

Genomic evidence for hatchery-induced domestication selection in Chinook salmon, *Oncorhynchus tshawytscha*



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Abstract: Salmon hatcheries are widely used across the Pacific Northwest to enhance fisheries and supplement declining wild populations. However, substantial evidence suggests that hatchery fish have reduced fitness compared to their wild counterparts. Domestication selection, or adaptation to the hatchery environment, poses a potential risk to wild populations if introgression between hatchery and wild fish occurs. While few studies have investigated domestication selection on a genomic level, none have done so in parallel across multiple hatchery-wild population pairs. In this study, we examined three separate hatchery populations of Chinook salmon, *Oncorhynchus tshawytscha*, and their corresponding wild progenitor populations using low-coverage whole genome sequencing. We sequenced 192 individuals from populations across Southeast Alaska and estimated genotype likelihoods at over six million loci. Each hatchery population, which was reared in a hatchery for approximately seven generations, was then compared to its wild progenitor population using multiple metrics of genomic divergence. While evaluating population-level genomic differentiation (F_{ST}), we discovered numerous outlier peaks in each hatchery-wild pair, although no outliers were shared across the three comparisons. Further analyses indicated that these relatively small (5 - 60 kilobase) peaks are likely due to genetic hitchhiking on hatchery-selected alleles, though the effects of these peaks on fitness are unknown. Overall, our genome-wide analyses demonstrate that domestication selection is prevalent in all hatchery facilities, but the genetic pathways differ across populations, possibly due to a polygenic basis of fitness related traits. These results provide fine-scale genetic evidence for domestication and highlight the need to assess if certain management practices, such as integration of wild broodstock, can universally mitigate genetic risks despite multiple pathways of domestication.

Introduction

- Salmon hatcheries are abundant in Alaska, and have been used for supplementing wild salmon populations since the 1970s
- In the past few decades, as we have seen declining salmon populations across the West Coast (1)
- Also, evidence for risks associated with hatchery salmon and supplementation
 - Genetic Drift & Inbreeding (2,3)
 - Domestication Selection (2)
 - 1. Relaxation of wild, natural selection
 - 2. Artificial selection due to environmental changes in hatchery-rearing environment
- Causes reduced fitness of hatchery fish when reintroduced into the wild (4)
 - This can negatively impact wild populations if they interbreed (5)
- Reason for fitness reduction is still unknown (6)

By comparing hatchery salmon lineages to the wild populations they were founded from, we can investigate if domestication selection is occurring in these hatchery facilities over approximately seven generations. Additionally, we can determine if selection is occurring at the same genomic regions across multiple hatchery facilities.



Figure 2 (right). The six study sites are located in Southeast Alaska: three hatchery facilities and three wild populations, along with main watersheds in the region. Matching colored borders represent the hatchery facility and its corresponding wild progenitor population by which that hatchery line was founded | Map Credit: Alaska Department of Fish & Game



Figure 1 (above). Chinook Salmon | NOAA Fisheries

Methods

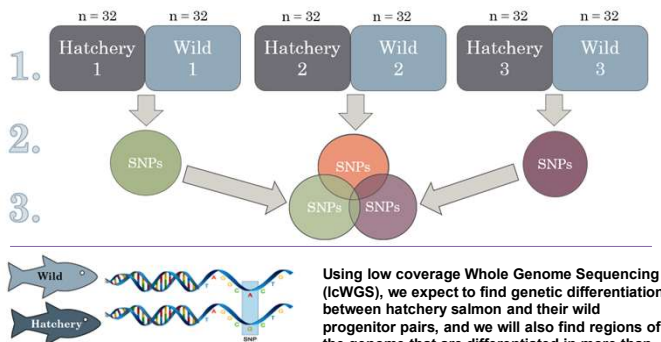


Figure 3. Single nucleotide polymorphisms (SNPs) are genetic differences in a DNA sequence at one nucleotide.

Using low coverage Whole Genome Sequencing (lcWGS), we expect to find genetic differentiation between hatchery salmon and their wild progenitor pairs, and we will also find regions of the genome that are differentiated in more than one hatchery-wild population pair.

Results

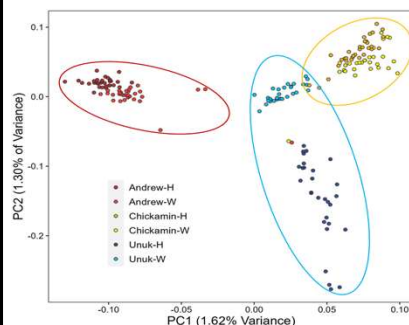


Figure 5. Principal component analyses show genome-wide population structure across all six populations, (H = Hatchery, W = Wild).

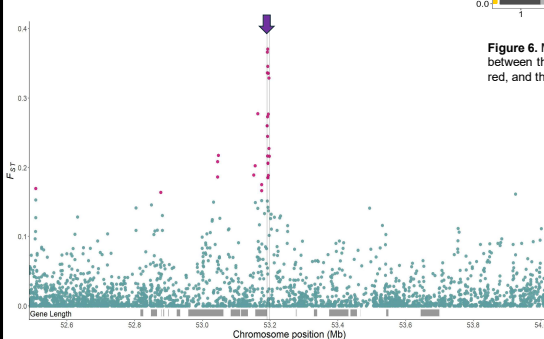


Figure 7. Manhattan plot of F_{ST} in the Unuk hatchery-wild comparison on Chromosome four at 53.2 million base pairs (Mb). Genes identified in the region of this outlier peak are delineated below F_{ST} values as gray bars.

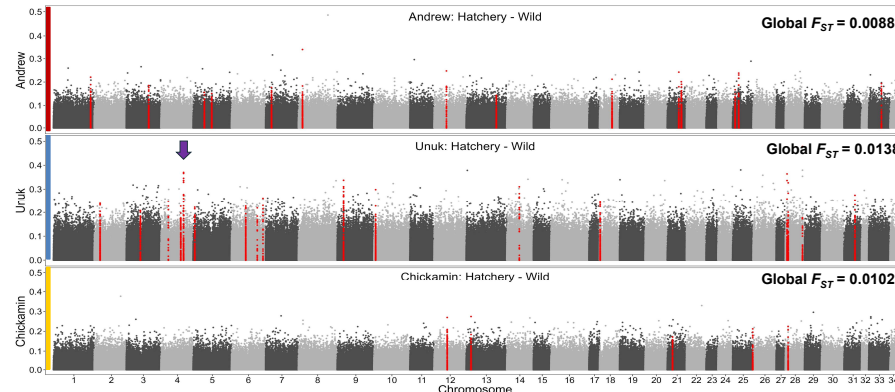


Figure 6. Manhattan plot of genome-wide F_{ST} on a per-SNP basis for each hatchery-wild population pair. Greater F_{ST} values are indicative of differing SNPs between the two populations (e.g., the allele is A in many wild salmon, but the allele is G for hatchery salmon at that same loci). Outlier F_{ST} peaks are shown in red, and the purple arrow represents the prolific peak, which is shown in greater detail in Figure 7.

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