FISHERY RESEARCH

WILD ADULT STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, SPAWN YEAR 2017

ANNUAL PROGRESS REPORT

Photo: IDFG

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2017 Annual Report

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ABBREVIATIONS AND ACRONYMS

BPA	Bonneville Power Administration
BY	Brood Year
CI	Confidence Interval
CHMBLN	Chamberlain Creek Genetic Stock
CLRWTR	Clearwater River Genetic Stock
CWT	Coded Wire Tag
DPS	Distinct Population Segment
EFGL	Eagle Fish Genetics Lab
ESA	Endangered Species Act
ESU	Evolutionarily Significant Unit
FALL	Snake River Fall Chinook Salmon
FL	Fork Length
FPC	Fish Passage Center
GRROND	Grande Ronde River Genetic Stock
GSI	Genetic Stock Identification
GT-seq	Genotyping-in-Thousands by Sequencing
H	Adipose Fin Clipped Hatchery
HELLSC	Hells Canyon Genetic Stock
HNC	Adipose Fin Intact Hatchery
IA	Individual Assignment
ICBTRT	Interior Columbia Basin Technical Recovery Team
IDFG	Idaho Department of Fish and Game
IMNAHA	Imnaha River Genetic Stock
IOSC	Idaho Office of Species Conservation
IPC	Idaho Power Company
LGR	Lower Granite Dam
LOCLWR	Lower Clearwater River Genetic Stock
LOSALM	Lower Salmon River Genetic Stock
LSNAKE	Lower Snake River Genetic Stock
LSRCP	Lower Snake River Compensation Plan
MFSALM	Middle Fork Salmon River Genetic Stock
MM	Mixture Modelling
MPG	Major Population Group
MY	Smolt Migration Year
NMFS	National Marine Fisheries Service
NOAA	National Oceanic and Atmospheric Administration
NWFCS	Northwest Fisheries Science Center
PBT	Parentage Based Tag
PCR	Polymerase Chain Reaction
PIT	Passive Integrated Transponder
PSMFC	Pacific States Marine Fisheries Commission
QCI	Quantitative Consultants, Inc.

SALMON	Salmon River Major Population Group
SAR	Smolt-to-adult return rate
SCOBI	Salmonid Compositional Bootstrap Intervals
SFCLWR	South Fork Clearwater River Genetic Stock
SFSALM	South Fork Salmon River Genetic Stock
SNP	Single Nucleotide Polymorphism
SY	Spawn Year
TAC	Technical Advisory Committee, *U.S. v. Oregon*
TUCANO	Tucannon River Genetic Stock
UPCLWR	Upper Clearwater River Genetic Stock
UPSALM	Upper Salmon River Genetic Stock
USACE	U. S. Army Corps of Engineers
VSP	Viable Salmonid Population
W	Wild
WDFW	Washington Department of Fish and Wildlife

