sampled previously i.e. some samples are already available, logistics have been tested, YOY fish are available for sampling, and port samplers at these locations have already received some training).
- 1 location in Indonesia’s EEZ in the eastern IO (e.g. Palabuhanratu, which was sampled previously under ACIAR project FIS/2009//059).
- 1 location in Indonesia’s EEZ along the Papua/West Papua coast adjacent to the Bismarck Sea (e.g. Jayapura, which was sampled previously under ACIAR project FIS/2009//059, or Biak, whose fishers fish in the WCPO as opposed to IAW).

- 3–4 locations within Philippines' EEZ (such that sampling covers the main fishing areas, including the East Philippine Sea, West Philippine Sea, Sulu Sea and Celebes Sea, to assess the connectivity among these areas and between these areas and Indonesia, Vietnam, and the WCPO).
- 1–2 locations within Vietnam's EEZ (potentially northern and southern Vietnam)
- Western Micronesia (e.g. Palau or the western extent of FSM's EEZ, as tagging data suggests some movement both of SKJ and YFT between the WPEA region and this region, and there is ongoing genetic sampling at some ports).
- Eastern Micronesia (e.g. Kiribati, Nauru, or RMI, as tagging data suggests some movement of both SKJ and YFT between the WPEA region and this region, and there are trained genetic samplers in these countries).
- Chinese Taipei/southern Japan (to test linkages between these fish and those in the WPEA region).
- Solomon Sea (as tagging data suggests some movement of both SKJ and YFT between the WPEA region and this region, and there is ongoing genetic sampling at major ports).
- Fiji/Tonga (as a southeast outlier, as tagging data indicate little/no movement of either SKJ or YFT to/from the WPEA region, and there is ongoing genetic sampling at major ports).

Discussion was then held on when to undertake sampling, and how to go about the large amount of work that this project would require. The workshop concluded that two sampling events be conducted in a given year to account for potential intra-annual variation. For each event, sampling should be done over as short a time period as possible across all areas. The workshop also recommended that sampling should be done in multiple years to investigate inter-annual stability of any observed patterns.

The workshop concluded that breaking up this task into smaller pieces of work, or phases, would be the most appropriate approach for implementation. A phased approach has considerable advantages in a project such as this, as it allows sampling to be flexible with respect to results and allows lessons learned during implementation to be actioned in subsequent phases. The workshop and following discussions recommended the work be broken into three distinct phases:

- 1) An initial analysis to understand the influence of different connectivity scenarios on the YFT stock assessment and resulting management advice through stock assessment modelling assuming different movement and recruitment distributions among regions, as well as initial explorations of the LCWGS approach using existing samples to assess sample size requirements and develop the necessary analytical pipelines (Phase 1).
- 2) A first round of sampling at broadly spaced locations, and pilot analyses of collected material to determine optimal directions for further sampling, training, and analysis (Phase 2).
- 3) A subsequent round of sampling at locations informed by the results of Phase 2, as well as final analyses to assess population structure and connectivity (Phase 3).

1.6. Utility of existing material in the Pacific Marine Specimen Bank to inform on population connectivity in the WPEA region

Workshop participants also reviewed the samples available through the Pacific Marine Specimen Bank curated by SPC to assess whether these could be used to investigate connectivity, thereby reducing the need for additional sampling. While large sample sizes of material are available for both SKJ and YFT from both Indonesia and Philippines (Table 3), these samples were not collected under current genetic sampling protocols. Consequently, cross contamination in these samples is likely to be high, and as such they are not recommended for use in genetic analyses. Overall, most SKJ samples were from large fish (Figure 12). Further investigation is required to determine which of these were from actively spawning fish. A range of YFT samples exist, including some from YOY fish from PNG and RMI (Figure 13), that could potentially be used in analysis.

Table 3. Genetic samples of SKJ and YFT in the Pacific Marine Specimen Bank.

EEZ	SKJ	YFT
Indonesia	71 muscle ¹ , 15 fin clips	187 muscle ¹ , 15 fin clips
Philippines	513 muscle ¹ , 96 fin clips	1,344 muscle ¹
Vietnam	-	-
Cook Islands	25	-
Fiji	65	4,162
FSM	72	24
Kiribati (Gilbert Is.)	409	68
New Caledonia		153
PNG	313	1,126
RMI	-	730
Solomon Islands	477	4,669
HSP2	64	33

¹ Not collected with biopsy/gene tagging tools and are unlikely to be suitable for genetic analysis.

