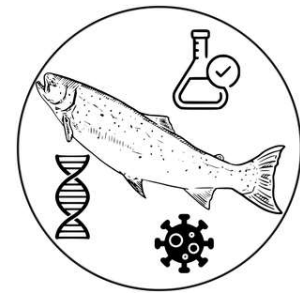


Relative reproductive success of hatchery- versus natural-origin salmon in Canadian integrated populations



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Locations
**Sarita River
Nitinat Hatchery**

Species
Chinook

Project ID
2451



Salmon
Enhancement



Genetics



Vancouver Island
West

There are risks associated with hatchery enhancement: differences between a hatchery and a natural habitat affect both the genetic and environmental factors that shape the performance and fitness of salmon. The relative fitness of hatchery-origin compared to natural-origin salmon has been estimated in a handful of systems through determination of Relative Reproductive Success (RRS). In these studies, returning adults are assigned back to their parents using genetic tags called parentage-based tags, and RRS is inferred by the number of returns per family from hatchery-origin compared to natural-origin parents.

In general, the results of RRS studies suggest that hatchery-origin fish have lower natural reproductive success than natural-origin fish, and this reduced RRS is potentially transferred across generations. The extent to which hatchery-origin fitness is lower than natural-origin fitness is likely dependent on current and historical factors impacting specific systems, including hatchery practices.

The objectives of the study are:

- 1) Initiate genetic sampling of both the escapement and broodstock for at least one population enhanced by the Salmonid Enhancement Program (SEP).
- 2) Use a genetic biomarker panel to genotype

Take-aways

- Salmon bred from a hatchery are often less fit in wild environments than naturally-bred salmon.
- However, this situation can change using different hatchery methods.
- This genetic study compares DNA samples from returning hatchery Chinook to natural Chinook in Sarita River to see if hatchery methods impact the spawning success of hatchery Chinook.

these natural-origin and hatchery-origin parents.

3) Explore alternative approaches to enable widespread RRS estimation across SEP hatcheries even in systems where extensively escapement sampling is infeasible.

Timeline

- ✓ Nov 2023: DNA samples collected from 900 potential natural-origin spawners
- ✓ Apr 2024: DNA samples collected from outmigrating smolts
- 🔄 to Mar 2025: Single-nucleotide polymorphism (SNP) genotype database of natural-origin spawners for future analyses on outmigrating smolts or returning adults.