11th MEETING OF THE SCIENTIFIC COMMITTEE

11 to 16 September 2023, Panama City, Panama

SC11 – JM02
Jack Mackerel Connectivity Research - Application for SPRFMO Funding

Jack Mackerel Connectivity Task Group

South Pacific Regional Fisheries Management Organisation

11th Meeting of the Scientific Committee

Panama City, Panama, 11-16 September 2022

Application form for SPRFMO project funding: *Characterization of the population variability of jack mackerel Trachurus murphyi on a spatio-temporal scale, in order to determine the existence of stocks or population units and their level of connectivity*

Fabrice Stephenson, Giovanna Sotil, Sebastián Vásquez

Foreword

We are pleased to present an application form for SPRFMO project funding titled *Characterization of the population variability of jack mackerel Trachurus murphyi on a spatio-temporal scale, in order to determine the existence of stocks or population units and their level of connectivity*. This funding application will be submitted for review at the COMM12 (Manta, Ecuador, 29 Jan – 2 Feb, 2024). In preparation for submission to COMM12, *we are inviting the SC to:*

- *Endorse the research proposal*
- *Recommend that COMM12 consider funding the research proposal*

Yours faithfully,

Jack Mackerel Connectivity Working Group co-chairs: Fabrice Stephenson, Giovanna Sotil, Sebastián Vásquez

APPLICATION FORM FOR SPRFMO PROJECT FUNDING

Characterization of the population variability of jack mackerel *Trachurus murphyi* on a spatio-temporal scale, in order to determine the existence of stocks or population units and their level of connectivity

Project Summary (250 words maximum)

To date, one of the major sources of uncertainty for the assessment and management of Chilean jack mackerel (CJM) *Trachurus murphyi* relates to its stock identity, as up to five stock structure hypotheses have been proposed, from a single population up to several discrete populations (SPRFMO, 2008; Gerlotto *et al.*, 2012; Bertrand *et al.*, 2016). Clarifying these aspects is of relevance for the assessment and management of the stock(s) and fisheries. A regional multidisciplinary analysis of the different aspects of the life-history of the CJM is proposed, including a scientifically robust sampling scheme, and the integration of factors that may affect changes in CJM abundance, distribution and genetic variability. Furthermore, the estimation of connectivity among possible populations units is critical for assessing the dynamics that occur within the species distribution range, including genetic divergence and adaptation, and improved knowledge of connectivity. To better understand the population structure and variability of CJM for the identification of stocks or population units, three main tasks are proposed: (1) Building on Gerlotto *et al.* (2012), Hintzen *et al.* (2014) and Cadrin *et al.* (2023) (amongst others), carry out a desk study in order to compile all available existing knowledge and data on the species and the stock identity issue, in order to identify the sources of information related to population structure and connectivity; (2) Develop a genetic research program, in accordance to what a genetic workshop could discuss and more specifically propose, including the analysis on NGS (Next Generation Sequencing) techniques like whole genome sequencing; and, (3) Develop a multidisciplinary research approach to tackle the gaps identified in the desk study.

This multidisciplinary project may include the analysis of different aspects, including genetic analyses, life-history, age and growth, habitat, migration, parasitology, trophic ecology, amongst others, for the interpretation of the population structure in a holistic approach, as well as through uniform sample sizes, protocols, analysis criteria along the species distribution.

The expected duration of the project is 5 years and the estimated total cost is NZ$ **1,567,428**, of which the equivalent of NZ$ **967,428** (equally provided by Peru and Chile) would be in-kind contributions from participating members and NZ$ **600,000** are being proposed for SPRFMO funding.