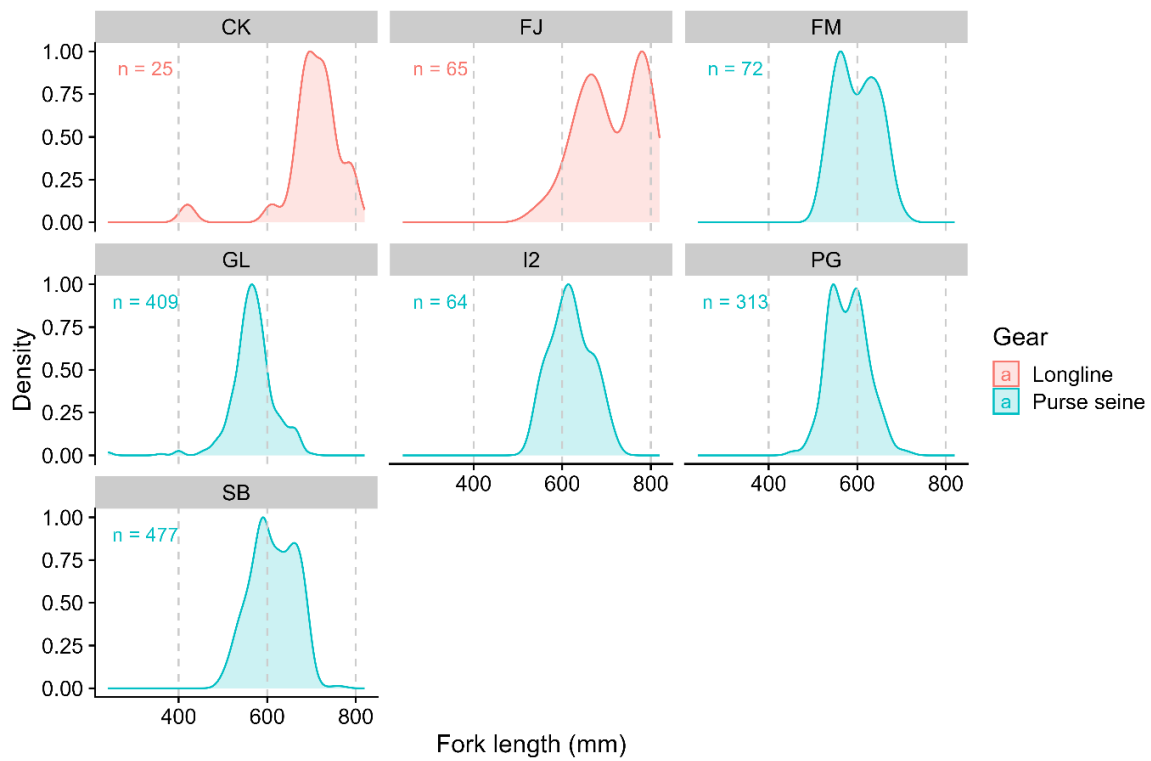


Figure 12. Summary of SKJ muscle samples available from the Pacific Marine Specimen Bank to inform on connectivity by gear and EEZ. GL = Gibert Islands (Kiribati), I2 = High Seas Pocket 2.

