FISHERY RESEARCH

# PARENTAGE BASED TAGGING OF SNAKE RIVER HATCHERY STEELHEAD AND CHINOOK SALMON

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# PARENTAGE BASED TAGGING OF SNAKE RIVER HATCHERY STEELHEAD AND CHINOOK SALMON

## Project Progress Report

**2013 Annual Report**

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## ABSTRACT

This report summarizes the progress in the continuing development and evaluation of a new genetic technology called Parentage Based Tagging (PBT), a versatile tool for genetically tagging steelhead *Oncorhynchus mykiss* and Chinook *O. tshawytscha* salmon in the Snake River basin. While PBT is potentially a more economical and efficient technique for tagging fish than coded wire tags (CWT), it also has the capability to address aspects of hatchery reform, salmonid life history, harvest patterns, and trait heritability. This report summarizes three objectives for this performance period of July 1, 2012 to June 30, 2013 that focused on the feasibility of developing and implementing PBT in the Snake River basin: Objective 1) annual sampling of hatchery broodstock, Objective 2) creation of genetic parental databases, and Objective 3) utilization of PBT to provide parentage assignments for hatchery fish of unknown origin. This project continues to sample and inventory nearly 100% of hatchery broodstock (Objective 1) for steelhead (~5,500 individuals annually) and spring/summer Chinook salmon (~8,000 individuals annually). In close collaboration with the Columbia River Inter-Tribal Fisheries Commission (CRITFC), we have used the PBT single nucleotide polymorphism (SNPs) identified for each species to genotype nearly 100% of the steelhead and spring/summer Chinook salmon broodstocks sampled in the Snake River basin from spawn year (SY) 2012 (Objective 2). In addition, summary data for Chinook broodstocks from SY2011 are presented. We then use the data generated from the broodstock baselines to provide parentage analysis for a variety of management objectives (Objective 3). Results, thus far, indicate that annual sampling, inventorying, and genotyping of all steelhead and spring/summer Chinook salmon broodstock in the Snake River basin is feasible and that the SNP sets identified for PBT are sufficient for accurate assignment of offspring to brood year and hatchery stock, thereby allowing an unprecedented ability to mark millions of Snake River smolts and an opportunity to address future objectives of parentage-based management.



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## INTRODUCTION

For over 40 years, researchers and managers in the Columbia River basin have used coded wire tags (CWTs) to monitor and assess harvest patterns and survival rates of salmon and steelhead in the Columbia River basin (Johnson 2004). Recovery of CWTs are one of the primary tools used by managers in Oregon, Washington, and Idaho to estimate the number of hatchery Chinook salmon *Oncorhynchus tshawytscha* and steelhead *O. mykiss* contributing to in-state and out-of-state fisheries and to estimate harvest of individual hatchery stocks.

Despite the predominance of CWT technology in addressing management concerns, it has several limitations. The process of physically tagging tens of thousands of juveniles from different hatchery stocks is logistically difficult, labor intensive, costly, and potentially increases physiological stress to the juveniles just prior to their release for downstream migration. All of these restrictions ultimately limit the total number of juveniles that are tagged each year, which in turn limits the number of CWT recoveries. The resulting small sample sizes greatly reduce statistical power to estimate stock contributions because the precision of these estimates are directly related to the number of CWTs recovered in fisheries or escapements (Hankin et al. 2009).

Parentage-based genetic tagging (described in Anderson and Garza [2005]), a technological alternative to CWT, would eliminate the problem of small sample sizes. Parentage-based tagging (PBT) involves annual sampling and genotyping of hatchery broodstock, creating a database of parental genotypes. Progeny from any of these parents (collected either as juveniles or adults), can be nonlethally sampled and, if genotyped, be assigned back to their parents, thus identifying their hatchery of origin and their exact brood year. The exceptional advantage that PBT has over CWT technology is increased sample size. By genotyping all parental broodstock, every juvenile is genetically "tagged."

While theoretically appealing (Anderson and Garza 2005; 2006), PBT technology still needs to be empirically tested and validated. Over the last several years, several committees and science review groups have recommended that two or more large-scale evaluations of the technology be performed (PFMC 2008; PSC 2008; ISRP/ISAB 2009).

Given these recent advancements, this project constructs the first PBT genetic baselines for steelhead and Chinook salmon hatcheries in the Snake River basin. It also addresses both current and future objectives in creating PBT baselines within the Snake River basin that can be used for monitoring harvest of hatchery stocks but also for addressing additional issues, such as the origin of hatchery strays and steelhead kelts, effectiveness of hatchery mitigation programs, broodstock integration, and relative reproductive success of hatchery fish.

## OBJECTIVES

For this performance period, the Snake River PBT project includes several objectives as follows:

### Objective 1: Genetic sampling of hatchery Chinook salmon and steelhead broodstock

Completion of this objective demonstrates the feasibility of sampling and inventorying all hatchery broodstock each year for steelhead and Chinook salmon and recording accurate biological information (e.g. sex, length, spawn day) for every fish.

## Objective 2: Creation of parental databases for Snake River hatcheries

Completion of this objective demonstrates the ability to genotype all sampled broodstock and to create a database of parental genotypes for each spawn year of steelhead and spring/summer Chinook salmon.

## Objective 3: Utilization of PBT methods to provide accurate parental assignments

We demonstrate the application of this technology through “back end” projects that use the PBT baselines to assign parentage to samples of unknown origin. We demonstrate the versatility of PBT by summarizing several of these “back end” projects including: 1.) Origin of hatchery steelhead harvested in the Zone 6 sport fishery, 2.) Origin of hatchery steelhead harvested in the Zone 6 tribal fishery, 3.) Hatchery proportions of steelhead at Lower Granite Dam, 4.) Origin of hatchery Chinook carcasses in S. Fk. Salmon River, 5.) Origin of Chinook harvested in lower Salmon river fishery, 6.) Hatchery proportions of Chinook at Lower Granite Dam.

# REPORT STRUCTURE

This report is divided into three sections, one for each of the objectives for this fiscal year. The first section reports on sampling efforts. The second section summarizes genetic data from the most recently genotyped broodstocks. The third section provides an overview of current implementation and results of PBT projects.

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## SECTION 1: ANNUAL SAMPLING OF HATCHERY STEELHEAD AND SPRING/SUMMER CHINOOK SALMON BROODSTOCK IN THE SNAKE RIVER BASIN

### INTRODUCTION

The implementation of PBT methods requires a complete sampling of broodstock from all hatcheries contributing to the production of steelhead and Chinook (Figure 1). This objective addresses the feasibility to annually sample tissue from 100% of the hatchery broodstock for spring/summer Chinook and steelhead in the Snake River basin.

### METHODS

The overall goal is to obtain high quality tissue samples and accurate biological data from every adult that contributes to spawning. This includes species, sex, hatchery/stock, date sampled/spawned, tag information, and markings. Hatcheries also record length and cross information whenever possible. Tissue samples are collected in the form of fin tissue or operculum punches, stored in 2 ml vials of 200-proof non-denatured ethanol, and shipped to the IDFG genetics lab in Eagle, Idaho. Care is taken to avoid contamination during sampling by rinsing scissors or hole-punch tools in water or ethanol and wiping with a paper towel in between each tissue sample.

An alternative dry-storage method is also being explored that would eliminate the use of ethanol. This method requires the tissue to be placed on or between sheets of absorptive chromatography paper. Tissue mounted on the paper, once completely dry, has been shown to yield high quality DNA while reducing processing time of samples in the lab (LaHood et al. 2008). Our future collections of broodstock may transition to this methodology if we verify a high genotyping success rate of samples collected using chromatography paper from our targeted broodstocks.

Each sample is labeled with a field identification number, which is used to track the samples until they arrive at the lab, at which time they are given a standardized lab database code. The associated data is reviewed at the lab to ensure accurate information was recorded for every fish sampled. Any discrepancies that are discovered are solved via correspondence with the hatchery employee in charge of recording data. Samples from spawned adults whose eggs were culled due to disease or surplus are not genotyped as they do not contribute to the offspring.

Once the samples are extracted and genotyped, genetic data are recorded into a Progeny SQL database and stored with collection information and individual fish data. Due to the scope of this project, this database was created to manage, organize, and track physical tissue samples along with their associated DNA extractions and genotypes. Progeny allows genetic data to be exported along with individual fish data in a variety of formats, which has proven to be essential for the transfer of data between the collaborating IDFG and CRITFC laboratories.

Complete sampling methods can be found at https://www.monitoringmethods.org/: *Tissue sampling for Parentage Based Tagging v1.0*, *Method ID# 1432.*

## RESULTS

For fiscal year 2012, we have collected and inventoried approximately 5,700 genetic samples from the steelhead broodstock (Table 1) spawned in the Snake River basin during SY2012, and approximately 17,500 samples (Table 2) from Chinook salmon broodstock spawned in the Snake River basin during spawn years 2011 and 2012. Most hatcheries provided biological information on all fish sampled (sex, length, etc.) as well as individual cross information.

## DISCUSSION

We continue to demonstrate the feasibility of large-scale sampling and inventorying of thousands of broodstock fish each year. The annual completion of this objective lays the foundation for the use of PBT baselines in the Snake River basin.

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## SECTION 2: CREATION OF GENETIC DATABASES FOR BROODSTOCKS OF STEELHEAD AND SPRING/SUMMER CHINOOK SALMON IN THE SNAKE RIVER BASIN

This section presents summary information for the genetic data collected from steelhead broodstocks in SY2012 and Chinook salmon broodstocks in SY2011 and SY2012.

### INTRODUCTION

A set of PBT single nucleotide polymorphism (SNPs) was identified for steelhead and Chinook salmon, and it was demonstrated that the selected SNPs would provide sufficient resolving power (Steele et al. 2011). These markers were used to genotype broodstock samples collected in 2011 and 2012 (Table 1 and 2).

During the third year of this project (FY2012), IDFG and CRITFC labs extracted and genotyped all samples for steelhead and Chinook salmon broodstocks (~12,000 IDFG, ~12,000 CRITFC = ~24,000 total samples). The backlog of samples collected in previous spawn years have now been genotyped and only samples collected in current spawn years will need to be genotyped.