Characterization of the population variability of Chilean jack mackerel *Trachurus murphyi* on a spatio-temporal scale, in order to determine the existence of stocks or population units and their level of connectivity

1. Proposal Narrative (6 pages maximum)

A. Introduction

Although Chilean jack mackerel (CJM) *Trachurus murphyi* is an important fishery species with a wide distribution in the South Pacific along South American coastal areas and across a 35° – 45° S band in the Pacific Ocean to New Zealand (Serra, 1991), its population structure is complex. Indeed, this complexity is a source of uncertainty for the assessment and management of this species stock(s) and fisheries. To date, up to five stock structure hypotheses have been proposed and are subject to discussion and consideration for the CJM. These include the four described in SPRFMO (2008), according to which (i) jack mackerel caught off the coasts of Peru and Chile each constitute separate stocks which straddle the high seas, or (ii) jack mackerel caught off the coasts of Peru and Chile constitute a single shared stock which straddles the high seas; and, (iii) jack mackerel caught off the Chilean area constitute a single straddling stock extending from the coast out to about 120°W, or (iv) jack mackerel caught off the Chilean area constitute separate straddling and high seas stocks. In addition, a fifth hypothesis of a metapopulation is proposed by Gerlotto *et al*. (2012, 2021), who suggest that in addition to any one of the previous four hypotheses the possible effects of long-term changing environmental conditions should be accounted for.

Using the best available information CJM stock assessment, since WG 2012 and SC 2013 SPRFMO has considered the working hypotheses (i) and (ii) (SPRFMO, 2012, 2013). However, there remains uncertainty as to which structure hypothesis should be used for fisheries management. In order to further explore the five stock structure hypotheses we propose a multidisciplinary regional study, that would include a genetic analysis, as well as other appropriate approaches related to the life history, population structure and connectivity of the CJM, and a scientifically robust sampling scheme which would account for potential environmental factors known to affect changes in the stock structure (e.g., in line with best practice proposed by Cadrin et al., 2023).

The aim of this project is to characterize the population structure and variability of CJM on a spatio-temporal scale, in order to disentangle its complex population structure and determine the existence of stocks or population units and their level of connectivity. A holistic approach is needed that, using tools with different and complementary resolution levels, to help to resolve population structure and connectivity (Randon *et al.*, 2020) and, in consequence, provide important information to take into account for managing marine resources that contrasts with the more conventional approach to management (Pikitch *et al.*, 2004). Consequently, it has been suggested in SC9-JM08 and SC9-JM04 (SPRFMO, 2021a, b) that genetic and genomic studies be complemented with other types of stock structure analyses, evaluated at different spatial and temporal levels, while expanding and updating previous studies in the region e.g., Serra and Glubokov (2008), SPRFMO (2008, 2012),Serra *et al.,* (2010; 2014) and Csirke & Ñiquen (2017).

A well stratified and robust (spatial and temporal) sampling design proposed to be considered, in order to properly capture the known dynamics and fluctuations in the distribution, abundance, and availability to the fisheries of the species throughout its distribution range, taking also into account the different hypothesis to be evaluated. During the five-year workplan, we are proposing: (1) to carry out a desk study in order to identify and select main sources of

information related to population structure and connectivity; (2) to develop a genetic research program for a genetic analysis of CJM along its distribution range using new NGS technologies (e.g. WGS); and, based on the gaps identified in the desk study, (3) to develop a multidisciplinary research program for CJM population structure evaluation taking into account spatial and temporal criteria.

B. Method and approach

Under SPRFMO research, a CJM Connectivity Research Task group was established in 2022, designating an independent chair (from New Zealand), and assisted by two co-chairs, from Peru and Chile. So, in accordance with the Terms of Reference already agreed (paragraph 102, Final report SC10), a working scheme has been proposed.

