



**CHINOOK SALMON AND STEELHEAD GENOTYPING
FOR GENETIC STOCK IDENTIFICATION AT LOWER
GRANITE DAM**

**ANNUAL PROGRESS REPORT
January 1, 2018 — December 31, 2018**



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**IDFG Report Number 19-08
January 2019**

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Project Progress Report

2018 Annual Report

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**Project Number 2010-026-00
Contract Number 79581**

**IDFG Report Number 19-08
January 2019**

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ABSTRACT

This report summarizes progress in the development and implementation of genetic stock identification (GSI) in the Snake River basin for natural-origin steelhead and spring/summer Chinook Salmon for the 01/01/2018 to 12/31/2018 reporting period. Four objectives for the GSI project are addressed in this report: 1) the maintenance and evaluation of single nucleotide polymorphism (SNP) panels for high-throughput genotyping of steelhead and Chinook Salmon in the Snake and Columbia river basins; 2) the updating, maintenance, and testing of SNP baselines to describe genetic variation and for use as a reference in conducting GSI for both species; 3) the implementation of GSI to estimate genetic stock composition and life history diversity of steelhead and spring/summer Chinook Salmon passing Lower Granite Dam (LGR); and 4) the summarization of life history and genetic diversity information for steelhead and spring/summer Chinook Salmon detected at PIT tag detection systems. For both species, panels of up to 379 SNPs have been in use for GSI and parentage-based tagging (PBT) at both Idaho Department of Fish and Game's Eagle Fish Genetics Lab, and its collaborating laboratory, the Columbia River Inter-Tribal Fish Commission's Hagerman Genetics Lab. Steelhead SNP baseline version v3.1 consists of 45 collections and 5,967 individuals. Chinook Salmon SNP baseline v3.1 consists of 30 collections and 4,356 individuals. SNP baselines are used to describe genetic diversity and structure of natural-origin populations throughout the Snake River. Based on population structure we have defined 10 genetic stocks for steelhead and 7 genetic stocks for Chinook Salmon for GSI analysis at LGR. We summarize GSI results for returning adults and emigrating juveniles during 2017-2018 at LGR using v3.1 baselines as reference. Finally, we describe the life history variation and genetic diversity of steelhead and Chinook Salmon detected at IPTDS. The information presented in this report provides critical data for viable salmonid population (VSP) monitoring of the Snake River steelhead DPS and the Snake River spring/summer Chinook Salmon ESU.

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Suggested citation:

Hargrove, J. S., T. A. Delomas, J. McCane, M. Davison, M. R. Campbell, R. L. Horn, and S. R. Narum. 2019. Chinook and Steelhead Genotyping for Genetic Stock Identification at Lower Granite Dam. Idaho Department of Fish and Game Report 19-08. Annual Report, BPA Project 2010-026-00.

INTRODUCTION

Abundance (i.e. number of adults on spawning grounds) is a primary metric needed for monitoring the status of steelhead and salmon populations in the Columbia River basin (McElhany et al. 2000). Estimates of abundance combined with age and sex information over time allows estimation of productivity (e.g. recruits-per-female). Both abundance and productivity metrics provide indicators of the resiliency of populations and allow assessments of extinction risk. Estimates of these metrics at the population or major population group (MPG) scale is information that fisheries managers can use to achieve sustainable harvest of larger populations, while protecting weaker stocks and the genetic diversity present within them.

Population-level assessments of abundance and productivity for ESA-threatened Snake River steelhead and Chinook Salmon can be particularly difficult due to the wide distribution and location of spawning areas (many populations are present in remote or wilderness areas). Additionally, environmental conditions at the time of spawning often prevent the use of traditional counting methodologies (weirs, and redd count surveys). For example, Snake River steelhead monitoring can be hampered due by high turbidity and changing flow conditions during the time of spawning (Thurow 1985). This is less of a problem for spring/summer Chinook Salmon, although turbid water conditions resulting from storms and forest fires have at times impacted the ability to estimate adult abundance using redd-based surveys in the Middle Fork and South Fork Salmon rivers (Thurow 2000). As a result, escapement estimates (and other demographic information) have not been available for most Snake River populations (Busby et al. 1996; Good et al. 2005) until recently.

In lieu of more detailed basin-level and population-specific information, steelhead in the Columbia River basin have traditionally been assigned to two groups (A-run and B-run), based on life history characteristics and bimodal passage timing at Bonneville Dam in the mid-Columbia River (Busby et al. 1996). By definition, A-run steelhead pass Bonneville Dam before August 25 and tend to return after one year in the ocean. B-run steelhead pass Bonneville Dam after August 25 and tend to return after two years in the ocean. B-run steelhead are thought to be larger at age than A-run steelhead. Upstream migrating steelhead adults at Lower Granite Dam (LGR) do not exhibit a bimodal passage distribution. A-run and B-run adults at LGR are enumerated based on length (A-run, ≤ 78 cm; B-run, > 78 cm) as a proxy for ocean age. A-run and B-run steelhead also exhibit differences in spawning distribution. A-run steelhead spawn throughout the Columbia basin, whereas the majority of B-run steelhead originate primarily from the Clearwater, Middle Fork Salmon, and South Fork Salmon rivers in Idaho. The putative differences in migration timing, morphology, and life history characteristics have been used as a surrogate for biodiversity in conservation planning for Snake River steelhead. However, the relationship between the morphological and life history characteristics to time of passage at Bonneville Dam is uncertain (Good et al. 2005). Further, the bimodal passage distribution at Bonneville Dam has become unimodal in recent years (Robards and Quinn 2002).