The continued creation of these parental genetic databases establishes an unprecedented ability to mark millions of Snake River smolts and an opportunity to address a variety of parentage-based research management objectives.

### METHODS

#### Laboratory protocol

Genomic DNA extraction and amplification and SNP genotyping using multiplex 5'-nuclease reactions followed the methods described in Matala et al. (2011). DNA was extracted using the Nexttec Genomic DNA Isolation Kit from XpressBio (Thurmont, Maryland) or Qiagen DNeasy (Valencia, California). Prior to DNA amplification of SNP loci using primer-probe sets (fluorescent tags), an initial polymerase chain reaction (PCR) "pre-amp" was implemented using whole genomic DNA to jumpstart SNP amplification via increased copy number of target DNA regions. The PCR conditions for the pre-amp step were as follows: an initial mixing step of 95°C for 15 min, followed by 14 cycles of 95°C for 15 seconds and 60°C for four minutes, ending with a final 4°C dissociation step. For steelhead, all individuals were genotyped at 95 SNPs and a Y-specific allelic discrimination assay that differentiates sex. For Chinook salmon, all individuals were genotyped at 95 SNPs (including one mtDNA SNP) and a Y-specific allelic discrimination assay that differentiates sex. Genotyping was performed using Fluidigm 96.96 Dynamic Array IFCs (chips). For each genotyping run, 96 samples (including an extraction negative control, a PCR negative control, and a PCR positive control) and 96 TaqMan SNP assays were either hand-pipetted or auto-pipetted onto the 96.96 chips. Sample cocktail and SNP assay cocktail recipes are available by request from mike.ackerman@idfg.idaho.gov. Each 96.96 chip was pressurized to load the DNA and SNP assays into the array using a Fluidigm IFC Controller HX. SNP amplification on the 96.96 chips were performed using either an Eppendorf Stand-Alone Thermal Cycler (protocol: thermal mixing step of 50°C for 2 min, 70°C for 30 min, and 25°C for 10 min, a hot-start step of 50°C for 2 min and 95°C for 10 min, followed by 50 cycles of 95°C for 15 sec and 60°C for 60 sec, and a final cooldown step of 25°C for 10 min) or a Fluidigm FC1 Fast-cycler (protocol: thermal mixing step of 70°C for 30 min and 25°C for 10 min, a hot-start

step of 95°C for 60 sec, followed by 50 cycles of 95°C for 5 sec and 25°C for 25 sec, and a final cooldown step of 25°C for 10 min). Chips were imaged on a Fluidigm EP1 system and analyzed and scored using the Fluidigm SNP Genotyping Analysis Software version 3.1.1.

Standardized parental genotypes were stored on a Progeny database server housed at Eagle Fish Genetics Laboratory (EFGL). Progeny software (http://www.progenygenetics.com/) is already used by the majority of Genetic Analysis of Pacific Salmon (GAPS) labs throughout the Pacific Northwest: Idaho Department of Fish and Game, University of Washington, NOAA-Northwest Fisheries Science Center, Washington Department of Fish and Wildlife, Columbia River Intertribal Fish Commission, and U.S. Fish and Wildlife Service.

Data quality was inferred from estimates of completion rate, missing data, poor performing loci, and error rates. The program ML-NULLFREQ (Kalinowski and Taper 2006) was used to identify loci with null alleles and estimate the proportion of null alleles per locus. Significance threshold were adjusted using the modified B-Y Method proposed by Narum (2006). Basic diversity indices were calculated for the brood years. This included estimates of average heterozygosity (observed $H_o$ and expected $H_e$) using ARLEQUIN (Excoffier and Lischer 2010), genetic structure ($F_{st}$) using GENEPOP (Rousset 2008), and effective population size (Ne) using LDNE (Waples and Do 2008).

### Sex locus

In an effort to increase the accuracy of the Chinook sex-determining SNP assay, a modified assay was used beginning with SY2010. The continuing accuracy of the sex-determining SNP assay for steelhead and Chinook were evaluated for hatchery stocks spawned in SY2012; comparisons were made between the phenotypic sex of samples, which was determined at time of spawning, and the genetically determined sex of samples.

### Tagging rate

Because genotypes from 100% of the broodstock are not always obtained for all hatchery stocks, this results in a small portion of hatchery-origin offspring that are genetically “un-tagged.” This “un-tagged” portion of hatchery-origin fish cannot be assigned back to their parental pair or hatchery of origin because genotypes are missing from one or both of their parents and genotypes from both parents are needed for accurate PBT assignment. However, we can easily estimate the proportion of “untagged” progeny of each hatchery stock for each brood year based on the proportion of successfully genotyped broodstock. Assuming that males and females are successfully genotyped at equal rates, the proportion of PBT-tagged offspring can also be estimated by squaring the total proportion of successfully genotyped broodstock. We use this method to estimate the proportion of PBT-tagged offspring from each stock (Tables 3 and 4).

## RESULTS

### Completion rate and missing data

If a sample failed to genotype at 10 or more SNPs it was re-extracted and regenotyped. If that sample failed a second time at 10 or more SNPs, it was automatically excluded from future PBT analyses because the excess missing data prevents accurate parentage assignment.

For steelhead SY2012, all 5,719 samples were extracted and genotyped with 95 PBT SNPs and the sex-identification assay. Of the 5,719 samples, 5,491 (96.0%) were genotyped with an acceptable level of missing data (Table 3). In this final SY2012 PBT baseline comprising the remaining 5,491 samples, there were just 2,590 missing genotypes due to SNP failure out of a possible 521,550 genotypes. This resulted in missing data for just 0.5% of the genotypes.

For Chinook SY2011, all 8,710 samples were extracted and genotyped with 95 PBT SNPs and the sex-identification assay. Of the 8,710 samples, 8,619 (99.0%) were genotyped with an acceptable level of missing data (Table 4). In this final SY2011 PBT baseline comprising the remaining 8,619 samples, there were just 7,101 missing genotypes due to SNP failure out of a possible 818,805 genotypes. This resulted in missing data for just 0.87% of the genotypes.

For Chinook SY2012, all 8,768 samples were extracted and genotyped with 95 PBT SNPs and the sex-identification assay. Of the 8,768 samples, 8,693 (99.1%) were genotyped with an acceptable level of missing data (Table 5). In this final SY2012 PBT baseline comprising the remaining 8,693 samples, there were just 4,704 missing genotypes due to SNP failure out of a possible 825,835 genotypes. This resulted in missing data for just 0.57% of the genotypes.

## Poor performing loci

Of the samples that genotyped with <10 missing SNPs, poor performing SNP assays were identified within the 95 PBT SNP panel.

For steelhead SY2012, two loci failed to genotype at >3% of samples. Locus Omy_99300-202 failed at 252 (4.6%) of the samples, OMS00039 failed to genotype 218 (4.0%) of the samples.

For Chinook SY2011, there were two loci that failed at >3% of the samples. Ots_ppie-245 failed at 288 (3.3%) of samples and Ots_txnip-321 failed at 280 (3.2%) of samples.

For Chinook SY2012, there were four loci that failed at >3% of the samples. Ots_ppie-245 and Ots_txnip-32 continued to perform poorly with failures at 1514 (17.4%) and at 862 (9.9%) samples, respectively. Additionally, Ots_101704-143 failed at 540 (6.2%) samples and Ots_112301-43 failed at 404 (4.6%) samples.

## Error rate (quality control)

For steelhead SY2012, a subset of 209 samples representing all extraction plates were rerun and checked for discrepancies. This resulted in 19,855 rerun genotypes being compared to the original PBT genotypes. Of these genotypes, 153 had a SNP failure either in the original genotype or the rerun genotype and could not be used in error estimation. This resulted in 19,702 genotypes with 162 discrepancies between the original and samples and a genotyping error rate of 0.82%.

For Chinook SY2011, a subset of 428 samples representing all extraction plates were rerun and checked for discrepancies. This resulted in 40,660 rerun genotypes being compared to the original PBT genotypes. Of these genotypes, 459 had a SNP failure either in the original genotype or the rerun genotype and could not be used in error estimation. This resulted in 40,201 genotypes with 453 unresolved discrepancies between the original and samples and a genotyping error rate of 1.1%.

For Chinook SY2012, a subset of 365 samples representing all extraction plates were rerun and checked for discrepancies. This resulted in 34,675 rerun genotypes being compared to the original PBT genotypes. Of these genotypes, 239 had a SNP failure either in the original genotype or the rerun genotype and could not be used in error estimation. This resulted in 34,436 genotypes with 75 unresolved discrepancies between the original and samples and a genotyping error rate of 0.22%.

## Null alleles

For steelhead SY2012, 37 of the 95 PBT loci were found to have a frequency of null alleles greater than zero, but only two loci had frequencies >5% (Table 6).

For Chinook SY2011, 40 of the PBT loci were found to have a frequency of null alleles greater than zero, but none had a frequency >5% although SNP Ots_OTALDBINT1SNP1 approached this threshold (Table 7).

For Chinook SY2012, 40 of the PBT loci were also found to have a frequency of null alleles greater than zero, but none had a frequency >5% although SNP Ots_OTALDBINT1SNP1 once again approached this threshold (Table 8).

## Sex markers

The sex-specific assay for steelhead matched phenotypic sex in 96.4% of the samples (Table 9). For instances in which genetically-determined sex did not correspond to the phenotypic sex, all but two were cases in which phenotypic females were misidentified by genotype as males. The assay either failed to genotype or provided ambiguous results for 5.7% of the samples.

The sex-specific assay for Chinook salmon matched phenotypic sex in 93.6% of the samples (Table 10). The majority of discrepancies were phenotypic females genetically identified as male. The assay produced ambiguous results, or failed to genotype, 4.1% of samples.

## Average He

Levels of observed heterozygosity within steelhead broodstocks was ~0.4 for all hatcheries broodstocks (Table 12). Levels of observed heterozygosity tended to be lower in Chinook (~0.35) in all stocks and across brood years (Table 12 and 13).