B.1. Generate a desk study

Building on Gerlotto *et al*. (2012), Hintzen *et al*. (2014) (amongst others) and following the framework of Cadrin *et al.* (2023), we will compile available existing knowledge and data related to the connectivity and the stock identity issue on the species. During the first year of the project, virtual meetings will be held between researchers from all SPRFMO delegations involved in the project, in order to:

- Review theoretical definitions in the literature of population structure and stocks for pelagic fish with the aim of providing appropriate terminology (that may include multiple relevant definitions) that will facilitate the sustainable management of CJM throughout its range.
- Analyze all evidence and establish priority research topics related to population identity and connectivity.
- Identify protocols, techniques and biological historical data, that could be considered for the multidisciplinary study.
- Explore feasibility of tagging methods (including providing a review of tagging methods) to provide additional information on the actual movements and migratory patterns of fish.
- Hierarchically analyze the evidence and identify the sources of information related to population connectivity.

This desk study will permit to identify priority lines for multidisciplinary research for CJM population structure and connectivity and propose a work plan based on the gaps identified in the desk study.

B.2. Sampling design

Considering the geographical distribution, dispersal capacity of the species, the different stocks hypothesis, the environmental changes and the low and high abundance periods over the years, among other variables, 16 sampling areas have been preliminary proposed (Fig 1), considering predominantly:

- Juveniles and adults from in and beyond areas of national jurisdiction of, Peru, Chile and New Zealand (and if available from Ecuador).
- Longitudinal distribution sampling: Coastal and oceanic individuals
- Sampling during winter and summer, during different years.

A virtual meeting will be held in order to define the proper operational spatio-temporal scale for the sampling plan, and discuss logistical feasibility of sampling, in agreement with all delegations

involved in the project. These samples will be evaluated during the multidisciplinary study with agreed protocols for the analysis in each of the prioritized lines of research from B.1.

Samples (whole fresh or frozen CJM fish) are expected to be collected by and purchased from fisheries, following a sampling protocol developed for this study (e.g., fish must be frozen within 24 hours of capture, properly labeled, amongst other considerations) within and beyond areas of national jurisdiction of, Peru, Chile and New Zealand (and if available from Ecuador), and finally delivered to involved laboratories. The lead researchers will work with identified fishers to ensure that appropriate metadata is collected, e.g., position of fishing tows, time, date, fishing gear used, etc. (the exact content of the metadata will be agreed upon at the virtual meeting and/or a workshop of the delegations involved in the project).

For the purposes of the multidisciplinary approach (see next section) a minimum of 50 whole fish (samples) will be collected from each of the 16 proposed sampling areas (numbered on Figure 1) in two seasons (summer and winter) and each year, totaling 4800 samples. In addition to these fisheries dependent data, additional fisheries independent samples will be opportunistically collected from aligned research activities in the study area (e.g., research surveys). The budget allocated to sampling will predominantly be used for purchasing samples from fishers, and subsequent storage and transportation.

Agreement from national research institutions and/or governing bodies to collect fishery dependent and independent data within their national waters will be sought (including eventual sampling of juveniles). It should be noted that there are already national research sampling programs within Peru and Chile which may need to be strengthened, adjusted or modified to fulfil the sampling requirements specified in this proposal. For waters beyond areas of national jurisdiction (SPRFMO), the fishery dependent collections will fall under the general catch limits of the vessels fishing outlines in CMM01 (CMM01 2022 *Trachurus-murphyi*). As for any research surveys (fisheries independent data), sampling will be carried out following fishing protocols and gears allowed in CMM 01 by flag States which have allocated quota within SPRFMO. That is, samples from either commercial fisheries or research surveys will conform to CMM 01.
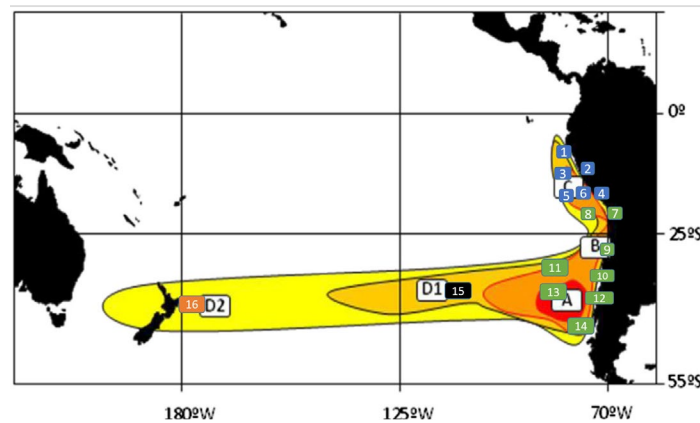

Figure 1. Sixteen proposed sampling areas off Peru (1 to 6), Chile (7 to 14) and New Zealand (16) along coastal and oceanic distribution of JM (modified from Gerlotto *et al*., 2012).