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ABSTRACT

This report summarizes the abundance and composition of wild steelhead and spring-summer Chinook Salmon returning to Lower Granite Dam in spawn year 2017. We used a combination of window counts and systematic biological samples from the fish trap to decompose each species by origin, body size, sex, age, and stock. These metrics were then used to calculate adult-to-adult productivity, expressed as recruits per spawner for each species, and smolt-to-adult return rate for spring-summer Chinook. The combined window count was 101,826 hatchery and wild steelhead. The estimated wild escapement was 15,576 fish and comprised 15% of the window count. Wild abundance decreased for all genetic stocks for the second consecutive year. The Grande Ronde River genetic stock was the most abundant followed by the Upper Clearwater River. Small steelhead (<78 cm, FL) dominated the total wild run; however, large fish (≥78 cm, FL) were as numerous as small fish in the Upper Clearwater River, South Fork Clearwater River, and South Fork Salmon River genetic stocks. Wild steelhead were female biased at 75%. Sex ratios for each genetic stock mirrored the aggregate wild run and ranged from 61% female for Lower Salmon River to 83% female for South Fork Salmon River. Sixteen different age classes were observed where age at spawn ranged from three to seven years, freshwater age ranged between one to four years, and saltwater age ranged from one to four years with additional fish returning as repeat spawners. Adult-to-adult productivity was completed for brood year 2009 at 0.96 returning recruits per spawner. The Upper Salmon River, South Fork Salmon River, Imnaha River, Grande Ronde River, and Lower Snake River genetic stocks were above replacement whereas the Middle Fork Salmon River, Lower Salmon River, and all Clearwater genetic stocks were below replacement. The combined window count was 48,192 hatchery and wild spring-summer Chinook Salmon. The estimated wild escapement was 5,793 fish and comprised 12% of the window count. Wild abundance decreased for most genetic stocks for the third consecutive year. The Hells Canyon genetic stock was the most abundant followed by the South Fork Salmon River. Large Chinook Salmon (≥57 cm, FL) dominated the total wild run; however, small fish (<57 cm, FL) were as numerous as large fish in the Tucannon River genetic stock. Wild Chinook Salmon were male biased at 57%. However, some genetic stocks were either female biased or not biased to either sex. Thirteen different age classes were observed where age at spawn ranged from two to six years, freshwater age ranged between zero to two years, and saltwater age ranged from zero (mini-jacks) to four years. Adult-to-adult productivity for brood year 2011 was completed at 1.07 returning recruits per spawner. The Upper Salmon River, Middle Fork Salmon River, Hells Canyon, and Tucannon River genetic stocks were above replacement whereas the South Fork Salmon River and Chamberlain Creek were below replacement. The smolt-to-adult return rate for the aggregate wild run was 2.82% for smolts crossing Lower Granite Dam in migration year 2013.

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INTRODUCTION

Populations of steelhead trout *Oncorhynchus mykiss* and Chinook Salmon *O. tshawytscha* in the Snake River basin declined substantially following the construction of hydroelectric dams in the Snake and Columbia rivers. Raymond (1988) documented a decrease in survival of emigrating steelhead trout and Chinook Salmon from the Snake River following the construction of dams on the lower Snake River during the late 1960s and early 1970s. Abundance rebounded slightly in the early 1980s, but escapements over Lower Granite Dam (LGR) into the Snake River basin declined again (Busby et al. 1996). In recent years, abundances in the Snake River basin have slightly increased. However, the increase has been dominated by hatchery fish, while the returns of naturally produced steelhead trout and Chinook Salmon remain critically low. As a result, Snake River steelhead trout (hereafter steelhead) were classified as threatened under the Endangered Species Act (ESA) in 1997. Within the Snake River steelhead distinct population segment (DPS), there are six major population groups (MPGs): Lower Snake River, Grande Ronde River, Imnaha River, Clearwater River, Salmon River, and Hells Canyon Tributaries (Table 1; Figure 1; ICBTRT 2003, 2005; NMFS 2016). The Hells Canyon MPG is considered to have been functionally extirpated. A total of 24 extant populations have been identified in the DPS. Snake River spring-summer Chinook Salmon (hereafter Chinook Salmon) were classified as threatened in 1992 under the ESA. Within the Snake River spring-summer Chinook Salmon evolutionarily significant unit (ESU), there are seven MPGs: Lower Snake River, Grande Ronde/Imnaha Rivers, South Fork Salmon River, Middle Fork Salmon River, Upper Salmon River, Dry Clearwater River, and Wet Clearwater River (Table 1; Figure 2). The Dry Clearwater River and Wet Clearwater River MPGs are considered to have been extirpated but have been refounded with stocks from other Snake River MPGs. A total of 28 extant populations have been identified in the ESU.