## Population structure ($F_{st}$)

Pairwise $F_{st}$ was calculated among the steelhead SY2012 hatchery broodstock (Table 14). Values ranged from a low of 0.002 between the Touchet and Tucannon stocks as well as between Dworshak and the newly created S.F. Clearwater stock. A high of 0.067 was observed between the Upper Salmon B-run stock and Little Sheep Crk. All $F_{st}$ values among stocks were significant.

For Chinook SY2011 pairwise $F_{st}$ values ranged from a low of 0.003 between Clearwater and Dworshak to a high of 0.049 between Sawtooth and Tucannon (Table 15). Chinook SY2012 had $F_{st}$ levels ranging from a low of 0.002 between the NPFH and the Dworshak stocks. A high

of 0.045 was observed between the Tucannon stock and the Sawtooth and Pahsimeroi stocks as well as between the Rapid River and Pahsimeroi stocks (Table 16). All Fst values among stocks were significant within each year.

### Effective population size (Ne)

Effective population size ($N_e$) and 95% CI for each steelhead hatchery broodstock and for subsets of a broodstock used for specific release sites programs (Table 17). Estimates of effective population size ranged from a low of 21.2 for the Upper Salmon B-run broodstock to a high of 244.5 for Dworshak production broodstock.

Effective population size and 95% CI for each Chinook hatchery stock in SY2011, and SY2012 was also calculated. Estimates of effective population size in SY2011 ranged from a low of 96.4 for Grande Ronde to a high of 499.2 for Rapid River (Table 18). In SY2012 estimates of effective population size ranged from a low of 62.0 for Grande Ronde to a high of 504 for Dworshak (Table 19).

## DISCUSSION

We have demonstrated the ability to routinely genotype the thousands of broodstock samples collected each year. Genotypes are stored and organized in an on-site database where they can be exported for PBT analysis. The creation of these PBT baselines also provides several measures of genetic diversity and relatedness among the broodstocks, which provide the added benefit of genetic monitoring of hatchery populations. The completion of this objective allows parental genotypes to be queried in parentage analyses resulting in the identification of hatchery fish originating from the Snake River basin.

### Sex markers

The steelhead sex marker performed well for most stocks. However, its accuracy was noticeably lower for stocks in the Grande Ronde (Wallowa, Little Sheep) suggesting that the marker may have stock-specific performance issues in this drainage.

The Chinook sex marker also performed well for most stocks. Two stocks (Dworshak and Lookingglass) had high levels of discrepancies between phenotypic sex and genetically-determined sex. In the case of Dworshak, the discrepancies were traced to scoring errors of the genotypes. This error arose simply because a large series of genotyped samples contained only one sex thereby producing only one cluster of genotypes. Without the other sex included in these samples there was not a second cluster of genotypes representing the other sex to provide perspective and the single cluster was misscored. In the case of the Lookingglass stock, the high level of discrepancies could not be traced back to a scoring error. Like the steelhead sex marker, the Chinook sex marker seems to perform poorly in the Grande Ronde drainage.

Aside from lower accuracy within certain stocks in the Grande Ronde drainage, the results are generally encouraging in that these assays can provide an accurate and nonlethal method of sex determination for these species.

## Completion rate and missing data

The high rate of genotyping success for samples and the low rate of missing data demonstrate the feasibility of collecting high quality data from nearly all Snake River basin broodstock samples.

## Poor performing loci

Both of the poor-performing steelhead loci (Omy_99300-202 and OMS00039) in SY2012 are known to have null alleles. To prevent null allele genotypes from being included in the database we have adopted scoring rules for these loci. If clustering patterns of samples at these loci suggest the presence of null alleles then the genotypes are manually 'no called', meaning that the genotype is not scored nor included in the data in order to minimize including null allele genotypes. The high proportion of failed samples at these loci is likely due to conservative scoring of genotypes.

Both of the poor-performing Chinook loci (Ots_ppie-245 and Ots_txnip-32) in SY2012 are also known to have either null alleles or poor clustering patterns. The high proportion of failed samples at these loci is likely due to samples being 'no called' because of ambiguous results.

## Error rate (quality control)

To minimize false negatives in parentage assignments, genetic markers need to exhibit low genotyping error rates and researchers should accommodate estimated error rates during data analysis (Kalinowski et al. 2007). Genotyping error rates for microsatellite markers are variable, but have often been reported between 1-2% (Pearse et al. 2009; Hauser et al. 2011). For the parentage software programs CERVUS and SNPPIT, the default error rate used is 1%. We consistently observed error rates ≤1% for both the steelhead and Chinook PBT panels of SNPs across several years.

## Null alleles

The three steelhead PBT loci that had the highest frequencies of null alleles (OMS00118, Omy_vatf406, Omy_113490159) are the same loci that had similar levels of null alleles in previous broodstock collections. These loci may need to be reevaluated or scoring rules for the loci may need to be modified to account for null alleles.

Within the Chinook SNP panel the locus Ots_OTALDBINT1SNP1 was identified as having a null allele frequency >5% for SY2008, SY2009, and SY2010 and was also ~5% in SY2011 and SY2012. This locus may need to be re-evaluated because of consistent presence of null alleles.

## Average He

The average expected heterozygosity was high and uniform across both steelhead hatchery stocks (~.40) and Chinook (~.35) demonstrating that the degree of variability in these SNP sets makes them useful for parentage analysis of hatchery stocks throughout the Snake River basin.

## Population structure

Within steelhead, the highest pairwise $F_{st}$ values are seen between the Dworshak Hatchery stock (and its derivatives such as the Upper Salmon B-run stock and SF Clearwater stock) and other locations. The larger degree of divergence between Dworshak and the other stocks reflects the distinctness of Clearwater origin fish to those in the Salmon and Snake rivers. The lowest $F_{st}$ values are also consistently seen between populations that are geographically proximate, such as the Touchet and Tucannon stocks in Washington State, or among stocks with shared population histories, such as the Oxbow, Sawtooth, and Pahsimeroi stocks. Low divergence among Oxbow, Sawtooth, and Pahsimeroi reflect their shared history of being recently derived from stocks whose brood source came from wild adult steelhead trapped at the Hells Canyon Dam on the Snake River in the late 1960s (Nielsen et al. 2009).

Within Chinook, the highest pairwise $F_{st}$ values are consistently seen among the most geographically distant stocks (e.g. Sawtooth/Pahsimeroi and Tucannon). This is a common pattern of isolation-by-distance indicating genetic differentiation increases with geographic distance. The lowest pairwise $F_{st}$ values tended to be among stocks within the Clearwater drainage (Dworshak, Powell, Nez Perce, and Clearwater). This perhaps reflects the current management practice of managing all Chinook in the Clearwater drainage as a single stock in which broodstock are moved among the different locations.

## Effective population size (Ne)

Effective population sizes generally corresponded to size of broodstock. Larger hatchery programs (e.g., steelhead stocks at Dworshak, Oxbow, Pahsimeroi, Sawtooth, and Wallowa or Chinook stocks at Clearwater and Rapid River) tended to have larger $N_e$, while programs with smaller broodstocks (steelhead stocks of Upper Salmon B-run and EFSR or Chinook stocks of the Grande Ronde) had a smaller $N_e$. The Touchet population had an unrealistic estimate of $N_e$ and an infinitely large CI that indicates an accurate estimate could not be made due to either small sample size of lack of linkage disequilibrium in the samples.

Sampling broodstock for PBT provides a unique opportunity to test the accuracy of $N_e$ estimation methods. A direct measurement of $N_e$ can be obtained through parental assignments of subsequent generations to previous generations of broodstock. This observed valued of $N_e$ through pedigree reconstruction can then be compared to estimates of $N_e$ from various software programs (e.g. LDNE, Colony) that are derived using genetic data from a single generation. Future research efforts will more thoroughly explore the correlations between these methods.

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## SECTION 3: UTILIZATION OF PBT TO PROVIDE PARENTAL ASSIGNMENTS

### INTRODUCTION

Several years' worth of broodstock genotypes have now been collected for both steelhead and spring/summer Chinook. Projects can now be implemented to use PBT in addressing a multitude of research and management questions involving hatchery stocks. We report the results from various projects that have utilized these PBT baselines for questions pertaining to Chinook and steelhead. All PBT projects presented here were instigated by fisheries managers and biologists in order to answer their specific research or monitoring questions. Brief descriptions of their projects are presented here but complete descriptions of the specific study objectives, design, results, and interpretation are presented in their respective reports.

For steelhead, the PBT baselines were used to determine the origin of: 1.) Samples from the sport fisheries in Columbia River Zones 1–5 during migration years 2011 and 2012 (SY2012 and SY2013), 2.) Samples from tribal fisheries in Columbia River Zone 6 during migration years 2011 and 2012 (SY2012 and SY2013), and 3.) Samples of adult ad-clipped fish crossing Lower Granite Dam (SY2013).

For Chinook, the PBT baselines were used to determine the origin of: 1.) Carcasses encountered in spawning-ground surveys on the South Fork Salmon River in 2012, 2.) Samples from the lower Salmon River fishery in 2012 (SY2012), and 3.) Samples of adult ad-clipped fish crossing Lower Granite Dam 2012 (SY2012).

### METHODS

Samples collected for these various "back end" projects were inventoried and genotyped using the same procedures as the broodstock. The program SNPPIT was used to conduct parentage analysis. Unless indicated otherwise, the criteria for accepting a PBT assignment was an LOD score (log of odds) >14.

#### Steelhead Sport Fisheries in Zones 1–5 of Columbia River

IDFG coordinated the sampling of steelhead harvested in the lower Columbia River sport fishery downstream of Bonneville Dam (River Sections 1–10) in 2011 and 2012. A total of 648 samples from 2011 and 839 samples from 2012 were processed for PBT assignment. A more detailed description of this project is presented in Byrne et al. (*In Prep. a*, *In Prep. b*)

#### Steelhead Tribal Fisheries in Zones 6 of Columbia River

IDFG also coordinated sampling of steelhead harvested in the tribal fishery between Bonneville Dam and McNary Dam (Zone 6) during 2011 and 2012. A total of 1,482 samples from clipped steelhead were analyzed in 2011 and 651 samples from clipped steelhead were analyzed in 2012. A more detailed description of this project is also presented in Byrne et al. (*In Prep. a*, *In Prep. b*).

