Project update: Dic 2025

Conservation of heavily fished species in the Patagonian seas: the case of hoki (*Macruronus magellanicus*) and southern blue whiting (*Micromesistius australis*)

Rufford I.D.

45039-1

Executive summary of the project

This project aims to address the knowledge gap about the population dynamics and structure of the ecologically and economically important hoki (*Macruronus magellanicus*) and southern blue whiting (*Micromesistius australis*) in the Patagonian seas. These species have faced intense fishing pressure, leading to population declines and stock depletion. This underscores the need for applied research to support sustainable management. We will use genomic analysis (RAD-seq) to robustly characterize the genetic structure, diversity, and connectivity of these two species. This will enhance stock identification and management strategies, ultimately contributing to improve the population status of both species.

Work progress

We have made significant progress in the following stages of the project:

1. Fieldwork, collection, processing, and preservation of samples.

Working together with researchers Dr. Analía Guissi and Specialist Anabela Zavatteri from the Argentine National Institute for Fisheries Research and Development (INIDEP), we collected and processed samples of hoki (*Macruronus magellanicus*) and southern blue whiting (*Micromesistius australis*) from different regions of the Southwestern Atlantic Ocean. These samples were obtained through the INIDEP Biological, Fisheries and Environmental Information Acquisition Program, as well as from both recent and previous research cruises carried out aboard INIDEP research vessels. Additional samples from Chilean waters and the Falkland/Malvinas Islands were provided by Dr. Canales Aguirre and Dr. Ferrada Fuentes.

For hoki, samples were collected from several areas, San Matías Gulf, San Jorge Gulf, the mid-shelf, and the southern shelf and slope (figure 3). Southern blue whiting samples were obtained from the southern continental shelf and slope, as well as from the Southeastern Pacific Ocean and the area surrounding the Falkland/Malvinas Islands (figure 4).

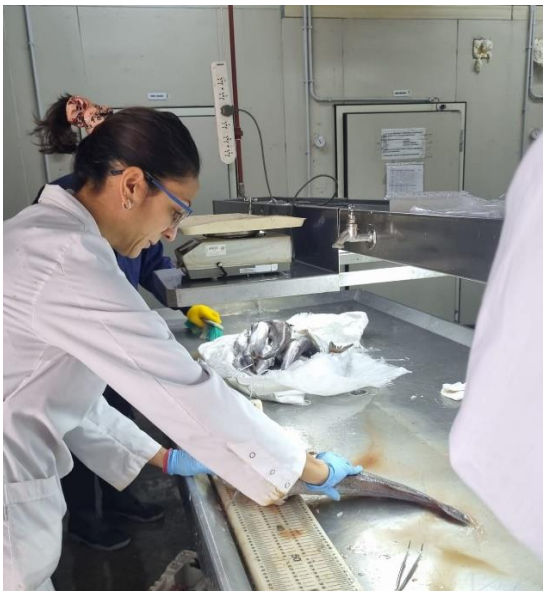

Figure 1. Sample processing of southern blue whiting (*Micromesistius australis*) specimens during laboratory work at the Instituto Nacional de Investigación y Desarrollo Pesquero (INIDEP, Mar del Plata, Argentina) © Alejandro Ezequiel Rojas.

Figure 2. Whole specimens of hoki (*Macruronus magellanicus*) collected for sampling © Alejandro Ezequiel Rojas.

Removed in online version

Figure 3. Map showing the sampling locations for hoki (*Macruronus magellanicus*) in the Southwestern Atlantic Ocean.

Removed in online version

Figure 4. Map showing the sampling locations for southern blue whiting (*Micromesistius australis*) in the in the Southwestern Atlantic and Southeastern Pacific Oceans.

2. DNA extraction, RAD library preparation, and sequencing

Genomic DNA was extracted from all available samples, and DNA integrity was assessed by agarose gel electrophoresis (figure 6). For RAD-seq library preparation, 96 samples per species were selected, prioritizing those with acceptable DNA quality (clear bands on the gel) and aiming to maximize their geographic representation. DNA concentration was subsequently quantified and normalized using a Qubit fluorometer.

RAD-seq libraries were prepared following a modified version of the protocol (Baird et al., PLOS ONE: https://doi.org/10.1371/journal.pone.0003376). In brief, genomic DNA from each sample was digested with a restriction enzyme, ligated to barcoded adapters, and then pooled for library construction. After fragmentation and size selection, libraries were amplified by PCR, purified, quantified, and diluted prior to sequencing.

Library preparation was performed independently for each species, and the final libraries were sent to an external sequencing service for high-throughput sequencing on an Illumina platform.

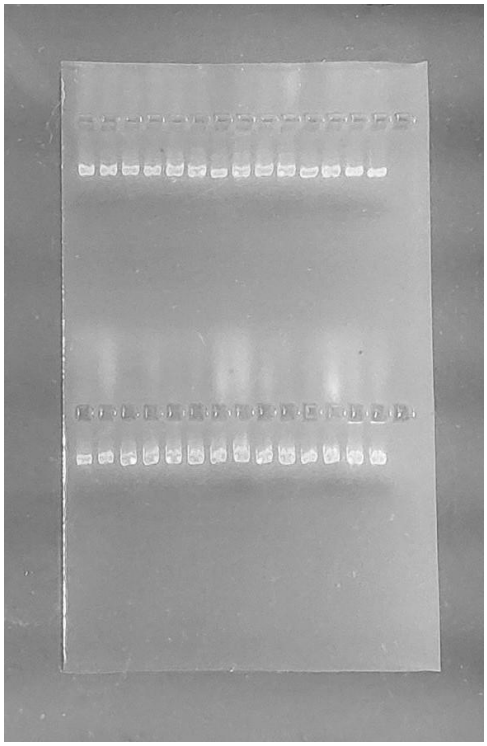

Figure 6. Gel electrophoresis image used to check the quality of DNA extracted from the samples.

Figure 7. Laboratory work during RAD-seq library preparation ©Agustina Caniguan (Centro Austral de Investigaciones Científicas – C.A.D.I.C).

Future steps

We are currently awaiting the RAD-seq data from the sequencing service. Once the data are received, we will proceed with bioinformatic analyses, followed by the preparation of scientific articles and reports, as well as the communication of results .

Obstacles to the original plan

One of the main challenges encountered was that a subset of samples showed signs of DNA degradation during quality assessment, appearing as smeared bands on agarose gels. This resulted in delays during the DNA extraction stage, as extractions had to be repeated several times, in some cases improving DNA quality.

In addition, we experienced difficulties in obtaining hoki samples from the Southeastern Pacific Ocean. Nevertheless, we continue to work in coordination with INIDEP to secure samples from this area and incorporate them into future analyses.