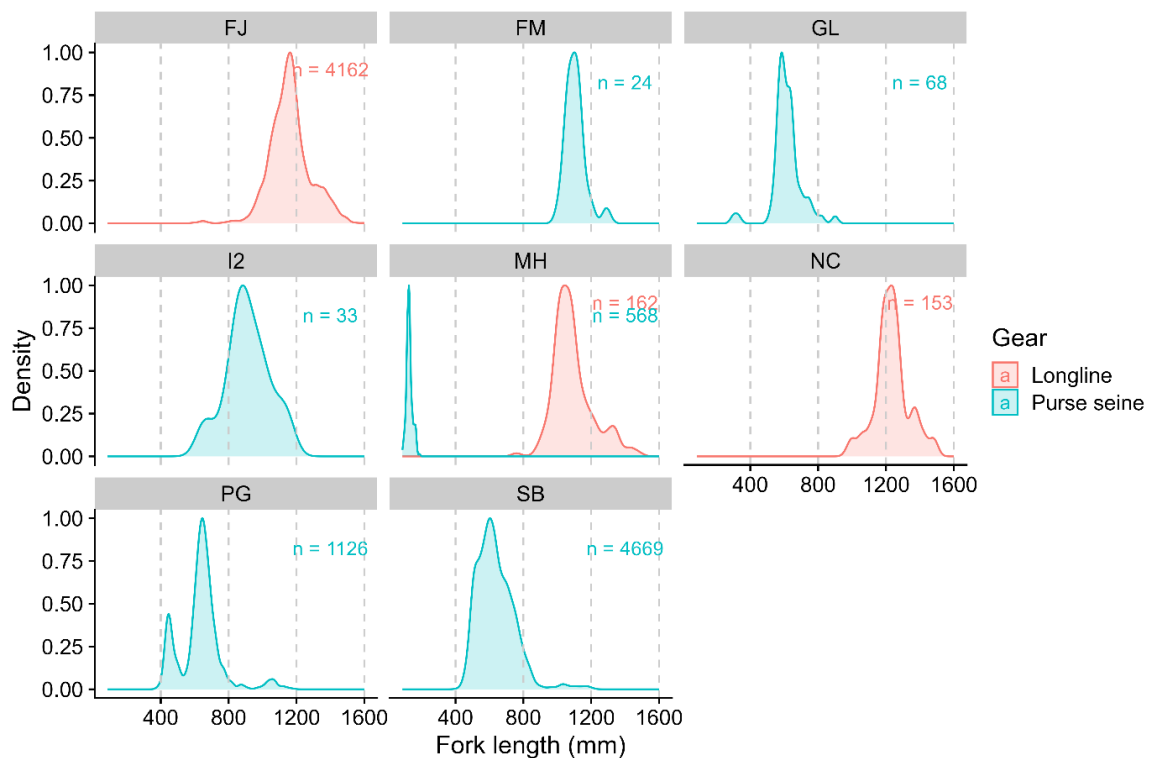


Figure 13. Summary of YFT muscle samples available from the Pacific Marine Specimen Bank to inform on connectivity by gear and EEZ. GL = Gibert Islands (Kiribati), I2 = High Seas Pocket 2.

Section 2: Draft Terms of Reference for a study to improve understanding of connectivity of skipjack and yellowfin tuna in WPEA region and the broader WCPO

2.1. Project introduction

The waters of the Western Pacific East Asia (WPEA) region, i.e. those surrounding Indonesia, Philippines, and Vietnam, support valuable fisheries for skipjack tuna (*Katsuwonus pelamis*; SKJ), yellowfin tuna (*Thunnus albacares*; YFT), and, to a lesser extent, bigeye tuna (*T. obesus*; BET). Millions of people in coastal communities across Indonesia, Philippines, and Vietnam are involved with tuna fisheries in some way, be it for food security, a source of employment and livelihood, or social endeavours (McDonald 2021³). These fisheries are managed both locally and regionally through the Western and Central Pacific Fisheries Commission (WCPFC), the latter being under the assumption that they form part of a single stock within the Western and Central Pacific Ocean (WCPO).

Collectively, catches from the three countries represent around 30% of the annual catches of key tuna species in the WCPO, including 40% of the total YFT catch (McDonald 2021). However, a lack of understanding of the degree of connectivity between the WPEA region and the WCPO has been highlighted as a key area of uncertainty in WCPO stock assessments for several years.

At present, YFT and SKJ in the WCPO are considered to represent single biological stocks for assessment and management purposes (Castillo Jordán et al 2022; Magnusson et al. 2023). However, there is some evidence to suggest YFT, SKJ and BET in at least some areas of the WPEA region may exhibit more spatial structure than is currently assumed. Differences in genetic markers have been observed between YFT and BET from within Indonesia's Archipelagic Waters (IAW) and the adjacent WCPO (Proctor et al. 2019), suggesting long-term reproductive isolation. Biological differences between Indonesia/Philippines and the broader WCPO have also been reported (Itano 2000, Farley et al. 2018), suggesting populations in these regions are demographically disconnected. Tagging data from the WCPO, largely restricted to smaller fish, indicate that while individual SKJ, YFT, and BET are capable of long-range movement, most individuals are generally recaptured within the region in which they were initially tagged (Moore et al. 2020).