Two management concerns regarding Snake River steelhead have arisen in the last several years. First, populations classified as "B-run" do not appear to be self-sustaining (NMFS 2007) and their presence in the basin has affected operation of the Columbia River hydrosystem and fisheries management in the lower Columbia River. In particular, harvest of fall Chinook Salmon is constrained in order to limit impacts to B-run steelhead concurrently present in the Columbia River fishery. Secondly, there are substantial data needs to refine population delineations and conservation assessments (ICTRT 2003), but data have been lacking. Although Snake River "B-run" steelhead are currently identified as a biologically significant and distinct component of the Snake River DPS, their management is confounded by the lack of a

clear and detailed understanding of their actual spawning distribution and population structure. Nielsen et al. (2009) found that steelhead in Idaho Snake River tributaries exhibit a complicated pattern of genetic structure with populations clustering according to drainage locality, not simply by “A-run” or “B-run” designations. Additionally, Copeland et al. (2017) identified a gradient of life history characteristics among traditional A- and B-run populations rather than a discrete, binary classification.

The above issues and similar conservation and management questions relating to Snake River steelhead and spring/summer Chinook Salmon may be addressed through genetic stock identification (GSI). GSI uses multilocus genotype data from reference populations (representing the contributing stocks) as a baseline and complimentary genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture (Shaklee et al. 1999; Anderson et al. 2008). GSI has been used extensively to understand and manage mixed stock fisheries for a variety of Pacific salmonids including Chinook Salmon (Smith et al. 2005), Sockeye Salmon (Habicht et al. 2010), Coho Salmon (Beacham et al. 2001), and steelhead (Beacham et al. 2000). In the Snake River basin, studies have indicated that both steelhead and Chinook Salmon exhibit significant genetic structuring at the watershed (or subbasin) level (Moran 2003; Narum et al. 2007; Nielsen et al. 2009; Matala et al. 2014). Previously, researchers have made use of this genetic structure to identify the genetic stock origin of kelt steelhead at LGR (Narum et al. 2008) and to estimate the stock composition of natural-origin and hatchery Chinook Salmon (Smith 2007) and natural-origin steelhead and Chinook Salmon (Ackerman et al. 2012; Campbell et al. 2012; Camacho et al. 2017; Camacho et al. 2018a; Camacho et al. 2018b) at LGR.

The results of the studies summarized above demonstrate the utility of GSI to obtain genetic stock abundance estimates for steelhead and Chinook Salmon in the Snake River basin. Continuation of GSI at LGR will allow us to 1) monitor genetic structure throughout the basin over time, and 2) estimate abundance, productivity, and life history diversity for genetic stocks throughout the Snake River. Sustained development and evaluation of GSI has been strongly recommended by regional research, monitoring, and evaluation (RME) workgroups. Similar work initiated at Bonneville Dam and in the lower Columbia River has been supported by the Independent Scientific Review Panel (<http://www.nwcouncil.org/library/isrp/isrp2008-15.pdf>).

REPORT STRUCTURE

This report contains four sections, one for each of the study objectives. Section 1 discusses the continued use of GT-Seq (Genotyping in Thousands by Sequencing) for more efficient and cost effective high-throughput genotyping for GSI in the Snake River basin. Section 2 summarizes efforts to update, maintain, and test SNP baselines for Snake River steelhead and spring/summer Chinook Salmon. These baselines are used to monitor genetic diversity and structure of natural-origin populations and are the reference for GSI at LGR. Section 3 addresses the use of GSI to estimate genetic stock proportions and life history diversity for natural-origin stocks at LGR. Section 4 directs readers to a separate stand-alone report that summarizes the life history and genetic diversity of steelhead and spring/summer Chinook Salmon detected at PIT tag detection systems.

In this report, we refer to adult steelhead and Chinook Salmon migrating past LGR using spawn years (SY). For steelhead, a spawn year refers to adults that migrate upstream past LGR during the fall of the previous calendar year and the spring of the current calendar year (e.g., SY2018 steelhead are adults that migrated past LGR between 7/1/17 – 6/30/18 and spawned in

spring of 2018). For spring/summer Chinook Salmon, a spawn year refers to adults that migrate past the dam prior to August 17 and spawn that same fall. We refer to juveniles of both species migrating past LGR using migratory years (MY). A migratory year refers to juveniles migrating downstream past LGR from the end of March to the end of July that year.

SECTION 1: EVALUATE AND MAINTAIN SNP MARKER PANELS

INTRODUCTION

The conclusion of calendar year 2018 marks our third full year of genotyping using the GT-seq platform for GSI and PBT applications. The current GT-seq marker panel consists of all markers developed on the previous Fluidigm platform as well as SNPs newly developed in 2017 and 2018. Both of the original Chinook Salmon and steelhead GT-seq panels consisted of 95 PBT loci, 96 GSI loci, and 1 sex marker. Beginning in 2017, in collaboration with the CRITFC Hagerman Genetics Lab, we expanded both the Chinook Salmon and steelhead GSI/PBT GT-seq panels to include an additional 107 and 77 new markers, respectively. These newly developed SNP panels consisted of 299 markers for Chinook Salmon and 269 markers for steelhead. Beginning in 2018, again in collaboration with CRITFC Hagerman Genetics Lab, an expanded SNP panel was developed for steelhead, which includes an additional 110 markers (new SNP panel total of 379 loci). Genetic stock identification and PBT work started in 2017 was performed using the 299 and 269 marker sets for Chinook Salmon and steelhead, respectively. Steelhead projects involving GSI and PBT initiated in 2018 have been genotyped at the 379 loci panel.

