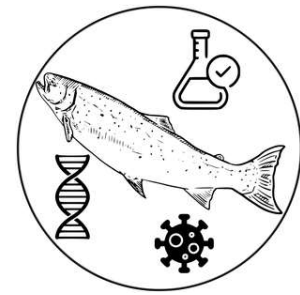


Epigenetic variation between hatchery- and natural-origin Canadian Chinook Salmon



Substantial epigenetic differences have been detected between hatchery-origin and natural-origin Pacific salmonids. Epigenetic variants are structural changes to DNA without a change in the DNA sequence itself. For example, DNA methylation is a commonly studied epigenetic mechanism in which a methyl group (-CH₃) is covalently added to a cytosine residue. These modifications to DNA can alter the function of the genome, particularly through the regulation of gene expression.

Given the extent of variation in epigenetic signatures between hatchery-origin and natural-origin salmon, the functional effects of epigenetic variants are excellent candidates to underlie the fitness consequences associated with hatchery enhancement. Additionally, it is possible for hatchery epigenetic variants to be inherited by the offspring of hatchery-origin fish, which aligns with the potential for long-term reductions in population fitness as hatchery-origin fish spawn in natural habitats. The study of epigenetic variation in Pacific salmonids is relatively in its infancy, but epigenetic biomarkers are a promising tool to facilitate managing hatchery enhancement.

The first-year objectives of the study are:

- 1) Identify hatchery- and natural-origin Chinook Salmon in broodstock from five SEP hatcheries through assignments of parentage-based tags.
- 2) Utilize enzymatic methyl sequencing to assess DNA methylation patterns among female and male hatchery- and natural-origin Chinook Salmon across difference age classes of return.

Take-aways

- There are few genetic differences between hatchery-bred and natural salmon in populations enhanced by the Salmonid Enhancement Program (SEP), but structural modifications to genes may affect gene expression and impact salmon fitness in the wild.
- This genetic sequencing study gathers Chinook samples from hatcheries at the Nicola, Quinsam, Sarita, Atnarko, and Chilliwack rivers to compare epigenetic (methylation) differences between hatchery and wild Chinook to better monitor the proportion of hatchery salmon in a river.

- 3) Determine hatchery-origin epigenetic variants that are: common across all hatcheries studied, specific to individual hatcheries, associated with physiological performance, associated with sex, or associated with age of return.
- 4) Identify candidate epigenomic biomarkers for use in high-throughput molecular tools to support monitoring and management decisions.

Timeline

- ✓ Apr 2024: data obtained and expected, and preliminary analysis for the Nicola and Sarita River populations completed
- 🔄 to Mar 2025: analysis of DNA methylation variation; pyrosequencing assay development; EM-seq analysis; transcriptomic analysis of gene expression

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Collaborations
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Locations
**Sarita, Chilliwack,
Nicola, Quinsam,
Atnarko Rivers**

Species
Chinook

Project ID
2453