An improved understanding of connectivity among the WPEA region and the broader WCPO would greatly help to reduce uncertainty in WCPO stock assessments and resulting management advice, including the development and testing of management procedures for harvest strategies. Such knowledge would also help to further develop spatial management and harvest strategies in each of the three WPEA countries and address open questions on whether collaborative management among them is required. An improved understanding of connectivity would also help to improve modelling work designed to estimate the impacts of climate change on tuna ecology and distribution in the WCPO and better inform the design of studies planned to mitigate the impacts of climate change on tuna stocks. The current modelling

³ References for this section can be found in [Appendix 2](#).

approach, based on the use of the Spatial Ecosystem and Population Dynamics Model (SEAPODYM), assumes that the tuna resources of the WCPO for a single stock (Bell et al. 2021). Moreover, significant investment is being made to improve the adaptation of the tuna dependent economies of the Pacific Islands region to the effects of climate change on tuna stocks. Understanding movement and connectivity is central to the success of these investments.

2.2. Aims and Objectives

The overall aim of this project is to assess the degree of connectivity of SKJ and YFT within the WPEA region and between the WPEA region and broader WCPFC Convention Area.

The specific objectives are to:

- i. Undertake modelling to assess the impact of different connectivity hypotheses on results of regional stock assessments and subsequent management advice.
- ii. Assess the utility of current sample collection Standard Operating Procedures (SOPs) for SKJ and YFT and train port samplers and observers in the WPEA region to undertake the necessary sampling.
- iii. Establish a sampling network linking the WPEA and broader WCPFC regions, commence large-scale tissue sample collection of SKJ and YFT (and BET), and test the effectiveness of sampling for DNA quality requirements.
- iv. Investigate and validate connectivity hypotheses for SKJ and YFT via Low Coverage Whole Genome Sequencing.
- v. Develop a sample library for potential future use as technologies develop.
- vi. Broaden the sampling and monitoring capacity among WCPFC Members by developing capacity in WPEA countries and linkages with adjacent areas.
- vii. Communicate project results, including providing advice to national governments and the WCPFC Scientific Committee on the degree of connectivity of SKJ and YFT within the WPEA region and between the WPEA region and the wider WCPFC-CA.

2.3. Impact

The expected direct outcomes of this work include: (i) reduced uncertainty in stock assessment models for key tuna species; (ii) improved understanding of the spatial considerations in domestic and broader WCPFC harvest strategy development; (iii) improved understanding of spatial considerations in climate modelling; and (iv) improved capacity within Indonesia, Philippines, and Vietnam to implement large scale sampling programs for highly migratory species and present results at domestic and international fisheries fora.

2.4. Scope of work

The proposed programme of work includes:

- Modelling to test different connectivity assumptions on stock assessment results and resulting management advice.

- Assessing the appropriateness of current sampling SOPs and revising these where necessary.
- Capacity building of local port samplers and observers in relevant countries where required in undertaking the necessary sampling.
- Collection and storage of muscle tissue for LCWGS analysis.
- Extraction, sequencing, and analysis of LCWGS data.
- Communication of project results, including through annual progress reports to the WCPFC SC, and the provision of advice to national governments and the WCPFC SC on the degree of connectivity of SKJ and YFT (and BET) between the WPEA region and the wider WCPFC-CA.

2.5. Assumptions

Achievement of the objectives is subject to the following assumptions:

- Resources are available within selected countries to undertake this work (except where specific provision has been made in the Project's budget).
- Staff are available to undertake this work, including in the SSP for modelling work.
- That adequate numbers of each species are available for sampling at each location during the sampling period.
- Necessary national approvals can be secured for sampling and genetic analyses.

2.6. Proposed activities and methodology

This project is proposed to be implemented in three phases. A summary of the proposed activities and methodology for each phase is described below and tabulated in Table 4.

