November 2021 Report

### Adult Salmonids Trap and Transport Success above Dams

Prepared for:

U. S. ARMY CORPS OF ENGINEERS

PORTLAND DISTRICT - WILLAMETTE VALLEY PROJECT

333 SW First Ave.

Portland, Oregon 97204

Prepared by:

Kathleen G. O’Malley, Sandra Bohn, Cristín K. Fitzpatrick, Dave Jacobson

Oregon State University

Department of Fisheries, Wildlife and Conservation Sciences

Coastal Oregon Marine Experiment Station

State Fisheries Genomics Lab

Hatfield Marine Science Center

2030 SE Marine Science Drive

Newport, Oregon 97365

INTRODUCTION

Adult spring Chinook salmon (*Oncorhynchus tshawytscha*) are released above USACE dams throughout the Upper Willamette River basin to increase the abundance, productivity, and diversity of naturally produced fish, such that this Evolutionarily Significant Unit (ESU) is self-sustaining and provides significant economic, ecological, recreational, cultural, social, and aesthetic benefits to the citizens of Oregon. Genetic parentage analysis is currently being used to evaluate the effectiveness of trapping and transport of adult spring Chinook salmon above and below the dams. This includes determining if returning spawners are progeny of previous transports and the total lifetime fitness of transported individuals. Current research efforts focus on reintroduction programs in the South Santiam River, McKenzie River, Fall Creek and North Santiam River.

The two main objectives of this work are to (1) maintain a tissue sample archive that will permit future studies to determine the number and proportion of unmarked adult spring Chinook salmon, sampled at various locations on the river (e.g. South Santiam River, South Fork McKenzie River, Fall Creek and North Santiam River) that can be assigned as progeny of Chinook salmon released above USACE dams and (2) estimate the total lifetime fitness and cohort replacement rate for adult spring Chinook salmon released above Detroit Dam on the North Santiam River in 2011, 2012, 2013, 2014 while evaluating the relative success of alternate reintroduction strategies (e.g. date and location of release).

This work will meet the specific information needs of Reasonable and Prudent Alternative (RPA) 9.5.1(4) of the Willamette Project Biological Opinion (NMFS 2008) in determining the reproductive success of hatchery fish in the wild. Results of the research will also address RPA 4.1 (restoration of productivity by outplanting Chinook above dams), RPA 4.7 (increase the percent of outplanted adults that successfully spawn through development of new release locations), RPA 6.2.3 (continue adult Chinook outplanting, Willamette basin-wide), and RPA 9.3 (monitoring the effectiveness of fish passage facilities and strategies at Willamette Project dams).

METHODS

*South Santiam River Sampling*

A tissue sample was collected from fish handled at the Foster Fish Collection Facility in 2019 including every unclipped, presumptive natural-origin spring Chinook salmon released above Foster Dam. Individual samples were stored in 95% ethanol as batch samples. For instance, tissue samples from all natural-origin salmon transported and released above Foster Dam on a given day were stored in a single container. This will permit an evaluation of the effect of release date and release location on the total lifetime fitness of adult spring Chinook salmon reintroduced above Foster Dam. A tissue sample was also collected from every individual used as hatchery broodstock. Samples from a given spawn day were stored in 95% ethanol as batch samples.

*McKenzie River Sampling*

A tissue sample was collected from hatchery-origin spring Chinook salmon at the McKenzie River Hatchery that were subsequently outplanted above Cougar Dam. In addition, tissue samples collected by USACE staff from presumptive natural-origin and hatchery-origin fish captured at the Cougar Trap and outplanted above Cougar Dam or released downstream were assembled and included in the tissue sample archive. Presumptive natural-origin fish incorporated into brood at McKenzie Hatchery were sampled as well. Individual samples were stored in 95% ethanol as batch samples. For instance, tissue samples from all salmon transported and outplanted above Cougar Dam on a given day were stored in a single container. This will permit an evaluation of the effect of release date and release location on the total lifetime fitness of adult spring Chinook salmon reintroduced above Cougar Dam.

*Fall Creek Sampling*

Tissue samples collected by USACE staff from presumptive natural-origin fish captured at the Fall Creek Fish Collection Facility and outplanted above Fall Creek Dam were assembled and included in the archive. A fin clip from every reintroduced individual was collected by the USACE and stored in single vial containing 95% ethanol. This will permit an evaluation of the effect of release date and release location on the total lifetime fitness of adult spring Chinook salmon reintroduced above the dam.