Data for the SNP marker panels described above can be accessed via the FishGen webpage (<https://www.fishgen.net/Home.aspx>). Once a user account has been set up with FishGen, the details of these panels can be accessed with the following link: (<https://www.fishgen.net/WebPages/CustomMarkerSet/MarkerExport.aspx>). Metadata for each marker include synonym of species, Vic probe, Vic allele, Fam probe, Fam allele, forward primer, and reverse primer. The new larger Chinook panel known as 'CRITFC/IDFG Chinook GTseq v3.0 299' consists of 95 PBT loci, 96 GSI loci, 1 sex marker, and 107 new SNP markers. The new larger steelhead panel known as 'CRITFC/IDFG Steelhead GTseq v3.0 379' consists of 95 PBT loci, 96 GSI loci, 1 sex marker, and 187 new SNP markers.

DISCUSSION

Marker panels have continued to expand since their inception in an effort to maximize the resolution of genetic data used in genetic stock identification and parentage based tagging. Because new panels include all previously used markers, the expansion of our marker panels does not affect backwards compatibility of our GSI/PBT work. In other words, direct comparisons can be made between currently analyzed samples and historic ones. We intend to perform a thorough evaluation over the next performance period to assess how newly added markers affect the accuracy and precision of GSI and PBT analyses. However, because fish from the past year are the only ones that have been genotyped on the larger marker panels we will continue to use the original 95 PBT marker panels for PBT work for the next several years.

SECTION 2: UPDATE, MAINTAIN, AND TEST SNP BASELINES FOR STEELHEAD AND CHINOOK SALMON IN THE SNAKE RIVER

INTRODUCTION

The Snake River SNP baselines for steelhead and Chinook Salmon serve two primary purposes: 1) to monitor genetic structure and diversity of natural-origin Snake River populations both spatially and temporally, and 2) to serve as a reference for GSI work at LGR.

First, the monitoring of genetic structure over time and space provides insight regarding gene flow, both historic and contemporary, from natural (successful straying) and manmade (i.e. out-of-basin hatchery stocking) causes. Monitoring genetic diversity of populations provides information about gain or loss in genetic diversity over time and provides insight into the adaptive potential of populations. Our GSI baselines provide genetic structure and diversity information for 23 extant steelhead Technical Recovery Team (TRT) populations and 28 extant Chinook Salmon TRT populations throughout the Snake River basin to aid in viable salmonid population (VSP; McElhany et al. 2000) monitoring of the Snake River steelhead distinct population segment (DPS) and spring/summer Chinook ESU.

Second, the Snake River SNP baselines serve as a reference for GSI conducted at LGR to estimate genetic stock composition of out-migrating smolts (e.g. Stark et al. 2016, Camacho et al. 2018b) and returning adults (e.g. Camacho et al. 2017, Camacho et al. 2018b). Genetic stock composition estimates of adults and juveniles at LGR, combined with sex and age data, will allow us to estimate abundance, productivity, and life history diversity of genetic stocks over time for VSP monitoring. For GSI, our objective is to periodically update and maintain the SNP baselines to accurately estimate contemporary allele frequencies (genetic structure) of natural-origin populations throughout the Snake River contributing to production at LGR.

DISCUSSION

For the current reporting period, we continued to use the GSI baselines v3.1 as described in Vu et al. (2015) to determine the source of origin for Snake River steelhead and Chinook Salmon sampled at LGR. Briefly, the current Chinook Salmon baseline consists of 4,356 samples from 30 populations genotyped at 173 loci. These collections represent 31 of 41 TRT populations and all five major population groups (MPG). The GSI baseline v3.1 for steelhead consists of all 23 TRT populations and all six major genetic stocks. Currently, there are 5,967 samples from 45 populations included in the steelhead individuals genotyped at 179 loci.

We are currently in the process of updating GSI baselines for steelhead in the Snake River basin and portions of the Columbia River. As outlined in Section 1 above, we have adopted an expanded SNP panel for steelhead (379 loci) and in the coming year we will perform the appropriate tests to optimize and update the associated baseline. As part of these efforts, we have begun to genotype historical samples (SY2017) with the newly expanded 379 loci SNP panel. Moving forward, we will use samples collected between SY2011 and SY2018 to construct a new GSI baseline for steelhead.

SECTION 3. IMPLEMENT GSI METHODS TO ESTIMATE PROPORTIONS AND BIOLOGICAL PARAMETERS OF NATURAL-ORIGIN STOCKS AT LOWER GRANITE DAM

INTRODUCTION

The long-range goal of the Idaho Department of Fish and Game's (IDFG) anadromous fish program is to preserve Idaho's salmon and steelhead runs and recover them to benefit all users (IDFG 2007). This goal is consistent with basinwide mitigation and recovery efforts. Fisheries management requires an understanding of how salmonid populations function as well as regular status assessments to document progress towards achieving these goals (McElhany et al. 2000). Estimates of abundance, combined with sex and age information over time, allow estimation of population growth rates; and both abundance and productivity metrics provide indicators of the resiliency and viability of populations. Estimates of these metrics at the genetic stock or MPG level can be used by fisheries managers to prescribe sustainable harvest rates for larger populations, while protecting weaker stocks and the genetic diversity within them.