Phase 1:

Comprising analyses to better understand the influence of different connectivity scenarios on the YFT stock assessment management advice, and initial explorations of the LCWGS approach using existing samples. Proposed activities include:

1. Modelling to test different connectivity assumptions on stock assessment results and resulting management advice, including consultation meeting involving the WPEA countries and interested parties to discuss the results.
2. Investigating the utility of LCWGS for assessing connectivity, using YFT as a test species, including the minimum sample size requirements and the necessary analytical pipelines for the analysis of LCWGS data.

Phase 2:

Comprising capacity building and initial sampling and analyses to determine optimal directions for further work. Proposed activities include:

1. Training of port sampling personnel in biological sampling and the collection and storage of muscle tissue for genetic analysis in each of Indonesia, Philippines, and Vietnam via a train-the-trainer approach.

2. Assessing the appropriateness of current sampling SOPs and revising these where necessary.
3. A first round of sampling of SKJ and YFT from locations in Indonesia, Philippines, Vietnam, and the Pacific Islands region (where required), with two sampling events conducted within a year at each location.
4. Extraction, sequencing, and analysis of genomic data.
5. Quarterly virtual and annual in-person Project Coordination Meetings.
6. Provision of annual progress reports to the WCPFC SC.

The scoping study conducted as part of WCPFC Project 128 (see Section 1) recommended that in Phase 2, young-of-the-year (YOY) YFT and SKJ, as small as possible, be sampled from broadly spaced locations within the WPEA region and adjacent WCPO countries and territories. Recommended sampling ports/area (with targeted fished areas in parentheses) identified include:

- Indonesia: e.g. Palabuhanratu (EIO off West Java), Kendari (Banda, Flores and Molucca Seas), Bitung (Molucca and Celebes Seas), Ambon (eastern Banda Sea), and Jayapura (Indonesia EEZ in WCPO).
- Philippines: e.g. Eastern Samar (East Philippine Sea), Puerto Princesa (Sulu Sea), General Santos City (Celebes Sea & HSP1), Subic (West Philippine Sea).
- Vietnam: e.g. Vũng Tàu (Southern Vietnam) and Thanh Hoa (northern Vietnam).
- WCPO: e.g. Yap (FSM EEZ), Majuro (RMI EEZ), Tongatapu (Tongan EEZ), Noro (Solomon Sea) and Chinese Taipei/southern Japan (Figure 14).

