Genetic analysis of New Zealand Chinook salmon

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In 2018 and 2021, researchers at the University of California Davis received Chinook salmon fin clips generously collected by New Zealand anglers. Two different genetic analyses were performed to better understand how New Zealand Chinook are related to existing runs of Chinook salmon in the Central Valley of California. These data will be used, along with other information, to support efforts to restore Chinook to the McCloud River in northern California.

The first genetic analysis to assign New Zealand fish to spawning run type was a testing method called SHERLOCK. SHERLOCK uses a protein called CRISPR Cas13a to detect target sequences of DNA in a sample. Researchers have identified a gene called GREB1L that contains two different alleles, or versions of the same gene, one unique to early migrating (winter and spring) Chinook and another found only in late migrating (fall and late fall) Chinook. We performed SHERLOCK tests targeting the early migrating and late migrating GREB1L sequences and found that 47% of Chinook sampled in 2018 and 39% in 2021 possessed two alleles of the late migrating Chinook (Figure 1). Seventeen and 22% had two early migrating alleles, and 32% and 24% of individuals had one of each allele (e.g. heterozygous for the early and late migrating alleles). We did some additional SHERLOCK testing to examine two other DNA sequences, one unique to present day spring run and one unique to present day winter run Chinook salmon in the Central Valley. Most individuals with two early migrating alleles also had the spring run sequence, while a few had neither sequence (unknown; Figure 1). No New Zealand Chinook had the sequence unique to present day Central Valley winter run Chinook.

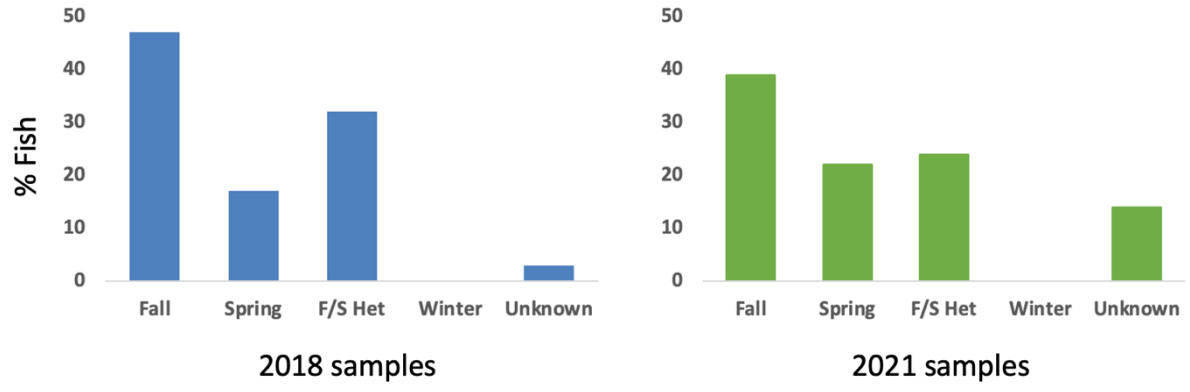

Figure 1. Percentage of Chinook assigning to different spawning run types (fall, spring, winter) using the SHERLOCK tests. F/S Het refers to individuals heterozygous for the late-migrating (fall) and early migrating alleles who assigned to spring run in the second test. Unknown individuals either had two early migrating alleles or were heterozygous for the late-migrating and early migrating alleles who could not be assigned to spring or winter run with the second test.

The second genetic analysis we performed, called microfluidic SNP genotyping, looked at 80 different genetic sequences scattered throughout the genomes of sampled fish to see how genetically similar each fish is to Chinook salmon from different populations found throughout the Central Valley of California. Only fish found to be early migrating or heterozygous in the SHERLOCK analysis were initially included in this analysis. We found that most of these early migrating fish were more genetically similar to fall run and late fall run Chinook salmon in the Central Valley than the other runs. Only a small percentage of fish were genetically similar to present day Central Valley spring runs. This result tells us that after Central Valley Chinook salmon were introduced to New Zealand, interbreeding occurred and GREB1L alleles were mixed among individuals from the different runs.

We plan to conduct additional genetic analysis of the New Zealand Chinook samples to better understand the origin of the fish and how they are related to current Central Valley Chinook salmon runs and populations. All New Zealand Chinook samples are now undergoing analysis at hundreds of different genetic sequences scattered throughout the Chinook salmon genome. This analysis will allow us to have a clearer understanding of the origin of New Zealand Chinook and their relationship to present day Central Valley runs and populations.