Intergenerational transfer and parental origins of DNA methylation variation in Coho and Chinook Salmon

Salmon Enhancement

Genetics

PBS Nanaimo

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The objective of this project is to document inheritance of DNA methylation and identify relative contribution of male and female parents to variation in methylation observed in their offspring. This project uses methylation sequencing of parents and offspring in hybrid crosses of hatchery and natural origin to document the presence of methylation in adult tissue that are present in their offspring. Knowledge of the parental origins and frequency of DNA methylation inheritance would inform specific breeding guidelines and allow management for reduced propagation of epigenetic effects.

Priorities are to:

1) Perform whole-genome methylation sequencing to characterize differential methylation between hatchery and natural origin fish.

Take-aways

- Chemical reactions in a salmon body decide which genes are expressed in a process called "DNA methylation."
- This hatchery genetics study sequences methylation across the genome to compare between hatchery and natural origin to see if salmon offspring inherit DNA methylation from parents (epigenetics) and how this could inform hatchery breeding methods.

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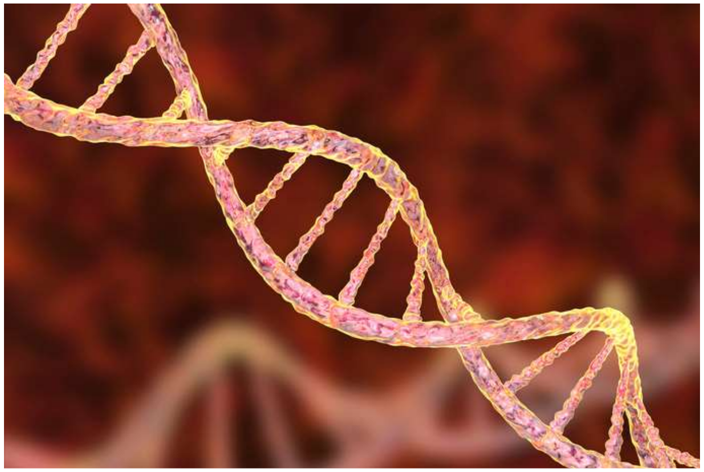
2) Use targeted bisulfite sequencing of specific regions identified in objective 1 in the offspring of breeding crosses made with the fish from objective 1 to detect parent of origin patterns in DNA methylation between different cross-types



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Timeline

- ✓ Adult methylation sequencing
- ✓ Jan – Mar 2024 Targeted sequencing

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Collaborations

UBC, Genome BC

Hatchery

Chehalis River

Species

Chinook

Coho

Project ID

2435