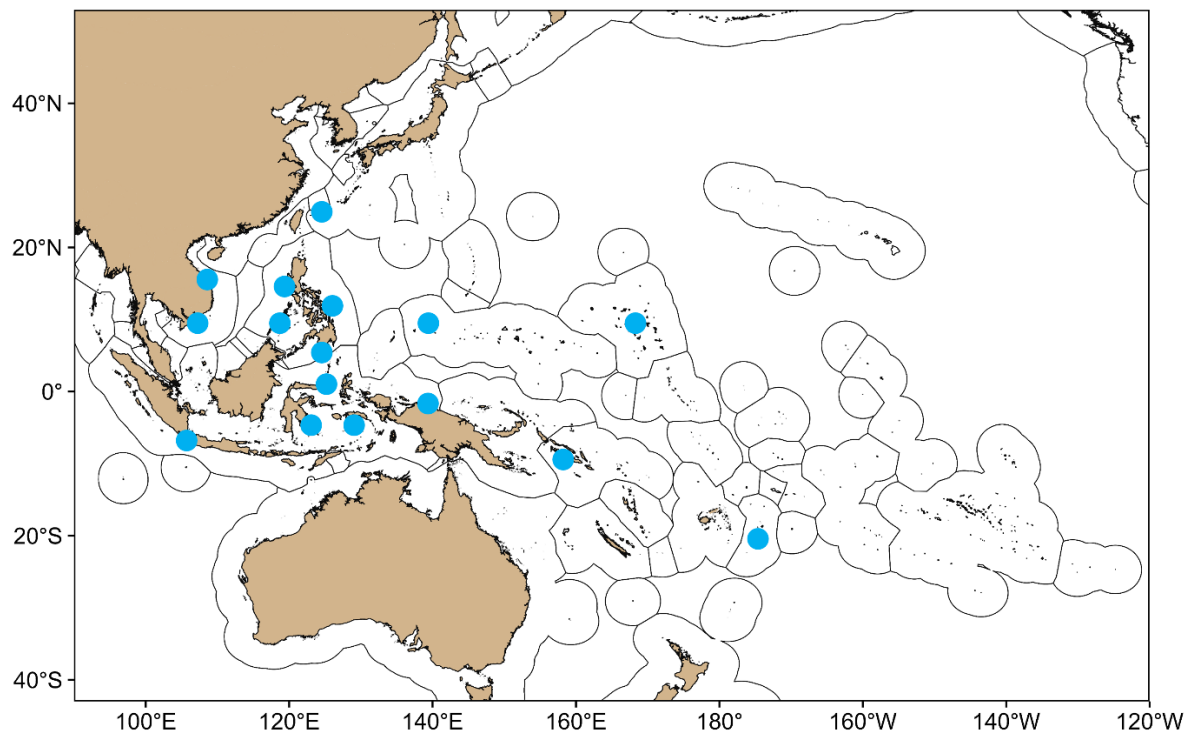


Figure 14. Indicative sampling locations for skipjack and yellowfin tuna recommended by Project 128 for Phase 2 of the proposed study.

To avoid duplication and coordinate efforts, it is recommended that sampling locations in the Pacific Islands region of the WCPO be closely linked with work undertaken in the existing Green Climate Fund (GCF) and Close-Kin Mark-Recapture (CKMR) initiatives within this region funded by the EU and partners.

The feasibility study conducted as part of WCPFC Project 128 recommended that the primary focus of sampling at these locations be on YOY (i.e. 0+) SKJ and YFT, with the aim of collecting muscle tissue from up to 100 samples per location. To avoid confusion and to streamline sampling, the same locations should be sampled for both species. Bigeye tuna (BET) should also be sampled opportunistically at each location. The intention of sampling YOY fish is that they will have had insufficient time to move far from their original spawning locations. Adult and larval SKJ and YFT should be sampled at a subset of locations to compare against signals observed in the YOY samples to assess the persistence of any observed population structure with ontogeny. Training on sampling protocols should be provided to sampling teams before sampling commences. Where possible, sampling should be done simultaneously over a short time period (ideally within a 3-month period) to reduce the likelihood of seasonal differences as a significant factor in any observed spatial differences. Two sampling events should be conducted within a 12-month period to test for any intra-annual (e.g. seasonal) differences. Collected samples should initially be transferred to centralised locations in each country where they should be stored frozen. Samples should then be transported to an appropriate laboratory for storage until processing for LCWGS.

Phase 3:

Comprising a subsequent round of sampling at locations informed by the results of Phase 2, training of sampling staff, sequencing and analysis of collected material, a capacity building workshop on the use of genomics in fisheries, and final analyses of all samples to assess population structure and connectivity. Proposed activities include:

1. Refresher training of port sampling personnel in biological sampling and repeated sampling of muscle tissue for genetic analysis at Phase 2 locations.
2. Training of port sampling personnel in biological sampling and a first round of sampling at additional locations (locations should be defined based on the results of Phase 2).
3. Extraction, sequencing, and analysis of genomic data.
4. Quarterly virtual and annual in-person Project Coordination Meetings.
5. Capacity building workshop on the use of genomics in fisheries.
6. Provision of annual progress reports and a final project report to the WCPFC SC.
7. Completion and submission of final project report and outputs (e.g. peer-reviewed journal articles) (Table 4).

During Phase 3, repeated sampling at selected locations sampled under Phase 2 should be conducted to assess the temporal stability of observed patterns. Should structure be found, finer-scale spatial sampling of locations within both the WPEA and WCPO regions should be conducted. The primary focus of sampling should again be on YOY (i.e. 0+) SKJ and YFT, with BET collected opportunistically. Adult and larval SKJ and YFT should be sampled at a

subset of locations to assess the persistence of any observed population structure with ontogeny.

2.7. Timeframe

It is envisioned that, including Phase 1, this project is expected to run over ~4 years:

- Phase 1: January to December 2026
- Phase 2: January 2027 to June 2028
- Phase 3: July 2028 to December 2029.

During Phases 2 and 3, the project team recommended that in-person Project Coordination Meetings (PCMs) be held regularly, with a total of three PCMs held over the course of the project. Virtual PCMs should be held quarterly (Table 4).