Anadromous fish management programs in the Snake River basin include large-scale hatchery programs – intended to mitigate for the impacts of hydroelectric dam construction and operation in the basin – and recovery planning and implementation efforts aimed at recovering ESA-listed wild steelhead and salmon stocks. The Idaho Department of Fish and Game's anadromous fish program long-range goals, consistent with basinwide mitigation and recovery programs, are to preserve Idaho's salmon and steelhead runs and recover them to provide benefit to all users (IDFG 2013). Management to achieve these goals requires an understanding of how salmonid populations function (McElhany et al. 2000) as well as regular status assessments. The key metrics to assessing viability of salmonid populations are abundance, productivity, spatial structure, and diversity (McElhany et al. 2000).

The aggregate escapement of Snake River steelhead and Chinook Salmon is measured at LGR, with the exception of the Tucannon River (Washington) population downstream of LGR. Some of the wild fish are headed to Washington or Oregon tributaries to spawn, but the majority are destined for Idaho. Age, sex, and stock composition data are important for monitoring recovery of wild fish for both species. Age data collected at LGR are used to assign returning adults to specific brood years, for cohort analysis, and to estimate productivity and survival rates (Camacho et al. 2017; Camacho et al. 2018). In addition, escapement estimates by cohort are used to forecast run sizes in subsequent years, and these forecasts are the basis for preliminary fisheries management plans in the Columbia River basin.

At Columbia River dams, U.S. Army Corps of Engineers (USACE) counts fish at viewing windows and designates jack Chinook Salmon as fish between 30 and 56 cm (12 and 22 inches) in length; salmonids under 30 cm (12 inches) in length are not identified to species. Mini-jacks are precocious salmon generally under 30 cm in length and thus are not counted (Steve Richards, WDFW, personal communication). Throughout this report, unless otherwise stated, adult Chinook Salmon refers to reproductively mature fish returning to spawn, including jacks but excluding mini-jacks less than 30 cm. Additionally, the USACE defines the Chinook Salmon run type by calendar date. Any Chinook Salmon counted at the window from March 1 to June 17 is considered spring run, June 18 to August 17 is considered summer run, and August 18 to December 31 is considered fall run. Fall-run Chinook Salmon passing LGR during the March 1 to August 17 time period are presented in this report for accounting purposes only and do not represent the entirety of the fall-run Chinook Salmon. For steelhead, the run year at LGR is defined to be from July 1 of the previous year to June 30. The steelhead run year dates were chosen to be consistent with the upriver steelhead run year at Bonneville Dam as defined in the *U.S. v. Oregon* management agreement. Most steelhead pass LGR in the fall but are assigned to their spawn year the following spring.

This goal of this report is to summarize the abundance and composition of wild steelhead and spring-summer Chinook Salmon returning to LGR during spawn year (SY) 2017 as defined by the USACE calendar date designations. We also update the adult-to-adult productivity series for both species last published by Camacho et al. (2017) and the smolt-to-adult return (SAR) rate series for Chinook Salmon last published by Stiefel et al. (2015). The objectives of this report are to:

1. Describe LGR adult trap operations and data collection during 2016-2017, which is the timeframe encompassing all steelhead and Chinook passing LGR for SY2017.

2. Estimate wild steelhead and Chinook Salmon escapement and age, sex, and size composition in aggregate and by genetic stock.

3. Evaluate wild steelhead and Chinook Salmon status using adult-to-adult productivity and replacement rates in aggregate and by genetic stock.

4. Estimate survival using smolt-to-adult return (SAR) rate for the aggregate return of wild Chinook Salmon.

METHODS

Adult Trap Operations at Lower Granite Dam

Systematic samples of steelhead and Chinook Salmon returning to LGR were collected during daily operation of the adult fish trap by National Marine Fisheries Service (NMFS; Ogden 2017, 2018). The trap is located in the LGR fish ladder upstream from the fish counting window. The trap captures a systematic random sample of fish by operating a trap gate according to a predetermined sample rate. The sample rate determines how long the trap gate remains open four times per hour; the trap is operational 24 hours per day. The sample rate is determined based on sample size goals of the various projects using the adult trapping data combined with forecasted abundance of the targeted species, run, and rear type. Ideally, the sample rate is apportioned equally across the entire sampling season. However, the trap does not operate during weekends from March 1 to August 17, and in-season adjustments to the sample rate are sometimes needed to accommodate limitations at the trapping facility, changes to the forecast, or sample size goal modifications. Additionally, high (≥21°C or ≥70°F) and low (below freezing) water temperatures require the trapping facility to temporarily modify or cease operations. During SY2017, high water temperatures did not limit trapping operations and the trap was closed