## Steelhead Hatchery Proportions at Lower Granite Dam

Samples representative of the adult steelhead run across Lower Granite dam were collected in the fall of 2012 and spring of 2013. A total of 1,133 samples were analyzed with PBT. Sampling methodology is summarized in Leth et al. (*In prep*).

## Chinook carcasses in S. Frk. Salmon R.

Chinook carcasses encountered during spawning-ground surveys of the South Fork Salmon River were sampled in 2012 to estimate the proportion of hatchery-origin spring/summer Chinook on the spawning grounds. A total of 218 carcasses were sampled and analyzed with PBT. Study rationale and design is more thoroughly presented in Hinrichsen et al. (*In Prep*.)

## Chinook Sport Fishery in Lower Salmon River

Fisheries managers within IDFG implemented PBT sampling of the lower Salmon River sport harvest in 2012. A total of 260 samples representative of the various time strata and river sections were analyzed with PBT. Results were also used to make comparisons between the PBT and CWT estimates of harvest contribution. Complete methodology is presented in Cassinelli et al. (2013).

## Chinook Hatchery Proportions at Lower Granite Dam

Samples representative of Chinook returning over Lower Granite Dam in 2012 were collected. A total of 1,025 samples were used to estimate stock and age composition of hatchery-origin spring/summer Chinook salmon at Lower Granite Dam. PBT-determined estimates of stock proportions were also compared to PIT-determined stock proportions for the same time period. Details of this project are also described in Cassinelli et al. (2013).

# RESULTS

## Steelhead Sport Fisheries in Zones 1–5 of Columbia River

Of the 648 samples collected in 2011, four were omitted from the analysis because they failed to meet genotyping criteria or were determined to be duplicate samples from the same fish. After expanding by PBT rates, 79% of the sport harvest samples in the lower Columbia River assigned to hatcheries in the Snake River basin. A detailed breakdown of stock composition in this fishery is presented in Byrne et al. (*In Prep. a*).

Of the 839 samples collected in 2012, nine were omitted from the analysis because they failed to meet genotyping criteria or were determined to be duplicate samples from the same fish. After expanding by PBT rates, 69% of the sport harvest samples in the lower Columbia River assigned to hatcheries in the Snake River basin. A detailed breakdown of stock composition in this fishery is presented in Byrne et al. (*In Prep. b*).

## Steelhead Tribal Fisheries in Zones 6 of Columbia River

Of the 1,482 samples collected from adipose-clipped fish in 2011, 19 samples were omitted from the analysis because they failed to meet genotyping criteria or were determined to

be duplicate samples from the same fish. After expanding by PBT rates, 96% of the Zone 6 samples assigned to hatcheries in the Snake River basin. A detailed breakdown of stock composition in this fishery is presented in Byrne et al. (*In Prep. a*).

Of the 651 samples collected from adipose-clipped fish in 2012, 30 samples were omitted from the analysis because they failed to meet genotyping criteria or were determined to be duplicate samples from the same fish. After expanding by PBT rates, 90% of the Zone 6 samples assigned to hatcheries in the Snake River basin. A detailed breakdown of stock composition in this fishery is presented in Byrne et al. (*In Prep*. *b*).

### Steelhead Hatchery Proportions at Lower Granite Dam

Of the 1,135 samples collected, three were omitted from the analysis because they failed to meet genotyping criteria or were determined to be duplicate samples from the same fish. After expanding by PBT rates, the origin of 98% of samples could be accounted for. A breakdown of stock and cohort proportions will be presented in Leth et al. (*In prep*).

### Chinook carcasses in S. Frk. Salmon R.

Using PBT assignments, the proportion of hatchery-origin fish on the spawning grounds of the South Fork Salmon River was 30.5% (SE = 3.1%) which could be broken into 4-year-olds (23.8%), 5-year-olds (6.2%), and 3-year-old jacks (0.6%). CWT recoveries provided similar estimates for the cohorts of hatchery-origin fish; however, the standard errors of estimates were smaller when the PBT data were used. Results are more thoroughly presented in Hinrichsen et al. (*In Prep*.)

### Chinook Sport Fishery in Lower Salmon River

All of the 260 samples genotyped completely, but two samples were omitted from the analysis because they were determined to be duplicate samples from the same fish. After expanding by PBT rates, the origin of 92% of the samples could be accounted for. The majority of unassigned fish had FL ≥80 cm suggesting that they were 5-year-olds (brood year 2007) that pre-dated PBT sampling. A detailed breakdown of stock composition in this fishery is presented in Cassinelli et al. (2013).

### Chinook Hatchery Proportions at Lower Granite Dam

Of the 1,025 tissue samples analyzed, 63 assigned to stocks from brood year 2009, 802 assigned to stocks from brood year 2008, and 160 did not assign to the baseline. A detailed breakdown of stock composition at Lower Granite Dam is presented in Cassinelli et al. (2013).

## DISCUSSION

The PBT baselines being developed and maintained are made available to fisheries managers to help address a variety of management questions for steelhead and Chinook. While specific implications and interpretations are presented in separate reports, the number and diversity of projects that made use of the PBT baselines is noteworthy.

## Steelhead Sport Fisheries in Zones 1–5 of Columbia River

This project represents some of the first comprehensive attempts to categorize the stock composition of the steelhead harvest in the Lower Columbia sport fishery. Implications of the results are more thoroughly explored in Byrne et al. (*In Prep. a*) and Byrne et al. (*In Prep. b*).

## Steelhead Tribal Fisheries in Zones 6 of Columbia River

This project also represents some of the first comprehensive attempts to categorize the stock composition of the steelhead harvest in the Zone 6 fishery. Implications of the results are more thoroughly explored in Byrne et al. (*In Prep. a*) and Byrne et al. (*In Prep. b*).

## Steelhead Hatchery Proportions at Lower Granite Dam

Expanding by PBT rates accounts for nearly 100% of samples in the collection, indicating that most fish crossing Lower Granite Dam are tagged with PBT. Additional discussion is presented in Leth et al. (*In prep*).

## Chinook carcasses in S. Frk. Salmon R.

This project demonstrated that PBT provides similar, and slightly more precise estimates, of pHOS (proportion of hatchery-origin fish on spawning grounds) as CWT. Results are used to design an efficient sampling protocol using PBT to determine pHOS in spawning grounds that have multiple contributing stocks with different marking rates (Hinrichsen et al., *In Prep*.).

## Chinook Sport Fishery in Lower Salmon River

This effort represents the agency's first implementation of PBT for estimating the stock and age composition of a Chinook salmon fishery. PBT provided several advantages over CWT. PBT accounted for a larger proportion of estimated harvest. Confidence intervals around harvest estimates were significantly smaller with PBT than for CWT. The PBT analysis identified two stocks that contributed to the fishery that were not identified with CWTs. These differences between PBT and CWT will ultimately provide managers the ability to more efficiently manage mixed stock fisheries particularly with regards as to how the stock composition changes temporally across the fisheries (Cassinelli et al. 2013).

## Chinook Hatchery Proportions at Lower Granite Dam

Managers have known that PIT-derived estimates of stock proportion at Lower Granite Dam tended to underestimate actual return numbers to the hatchery, likely due to shedding of tags or mortality. The comparison of PIT-derived estimates to PBT-estimates showed PBT provides a more precise estimate of stock proportions that more closely match rack returns (Cassinelli et al. 2013).

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**TABLES**

Table 1. Total steelhead hatchery broodstock genetically sampled in spawn year 2012 in the Snake River basin. Broodstock are sampled at 100% but only samples from broodstock producing offspring were included (samples from broodstock whose eggs were culled were not included).

| Snake River Hatchery | SY2012 |
|---|---|
| LSRCP/IDFG Sawtooth (IDFG & SBT) | 744 |
| LSRCP/IDFG Sawtooth (EFSR) | 72 |
| LSRCP/IDFG Sawtooth (USB/Squaw) | 42 |
| Idaho Power/IDFG, Oxbow F.H. | 477 |
| Idaho Power/IDFG, Pahsimeroi F.H. | 1012 |
| Idaho Power/IDFG, Pahsimeroi F.H (SBT) | 288 |
| LSRCP/IDFG/USFWS Dworshak/C.W. | 1981 |
| LSRCP/ODFW-Wallowa F.H. | 492 |
| LSRCP/WDFW-Lyons Ferry | 193 |
| LSRCP/ODFW- Little Sheep Crk | 134 |
| LSRCP/WDFW-L.F. (Tucannon) | 39 |
| LSRCP/WDFW-L.F. (Touchet) | 32 |
| LSRCP/WDFW-L.F. (G.R. cottonwood) | 213 |
| Total | 5719 |

Table 2. Total Chinook salmon hatchery broodstock sampled in spawn years 2011 and 2012 in the Snake River basin. Broodstock are sampled at 100% but only samples from broodstock producing offspring were included (samples from broodstock whose eggs were culled were not included).

| Snake River Hatchery | SY2011 | SY2012 |
|---|---|---|
| Idaho Power/IDFG, Rapid River | 2180 | 1454 |
| LSRCP/USFWS, Dworshak | 1399 | 2095 |
| LSRCP/IDFG, Clearwater (Powell) | 962 | 775 |
| LSRCP/IDFG, Clearwater (SF) | 676 | 738 |
| LSRCP/IDFG, Sawtooth | 326 | 967 |
| Idaho Power/IDFG, Pahsimeroi River | 707 | 410 |
| LSRCP/WDFW-L.F. (Tucannon) | 167 | 164 |
| LSRCP/IDFG, McCall (SFSR) | 953 | 1030 |
| LSRCP/ODFW, Imnaha | 255 | 244 |
| LSRCP/ODFW/NPT, Lostine | 123 | 125 |
| LSRCP/ODFW, Catherine Crk. | 75 | 87 |
| LSRCP/ODFW, Grande Ronde | 318 | 149 |
| LSRCP/ODFW, Lookingglass Crk. | 148 | 152 |
| Nez Perce Tribal Hatchery (NPTH) | 356 | 378 |
| Johnson Crk. (EFSR Salmon River) | 65 | 0 |
| Total | 8710 | 8768 |