In-country sampling is proposed to occur for Quarters 1 and 3 of 2027 (Phase 2) and 2028 (Phase 3). Processing (i.e. DNA extraction, sequencing) and analysis of resulting sequence data is planned for Quarters 2 to 4.

Progress reports should be provided to and presented at the WCPFC SC meetings in August 2026 (SC22), August 2027 (SC23), and August 2028 (SC24), and final project results should be presented to the WCPFC SC in August 2029 (SC25) (Table 4).

Under this timeframe, provisional results are expected to be available for the 2028 SKJ and 2029 YFT WCPFC stock assessments, provided funding is sourced to allow activities to commence in Quarter 1 of 2026.

2.8. Budget

We estimate costing for the work as described above to be approximately \$1.1 million USD. These costs should be considered indicative at this stage and will change depending on results from the Phase 1 analyses and if increased sampling locations are required in Phase 3.

Table 4. Proposed timeline for implementation of the project.

Phase / Activity	2026				2027				2028				2029			
	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
Phase 1																
1. Modelling																
a. Analysis																
2. LCWGS trials																
a. Processing of samples																
b. Analysis																
3. Reporting and presentation to WCPFC SC																
4. Virtual (V) Project Coordination meetings and in-person (IP) workshop	V	V	V	IP												
5. Delivery of final report to WCPFC Secretariat																
Phase 2																
1. In-country training and sample collection																
2. Processing of samples																
3. Analysis of samples																
4. Progress report to WCPFC SC							P									
5. Virtual (V) and In-person (IP) Project Coordination meetings					V	V	V	IP								
Phase 3																
1. In-country training and sample collection																
2. Processing of samples																
3. Analysis of samples																
4. Capacity building workshop for IDN, PHL, VNM in fisheries genomics																
5. Progress (P) and final (F) report to WCPFC SC											P				F	
6. Virtual (V) and In-person (IP) Project Coordination meetings									V	V	V	V	IP			
7. Delivery of final project reports, outputs																

Table 5. Estimated costs for each proposed phase of the project.

Phase	Component	Cost estimate (USD)
Phase 1	Stock assessment modelling	\$10,000
	LCWGS and analysis	\$90,000
	Stakeholder workshop	\$25,000
	Phase 1 total cost	\$125,000
Phase 2	Sampling + in-country training (includes travel, equipment and staff time) and coordination meetings	\$165,000
	Sample processing and reporting ¹	\$235,000
	Phase 2 total cost	\$400,000
Phase 3	Sampling + in-country training (includes travel, equipment and staff time) and coordination meetings	\$237,000
	Sample processing and reporting + genomics workshop	\$322,000
	Phase 3 total cost	\$559,000
Total project cost estimate		\$1,084,000

¹Budget accounts for processing and analysis of 16 sampling locations for YFT and 8 for SKJ in each of two sampling events in the phase.

Section 3: TOR for Phase 1 work to undertake the necessary first steps to support further proposal development and funding acquisition for the full project

Project XX	Initial analyses to support investigations of the connectivity of key tuna species between the Western Pacific East Asia (WPEA) region and broader WCPFC-CA
Objectives	<p>The aim of this project is to undertake some of the necessary supporting analyses to: 1) understand the influence of different connectivity scenarios between the Western Pacific East Asia (WPEA) region and the broader WCPFC Convention Area (WCPFC-CA) on regional stock assessments and management advice in the WCPO and 2) assess the feasibility of using a novel genomic approach - Low Coverage Whole Genome Sequencing (LCWGS) - for assessing connectivity (including minimum sample size and analytical requirements).</p> <p>The specific objectives are to:</p> <ol style="list-style-type: none"> Undertake modelling to assess the impact of different connectivity assumptions on the results of regional stock assessments and subsequent management advice for yellowfin tuna (and possibly skipjack tuna). Undertake a preliminary examination of the utility and sample size requirements of using LCWGS for investigating connectivity of yellowfin tuna as a test species within the WPEA region and adjacent waters using pre-existing genetic material.
Rationale	<p>The WPEA region supports valuable fisheries for skipjack tuna (<i>Katsuwonus pelamis</i>; SKJ) and yellowfin tuna (<i>Thunnus albacares</i>; YFT), collectively accounting for over 30% of the annual catch of tuna species in the WCPFC-CA. These fisheries are assumed to form part of a larger Western and Central Pacific Ocean (WCPO) stock for assessment and management purposes. However, evidence suggests SKJ and YFT in at least some areas of the WPEA region may represent separate demographic stocks from those in the broader WCPO (see Proctor et al. 2019, Moore et al. 2020, Hamer et al. 2023). Dedicated studies are required to address this hypothesis.</p> <p>Before embarking on a costly field sampling project, it is important to understand the influence of different connectivity scenarios between the WPEA region and the broader WCPFC-CA on the stock assessment and management advice for YFT in the WCPO, as well as to assess the feasibility of using the LCWGS approach for detecting connectivity, based on existing samples (including sample size and analytical requirements).</p>
Assumptions	<ul style="list-style-type: none"> Personnel are available to undertake this work
Scope	<p>The proposed activities include:</p> <ol style="list-style-type: none"> Modelling to assess the impact of different connectivity hypotheses on the results of the regional YFT (and potentially SKJ) stock assessments and subsequent management advice. Low Coverage Whole Genome Sequencing (LCWGS) and analysis of resulting data from a subset of YFT samples, collected at key locations during ACIAR project FIS/2009/095, using LCWGS (up to 50