November 21, 2017 through March 13, 2018 for the winter (Appendix A-1). During SY2017, 94.0% of the steelhead run passed the window while the trap was open. The majority of the steelhead run crossed LGR in the fall season, but a second small pulse occurred in late March and April (Appendix A-2). Weekend trap closures resulted in the trap operating when 71.8% of the Chinook Salmon run crossed LGR (Appendix A-3). Additional details on the trap can be found in Harmon (2003), Steinhorst et al. (2010), and USACE (2016, 2017).

Standard methods were used by NMFS and IDFG staff to process and biologically sample fish at the trap. All fish captured were anesthetized; examined for external marks, tags, and injuries; scanned for an internal coded wire tag (CWT) or passive integrated transponder (PIT) tag; and measured for fork length (FL, nearest cm).

All fish were classified by origin (hatchery or wild) based on a hierarchical key of external and internal marks identified at LGR and after post hoc genetic analysis conducted in the laboratory (Appendix A-4). At the LGR trap, the presence or absence of an adipose fin was examined first. All fish considered to have a clipped adipose fin (absent or partial clip evident by a healed scar) were classified as ad-clipped hatchery fish. Although most hatchery steelhead and Chinook Salmon have a clipped adipose fin (hereafter ad-clipped), some are released with an unclipped adipose fin (hereafter ad-intact) for supplementation or broodstock management purposes. All ad-intact fish were subsequently scanned for CWT and examined for ventral fin clips. Additionally, ad-intact steelhead were inspected for dorsal fin erosion, which is assumed to occur only in hatchery fish (Latremouille 2003). Any ad-intact fish with the presence of a CWT, ventral fin clip, and/or dorsal fin erosion (steelhead only) were classified as ad-intact hatchery fish. The trap crew sampled fin tissue from fish determined to be phenotypically wild; genotyping for PBT analysis was conducted post hoc to further classify ad-intact hatchery fish. In sum, final classification of hatchery fish was made using any of five marks or tags: adipose fin clip (complete removal or partial clip), CWT, ventral fin clip, dorsal or ventral fin erosion (steelhead only), or PBT. Information from fish previously PIT tagged was not used to determine origin.

For all phenotypically wild fish, scale samples were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG Nampa Research Anadromous Ageing Laboratory. For all ad-intact fish, tissue samples were taken from a small clip of the anal fin. Tissues were stored on a dry Whatman paper medium (LaHood et al. 2008) for transport to the IDFG Eagle Genetics Laboratory. All ad-intact fish captured were also PIT tagged if not previously tagged for abundance estimation at instream PIT detectors upstream of LGR (Beasley and White 2010; QCI 2013; See 2016; Orme and Kinzer 2018).

After processing, all fish were returned to the adult fish ladder to resume their upstream migration.

Trap Data Management

All data were entered into a NMFS cloud-based database via touch-screen computer systems located in the trap work area. This system allowed interested parties to access the data they need at the end of each day and eliminated transcription errors from paper data sheets to electronic form. The IDFG LGR SQL server database automatically queries the NMFS database daily to populate tables used by IDFG for reporting purposes.