Table 3. Sample sizes and genotyping completion rate of SY2012 steelhead broodstock. Samples with ≥10 failed PBT SNPs are not considered successfully genotyped. The PBT-tagging rate for each stock is calculated by squaring the proportion of successfully genotyped broodstock.

| | 2012 | | |
|---|---|---|---|
| **Snake River Hatchery Stocks** | **Sampled** | **Genotyped (%)** | **Tagging Rate** |
| Sawtooth | 332 | 332 (100%) | 100% |
| Sawtooth supply to Sho-Ban Tribe Egg Boxes | 208 | 208 (100%) | 100% |
| Sawtooth supply to Yankee Frk release | 204 | 204 (100%) | 100% |
| E. Fk. Salmon R (Sawtooth) | 72 | 70 (97.2%) | 94.5% |
| Upper Salmon B (Sawtooth) | 42 | 42 (100%) | 100% |
| Oxbow Hatchery | 477 | 456 (95.6%) | 91.4% |
| Pahsimeroi Hatchery | 748 | 738 (98.7%) | 97.3% |
| Pahsimeroi Hatchery supply to Sho-Ban Tribe | 240 | 236 (98.3%) | 96.7% |
| Pahsimeroi supply to Sawtooth Hatchery | 312 | 311 (99.7%) | 99.4% |
| Dworshak Hatchery | 1037 | 1012 (97.6%) | 95.2% |
| Dworshak supply to Clearwater Hatchery | 323 | 294 (91.0%) | 82.9% |
| Dworshak supply to Magic Valley Hatchery | 497 | 377 (75.9%) | 57.5% |
| S.F. Clearwater (Dworshak) | 124 | 116 (93.6%) | 87.5% |
| Little Sheep Crk (Wallowa Hatchery) | 134 | 131 (97.8%) | 95.6% |
| Lyons Ferry Hatchery | 204 | 204 (100%) | 100% |
| Tucannon (Lyons Ferry Hatchery) | 34 | 30 (88.2%) | 77.9% |
| Touchet (Lyons Ferry Hatchery) | 30 | 30 (100%) | 100% |
| Cottonwood Crk (Lyons Ferry Hatchery) | 209 | 209 (100%) | 100% |
| Wallowa Hatchery | 492 | 490 (99.6%) | 99.2% |
| Total | 5719 | 5490 (96.0%) | 92.2% |

Table 4. Sample sizes and genotyping completion rate of SY2011 Chinook broodstock. Samples with ≥10 failed PBT SNPs are not considered successfully genotyped. The PBT-tagging rate for each stock is calculated by squaring the proportion of successfully genotyped broodstock.

| | 2011 | | |
|---|---|---|---|
| **Snake River Hatcheries** | **Sampled** | **Genotyped (%)** | **Tagging Rate** |
| Rapid River | 2180 | 2162 (99.2%) | 98.4% |
| Dworshak | 766 | 762 (99.5%) | 99.0% |
| Dworshak (supplied to Clearwater) | 150 | 150 (100%) | 100% |
| Dworshak (Kooskia stock) | 483 | 479 (99.2%) | 98.4% |
| Powell | 278 | 277 (99.6%) | 99.3% |
| Powell (released in Clear Crk.) | 130 | 129 (99.2%) | 98.5% |
| Powell (parr release in Selway) | 188 | 187 (99.5%) | 98.9% |
| Powell (smolt release in Selway) | 244 | 242 (99.2%) | 98.4% |
| Powell (supplied to NPTH) | 122 | 120 (98.4%) | 96.7% |
| Clearwater (SF Clearwater stock) | 676 | 661 (97.8%) | 95.6% |
| Sawtooth | 263 | 258 (98.1%) | 96.2% |
| Sawtooth (Integrated Broodstock) | 63 | 63 (100%) | 100% |
| Pahsimeroi | 641 | 632 (98.6%) | 97.2% |
| Pahsimeroi (Integrated Broodstock) | 66 | 65 (98.5%) | 97.0% |
| Lyons Ferry (Tucannon stock) | 167 | 165 (98.8%) | 97.6% |
| McCall | 589 | 587 (99.7%) | 99.3% |
| McCall (Integrated Broodstock) | 150 | 149 (99.3%) | 98.7% |
| McCall (supplied to Clearwater) | 140 | 140 (100%) | 100% |
| McCall (supplied to Sho-Ban Tribe) | 74 | 74 (100%) | 100% |
| Lookingglass | 148 | 146 (98.6%) | 97.3% |
| Lookingglass (Captive Broodstock) | 244 | 243 (99.6%) | 99.2% |
| Lookingglass (Imnaha stock) | 255 | 247(96.7%) | 93.8% |
| Lookingglass (Lostine stock) | 123 | 118 (95.9%) | 92.0% |
| Lookingglass (Catherine Crk stock) | 75 | 72 (96%) | 92.2% |
| Lookingglass (Grande Ronde stock) | 74 | 74 (100%) | 100% |
| Nez Perce Tribal Hatchery | 356 | 354 (99.4%) | 98.9% |
| Johnson Crk | 65 | 63 (96.9%) | 93.9% |
| Total | 8710 | 8619 (99.0%) | 97.9% |

Table 5. Sample sizes and genotyping completion rate of SY2012 Chinook broodstock. Samples with ≥10 failed PBT SNPs are not considered successfully genotyped. The PBT-tagging rate for each stock is calculated by squaring the proportion of successfully genotyped broodstock.

| | 2012 | | |
|---|---|---|---|
| **Snake River Hatcheries** | **Sampled** | **Genotyped (%)** | **Tagging Rate** |
| Rapid River | 1454 | 1430 (98.3%) | 96.7% |
| Dworshak | 1410 | 1407 (99.8%) | 99.6% |
| Kooskia | 685 | 684 (99.9%) | 99.7% |
| Powell (reared at Clearwater) | 576 | 573 (99.5%) | 99.0% |
| Powell (parr release in Selway) | 199 | 197 (99.0%) | 98.0% |
| Clearwater (SF Clearwater stock) | 738 | 723 (98.0%) | 96.0% |
| Sawtooth | 886 | 886 (100%) | 100% |
| Sawtooth (Integrated Broodstock) | 81 | 80 (98.8%) | 97.5% |
| Pahsimeroi | 354 | 353 (99.7%) | 99.4% |
| Pahsimeroi (Integrated Broodstock) | 56 | 56 (100%) | 100% |
| Lyons Ferry (Tucannon stock) | 164 | 161 (98.2%) | 96.4% |
| McCall | 634 | 634 (100%) | 100% |
| McCall (Integrated Broodstock) | 124 | 124 (100%) | 100% |
| McCall (supplied to Clearwater) | 272 | 270 (99.3%) | 98.5% |
| Lookingglass | 152 | 148 (97.4%) | 94.8% |
| Lookingglass (Imnaha stock) | 244 | 243 (99.6%) | 99.2% |
| Lookingglass (Lostine stock) | 125 | 125 (100%) | 100% |
| Lookingglass (Catherine Crk stock) | 87 | 83 (95.4%) | 91.0% |
| Lookingglass (Grande Ronde stock) | 149 | 149 (100%) | 100% |
| Nez Perce Tribal Hatchery | 378 | 367 (97.1%) | 94.3% |
| Total | 8768 | 8693 (99.1%) | 98.3% |

Table 6. Ranked estimates of null allele frequencies for 37 loci from the steelhead 2012 PBT broodstock.

| SNP Name | Freq of null allele | SNP Name | Freq of null allele |
|---|---|---|---|
| OMS00039 | 0.002 | OMS00078 | 0.024 |
| OMS00057 | 0.013 | Omy_BACB4324 | 0.024 |
| Omy_b1266 | 0.013 | Omy_metA161 | 0.024 |
| OMS00068 | 0.015 | OMS00089 | 0.025 |
| Omy_hsc71580 | 0.015 | Omy_u0954311 | 0.026 |
| Omy_101832195 | 0.017 | Omy_101993189 | 0.028 |
| OMS00180 | 0.018 | Omy_Ogo4212 | 0.028 |
| Omy_nkef241 | 0.019 | OMS00106 | 0.029 |
| Omy_97660230 | 0.021 | OMS00053 | 0.032 |
| Omy_cd59206 | 0.021 | OMS00101 | 0.032 |
| Omy_bcAKala380rd | 0.021 | Omy_anp17 | 0.032 |
| Omy_stat3273 | 0.021 | Omy_105105448 | 0.034 |
| Omy_U11_2b154 | 0.021 | OMS00064 | 0.036 |
| OMS00024 | 0.022 | OMS00070 | 0.037 |
| M09AAJ163 | 0.023 | Omy_crb106 | 0.039 |
| OMS00175 | 0.023 | Omy_Il1b198 | 0.039 |
| Omy_105714265 | 0.023 | OMS00118 | 0.044 |
| OMS00077 | 0.024 | Omy_vatf406 | 0.053 |
| | | Omy_113490159 | 0.063 |

Table 7. Ranked estimates of null allele frequencies for 40 loci from the combined Chinook 2011 PBT broodstock.

| SNP Name | Freq of null allele | SNP Name | Freq of null allele |
|---|---|---|---|
| Ots_ppie245 | 0.008 | Ots_u0725325 | 0.018 |
| Ots_unk526 | 0.009 | Ots_105385421 | 0.018 |
| Ots_GPH318 | 0.011 | Ots_NOD1 | 0.019 |
| Ots_txnip321 | 0.011 | Ots_11820561 | 0.019 |
| Ots_mapK3309 | 0.012 | Ots_TLR3 | 0.019 |
| Ots_12875761R | 0.013 | Ots_ARNT | 0.019 |
| Ots_101704143 | 0.013 | Ots_IL8R_C8 | 0.02 |
| Ots_ETIF1A | 0.013 | Ots_TAPBP | 0.02 |
| Ots_109525816 | 0.013 | Ots_S71 | 0.02 |
| Ots_GCSH | 0.014 | Ots_u675 | 0.022 |
| Ots_113242216 | 0.014 | Ots_E2275 | 0.023 |
| Ots_pop596 | 0.014 | Ots_105407117 | 0.023 |
| Ots_SWS1op182 | 0.014 | Ots_129458451 | 0.024 |
| Ots_Prl2 | 0.014 | Ots_11230143 | 0.024 |
| Ots_GDH81x | 0.015 | Ots_102414395 | 0.024 |
| Ots_117432409 | 0.015 | Ots_mapKpr151 | 0.026 |
| Ots_110064383 | 0.015 | Ots_MHC2 | 0.027 |
| Ots_cox1241 | 0.016 | Ots_u100275 | 0.027 |
| Ots_mybp85 | 0.016 | Ots_TGFB | 0.029 |
| Ots_94857232R | 0.018 | Ots_OTALDBINT1SNP1 | 0.049 |