	<p>samples from each of Maldives, Palabuhanratu (IDN), Kendari (IDN), Ambon (IDN), Bitung (IDN), Jayapura (IDN), and Noro (SLB).</p> <p>iii. An in-person stakeholder workshop involving participants from each of IDN, PHL, VNM, SPC, and CSIRO to discuss results of i and ii and progress full project proposal development.</p> <p>iv. Preparation and presentation of a project report to SC22 and a final report to the WCPFC Secretariat.</p>								
Timeframe	12 months (from January 2026 to December 2026)								
Budget	<p>This TOR would require a budget of 125k USD.</p> <table border="1"> <thead> <tr> <th>Component</th><th>Cost (USD)</th></tr> </thead> <tbody> <tr> <td>Stock assessment modelling</td><td>\$10,000</td></tr> <tr> <td>LCWGS and analysis</td><td>\$90,000</td></tr> <tr> <td>Stakeholder workshop¹</td><td>\$25,000</td></tr> </tbody> </table> <p>¹ Budgeted as an in-person, 3-day workshop occurring in Australia with two participants from each of IDN, PHL, VNM, and SPC attending.</p> <p>It is proposed that CSIRO be the implementing agency for this work.</p>	Component	Cost (USD)	Stock assessment modelling	\$10,000	LCWGS and analysis	\$90,000	Stakeholder workshop ¹	\$25,000
Component	Cost (USD)								
Stock assessment modelling	\$10,000								
LCWGS and analysis	\$90,000								
Stakeholder workshop ¹	\$25,000								
References	<p>Hamer P, Macdonald J, Potts J, Vidal T, Teears T, Senina I. (2023). Review and analyses to inform conceptual models of population structure and spatial stratification of bigeye and yellowfin tuna assessments in the Western and Central Pacific Ocean. Working Paper WCPFC-SC19-SA-WP-02 presented to the Nineteenth Regular Session of the Scientific Committee of the Western and Central Pacific Fisheries Commission, Koror, Palau. https://meetings.wcpfc.int/node/19350</p> <p>Moore BR, Bell JD, Evans K, Farley JH, Grewe P, Hampton J, Marie AD, Minte-Vera CV, Nicol S, Pilling G, Scutt Phillips J, Tremblay-Boyer L, Williams A, Smith N (2020). Defining the stock structure of key commercial tunas in the Pacific Ocean I: Current knowledge and main uncertainties. <i>Fisheries Research</i> 230: 105525. https://doi.org/10.1016/j.fishres.2020.105525</p> <p>Proctor C, Lester RJG, Clear NP, Grewe PM, Moore B, Eveson JP, et al. (2019). Population structure of yellowfin tuna (<i>Thunnus albacares</i>) and bigeye tuna (<i>T. obesus</i>) in the Indonesian region. Final Report as output of ACIAR Project FIS/2009/059. Australian Centre for International Agricultural Research, Canberra, 139 pp. https://www.aciar.gov.au/sites/default/files/project-page-docs/fis-2009-059_popstructurestudy_final_report.pdf</p>								

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Appendix 2: References used in Section 2

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