Valid Sample Selection

Not all trapped fish were deemed valid by IDFG for sample selection or analysis. Trapped fish that were missing data for any of the following five fields were considered invalid: date of collection, species, FL, origin (hatchery or wild), or adipose fin status (ad-clipped or ad-intact). Trapped fish less than 30 cm (FL) were considered invalid as they are not identified to species at the USACE fish-counting window. Further, the trap was not designed to efficiently trap these smaller fish (Darren Ogden, NMFS, personal communication); for Chinook Salmon, this includes all mini-jacks less than 30 cm. Finally, any sort-by-code PIT-tagged fish trapped outside the normal trap sampling timeframe were considered invalid. A computer program written by Tiffani Marsh (NMFS) was used to make this determination. Sort-by-code, or separation-by-code, is the process whereby PIT-tagged fish ascending the LGR fish ladder are diverted into the trap box using predetermined PIT-tag codes programmed into the trap gate computer.

Our goal was to age and genotype approximately 2,000 wild steelhead and 2,000 wild Chinook Salmon. In collaboration with our work, approximately 4,000 wild steelhead and 4,000 wild Chinook Salmon were PIT tagged and scale and genetic tissue samples were collected to estimate abundance at instream PIT detectors. We emphasize that both goals were complimentary and not mutually exclusive. To simplify collaborative logistics and increase accuracy and precision of abundance estimates using GSI and PBT, every ad-intact steelhead and Chinook Salmon trapped at LGR was genotyped. All valid trap wild fish samples were systematically subsampled if more than approximately 2,000 samples were available for each species. The result was a pool of samples collected systematically across the spawning run of each species and generally in constant proportion to their abundance. Hence, for either species, the sample pool can be considered a daily systematic sample (Steinhorst et al. 2017).

Scale Processing, Analysis, and Age Validation

Technicians processed scale samples in the IDFG Nampa Research Anadromous Ageing Laboratory according to protocols detailed in Wright et al. (2015). Ages are formatted using the European system where freshwater (FW) age is separated from saltwater (SW) age by a decimal. For steelhead repeat spawners, an ‘R’ is added to the saltwater age to designate the winter spent in freshwater while on the first spawning run. Age classes are defined as the unique combinations of SW, FW, and repeat spawning ages. Brood year (BY) is the migration year minus the total age at spawning (sum of freshwater and saltwater ages, plus 1). Fish lacking either a freshwater or saltwater age were not used for analysis.

We validated wild fish saltwater-age assignments with known saltwater-ages from hatchery and wild fish PIT-tagged as juveniles and hatchery fish with CWT. Accuracy of age assignments was estimated by percent agreement between saltwater-age and known emigration date determined from juvenile PIT-tag detection in the hydrosystem. Known saltwater-age fish were used to compute accuracy rates for Chinook Salmon and steelhead ages.

Genetics Tissue Processing and Analysis

Detailed methods for extraction of genomic DNA from tissue samples, DNA amplification, and SNP genotyping are described in Vu et al. (2015) and Campbell et al. 2015. Briefly, samples were processed using “Genotyping-in-Thousands by sequencing” (GT-seq) technique at either the IDFG genetics laboratory in Eagle, Idaho (EFGL), or the Columbia River Inter-Tribal Fish Commission’s genetics laboratory in Hagerman, Idaho. Steelhead were examined at a 268 SNP marker panel and Chinook Salmon were examined at a 298 SNP marker panel. Each panel contains SNPs for parental based tagging (PBT) and genetic stock identification (GSI), and sex-determination analysis.

Parental based tag analysis was conducted on all ad-intact adults to identify hatchery fish that were phenotypically wild. Since 2008, fin tissue has been sampled from nearly all adult steelhead and spring-summer Chinook Salmon broodstock spawned at Snake River hatcheries in Idaho, Oregon, and Washington (Steele et al. 2016). The PBT project essentially “tags” all hatchery steelhead and spring-summer Chinook Salmon smolts released in the Snake River basin. This allows researchers to identify the exact parents of an individual, and thus its origin and total age (Steele et al. 2013). PBT is a critical tool to differentiate hatchery fish when all other physical tags (e.g., CWT and fin clips) are not present.