B.3. Genetic Research program

In order to analyze samples under the same criteria and method:

- A virtual Genetic Workshop will be organized to examine and discuss background and experiences from different ongoing and completed genetic programs done in fishery resources, with participation of colleagues from different countries. Different sampling scheme and genetic NGS methods will be discussed, including the analysis of NGS (Next Generation Sequencing) techniques, like whole genome sequencing. So, a genetic research workplan will be developed, including the number of samples, method and criteria for SNPs (Single Nucleotide Polymorphisms).
- Samples collected for genetic analysis from each delegation will be sent to an independent commercial genetic laboratory for processing them (DNA library preparation and NGS technique application). The Whole Genome Sequencing (WGS) analysis will be considered.
- A single report will be produced, including all the samples collected and analyzed using the same criteria.

B.4. Topics for multidisciplinary study

A list of topics is initially proposed below for the characterization of the structure and variability of CJM population on a spatial-temporal scale, in order to determine the existence of stocks or population units and their level of connectivity. As part of the desk study, each topic will be systematically reviewed and will provide a concise summary (4-5 pages total) covering: the background and rationale for the use of the approaches / field of study; a description and critical appraisal of methods described in the international literature; whether these methods have previously been applied to CJM or other small pelagic (and their effectiveness); and the feasibility / limitations of these methods within the proposed multidisciplinary study. The final list of topics will be ratified and prioritized as a result of the desk study (B1).

Topics	Main goals
Accompanying fauna	Evaluation of the composition, structure and function of the pelagic fauna associated with CJM
Age and growth	Determination of age and growth in juveniles and adults
Early stages	Age and growth evaluation of larval stages and/or early juveniles
Fisheries dynamics	Historical trends in spatio-temporal fishing indicators (e.g. catch, yield, size/age structure)
Genetics (detailed in item B.3)	Determination of the structure and the spatial and temporal population genetic variability
Geometric morphometry	Characterization and comparison of the morphometry of jack mackerel individuals and otoliths from different areas
Habitat	Habitat characterization at different stages (in conjunction with data from early-stage zones, and associated with oceanographic characteristics, e.g., Species Distribution Modelling of CJM in collaboration with the Habitat Monitoring WG).
Microchemistry	Trace elements incorporated into otolith growth may inform migration patterns
Parasitology	Comparative evaluation of the parasitic fauna between areas and/or population units
Reproduction	Evaluation of reproductive aspects and the spatio-temporal variation.

Resource condition	Evaluation of the resource condition and its spatio-temporal relationship with oceanographic variables.
Tagging methods	Review and evaluation of tagging methods (e.g., spaghetti tags, pop-up tags) to provide additional information on fish movements and migration.
Trophic ecology	Evaluation of the spatio-temporal variability of diets

These topics will be prioritized according to the desk study (and specific research budget allocated), and samples will be collected and analyzed considering protocols previously agreed for its use during this multidisciplinary study. Prioritization of research topics and/or articulating how outputs from each of the topics will be considered for decision making will be summarized (e.g., as a decision tree / flow diagram, designing sensitivity analyses to investigate the effect of different outputs) and agreed-upon by members of the CJM connectivity task group and approved by the SC. This key task will be completed before undertaking the sampling and subsequent interdisciplinary research tasks.