Table 8. Ranked estimates of null allele frequencies for 40 loci from the combined Chinook 2012 PBT broodstock.

| SNP Name | Freq of null allele | SNP Name | Freq of null allele |
|---|---|---|---|
| Ots_11230143 | 0.002 | Ots_u21185 | 0.015 |
| Ots_101704143 | 0.007 | Ots_100884287 | 0.016 |
| Ots_mybp85 | 0.011 | Ots_TAPBP | 0.017 |
| Ots_105105613 | 0.012 | Ots_OTSTF1SNP1 | 0.017 |
| Ots_105407117 | 0.012 | Ots_u100275 | 0.018 |
| Ots_Est740 | 0.012 | Ots_txnip321 | 0.018 |
| Ots_hsc713488 | 0.012 | Ots_SWS1op182 | 0.019 |
| Ots_pigh105 | 0.013 | Ots_MHC1 | 0.019 |
| Ots_GTH2B550 | 0.013 | Ots_112820284 | 0.019 |
| Ots_102414395 | 0.013 | Ots_Prl2 | 0.02 |
| Ots_IGFI176 | 0.013 | Ots_RAG3 | 0.02 |
| Ots_NFYB147 | 0.013 | Ots_u675 | 0.022 |
| Ots_12875761R | 0.014 | Ots_129458451 | 0.022 |
| Ots_GCSH | 0.014 | Ots_mapK3309 | 0.023 |
| Ots_ntl255 | 0.014 | Ots_94857232R | 0.024 |
| Ots_vatf251 | 0.014 | Ots_115987325 | 0.025 |
| Ots_P53 | 0.014 | Ots_u0725325 | 0.025 |
| Ots_110064383 | 0.014 | Ots_HSP90B100 | 0.035 |
| Ots_brp1664 | 0.015 | Ots_MHC2 | 0.038 |
| Ots_110201363 | 0.015 | Ots_OTALDBINT1SNP1 | 0.056 |

Table 9. Results of comparisons between phenotypic sex and genetically determined sex using the sex-specific assay for SY2012 steelhead (Omy1_2SEXY).

| | **Total Samples** | **Missing Genetic Data** | **Total Successful Genotypes** | **Corresponding** | **Non-corresponding** | **Phenotypic males misidentified as female** | **Phenotypic females misidentified as male** | **Total phenotypic males** | **Total phenotypic females** |
|---|---|---|---|---|---|---|---|---|---|
| Dworshak | 1981 | 192 (9.7%) | 1789 (90.3%) | 1789 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 853 (43.1%) | 1128 (56.9%) |
| Squaw Cr. | 42 | 2 (4.8%) | 40 (95.2%) | 36 (90%) | 4 (10.0%) | 1 (25.0%) | 3 (75.0%) | 15 (35.7%) | 27 (64.3%) |
| E Fk Sal. R | 72 | 4 (5.6%) | 68 (94.4%) | 65 (95.6%) | 3 (4.4%) | 1 (33.3%) | 2 (66.7%) | 37 (51.4%) | 35 (48.6%) |
| Pahsimeroi | 1300 | 59 (4.5%) | 1241 (95.5%) | 1241 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 650 (50.0%) | 650 (50.0%) |
| Sawtooth | 744 | 15 (2.0%) | 729 (98.0%) | 721 (98.9%) | 8 (1.1%) | 0 (0.0%) | 8 (100.0%) | 372 (50.0%) | 372 (50.0%) |
| Wallowa | 492 | 24 (4.9%) | 468 (95.1%) | 335 (71.6%) | 133 (28.4%) | 0 (0.0%) | 133 (100.0%) | 245 (49.8%) | 247 (50.2%) |
| Lyons Ferry | 477 | 19 (4.0%) | 458 (96.0%) | 458 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 224 (47.0%) | 253 (53.0%) |
| Little Sheep | 134 | 6(4.5%) | 128 (95.5%) | 94 (73.4%) | 34 (26.6%) | 0 (0.0%) | 34(100%) | 67 (50.0%) | 67 (50.0%) |
| Oxbow | 477 | 3 (0.6%) | 474 (99.4%) | 462 (97.5%) | 12 (2.5%) | 0 (0.0%) | 12 (100%) | 234 (49.1%) | 243 (50.9%) |
| *Total* | 5719 | 324 (5.7%) | 5395 (94.3%) | 5201 (96.4%) | 194 (3.6%) | 2 (1.0%) | 192 (99.0%) | 2697 (47.2%) | 3022 (52.8%) |

Table 10. Results of comparisons between phenotypic sex and genetically determined sex using the modified sex-specific assay for Chinook salmon (IDFG-OTS-SEX) from the SY2012 broodstocks.

| | **Total Samples** | **Missing Genetic Data** | **Total Successful Genotypes** | **Corresponding** | **Non-corresponding** | **Phenotypic males misidentified as female** | **Phenotypic females misidentified as male** | **Total phenotypic males** | **Total phenotypic females** |
|---|---|---|---|---|---|---|---|---|---|
| Clearwater | 738 | 18 (2.4%) | 720 (97.6%) | 720 (100%) | 0 (0%) | 0 (0.0%) | 0 (0.0%) | 374 (50.7%) | 364 (49.3%) |
| Dworshak | 2095 | 204 (9.7%) | 1891 (90.3%) | 1430 (75.6%) | 461 (24.4%) | 2 (0.1) | 459 (24.3%) | 727 (34.7%) | 1368 (65.3%) |
| Catherine Crk | 87 | 4 (4.6%) | 83 (95.4%) | 82 (98.8%) | 1 (1.2%) | 1 (1.2%) | 0 (0.0%) | 42 (48.3%) | 45 (51.7%) |
| Grande Ronde | 149 | 1 (0.7%) | 148 (99.3%) | 148 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 75 (50.3%) | 74 (49.7%) |
| Lookingglass | 152 | 7 (4.6%) | 145 (95.4%) | 77 (53.1%) | 68 (46.9%) | 31 (20.4%) | 31 (20.4%) | 65 (42.8%) | 81 (53.3%) |
| Lostine | 125 | 0 (0.0%) | 125 (100%) | 125 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 63 (50.4%) | 62 (49.6%) |
| Imnaha | 244 | 11 (4.5%) | 233 (95.5%) | 232 (99.6%) | 1 (0.4%) | 1 (0.4%) | 0 (0.0%) | 135 (55.3%) | 109 (44.7%) |
| Rapid River | 1454 | 26 (1.8%) | 1428 (98.2%) | 1426 (99.9%) | 2 (0.1%) | 0 (0.0%) | 2 (0.1%) | 693 (47.7%) | 761 (52.3%) |
| Powell | 775 | 14 (1.8%) | 761 (98.2%) | 759 (99.7%) | 2 (0.3%) | 0 (0.0%) | 2 (0.3%) | 393 (50.7%) | 382 (49.3%) |
| Sawtooth | 967 | 22 (2.3%) | 945 (97.7%) | 945 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 470 (48.6%) | 497 (51.4%) |
| Pahsimeroi | 410 | 8 (0.2%) | 402 (98.0%) | 402 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 164 (40.0%) | 246 (60.0%) |
| Lyons Ferry (Tucannon) | 164 | 10 (6.1%) | 154 (93.9%) | 154 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 69 (42.1%) | 95 (57.9%) |
| McCall | 1030 | 15 (1.5%) | 1015 (98.5%) | 1013 (99.8%) | 2 (0.2%) | 2 (0.2%) | 0 (0.0%) | 507 (49.2%) | 523 (50.8%) |
| NPTH | 378 | 17 (4.5%) | 361 (95.5%) | 361 (100%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 196 (51.9%) | 182 (48.1%) |
| *Total* | 8768 | 357 (4.1%) | 8411 (95.9%) | 7874 (93.6%) | 537 (6.4%) | 37(0.4%) | 494 (5.9%) | 3973 (45.3%) | 4795 (54.7%) |

Table 11. Average observed and expected heterozygosity of hatchery steelhead stocks for SY2012.

| | 2012 | | | |
|---|---|---|---|---|
| | **Avg het (Obs)** | **SD** | **Avg het (Exp)** | **SD** |
| Dworshak | 0.395 | 0.0937 | 0.397 | 0.092 |
| Dworshak (supplied to Clearwater) | 0.394 | 0.094 | 0.398 | 0.091 |
| Dworshak (supplied to Magic Valley) | 0.394 | 0.093 | 0.4 | 0.092 |
| S.F. Clearwater | 0.40 | 0.102 | 0.401 | 0.089 |
| Lyons Ferry | 0.419 | 0.0950 | 0.418 | 0.087 |
| Cottonwood Crk | 0.426 | 0.093 | 0.424 | 0.08 |
| Touchet | 0.425 | 0.123 | 0.429 | 0.091 |
| Tucannon | 0.445 | 0.124 | 0.429 | 0.088 |
| Little Sheep Crk. | 0.423 | 0.097 | 0.421 | 0.087 |
| Little Sheep Crk (above Weir) | 0.438 | 0.154 | 0.434 | 0.096 |
| Oxbow | 0.432 | 0.082 | 0.429 | 0.075 |
| Pahsimeroi | 0.432 | 0.077 | 0.429 | 0.072 |
| Pahsimeroi (supplied to Sawtooth) | 0.429 | 0.082 | 0.428 | 0.076 |
| Pahsimeroit (supplied to SBT) | 0.436 | 0.08 | 0.43 | 0.073 |
| Sawtooth | 0.426 | 0.071 | 0.428 | 0.067 |
| Sawtooth (Yankee Frk Release) | 0.43 | 0.081 | 0.427 | 0.07 |
| Sawtooth (SBT Egg Box Release) | 0.426 | 0.079 | 0.427 | 0.069 |
| EFSR | 0.417 | 0.093 | 0.42 | 0.083 |
| Squaw Crk. | 0.409 | 0.139 | 0.392 | 0.109 |
| Wallowa | 0.434 | 0.079 | 0.428 | 0.075 |