However, population level or MPG assessments of abundance and productivity for ESA-listed Snake River steelhead and spring/summer Chinook Salmon can be particularly difficult (see Report Introduction). Specific data on Snake River steelhead and Chinook Salmon MPGs and populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICTRT 2003). Genetic Stock Identification is one potential means for estimating these parameters at a finer-scale (e.g., MPG, genetic stock [reporting group], or population). Genetic Stock Identification uses multilocus genotype data from reference populations (representing potential contributing stocks) as a baseline and a complimentary set of genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture and to estimate stock of origin of individual fish (Shaklee et al. 1999). Section 2 of Vu et al. (2015) presents the SNP baselines used for GSI in the Snake River basin. Here we use complementary sets of genotype data from adults sampled at the Lower Granite Dam (LGR) adult trap and juveniles sampled at the LGR juvenile bypass facility to estimate the genetic stock of origin of upstream migrating adults and emigrating juveniles. We then provide life history diversity (sex, length, age, migration timing) information of individuals assigning to the various Snake River genetic stocks.

In this report, we present individual genetic assignments and life history diversity information for SY2018 adults and MY2018 juveniles (both steelhead and Chinook Salmon) sampled at LGR.

METHODS

Adult Trap Operations

Detailed methods for operation of the LGR adult trap can be found in Camacho et al. (2017) and citations within. Briefly, adult steelhead and spring/summer Chinook Salmon migrating upstream past LGR may be intercepted at a trapping facility, located on the adult fish ladder above the counting window, according to a predetermined sampling rate. Trapping rates that achieve sample requirements for various projects while balancing fish handling concerns are determined by a committee of collaborating management agencies. Sample rates are typically 10–20%. The sample rate determines how long a trap gate remains open four times per hour; the trap is operational 24 hours per day.

Juvenile Trap Operations

Detailed methods for operation of the LGR juvenile trap can be found in Camacho et al. (2018b) and citations within. The juvenile trap is located on the LGR juvenile bypass system. The trap captures a systematic sample of fish by operating two trap gates according to a predetermined sample rate. The sample rate determines how long the trap gates remain open, up to six times per hour. The trap is operational 24 hours per day and fish are processed every morning. Sample rate is predetermined daily to collect 250-750 fish per day (all species combined) and is based on the expected number of fish entrained in the bypass system that day.

Fish Handling Protocols (Adults and Juveniles)

Fish handling procedures are detailed in Camacho et al. (2017) for adults and Camacho et al. (2018b) for juveniles (and citations within both reports). Fish captured at the LGR adult or juvenile trap are anesthetized; identified to species; examined for external marks, tags, and injuries; scanned for an internal CWT or PIT tag; and measured for fork length (FL). All fish are examined for the presence (unclipped) or absence (clipped) of the adipose fin and classified to putative origin (hatchery or natural). All natural-origin fish have an unclipped adipose fin because they spend their entire life cycle in the natural environment. Most hatchery-origin fish have a clipped adipose fin. However, some hatchery fish may be released with an unclipped adipose fin for supplementation or tribal harvest opportunities. Thus, unclipped fish are also examined for a CWT or a PIT tag. The presence of a CWT definitively identifies an unclipped fish as hatchery origin. For unclipped adult steelhead, hatchery origin may also be determined by the presence of dorsal and/or ventral fin erosion, which is assumed to occur only in hatchery-reared steelhead (Latremouille 2003). Captured fish determined to be putatively natural-origin or unclipped hatchery with no CWT are sampled for scales (for age; except juvenile Chinook). Tissue from adults sampled at LGR for sex and genotype data are collected from fish with either an unclipped or a clipped adipose fin. For juveniles, fish bearing PIT tags and/or diseased or injured fish were omitted from the subsample, as were Chinook deemed to be yearling fall Chinook based on external morphology (Tiffan et al. 2000).

Scales were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG ageing laboratory in Nampa, Idaho. Tissue samples were taken from a small clip of the anal fin. Tissues were stored on a Whatman sheet for transport to the IDFG Eagle Fish Genetics Laboratory. Gender was not visually determined at the trap, but was assessed using Y-specific genetic assays (Campbell et al. 2012). After processing, all fish were returned to the fish ladder to resume upstream migration (adults) or the bypass system to resume downstream migration (juveniles).

Scale Age Protocol

Protocols for determining a fish's age from scales are detailed in Wright et al. (2015).

Genetics Laboratory Protocol

Laboratory protocols for DNA extraction, amplification, and SNP genotyping are detailed in Section 2 of Vu et al. (2015). MY2018 steelhead and Chinook Salmon juveniles and SY2018 steelhead and Chinook Salmon adults were processed at IDFG's Eagle Fish Genetics Lab (EFGL) in Eagle, Idaho.

Parentage-Based Tagging

Beginning in 2008, parentage-based tagging (PBT; Anderson and Garza 2005) has been used to genetically tag nearly all hatchery-origin steelhead in the Snake River basin (Steele et al. 2013a, 2013b). This genetic tagging technique is accomplished by genotyping all parental broodstock each spawn year, thereby allowing any offspring to be assigned back to their parents and identifying the hatchery of origin and age of offspring. The implementation of PBT provides an alternative to coded-wire tags (CWT) for identifying the origin and age of fish harvested in mixed-stock fisheries or that stray into natural spawning areas.

We conducted PBT analysis for all unclipped juvenile fish sampled in MY2018 and adult fish sampled in SY2018. In using PBT to evaluate all the fish, we are better able to identify putative natural-origin (unmarked, untagged) fish that are truly of hatchery origin. Any individuals identified as unmarked hatchery origin adults with a PBT were removed from the dataset before performing GSI and evaluating life history diversity of genetic stocks.