Genetic stock identification is another genetic technique that estimates the reporting group (referred to here as genetic stocks) for wild fish. Genotypes were analyzed against genetic baseline populations to assign each individual to the genetic stock in which the probability of its genotype occurring is the greatest. Vu et al. (2015) provides a detailed description of the Snake River genetic baselines used for both steelhead and Chinook Salmon GSI analyses (also see Figures 1 and 2). Genetic stocks are assemblages of baseline populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and management units (Ackerman et al. 2012). Individuals were assigned to genetic stocks using the maximum likelihood estimation method of Smouse et al. (1990) as implemented in the program gsi_sim (Anderson et al. 2008; Anderson 2010). The probability of membership to each population is summed within reporting units (allocate-sum procedure; Wood et al. 1987), and an individual’s genetic stock is assigned as the reporting unit with the maximum probability of membership.

Ten wild steelhead genetic stocks were used. The genetic stocks include: 1) UPSALM: upper Salmon River (including North Fork Salmon River and upstream); 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: Little Salmon River and tributaries of the 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: tributaries of the lower Snake River both above (e.g., Alpowa and Asotin creeks) and below (primarily Tucannon River) LGR. Some Tucannon River steelhead ascend LGR dam and either stay upriver to spawn or fall back and spawn downriver. Results from some genetic stocks are aggregated to report by Snake River steelhead MPGs (Table 1).

Seven wild Chinook Salmon genetic stocks were used. The genetic stocks include: 1) UPSALM: upper Salmon River (including North Fork Salmon River and upstream); 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: Hells Canyon stock, an aggregate genetic stock that includes the Clearwater, Little Salmon, lower Salmon, Grande Ronde, Imnaha, and lower Snake rivers; 6) TUCANO: Tucannon River; and 7) FALL: Snake River fall Chinook Salmon. Chinook Salmon populations in TUCANO can be distinguished from HELLSC in GSI analyses because they exhibit low levels of introgression with fall Chinook Salmon (Narum et al. 2010). The TUCANO genetic stock was included in the baseline to represent fish that originated below LGR, but ascend the dam and either stay upriver to spawn or fall back and spawn downriver. Except for fall Chinook Salmon, these genetic stocks largely correspond to Snake River spring-summer Chinook Salmon MPGs (Table 1). The MFSALM and CHMBLN genetic stock results were aggregated to report the Middle Fork Salmon River MPG. Three collections of Snake River fall Chinook Salmon (Clearwater River, Nez Perce Tribal Hatchery, and Lyons Ferry Hatchery) were included in the baseline to distinguish fall Chinook Salmon trapped prior to August 18 from spring-summer Chinook Salmon using genetic data (Ackerman et al. 2014).

The resolution of the Snake River genetic baselines was evaluated in Vu et al. (2015). The GSI project continues to update the genetic baselines periodically in an effort to improve resolution. Further, the GSI project continues to develop methods and evaluate available tools to assess and improve the accuracy and precision of genetic stock proportion and abundance estimates. These efforts are reported separately in the annual progress reports for the GSI project.

Sex was not and generally cannot be reliably determined by personnel at the LGR trap, as fish typically do not exhibit sexually dimorphic characteristics when crossing LGR. A sex-determination assays developed by Campbell et al. (2012) was used and included in the genotyping process. The accuracy of the sex-determination assays was evaluated in Steele et al. (2016). Further details can be found in Campbell et al. (2012).

Wild Escapement by Origin, Genetic Stock, Size, Sex, and Age

The USACE daily window counts, which occur in the fish ladder downstream of the trap, were assumed to be the daily aggregate escapement to LGR for each species. Count data were downloaded from the FPC website: http://www.fpc.org/environment/home.asp. Additional daily window count operation information was obtained from USACE annual fish passage reports (USACE 2016, 2017). For Chinook Salmon, the adult count was combined with the jack count to derive the total count on a daily basis.

