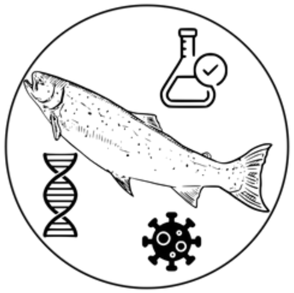
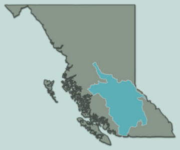
Chum whole genome sequencing for improved stock delineation

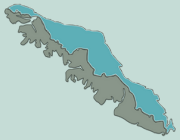


Salmon Enhancement

Genetics



Fraser



Vancouver Island East

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The objective of this study is to better understand the population structure of Chum salmon in British Columbia, by using low-coverage whole genome sequencing, in order to strengthen genetic stock delineation and improve genetic stock identification methods across the region – this includes hatchery-enhanced populations in systems where they are collected.

The project began in the Salish Sea and Fraser River, where there remains important stock structure delineations that cannot be reliably assigned. In particular, splitting the assignment of the Chilliwack River and the remainder of the Lower Fraser River has been a long-standing management objective that cannot achieve the necessary reliability within the current genetic stock identification panel. Within the Strait of Georgia, examining the population structure that delineates the East Coast Vancouver Island, Sunshine Coast, and Howe Sound regions has been paramount. In each case, while the existing panel suggests genetic delineation exists, the genetic markers within the current panel are not sufficient to assign to these regions reliably.

Analyses are being run to determine what portions of the genome might be different among the regions under focus. A deep dive into the full genomic allele frequencies will allow for a full-scale re-examination of the population structure and identify the genetic markers that underlie these differences. Once complete, the existing SNP-based genetic stock identification panel will be re-designed to incorporate these markers, to ensure future analyses are targeting the greatest resolution that can be achieved.

Take-aways

- Genetic sequencing is an effective tool to identify salmon species by stock, but this method is only available where enough genetic information has been gathered and sufficient differentiation has been detected.
- South Coast chum salmon have not been sequenced intensely enough to fully describe population structure delineation, so this genome sequencing study gathers DNA from across the region to assess differences in genetic markers that could be used to maximize the resolution.

This initial effort will be built upon over the duration of the project by extending sampling to additional regions where further stock delineation is necessitated to meet assessment and enhancement objectives; next up will likely include West Coast Vancouver Island, Johnstone Strait, and the Central Coast of BC.

Timeline

✓ Jul 2023-Mar 2024:generation of the lcWGS data from the targeted South Coast and Fraser River Chum populations

↻ to March 2025: Chum lcWGS sequencing; whole-genome analysis of differentiation among South Coast Chum populations

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Locations

Fraser Valley
Salish Sea

Species

Chum

Project ID

2436