Genetic Stock Identification

Individual assignment (IA) tests were conducted on all unmarked juveniles and adults that did not receive a PBT assignment in MY2018 and SY2018 using the Snake River SNP baselines v3.1 described in Section 2 of Powell et al. (2017). SNP allele frequency estimates from baseline collections serve as the reference information for IA tests. Fish sampled at the LGR adult and juvenile trapping facilities were genotyped at the same SNPs, and multilocus genotype data were used to assign individual fish back to their estimated population (and genetic stock) of origin (Pella and Milner 1987; Shaklee et al. 1999). In IA, the probability that each fish originates from a baseline population is calculated based on the likelihood that the individual's genotype belongs to that population, given baseline allele frequency estimates. Individual population estimates were first calculated and then summed into genetic stock estimates (allocate-sum procedure; Wood et al. 1987). Genetic stocks (aka reporting groups) are assemblages of reference (baseline) populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and/or management units (Ackerman et al. 2011). IA procedures assign an individual's genotype to the reporting group from which it is most likely to have originated.

Ten genetic stocks were used for natural-origin steelhead IA analyses. Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: lower Salmon River; 5) UPCLWR: upper Clearwater River (Lochsa and Selway rivers); 6) SFCLWR: South Fork Clearwater River (including Clear Creek); 7) LOCLWR: lower Clearwater River; 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSNAKE: Asotin Creek and tributaries to the Snake River downstream of the Clearwater River confluence.

Seven natural-origin Chinook Salmon genetic stocks were used during IA analyses. Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: an aggregate reporting group that includes the Little Salmon, Clearwater, Grande Ronde, and Imnaha rivers; 6) TUCANO: Tucannon River, and 7) FALL: Snake River fall Chinook Salmon. Three collections of Snake River fall Chinook Salmon (see Table 2 in Ackerman et al. 2012) are included in the SNP baselines (FALL genetic stock); we are able to identify fall Chinook within mixtures of spring/summer Chinook with 100% accuracy.

After performing IA, we estimated genetic stock compositions of all samples analyzed and evaluated life history diversity for each genetic stock. We summarize results for four sample groups:

- SY2018 steelhead adults
- MY2018 steelhead juveniles
- SY2018 Chinook adults
- MY2018 Chinook juveniles

RESULTS

We inventoried a total of 8,303 samples (including both steelhead and Chinook Salmon) from SY2018 adults and MY2018 juveniles at LGR (Table 1). Of the 8,303 inventoried samples, 8,296 were queued for genotyping. The seven individuals that were inventoried but not queued for genotyping were missing a fin clip sample for extraction. We failed to successfully genotype 555 (6.7%) of the queued samples. We assigned 1,524 (19.7%) samples to hatchery parents in our PBT baseline despite all samples being collected from fish with intact adipose fins. For the remaining 6,225 samples, we performed IA, which are summarized below and in Tables 1-5.

SY2018 Steelhead Adults

Of the 3,025 unclipped adult steelhead sampled in SY2018, 2,573 (85.1%) were phenotypically identified as natural-origin because they had no apparent dorsal or ventral fin erosion (Table 1). The remaining 452 (14.9%) fish were identified as hatchery origin due to the presence of dorsal and/or ventral fin erosion. Of the 3,025 total samples collected in SY2018, 3,018 samples were queued for genotyping, and 2,895 (95.9%) of the queued samples were successfully genotyped. We assigned 179 (7.3%) of the 2,454 successfully genotyped, phenotypically natural-origin fish to hatchery parents. Of the 441 fish that were successfully genotyped and phenotypically identified as hatchery origin fish, 379 (85.9%) individuals were assigned via PBT to hatchery parents. All remaining successfully genotyped, phenotypically natural-origin (2,275), and phenotypically hatchery (62) adult steelhead that failed to assign to hatchery parents were assigned to a genetic stock via IA.

Life history diversity information (sex, length, and ocean age) for the 2,275 unclipped, phenotypically wild adult steelhead sampled in SY2018 and assigned a genetic stock is summarized in Table 2. Of the 2,275 steelhead assigned a genetic stock, 219 (10%) assigned to UPSALM, 156 (6.9%) to MFSALM, 42 (1.8%) to SFSALM, 42 (1.8%) to LOSALM, 157 (6.9%) to UPCLWR, 72 (3.2%) to SFCLWR, 132 (5.8%) to LOCLWR, 154 (6.8%) to IMNAHA, 856 (37.6%) to GRROND, and 445 (19.6%) to LSNAKE.

MY2018 Steelhead Juveniles

All 1,062 unclipped juvenile steelhead samples for MY2018 were queued for genotyping (Table 1). A total of 782 (73.6%) juveniles were genotyped successfully, with 3 (0.4%) assigning back to hatchery parents. The remaining 779 (99.6%) were assigned a genetic stock via IA.

Life history diversity information for the 779 emigrating steelhead smolts that were assigned to a genetic stock is summarized in Table 3. Of the 779 steelhead smolts assigned a genetic stock, 147 (18.9%) assigned to UPSALM, 37 (4.7%) to MFSALM, 31 (4.0%) to

SFSALM, 25 (3.2%) to LOSALM, 85 (10.9%) to UPCLWR, 71 (9.1%) to SFCLWR, 24 (3.1%) to LOCLWR, 64 (8.2%) to IMNAHA, 213 (27.3%) to GRROND, and 82 (10.5%) to LSNAKE.

SY2018 Chinook Salmon Adults

We inventoried 2,275 unclipped adult Chinook Salmon samples for SY2018, all of which were queued for genotyping (Table 1). A total of 2,262 (99.4%) adults were successfully genotyped, of which 746 (33.0%) were assigned back to hatchery parents and 1,516 (67.0%) were assigned back to a genetic stock via IA.

Life history diversity information for the 1,516 Chinook Salmon adults that were assigned to a genetic stock is summarized in Table 4. Of the 1,516 samples, 255 (16.8%) assigned to UPSALM, 224 (14.8%) to MFSALM, 37 (2.4%) to CHMBLN, 254 (16.8%) to SFSALM, 649 (42.8%) to HELLSC, 81 (0.1%) to TUCANO, and 96 (6.3%) to FALL.

