

Genetic Stock Identification for the Chinook Columbia River Pound Net Evaluation Project

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In the lower Columbia River just below the Bonneville dam, 2072 Chinook salmon were captured, passive integrated transponder (PIT) tagged, and fin clipped during August-October 2017 via pound net fish traps to evaluate the efficiency of this capture method to maintain low post-release mortality rates as opposed to the traditional gillnet method. Approximately equal numbers of these fish were captured in a control and a treatment setting. PIT tags were used to identify individuals that survived capture by detecting them at fish ladders as they moved upstream through the Bonneville dam.

Single nucleotide polymorphism (SNP) genotyping was used to identify how many individuals were bound for tributaries below the Bonneville dam in order to exclude those individuals when estimating pound net mortality rates. A random subset of 507 Chinook fin clips were genotyped by the Eagle Fish Genetics Lab (Idaho Fish and Game) and assigned to reporting groups of individual's origins using the Chinook salmon Columbia River Basin baseline version 3.1 in order to estimate post-release survival rates of the pound net equipment. Genotyped individuals were screened to determine if they were hatchery fish using a parentage-based tag (PBT) at 298 SNP loci against the Columbia Basin Chinook PBT baseline (see CRITFC citation below). Fish were tested at 95 additional SNP loci using the Snake River spring/summer Chinook PBT baseline. Wild fish were assigned to a genetic stock at 299 SNP loci using a Chinook salmon genetic stock identification (GSI) baseline from the Columbia River basin developed by the Columbia River Inter-Tribal Fish Commission (CRITFC; Hess et al 2015).

We are currently unable to provide a list of the PBT broodstocks used in this project because they are in the process of being updated on FishGen (the database of IDF&G at www.fishgen.net). Parentage assignments were made using the program SNPPIT and assignments were accepted if the identified parents were of opposite sex and the LOD score was at least 14 (Hess et al 2015). Wild fish populations were assigned back to 19 different possible reporting groups including: : Young's Bay-Columbia Rouge "YOUNGS", West Cascade spring-run "WCASSP", West Cascade fall-run "WCASFA", Willamette River spring-run "WILLAM", Spring Creek Group Tule fall-run "SPCRTU", Klickitat River spring-run "KLICKR", Deschutes River spring-run "DESCSP", John Day River spring-run "JOHNDR", Yakima River spring-run "YAKIMA", upper Columbia River spring-run "UCOLSP", Tucannon River spring-run "TUCANO", Hells Canyon spring-run "HELLSC", South Fork Salmon River spring-run "SFSALM", Chamberlain Creek spring-run "CHMBLN", Middle Fork Salmon River spring-run "MFSALM", upper Salmon River spring-run "UPSALM", Deschutes River fall-run "DESCFA", upper Columbia River summer/fall-run "UCOLSF", and Snake River fall-run "SRFALL." For more details on reporting groups see Hess et al 2015.

Of the 507 fin clips, 86 of the total genotyped samples had a PBT tag (17.3% hatchery origin) from the following hatcheries: 21 from Little White Salmon National Fish Hatchery (summer/fall), 17