*North Santiam Sampling*

A tissue sample was collected from fish handled at the Minto Fish Collection Facility in 2019 including every hatchery-origin spring Chinook salmon outplanted above Detroit Dam as well as every presumptive natural-origin spring Chinook salmon released above Minto, or elsewhere, and every presumptive natural-origin salmon incorporated into broodstock. Individual samples were stored in 95% ethanol as batch samples. For instance, tissue samples from all hatchery-origin salmon transported and outplanted above Detroit Dam on a given day were stored in a single container. Similarly, tissue samples from all natural-origin salmon released above Minto Dam on a given day were stored in a single container. This will permit an evaluation of the effect of release date and release location on the total lifetime fitness of adult spring Chinook salmon. A tissue sample from every individual used as hatchery broodstock was collected and samples from a given spawn day were stored in 95% ethanol as batch samples.

*North Santiam Genetic Pedigree Analysis*

Tissue samples have been collected from (most) spring Chinook salmon released above Detroit Dam since 2007. These samples constitute potential parents of unmarked, presumed natural-origin adult spring Chinook salmon sampled at the Bennett Dam fish trap (2011 and 2012), Minto fish trap, and on spawning grounds of the North Santiam River, below Big Cliff Dam. Samples collected from these hatchery-origin outplants in 2007-2012 were previously genotyped at 11 microsatellite markers and one sex identification marker. Here, samples collected from hatchery-origin salmon outplanted above Detroit Dam in 2013 (N =1149), 2014 (N = 880), 2015 (N = 1,030), and 2016 (N = 1,322) were genotyped at 11 microsatellite markers and one sex identification marker. These samples constitute potential parents of unmarked, presumed natural-origin adult spring Chinook salmon sampled at the Minto Fish Collection Facility (2016-2019), and on spawning grounds of the North Santiam River, below Big Cliff Dam in 2016-2019.

Samples collected from unmarked, presumed natural-origin adult spring Chinook salmon at the Minto Fish Collection Facility in 2016 (N = 531), 2017, (N =519), 2018 (N =257), and 2019 (N = 550) were genotyped at 11 microsatellite markers and one sex identification marker to assign parentage. These individuals are putative offspring of hatchery-origin spring Chinook salmon released above Detroit Dam in 2011-2016.

Samples collected from unmarked, presumed natural-origin adult spring Chinook salmon carcasses below Big Cliff Dam in 2016 (N = 48 ), 2017, (N = 31), 2018 (N = 17), and 2019 (N = 30) were genotyped at 12 microsatellite markers and one sex identification marker to assign parentage. These individuals are putative offspring of hatchery-origin spring Chinook salmon released above Detroit Dam in 2011-2016.

Whole genomic DNA was isolated from tissue samples using the protocol of Ivanova *et al.* (2006). Each DNA sample was then genotyped at 12 microsatellite loci: *Ots201*, *Ots211*, *Ots212*, *Ots215*, *OtsG249*, *OtsG311*, *OtsG409*, *OtsG474*, *Ots515*, *Ssa408*, *Ogo4*, and *Ogo2* (Olsen *et al.* 1998, Cairney *et al.* 2000, Naish and Park 2002, Williamson *et al.* 2002, Greig *et al.* 2003) and at the sex-linked marker, *Oty3*, to determine sex (Brunelli *et al.* 2008). Loci were amplified using polymerase chain reaction (PCR), PCR products were visualized on an ABI 3730xl DNA analyzer, and allele sizes scored using GENEMAPPER software (Version 5.0, Applied Biosystems, Inc., Foster City, CA).

Genetic-based parentage assignments were made for all unmarked adult spring Chinook salmon sampled in the North Santiam River (2016-2019) at the Minto Fish Collection Facility or on the spawning grounds using genotypes from hatchery-origin salmon previously outplanted above Detroit Dam as potential parents (2011-2016). Two analytical approaches were used as implemented in the software programs: CERVUS (Kalinowski *et al.* 2007), and COLONY (Jones and Wang 2010).

Genetic-based parentage assignments were made for all unmarked adult spring Chinook salmon sampled in the North Santiam River (2016-2019) at the Minto Fish Collection Facility or on the spawning grounds using genotypes from unmarked, presumed natural-origin salmon released into the North Santiam River below Big Cliff Dam as potential parents (2013-2016).

Genetic-based parentage assignments were made for all unmarked adult spring Chinook salmon sampled on the spawning grounds (i.e. carcass samples) in the North Santiam River (2016-2019) using genotypes from unmarked, presumed natural-origin salmon sampled on the spawning grounds in the North Santiam River below Big Cliff Dam as potential parents (2013-2016).

RESULTS

*South Santiam River Sampling*

In 2019, tissue samples were collected from adult spring Chinook salmon transported above Foster Dam (N = 133) as well as from unmarked spring Chinook salmon on the spawning grounds (N = 65). Tissue samples were collected from 798 hatchery-origin adult spring Chinook salmon that were used as broodstock at the South Santiam Hatchery. The tissues samples have been archived and the data has been entered in the State Fisheries Genomics Lab tissue sample database.