MY2018 Chinook Salmon Juveniles

We inventoried 1,941 unclipped juvenile Chinook Salmon for MY2018. All inventoried juvenile Chinook Salmon (1,941) were queued for genotyping and 1,815 (93.5%) of those individuals were successfully genotyped (Table 1). Of the juveniles that were successfully genotyped, 217 (12.0%) were assigned back to hatchery parents and the remaining 1,598 (88.0%) were assigned a genetic stock via IA.

Life history diversity information for the 1,598 Chinook Salmon smolts assigned a genetic stock is summarized in Table 5. Of the 1,598 Chinook Salmon smolts assigned a genetic stock, 298 (18.6%) assigned to UPSALM, 313 (19.6%) to MFSALM, 16 (1.0%) to CHMBLN, 279 (17.5%) to SFSALM, 671 (42.0%) to HELLSC, 0 (0.0%) to TUCANO, and 21 (1.3%) to FALL.

DISCUSSION

Adult steelhead and spring/summer Chinook Salmon are intercepted at the LGR adult trapping facility at approximately a 10–20% trapping rate. Tissue samples are taken from trapped fish as part of this project to estimate abundance and life history diversity metrics at the genetic stock and/or MPG scale. This work allows estimation of abundance and productivity by the Idaho Department of Fish and Game for both steelhead and Chinook Salmon at the genetic stock scale across the entire Snake River basin. These metrics are critical components of VSP monitoring and are reported in the wild adult and juvenile steelhead and Chinook Salmon abundance and composition reports (e.g., Camacho et al. 2017, Camacho et al. 2018a, Camacho et al. 2018b).

Trapped adult fish are also PIT-tagged by the Integrated Status and Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00). Detection of these PIT-tagged fish throughout the Snake River basin are used in a Bayesian branching model to provide reliable and unbiased estimates of abundance at the tributary scale (QCI 2013; See et al. 2016). A multi-agency collaboration has been initiated to utilize information generated from these two innovative technologies (SNP genotyping and PIT tag detections). The goal of this collaboration is to synthesize available data regarding abundance, life-history diversity, and genetic structure and diversity of Snake River steelhead and spring/summer Chinook Salmon. This information is available from the PIT tagging and biological sampling of adults at LGR and the subsequent

detection of those adults throughout the Snake River basin. We discuss where the results of this collaboration are reported in Section 4.

The Columbia River Inter-Tribal Fish Commission conducts PBT and GSI of adult steelhead and Chinook Salmon at Bonneville Dam to estimate stock composition and abundance and to evaluate life history information for stocks migrating above Bonneville Dam. In the future, we intend to combine information from GSI at both LGR and Bonneville Dam to evaluate straying and survival between the two dams for both species. Further, we will evaluate adults captured in the Zone 6 fishery (between Bonneville Dam and McNary Dam) using a combination of PBT and GSI. The above information combined will also greatly assist run reconstruction efforts.

Parentage-based tagging is another important genetic technology implemented on all fish with intact adipose fins sampled at LGR prior to GSI. Using this technology, we can remove unmarked, untagged hatchery origin individuals from the natural-origin sample used to estimate abundance at the genetic stock, MPG, population, and/or subpopulation levels. Failing to remove these unidentified hatchery individuals will result in overestimating abundance of natural-origin stocks. This overestimate is likely the largest potential source of bias in abundance estimation within the Snake River basin. We illustrate the importance of this filtering step with returning steelhead. Hatchery steelhead can potentially be identified through the presence of dorsal and/or ventral fin erosion that is assumed absent from natural-origin individuals (Latreuille 2003) in addition to any physical marks (e.g., coded wire tags, adipose fin clip) applied at the hatchery. Despite this additional “mark,” using PBT we identified an additional 7.63% of the phenotypically natural-origin steelhead trapped at LGR as hatchery origin in SY2018 (Table 1). Because there is no additional phenotypic hatchery “mark” for Chinook Salmon, the rate of adipose-intact hatchery fish identified via PBT-only is higher than for steelhead. Thus, the application of PBT is instrumental in accurately estimating abundance of natural-origin stocks in the Snake River basin.

Continuation of GSI efforts at LGR will allow us to 1) monitor genetic structure and diversity throughout the basin over time, and 2) estimate productivity parameters and related life history diversity information for genetic stocks throughout the Snake River basin.

SECTION 4: SUMMARIZE LIFE HISTORY AND GENETIC DIVERSITY OF NATURAL-ORIGIN STEELHEAD AND SPRING/SUMMER CHINOOK SALMON THAT ARE DETECTED AT PIT TAG DETECTIONS SYSTEMS IN THE SNAKE RIVER BASIN SY2018

Powell et al. (2017, 2018) synthesized life history and genetic diversity of 15 of the 24 extant independent steelhead populations within the Snake River DPS, 17 of the 28 extant Snake River spring/summer Chinook Salmon populations, and 4 extirpated Snake River spring/summer Chinook Salmon populations for SY2010–2017. Hargrove and others are presenting this information for SY2018 in a companion report titled “Abundance, life history, and genetic diversity of natural-origin steelhead and spring/summer Chinook Salmon detected at instream PIT tag detection systems in the Snake River basin.”