A repository managed by the SPRFMO secretariat is suggested to be created, to share all the project databases with the researchers of the delegations involved in this work program (including those involved in joint analyses). Joint analyses and reports of CJM stock structure and connectivity study, integrating data analyzed considering the same criteria between delegations, will be presented during the SC meetings. Each member will take care of the storage of tissue samples under standard preservation methods for DNA analysis as back-up and consideration for future studies.

Research budget provided by the SPRFMO Secretariate for this task will largely go towards analyses required to be undertaken at external laboratories (e.g., isotopes, otoliths microchemistry, parasitology, and others). In addition, we propose that two (2-year fixed term) researchers are recruited to support the research team and provide additional capacity to deliver on analyses and reports.

B.5. Workplan and estimated budget

Years	1 (2023)	2 (2024)		3(2025)		4 (2026)		5 (2027)	
Budget (NZD)	In kind	in-kind	SPRFMO	in-kind	SPRFMO	in-kind	SPRFMO	in-kind	SPRFMO
Funding proposal	$10,000								
Submit funding proposal to SC11	X								
Review funding proposal for submission to COMM12	X								
Desk study	$10,000	$58,848							
Systematic review of multidisciplinary topics (e.g., Fisheries dynamics, Genetics, Habitat) – submission as SC11 paper	X								
Systematic review of multidisciplinary topics (all remaining topics) - submission as SC12 paper		X							
Review theoretical definitions in the literature of population structure and stocks for pelagic fish		X							
Virtual meeting/workshop between researchers from different delegations		X							
Identification of priority lines list of multidisciplinary research		Critical milestone must be achieved before tasks are undertaken in Years 3 - 5							
List of gaps identified in CJM research for connectivity study		X							

Activity					
Submit joint report to SC on final recommendations for the multidisciplinary study			X		
Sampling	$30,000	$31,600 $5,000	$61,600 $5,000	$61,600 $5,000	
Development of a sampling protocol; Virtual meeting between researchers from different delegations to input on sampling protocol; Submission to SC11 for review)	X				
Elaboration of the proper operational spatio-temporal scale for the sampling plan		X			
Sampling activities		X	X	X	
Submit joint sampling reports to SC			X	X	X
Genetic research program		$13,860 $10,000	$13,860 $50,000	$13,860 $50,000	$46,200 $ 50,000
Genetic workshop		X			
Samples processing for good quality of DNA extraction		X	X	X	
DNA sequencing (Whole Genome Sequencing analysis) undertaken by an independent facility			X	X	X
Joint population genetic analysis and report submitted to SC				X	X
Multidisciplinary research program			$204,000 $156,000	$204,000 $155,000	$204,000 $114,000

Elaboration of protocols (and or validation) for sample processing and analysis (if necessary)				X		X		
Processing of samples for prioritized research topics				X		X		X
Creation of a database repository for participating delegations involved in the joint analysis and reporting				X		X		
Report of preliminary results integrating data from delegations								X
TOTAL BUDGET		$308,308	$161,000	$229,460	$162,000	$229,460	$161,000	$200,200	$116,000

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C. Project management

Administrative and logistic responsibilities will be carried out by the chair and co-chairs designated during SC10 meeting. Researchers from the Peruvian and Chilean SPRFMO delegations, will form the core research team noting that all interested SPRFMO delegates are encouraged to be involved in this multidisciplinary study. Currently, the core research is expected to include (but is not limited to):

Chair and co-chairs	Research Team	
- Fabrice Stephenson (New Zealand) - Giovanna Sotil (Peru) - Sebastián Vásquez (Chile)	*Peru delegation*: - Ana Alegre - Patricia Ayón - Betsy Buitrón - Erich Díaz - Pepe Espinoza - Elisa Goya - Daniel Grados - Luis Usca	*Chile delegation:* - Cristian Canales-Aquirre - Victor Espejo - Sandra Ferrada - Sergio Núñez - Ignacio Payá - Aquiles Sepúlveda

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