*McKenzie River Sampling*

In 2019, tissue samples were collected from unmarked, presumed natural-origin, adult spring Chinook salmon sampled at the Cougar Trap and released below the Cougar Dam at either Forest Glen Landing in the mainstem McKenzie or in the South Fork McKenzie just below the dam (N = 166). Tissue samples were collected from hatchery-origin adult spring Chinook salmon collected at the Cougar Trap and transported above the dam (N = 8). Tissue samples were also collected from hatchery-origin spring Chinook sampled at the McKenzie Hatchery and outplanted above Cougar Dam (N = 381) and above Trailbridge Dam (N = 70), as well as from natural-origin (N = 100) and hatchery-origin (N = 554) spring Chinook salmon sampled at the McKenzie Hatchery that were incorporated into broodstock in 2019 and not released. Additional tissue samples were collected from 18 natural-origin spring Chinook salmon carcasses during spawning ground surveys conducted below the Cougar Dam. All tissues samples have been archived and the data has been entered in the State Fisheries Genomics Lab tissue sample database.

*Fall Creek Sampling*

In 2019, tissue samples were collected from adult spring Chinook salmon transported above Fall Creek Dam (N = 250). The tissues samples have been archived and the data has been entered in the State Fisheries Genomics Lab tissue sample database.

*North Santiam Sampling*

In 2019, tissues samples were collected from 832 natural-origin spring Chinook salmon sampled at the Minto Fish Collection Facility. Tissue samples were also collected from 73 natural-origin spring Chinook salmon carcasses during spawning ground surveys below Big Cliff Dam. Tissue samples were collected from 959 hatchery-origin spring Chinook salmon that were used as broodstock at Marion Forks Fish Hatchery.

*North Santiam Genetic Pedigree Genotyping*

2016 - Of the 579 NOR tissue samples collected during 2016, one batch-collected sample failed to genotype and DNA was severely degraded for 18 carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2016 revealed 21 duplicate genotypes , which were subsequently removed from the analysis (Table 1). The remaining 539 NOR samples were then used in parentage analysis as putative adult progeny.

2017 - Of the 544 NOR tissue samples collected during 2017, one batch-collected sample failed to genotype and DNA was severely degraded for seven carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2017 revealed 17 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 519 NOR samples were then used in parentage analysis as putative adult progeny.

2018 - Of the 266 NOR tissue samples collected during 2018, DNA was severely degraded for four carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2018 revealed 11 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 251 NOR samples were then used in parentage analysis as putative adult progeny.

2019 - Of the 905 NOR tissue samples collected during 2019, six batch-collected samples failed to genotype and DNA was severely degraded for 30 carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2019 revealed 50 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 819 NOR samples were then used in parentage analysis as putative adult progeny.

Since the USACE has decided to fund inclusion of the 2020 spring Chinook salmon samples into the genetic pedigree analysis, a subequent report detailing all of the results will be submitted to the USACE in February 2022.

REFERENCES

Brunelli, J. P., K. J. Wertzler, K. Sundin, and G. H. Thorgaard. 2008. Y-specific sequences and polymorphisms in rainbow trout and Chinook salmon. Genome 51:739-48.

Cairney, M., J. Taggart, and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon and cross-species amplification in other salmonids. Molecular Ecology 9:2175-2178.

Greig, C., D. P. Jacobson, and M. a. Banks. 2003. New tetranucleotide microsatellites for fine scale discrimination among endangered chinook salmon. Molecular Ecology Notes 3:376379.

Ivanova, N., J. R. Dewaard, and P. D. N. Hebert. 2006. An inexpensive, automation-friendly protocol for recovering high-quality DNA. Molecular Ecology Notes 6:998-1002.

Jones, O. R., and J. Wang. 2010. COLONY: a program for parentage and sibship inference from multilocus genotype data. Molecular Ecology Resources 10:551-555.

Kalinowski, S. T., M. L. Taper, and T. C. Marshall. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular Ecology 16:1099-1106.

Naish, K. A., and L. K. Park. 2002. Linkage relationships for 35 new microsatellite loci in Chinook salmon. Animal Genetics 33:316-8.

NMFS. 2008. Endangered species act-section 7 consultation biological opinion and MagnusonStevens fishery conservation and management act consultation on the Willamette River basin flood control project. Portland, OR.

Olsen, J. B., P. Bentzen, and J. E. Seeb. 1998. Characterization of seven microsatellite loci derived from pink salmon. Molecular Ecology 7:1087-1089.

Williamson, K. S., J. F. Cordes, and B. May. 2002. Characterization of microstellite loci in Chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. Molecular Ecology Notes 2:17-19.