ACKNOWLEDGEMENTS

The authors would like to thank the many individuals who contributed time and expertise towards implementing this project (alphabetical):

IDFG Eagle Fish Genetics Lab:

- John Powell (IDFG)
- Amanda Boone (PSMFC)
- Grant Bruner (IDFG)
- Dan Eardley (PSFMC)
- Kelly Heindel (PSMFC)
- Dylan Kovis (PSMFC)
- Laura Redfield (PSMFC)
- Lynn Schrader (PSMFC)
- Thea Wickersham (PSMFC)

Idaho Department of Fish and Game:

- Carlos Camacho
- Tim Copeland
- J. Lance Hebdon
- Bill Schrader

Columbia River Inter-Tribal Fish Commission:

- Nate Campbell
- Stephanie Harmon
- Nick Hoffman
- Vanessa Jacobson
- Amanda Matala
- Andrew Matala
- Lori Maxwell
- Megan Moore
- Jeff Stephenson

Quantitative Consultants, Inc. (QCI)

- Chris Beasley
- Mike Ackerman
- Kevin See

NOAA Northwest Fisheries Science Center:

- Darren Ogden

Oregon Department of Fish and Wildlife

Washington Department of Fish and Wildlife

US Fish and Wildlife Service

Nez Perce Tribe

Shoshone-Bannock Tribes

Bonneville Power Administration

- Dorothy Welch
- Barbara Shields

Primary funding for this project comes from the Bonneville Power Administration (Project #2010-026-00).

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TABLES

Table 1. Summary of SY2018 adult and MY2018 juvenile steelhead and Chinook Salmon samples from Lower Granite Dam (LGR). Summary includes the number of samples that arrived from LGR (inventoried) and the number inventoried that were queued for genotyping. Of queued samples, we show the number that genotyped successfully and the number that failed genotyping. For samples that genotyped successfully, we show the number of individuals with a parentage based tag (PBT; i.e., of hatchery origin) and the number that were assigned a genetic stock based on individual assignment (IA) using SNP baselines v3.1.

Sample Group	Total Samples Inventoried	Samples Queued for Genotyping	Failed Genotyping (NG)	Successfully Genotyped	PBT Assignments	GSI Assignments
<i>Steelhead</i>						
SY2018 Adults (Natural-origin Phenotype)	2,573	2,566	112 (4.4%)	2,454 (95.6%)	179 (7.3%)	2,275 (92.7%)
SY2018 Adults (Hatchery Phenotype)	452	452	11 (2.4%)	441 (97.6%)	379 (85.9%)	62 (14.1%)
MY2018 Juveniles	1,062	1,062	280 (26.4%)	782 (73.6%)	3 (0.4%)	779 (99.6%)
<i>Chinook</i>						
SY2018 Adults	2,275	2,275	13 (0.6%)	2,262 (99.4%)	746 (33.0%)	1,516 (67.0%)
MY2018 Juveniles	1,941	1,941	126 (6.5%)	1,815 (93.5%)	217 (12.0%)	1,598 (88.0%)
TOTAL:	8,303	8,296	542 (6.5%)	7,741 (93.3%)	1,524 (19.7%)	6,225 (80.3%)

Table 2. Summary of Lower Granite Dam (LGR) natural-origin adult steelhead samples from SY2018 assigned to a genetic stock using individual assignment based on the Snake River steelhead SNP baseline v3.1. Summaries of life history diversity information (sex, length, and ocean age) for each genetic stock are shown. The 'Other' saltwater age category includes fish that were not queued to be aged, fish that could not be aged, and fish with spawn checks.

SY	Genetic Stock	Total Assignments	% Stock Composition	Sex			Length						Ocean (Saltwater) Age									
				Frequency		Percentage	Mean Length (cm FL) by Ocean Age			Frequency		Percentage		Frequency			Percentage					
				F	M	U	F	M	1	2	3	A-Run	B-Run	A-Run	B-Run	1	2	3	Other	1	2	3
2018	UPSALM	219	10%	137	79	3	63%	37%	59.8	69.1	-	218	1	100%	0%	186	28	0	5	87%	13%	0%
	MFSALM	156	7%	103	48	5	68%	32%	62	70.3	79	150	2	99%	1%	123	22	2	9	84%	15%	1%
	SFSALM	42	2%	29	13	0	69%	31%	64.7	76	85	37	5	88%	12%	29	7	2	4	76%	18%	5%
	LOSALM	42	2%	31	9	2	78%	22%	60.4	69.1	-	42	0	100%	0%	32	10	0	0	76%	24%	0%
	UPCLWR	157	7%	95	59	3	62%	38%	66.1	77.1	88.5	133	23	85%	15%	114	32	4	7	76%	21%	3%
	SFCLWR	72	3%	44	26	2	63%	37%	64.3	76.6	81.5	58	14	81%	19%	36	25	6	5	55%	36%	9%
	LOCLWR	132	6%	84	44	4	66%	34%	60.5	71.3	77	130	2	98%	2%	95	30	1	6	75%	24%	1%
	IMNAHA	154	7%	101	52	1	66%	34%	58.9	-	-	151	1	99%	1%	128	21	0	5	86%	14%	0%
	GRROND	856	38%	556	287	13	66%	34%	59.9	69.5	70	850	5	99%	1%	649	173	1	33	79%	21%	0%
	LSNAKE	445	20%	288	154	3	65%	35%	59.8	68.9	77	440	3	99%	1%	343	88	1	13	79%	21%	0%
<i>SY2018 Total:</i>		<i>2,275</i>		<i>1,468</i>	<i>771</i>	<i>36</i>	<i>66%</i>	<i>34%</i>	<i>60.6</i>	<i>70.7</i>	<i>82.1</i>	<i>2,209</i>	<i>56</i>	<i>98%</i>	<i>2%</i>	<i>1,735</i>	<i>436</i>	<i>17</i>	<i>87</i>	<i>79%</i>	<i>20%</i>	<i>1%</i>

Table 3. Summary of Lower Granite Dam (LGR) juvenile steelhead samples from MY2018 assigned to a genetic stock using individual assignment based on the Snake River steelhead SNP baseline v3.1. Summaries of life history diversity information (sex, length, and freshwater age) for each genetic stock are shown. The 'Other' freshwater age category includes fish that were not queued to be aged or could not be aged.

