



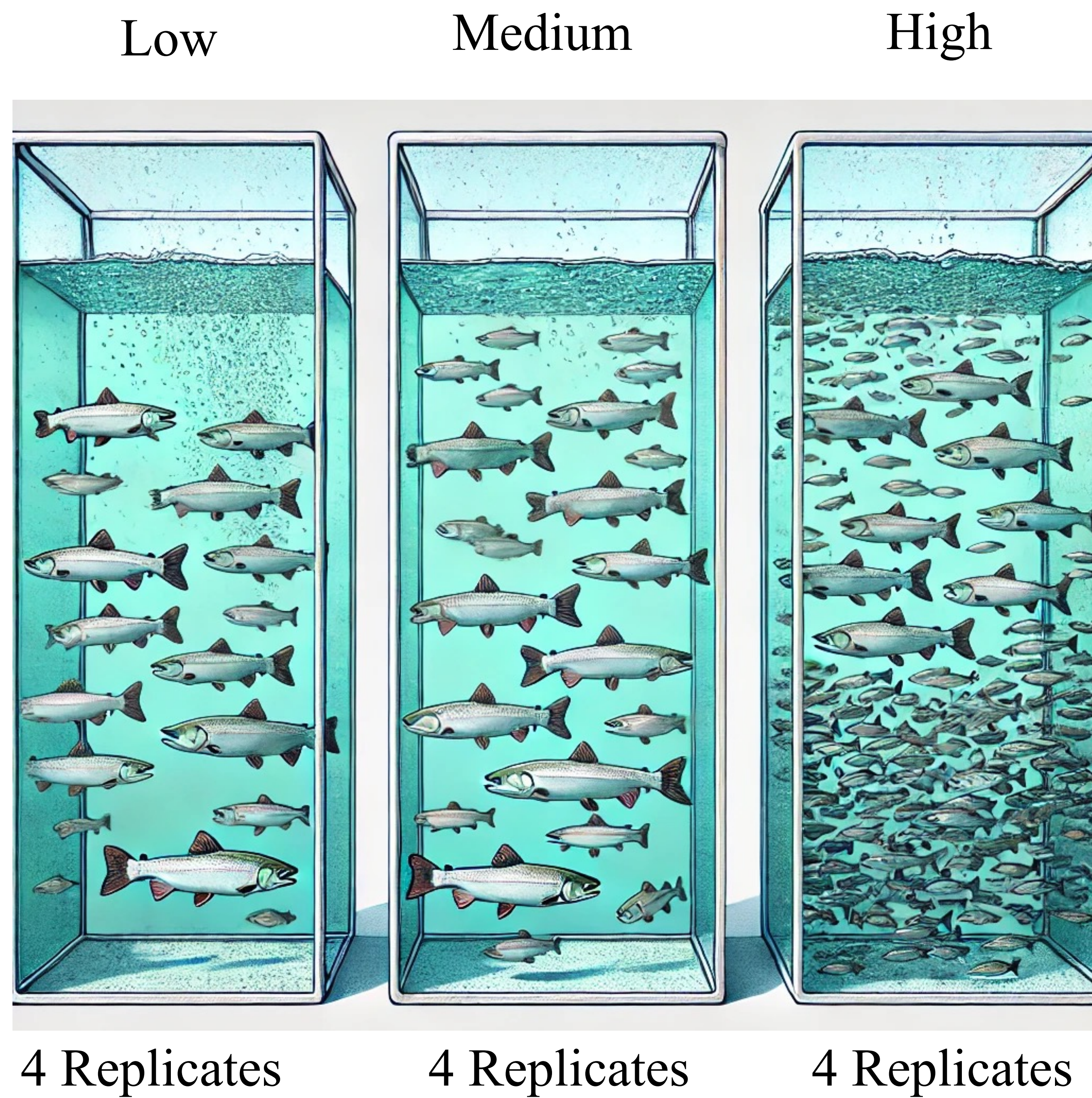
An epigenetics pilot study to evaluate effects of rearing density on methylation patterns in Chinook salmon



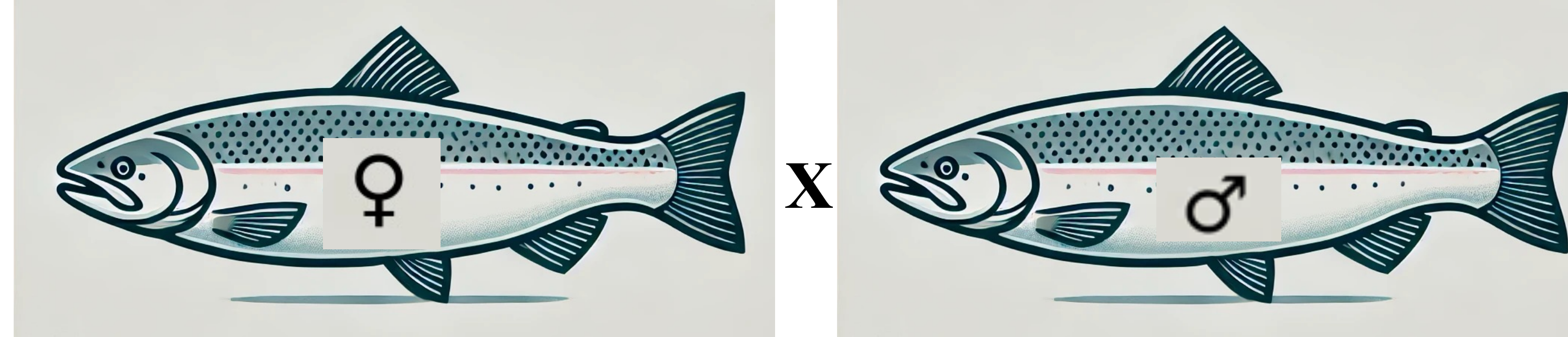
Ilana Koch, Hayley Nuetzel, Shawn Narum

Primary Question: Does hatchery rearing density influence methylation patterns in Chinook salmon?

