

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

from Lyons Ferry Fish Hatchery, 6 from Nez Perce Tribal Fish Hatchery (fall), 33 from Priest Rapids Hatchery, and 9 from Spring Creek National Fish Hatchery. 11 individuals were not genotyped successfully. Of the remaining 410 putatively wild fish, assignments were successfully made to the following GSI reporting groups: 19 from Young's Bay- Columbia Rouge "YOUNGS", 80 from West Cascade fall-run "WCASFA", 107 from Spring Creek Group Tule fall-run "SPCRTU", 2 from Deschutes River fall-run "DESCFA", 186 from upper Columbia River summer-/fall-run "UCOLSF", and 16 from Snake River fall-run "SRFALL."

Three hundred and ninety-seven fish were successfully assigned to populations above the Bonneville dam through both PBT and GSI. One hundred and five of those 397 individuals did not check in at the Bonneville fish ladder or above and had no PIT tag information in the metadata file (Table 1). In total 292 fish (of 397) are known to have survived to climb the fish ladder. There are 5 individuals that did not check in at a fish ladder and were also not genotyped successfully, thus we cannot determine if they belong to populations above or below Bonneville dam. In addition, 97 individuals did not check in at any ladder and were assigned to populations below Bonneville (WCASFA or YOUNGS). Two fish were assigned to populations below Bonneville but checked in at the Bonneville Bradford and Cascades Island ladders.

Of all fish that did not check in at a fish ladder, 5 individuals have a low probability of best GSI reporting unit (below 90%), thus we cannot assign them with high confidence to reporting groups either above or below Bonneville dam (Table 2). A threshold of 90% probability has been chosen to ensure high confidence in assignment probability for individuals who were potentially assigned to both lower and upper Columbia River populations. Four of those individuals have been assigned to WCASFA (below) but also have a fairly high potential to be assigned above Bonneville. One individual was assigned above Bonneville at SPCRTU, but has a 40% chance of being from WCASFA. It is recommended that these fish be omitted from the dataset, as they are below the threshold for assignment probability which has potential to reassign them to originating from either above or below the Bonneville dam. Additional fish had an assignment probability below 90%; however, their possibilities for population of origin were all above the Bonneville dam, not affecting their end result.

The DNA of 32 individuals was extracted both by Montana Conservation Genomics Lab and Eagle Fish Genetics Lab in order to serve as a control for the SNP genotyping data. Thirty-one of those individuals had 100% identical loci between duplicates. The remaining duplicate extraction was 99.65% identical with only one discordant locus.

Overall, 97 of the individuals that did not check in to a fish ladder were assigned to populations of origin below the Bonneville dam from genetic stock identification based on the Chinook salmon Columbia River GSI baseline (Table 1). These fish could be assumed to be bound for tributaries below the Bonneville dam and thus excluded from pound net mortality estimates. However, sources of uncertainty for both PBT and GSI data still remain. We are uncertain whether all of the lower Columbia River hatcheries are included in the PBT baseline and if not, which hatcheries have been omitted from

the baseline. It is also unknown how accurate the GSI assignment accuracy is for fish belonging to any excluded hatcheries/populations. We are currently working to obtain this information from CRITFC.

Table 1. Summary of total number of individuals that were assigned above/below Bonneville or were not able to be successfully genotyped. The number of fish in each assignment group that were part of the treatment or control group is noted under the “Treatment” and “Control” columns. Individuals that were assigned to a reporting group based on either genetic stock identification or parentage based tagging are indicated under “GSI Assignment” and “PBT Assignment,” respectively. Fish were able to “check in” at a location (Bonneville, The Dalles, and McNary dam fish ladders) using the PIT tag implanted at time of capture in order to track fish movement.

Assignment Type	Treatment	Control	GSI Assignment	PBT Assignment	Total Number of Individuals
Successfully Assigned Above Bonneville	209	188	311	86	397
Assigned Above Bonneville- Checked in at Ladder	149	143	219	73	292
Assigned Above Bonneville- Did Not Check in at Ladder	60	45	92	13	105
Successfully Assigned Below Bonneville	52	47	99	0	99
Assigned Below Bonneville- Checked in at Ladder	0	2	2	0	2
Assigned Below Bonneville- Did Not Check in at Ladder	52	45	97	0	97
Not Able to be Genotyped	5	6	NA	NA	11
Not Able to be Genotyped- Checked in at Ladder	4	2	NA	NA	6
Not Able to Be Genotyped- Did Not Check in at Ladder	1	4	NA	NA	5

Table 2. The five individuals that did not check in at a Bonneville dam fish ladder or above and with a probability of best GSI reporting unit below 90% in which having a low assignment probability may affect the outcome of whether the individual is assigned to an origin population above or below the Bonneville dam. Spring Creek Group Tule fall-run “SPCRTU” is located above the Bonneville dam. West Cascade fall-run “WCASFA” is located below the Bonneville dam. The remaining 14 GSI reporting groups are not included in the table because these individuals did not assign to the groups at any percentage.

Genetic ID	Best GSI Reporting Unit	Probability Best GSI Reporting Unit	Amplified GSI Loci	%WCASFA	%SPCRTU	%DESCFA	%UCOLSF	%SRFALL
2396	WCASFA	0.51	178	0.51	0	5.10E-07	0.10	0.39
1498	WCASFA	0.53	178	0.53	0.47	0	0	0
2843	SPCRTU	0.60	179	0.40	0.60	0	0	0
779	WCASFA	0.66	175	0.66	0.34	0	0	0
1968	WCASFA	0.72	177	0.72	0.28	0	0	0

References Cited

Jon E. Hess Nathan R. Campbell Andrew P. Matala Daniel J. Hasselman Shawn R. Narum, GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS, 4/1/2014 - 3/31/2015 Annual Report, 2008-907-00.