Table 12. Average observed and expected heterozygosity of hatchery Chinook stocks in 2011.

| | 2011 | | | |
|---|---|---|---|---|
| | **Avg het (Obs)** | **SD** | **Avg het (Exp)** | **SD** |
| Clearwater | 0.341 | 0.120 | 0.346 | 0.121 |
| Catherine Crk. | 0.351 | 0.144 | 0.346 | 0.130 |
| Dworshak | 0.339 | 0.129 | 0.337 | 0.123 |
| Dworshak (supplied to Clearwater) | 0.344 | 0.133 | 0.338 | 0.129 |
| Dworshak (Kooskia stock) | 0.338 | 0.126 | 0.338 | 0.125 |
| Grande Ronde | 0.342 | 0.151 | 0.338 | 0.135 |
| Grande Ronde (Captive) | 0.347 | 0.136 | 0.339 | 0.126 |
| Imnaha | 0.345 | 0.129 | 0.343 | 0.125 |
| Johnson Crk | 0.323 | 0.150 | 0.324 | 0.136 |
| Lookingglass | 0.349 | 0.131 | 0.348 | 0.127 |
| Lostine | 0.335 | 0.134 | 0.331 | 0.130 |
| S Fk Sal. R. | 0.328 | 0.132 | 0.331 | 0.132 |
| S Fk Sal R (IBS) | 0.332 | 0.134 | 0.333 | 0.133 |
| S FK Sal R (SBT) | 0.333 | 0.140 | 0.332 | 0.132 |
| S Fk Sal R (Clearwater) | 0.319 | 0.136 | 0.324 | 0.139 |
| Nez Perce FH | 0.340 | 0.119 | 0.345 | 0.120 |
| Pahsimeroi | 0.334 | 0.131 | 0.333 | 0.129 |
| Pahsimeroi (IBS) | 0.334 | 0.146 | 0.331 | 0.132 |
| Pahsimeroi to Sawtooth | 0.335 | 0.150 | 0.327 | 0.138 |
| Powell | 0.357 | 0.132 | 0.351 | 0.122 |
| Powell (Clear Crk release) | 0.357 | 0.141 | 0.351 | 0.130 |
| Powell (NPTH) | 0.362 | 0.141 | 0.352 | 0.128 |
| Powell (Selway Parr) | 0.360 | 0.131 | 0.354 | 0.120 |
| Powell (Selway FTS) | 0.348 | 0.127 | 0.347 | 0.125 |
| Powell (IBS) | 0.333 | 0.151 | 0.331 | 0.142 |
| Rapid River | 0.340 | 0.124 | 0.339 | 0.123 |
| Sawtooth | 0.327 | 0.136 | 0.331 | 0.134 |
| Tucannon | 0.343 | 0.143 | 0.340 | 0.138 |

Table 13. Average observed and expected heterozygosity of hatchery Chinook stocks in 2012.

| | 2012 | | | |
|---|---|---|---|---|
| | **Avg het (Obs)** | **SD** | **Avg het (Exp)** | **SD** |
| Clearwater | 0.345 | 0.127 | 0.343 | 0.124 |
| Catherine Crk. | 0.361 | 0.140 | 0.357 | 0.126 |
| Dworshak | 0.346 | 0.122 | 0.347 | 0.121 |
| Dworshak (Kooskia stock) | 0.339 | 0.124 | 0.339 | 0.121 |
| Grande Ronde | 0.347 | 0.136 | 0.342 | 0.127 |
| Imnaha | 0.348 | 0.126 | 0.348 | 0.124 |
| Lookingglass | 0.360 | 0.133 | 0.354 | 0.124 |
| Lostine | 0.339 | 0.135 | 0.337 | 0.130 |
| S Fk Sal. R. | 0.333 | 0.133 | 0.334 | 0.133 |
| S Fk Sal R (IBS) | 0.333 | 0.136 | 0.334 | 0.133 |
| S Fk Sal R (Clearwater) | 0.336 | 0.133 | 0.336 | 0.132 |
| Nez Perce FH | 0.350 | 0.125 | 0.348 | 0.120 |
| Pahsimeroi | 0.334 | 0.130 | 0.331 | 0.126 |
| Pahsimeroi (IBS) | 0.341 | 0.133 | 0.338 | 0.122 |
| Powell | 0.338 | 0.139 | 0.335 | 0.134 |
| Powell (Selway Parr) | 0.340 | 0.132 | 0.338 | 0.128 |
| Rapid River | 0.342 | 0.128 | 0.341 | 0.127 |
| Sawtooth | 0.337 | 0.144 | 0.337 | 0.142 |
| Sawtooth (IBS) | 0.333 | 0.148 | 0.334 | 0.144 |
| Tucannon | 0.340 | 0.139 | 0.345 | 0.137 |

Table 14. Population structure (Fst) among steelhead hatchery stocks sampled in 2012. Asterisks (*) indicate that Fst values were significantly different from zero.

| Population | Oxbow | Wallowa | EFSR | USB | Sawtooth | Pahs. | Dwor. | SF Clearwater | Cottonwood | Lyons Ferry | Touchet | Tucan. | Little Sheep |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Oxbow | --- | * | * | * | * | * | * | * | * | * | * | * | * |
| Wallowa | 0.020 | --- | * | * | * | * | * | * | * | * | * | * | * |
| EFSR | 0.018 | 0.029 | --- | * | * | * | * | * | * | * | * | * | * |
| USB | 0.053 | 0.056 | 0.049 | --- | * | * | * | * | * | * | * | * | * |
| Sawtooth | 0.005 | 0.020 | 0.018 | 0.056 | --- | * | * | * | * | * | * | * | * |
| Pahsimeroi | 0.005 | 0.020 | 0.016 | 0.061 | 0.005 | --- | * | * | * | * | * | * | * |
| Dworshak | 0.045 | 0.046 | 0.030 | 0.024 | 0.046 | 0.048 | --- | * | * | * | * | * | * |
| SF Clearwater | 0.038 | 0.039 | 0.025 | 0.031 | 0.038 | 0.041 | 0.002 | --- | * | * | * | * | * |
| Cottonwood Crk | 0.022 | 0.006 | 0.033 | 0.060 | 0.021 | 0.024 | 0.050 | 0.044 | --- | * | * | * | * |
| Lyons Ferry | 0.025 | 0.022 | 0.035 | 0.061 | 0.025 | 0.026 | 0.050 | 0.044 | 0.028 | --- | * | * | * |
| Touchet | 0.015 | 0.011 | 0.022 | 0.056 | 0.019 | 0.017 | 0.044 | 0.037 | 0.016 | 0.014 | --- | * | * |
| Tucannon | 0.015 | 0.013 | 0.019 | 0.045 | 0.014 | 0.015 | 0.040 | 0.034 | 0.023 | 0.014 | 0.002 | --- | * |
| Little Sheep | 0.021 | 0.023 | 0.033 | 0.067 | 0.024 | 0.022 | 0.056 | 0.048 | 0.026 | 0.022 | 0.011 | 0.019 | --- |

Table 15. Population structure ($F_{st}$) among SY2011 Chinook hatcheries. Asterisks (*) indicate $F_{st}$ values are significantly different from zero (p <0.01).

| | **Clearwater** | **Catherine** | **Imnaha** | **Johnson** | **Looking.** | **Lostine** | **NPTH** | **Rapid** | **Tucann.** | **Pahsim.** | **SFSR** | **Grande Ronde** | **Dwor.** | **Powell** | **Sawt.** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Clearwater | --- | * | * | * | * | * | * | * | * | * | * | * | * | * | * |
| Catherine | 0.009 | --- | * | * | * | * | * | * | * | * | * | * | * | * | * |
| Imnaha | 0.012 | 0.016 | --- | * | * | * | * | * | * | * | * | * | * | * | * |
| Johnson Crk | 0.029 | 0.031 | 0.032 | --- | * | * | * | * | * | * | * | * | * | * | * |
| Lookingglass | 0.009 | 0.004 | 0.012 | 0.039 | --- | * | * | * | * | * | * | * | * | * | * |
| Lostine | 0.024 | 0.028 | 0.018 | 0.054 | 0.024 | --- | * | * | * | * | * | * | * | * | * |
| NPTH | 0.002 | 0.011 | 0.014 | 0.035 | 0.011 | 0.021 | --- | * | * | * | * | * | * | * | * |
| Rapid River | 0.011 | 0.018 | 0.015 | 0.040 | 0.016 | 0.031 | 0.013 | --- | * | * | * | * | * | * | * |
| Tucannon | 0.024 | 0.025 | 0.030 | 0.048 | 0.030 | 0.038 | 0.025 | 0.042 | --- | * | * | * | * | * | * |
| Pahsimeroi | 0.030 | 0.031 | 0.029 | 0.044 | 0.035 | 0.039 | 0.031 | 0.040 | 0.048 | --- | * | * | * | * | * |
| SFSR | 0.018 | 0.019 | 0.017 | 0.015 | 0.024 | 0.027 | 0.021 | 0.028 | 0.038 | 0.029 | --- | * | * | * | * |
| Grande Ronde | 0.010 | 0.011 | 0.013 | 0.036 | 0.009 | 0.027 | 0.010 | 0.014 | 0.031 | 0.038 | 0.024 | --- | * | * | * |
| Dworshak | 0.003 | 0.010 | 0.016 | 0.033 | 0.010 | 0.026 | 0.004 | 0.018 | 0.025 | 0.032 | 0.020 | 0.011 | --- | * | * |
| Powell | 0.004 | 0.010 | 0.014 | 0.033 | 0.011 | 0.025 | 0.005 | 0.018 | 0.023 | 0.032 | 0.021 | 0.014 | 0.005 | --- | * |
| Sawtooth | 0.027 | 0.026 | 0.028 | 0.035 | 0.030 | 0.036 | 0.030 | 0.031 | 0.049 | 0.023 | 0.019 | 0.033 | 0.029 | 0.029 | --- |