Treatment Groups:



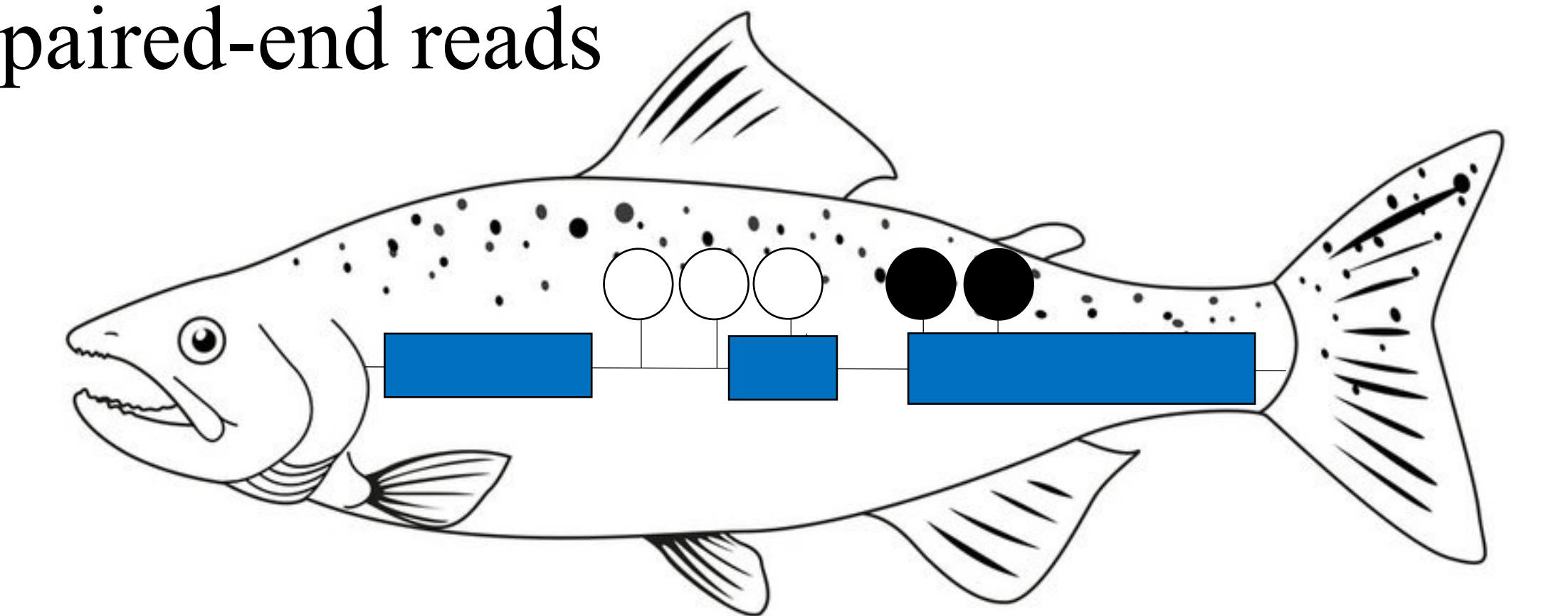
8 Families Distributed in Each Treatment:



N=2	Hatchery-Origin	X	Natural-Origin
N=2	Natural-Origin	X	Hatchery-Origin
N=2	Hatchery-Origin	X	Hatchery-Origin
N=2	Natural-Origin	X	Natural-Origin

Whole Genome Bisulfite Sequencing:

- 8X minimum coverage from Illumina 150 bp paired-end reads



N=40

Identical Tank Conditions:

- Food (% body weight)
- Temperature
- Light



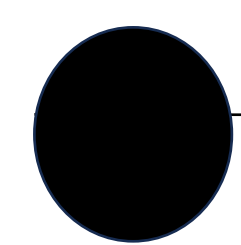
Samples Collected From Parents & Study Fish (i.e., offspring):

- Heart
- Liver
- Gonad
- Fin Clip

Additional Study Questions:

- Are there functional genomic regions that are differentially methylated in response to different density treatments?
- How does methylation change during development?
- How heritable are these methylation marks?
- How does parental origin (hatchery or natural) affect methylation patterns?

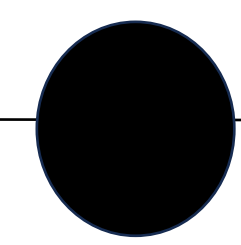
Sampled parents



August 2024

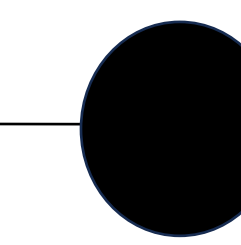
Obtained eggs & milt from Umatilla Hatchery spring Chinook stock. Crossed gametes & incubated at Oregon State University – Fish Performance Genetics Lab.

Sample 20 fish per tank



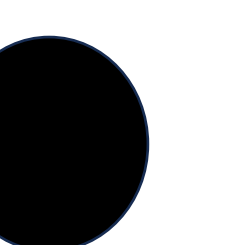
February 2025

Progeny reached button-up fry stage. Moved from incubation trays & distributed across 12 treatment tanks (3 treatments, 4 replicates).



September 2025

Study fish reach parr stage.



Sample all remaining fish

April 2026

Study fish reach smolt stage. Experiment ends.