Genetic Stock	Total Assignments	% Stock Composition	Sex			Length					Freshwater Age								
			Frequency			Percentage		Frequency					Percentage						
			F	M	U	F	M	Mean Length (mm FL)	1	2	3	4	5	Other	1	2	3	4	5
UPSALM	147	19%	77	54	16	59%	41%	184	14	100	29	3	0	1	10%	68%	20%	2%	0%
MFSALM	37	5%	20	15	2	57%	43%	178	0	17	17	3	0	0	0%	46%	46%	8%	0%
SFSALM	31	4%	23	8	0	74%	26%	179	1	5	24	0	0	1	3%	17%	80%	0%	0%
LOSALM	25	3%	16	8	1	67%	33%	177	1	17	6	1	0	0	4%	68%	24%	4%	0%
UPCLWR	85	11%	53	27	5	66%	34%	173	2	35	42	3	0	3	2%	43%	51%	4%	0%
SFCLWR	71	9%	33	28	10	54%	46%	171	7	48	16	0	0	0	10%	68%	23%	0%	0%
LOCLWR	24	3%	13	9	2	59%	41%	177	0	19	3	0	0	2	0%	86%	14%	0%	0%
IMNAHA	64	8%	39	19	6	67%	33%	177	2	46	13	0	0	3	3%	75%	21%	0%	0%
GRROND	213	27%	126	71	16	64%	36%	181	26	132	47	0	0	8	13%	64%	23%	0%	0%
LSNAKE	82	11%	45	30	7	61%	39%	186	10	51	16	1	0	4	13%	64%	21%	1%	0%
<i>Total:</i>	<i>779</i>		<i>445</i>	<i>269</i>	<i>65</i>	<i>62%</i>	<i>38%</i>	<i>179.5</i>	<i>63</i>	<i>470</i>	<i>213</i>	<i>11</i>	<i>0</i>	<i>22</i>	<i>8%</i>	<i>62%</i>	<i>28%</i>	<i>2%</i>	<i>0%</i>

Table 4. Summary of Lower Granite Dam (LGR) adult Chinook Salmon samples from SY2018 assigned to a genetic stock using individual assignment based on the Snake River Chinook Salmon SNP baseline v3.1. Summaries of life history diversity information (sex, length, and ocean age) for each genetic stock are shown. MJ = minijack.

Genetic Stock	Total Assignments	% Stock Composition	Sex						Ocean (Saltwater) Age						Length					
			Frequency			Percentage			Frequency			Percentage			Mean Length (cm FL) by Ocean Age					
			F	M	U	F	M	MJ	1	2	3	U	MJ	1	2	3	MJ	1	2	3
UPSALM	255	17%	106	149	0	42%	58%	0	22	223	7	3	0%	9%	88%	3%	-	54.7	73.2	83.8
MFSALM	224	15%	73	151	0	33%	67%	0	14	198	6	6	0%	6%	91%	3%	-	46.3	71.8	91.7
CHMBLN	37	2%	19	18	0	51%	49%	0	1	33	1	2	0%	3%	94%	3%	-	52.5	72.4	-
SFSALM	254	17%	115	139	0	45%	55%	0	4	238	6	6	0%	2%	96%	2%	-	55.5	73.5	84.8
HELLSC	649	43%	296	353	0	46%	54%	0	40	569	13	27	0%	6%	91%	2%	-	-	72.1	79.8
TUCANO	1	0%	1	0	0	100%	0%	0	0	1	0	0	0%	0%	100%	0%	-	-	-	-
FALL	96	6%	49	47	0	51%	49%	6	10	34	40	6	7%	11%	38%	44%	38.2	51.2	74.8	84.5
<i>Total:</i>	<i>1,516</i>		<i>659</i>	<i>857</i>	<i>0</i>	<i>43%</i>	<i>57%</i>	<i>6</i>	<i>91</i>	<i>1296</i>	<i>73</i>	<i>50</i>	<i>1%</i>	<i>6%</i>	<i>88%</i>	<i>5%</i>	<i>38.2</i>	<i>51.2</i>	<i>71.7</i>	<i>84.4</i>

Table 5. Summary of Lower Granite Dam (LGR) juvenile Chinook Salmon samples from MY2018 assigned to a genetic stock using individual assignment based on the Snake River Chinook Salmon SNP baseline v3.1. Summaries of life history diversity information (sex and length) by genetic stock are shown. Freshwater age is not summarized because scales were not collected from juvenile Chinook Salmon at Lower Granite Dam.

Genetic Stock	Total Assignments	% Stock Composition	Sex					Length
			Frequency			Percentage		Mean Length (mm FL)
			F	M	U	F	M	
UPSALM	298	19%	143	155	0	48%	52%	113
MFSALM	313	20%	169	144	0	54%	46%	110
CHMBLN	16	1%	10	6	0	62%	38%	107
SFSALM	279	17%	151	128	0	54%	46%	111
HELLSC	671	42%	387	282	2	58%	42%	116
TUCANO	0	0%	0	0	0	-	-	-
FALL	21	1%	10	11	0	48%	52%	113
<i>MY2018 Total:</i>	<i>1,598</i>		<i>870</i>	<i>726</i>	<i>2</i>	<i>55%</i>	<i>44%</i>	<i>113</i>

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