Table 16. Population structure (Fst) among Chinook hatchery stocks sampled in 2012. Asterisks (*) indicate that Fst values were significantly different from zero (p <0.01).

| | Clearwater | Tucannon | NPFH | Rapid R | Dworshak | Pahsimeroi | McCall | Grande Ronde | Imnaha | Looking. | Lostine | Powell | Sawtooth | Catherine |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Clearwater | --- | * | * | * | * | * | * | * | * | * | * | * | * | * |
| Tucannon | 0.027 | --- | * | * | * | * | * | * | * | * | * | * | * | * |
| NPFH | 0.002 | 0.025 | --- | * | * | * | * | * | * | * | * | * | * | * |
| Rapid R | 0.013 | 0.044 | 0.012 | --- | * | * | * | * | * | * | * | * | * | * |
| Dworshak | 0.003 | 0.026 | 0.001 | 0.015 | --- | * | * | * | * | * | * | * | * | * |
| Pahsimeroi | 0.033 | 0.045 | 0.033 | 0.045 | 0.033 | --- | * | * | * | * | * | * | * | * |
| McCall | 0.02 | 0.033 | 0.019 | 0.029 | 0.017 | 0.029 | --- | * | * | * | * | * | * | * |
| Grande Ronde | 0.009 | 0.024 | 0.009 | 0.016 | 0.010 | 0.035 | 0.021 | --- | * | * | * | * | * | * |
| Imnaha | 0.015 | 0.028 | 0.011 | 0.019 | 0.013 | 0.031 | 0.019 | 0.012 | --- | * | * | * | * | * |
| Lookingglass | 0.009 | 0.029 | 0.008 | 0.017 | 0.009 | 0.034 | 0.021 | 0.010 | 0.013 | --- | * | * | * | * |
| Lostine | 0.021 | 0.038 | 0.019 | 0.026 | 0.022 | 0.038 | 0.026 | 0.020 | 0.021 | 0.024 | --- | * | * | * |
| Powell | 0.010 | 0.033 | 0.010 | 0.033 | 0.010 | 0.039 | 0.029 | 0.021 | 0.022 | 0.019 | 0.035 | --- | * | * |
| Sawtooth | 0.028 | 0.045 | 0.028 | 0.035 | 0.028 | 0.024 | 0.021 | 0.029 | 0.032 | 0.033 | 0.039 | 0.033 | --- | * |
| Catherine Crk. | 0.012 | 0.027 | 0.011 | 0.017 | 0.010 | 0.036 | 0.024 | 0.013 | 0.016 | 0.005 | 0.020 | 0.024 | 0.033 | --- |

Table 17 Estimates of effective population size ($N_e$) and 95% confidence intervals for steelhead hatchery stocks and release groups in SY2012.

| | 2012 | |
|---|---|---|
| | **$N_e$** | **95% CI** |
| Grande Ronde | | |
| Dworshak | 244.5 | 227.4–263.1 |
| Dworshak (supplied to Clearwater) | 209.6 | 184.1–240.9 |
| Dworshak (SF Clearwater stock) | 101.3 | 86.9–119.8 |
| Dworshak (supplied to Magic Valley) | 136.9 | 125.3–149.9 |
| EFSR | 71.1 | 59.7–86.5 |
| Little Sheep Crk. | 100.4 | 86.2–118.7 |
| Lyons Ferry | 91.0 | 82.3–100.9 |
| Oxbow | 184.9 | 168.4–203.4 |
| Pahsimeroi | 287.2 | 262.3–315.3 |
| Pahsimeroi (supplied to Sawtooth) | 139.8 | 126.5–154.9 |
| Pahsimeroi (SBT) | 187.8 | 163.2–218.7 |
| Sawtooth | 240.6 | 211.1–276.7 |
| Sawtooth (Egg Box Release) | 188.3 | 161.7–222.8 |
| Sawtooth (Yankee Frk Release) | 169.9 | 147.0–198.9 |
| Upper Salmon B-run | 21.2 | 18.6–24.2 |
| Cottonwood Crk | 65.6 | 60.2–71.4 |
| Touchet | -1100.6 | 236.1 – Inf. |
| Tucannon | 137.7 | 76.9–506.3 |
| Wallowa | 180.9 | 165.6–198.2 |

Table 18. Estimates of effective population size and 95% confidence intervals for SY2011 Chinook hatchery stocks.

| | 2011 | |
|---|---|---|
| | **Ne** | **95% CI** |
| Clearwater | 286.0 | 259.7–315.9 |
| Catherine Crk | 110.2 | 87.3–145.8 |
| Dworshak | 446.8 | 411.7–490.8 |
| Grande Ronde | 96.4 | 88.8–104.9 |
| Imnaha | 216.9 | 186.5–255.9 |
| Johnson Crk | 138.7 | 102.1–207.7 |
| Lookingglass | 217.7 | 174.6–283.1 |
| Lostine | 159.0 | 128.8–203.5 |
| SF Salmon | 442.8 | 400.8–491.1 |
| Nez Perce FH | 101.2 | 93.4–109.7 |
| Pahsimeroi | 181.5 | 168.3–196.0 |
| Powell | 135.9 | 127.8–126.8 |
| Rapid | 499.2 | 464.8–536.5 |
| Sawtooth | 129.3 | 117.6–142.4 |
| Tucannon | 142.7 | 122.3–169.1 |

Table 19. Estimates of effective population size and 95% confidence intervals for SY2012 Chinook hatchery stocks.

| | 2012 | |
|---|---|---|
| | **Ne** | **95% CI** |
| Clearwater | 188.5 | 174.8–203.4 |
| Catherine Crk | 125.9 | 100.3–165.2 |
| Dworshak | 504.0 | 469.1–542 |
| Grande Ronde | 62.0 | 56.1–68.6 |
| Imnaha | 238.3 | 260.5–399.7 |
| Lookingglass | 170.5 | 141.9–210.1 |
| Lostine | 150.8 | 124.7–187.4 |
| SF Salmon | 366.2 | 336.0–400.1 |
| Nez Perce FH | 210.5 | 187.9–237.2 |
| Pahsimeroi | 198.1 | 178.7–220.5 |
| Powell | 115.9 | 108.9–123.4 |
| Rapid | 498.0 | 457.4–543.3 |
| Sawtooth | 276.2 | 255.4–298.9 |
| Tucannon | 177.8 | 149.1–216.9 |

**FIGURES**

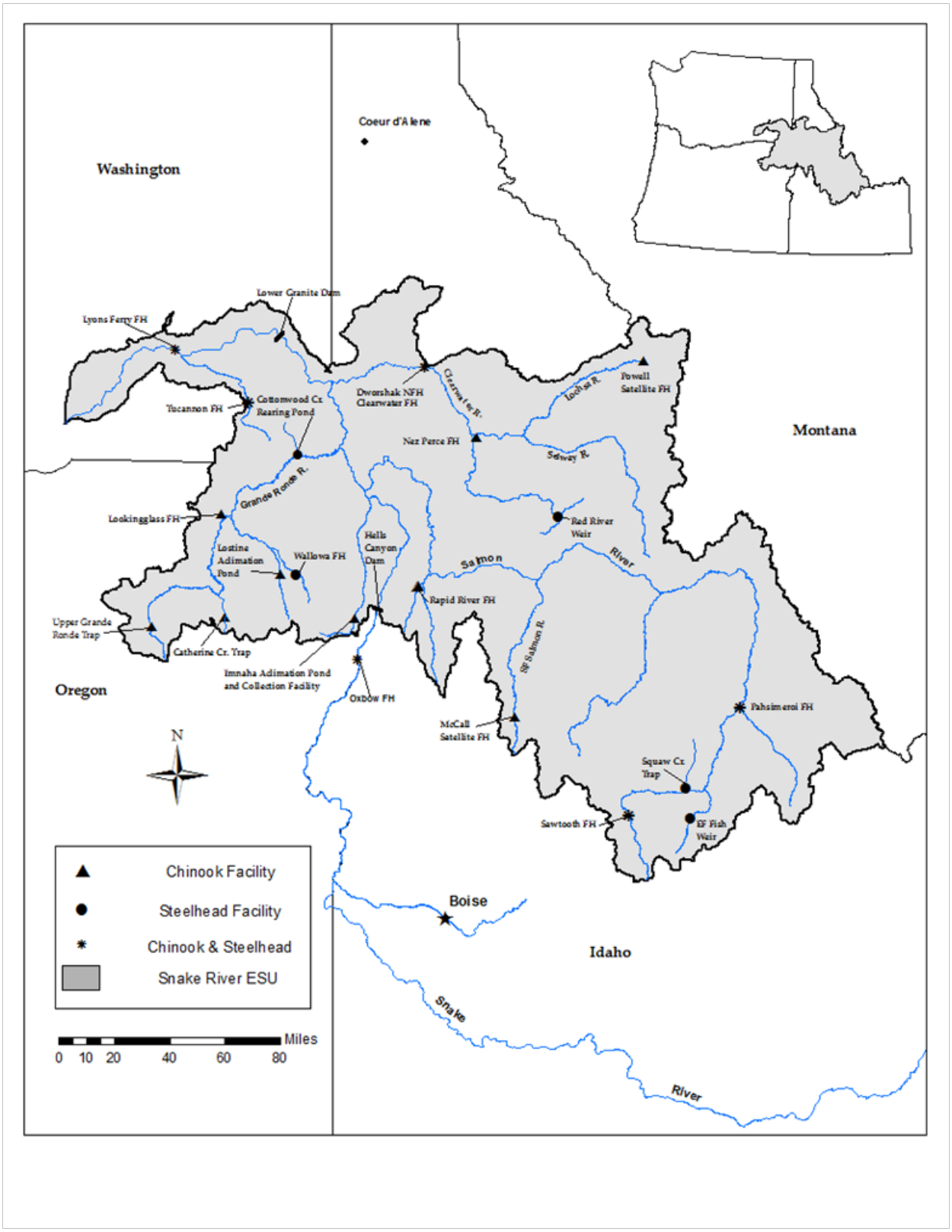


Figure 1. Location of sampled fish hatcheries in the Snake River basin.

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