Window counts were decomposed into escapement estimates for reporting groups of interest with 90% confidence intervals (CI). The basic methods were developed by Steinhorst et al. (2017) and implemented in the SCOBI (Salmonid Composition Bootstrap Intervals) function in the SCOBI R package (https://github.com/mackerman44/SCOBI; Ackerman et al. *In Preparation*; R Development Team 2008; Steinhorst et al. 2017). SCOBI combined the window count with the adult trap sample data on a temporally stratified basis to account for changes in the trapping rate and run characteristics through time. The spawn year for each species was divided into “statistical week” strata with each stratum defined as a week (starts on Monday and ends on Sunday) or a series of adjacent weeks with sufficient trap numbers (n ≥100) to adequately estimate all proportions. Escapement by stratum was estimated by multiplying the window counts by the trap proportions. The total escapement to LGR was the sum of escapement estimates from each stratum, which equals the total window count for the spawn year. In essence, the stratum proportions were weighted by stratum run size of all fish from each species as counted at the window. We assumed 1) window counts represent true abundance, and 2) proportions are constant within each stratum.

The analysis decomposes total escapement (i.e. window count) into rearing type, primary, and secondary categories. These are hierarchical and each category was nested within the previous category (Figure 3). First, the total escapement is decomposed into rearing type. Fish from each rearing type are then divided into primary categories. Wild fish were further decomposed into secondary categories (size, sex, brood year, saltwater age, and age class).

Abundance estimates by rear type were calculated by multiplying the trapping proportions of each rear type for each stratum by the window count for that stratum and summing over the season. A parametric bootstrap is used to find 90% CIs on the estimated abundance of wild (W), ad-clipped hatchery (H), and ad-intact hatchery (HNC). The parametric bootstrap uses the number of adults trapped in each stratum along with the three estimated multinomial proportions for W, H, and HNC in that stratum to produce bootstrap pseudo values for numbers of fish by rearing category. These are converted to pseudo proportions by stratum and multiplied by weekly window counts to produce bootstrap estimates of totals by W, H, and HNC. The three bootstrap series of estimates are ordered and the fifth and ninety-fifth ordered values give the three one-at-a-time confidence intervals. All CIs are generated for the spawn year total rather than for individual strata.

The trap data are then categorized to one of the rearing types. Proportions by stratum are computed for the primary classification variable (size for H and HNC and genetic stock for W). Estimates of numbers of fish in each primary category are found by multiplying the stratum proportions by the stratum numbers of fish of that rearing type and summing over strata. Pseudovalues for numbers of fish of the given rearing type for each primary category for each stratum are produced by a second parametric bootstrap, which leads to confidence intervals for estimates of fish in the primary categories.

Finally, for each stratum a two-way table of proportions was calculated for combinations of the primary and secondary variable categories. For each stratum these proportions are applied to estimated numbers of fish of the given rearing type and primary category to get estimates of numbers of fish for each level of the secondary category. That is, if one fixes a primary category, then the estimated number of fish of that primary category is decomposed into estimates for each of the secondary categories. Summing over primary categories, the resulting estimate of fish in each secondary category is constrained to sum to the total fish found in the primary categories. Each row of a table of proportions for fixed stratum and primary category was used to produce multinomial parametric bootstrap pseudo values for numbers of fish in each secondary category leading to confidence intervals for the corresponding estimates.

Point estimates from all nested categories must sum to equal the parent category. Due to rounding error in the final output of data, additional steps were developed to adjust point estimates. First, all rear types must sum to the window count obtained from the FPC website (http://www.fpc.org/environment/home.asp). If rear types do not sum to window count, fish were added or subtracted from the rear type with the largest number of fish. Second, genetic stock estimates must sum to the wild fish estimate. If not, fish were added or subtracted from the genetic stock with the largest number of fish. The adjusted estimates for the genetic stocks were used to further adjust the MPG and composition estimates. Estimates for MPGs were adjusted to match the summation of corresponding genetic stocks (e.g., all CLWR genetic stocks combine to CLRWTR, all SALM genetic stocks combine to SALMON). For composition estimates (size, sex, age class), fish were added or subtracted from the group with the largest number of fish (e.g., male and female CHMBLN need to add up to the total genetic stock estimate for CHMBLN). For total age and saltwater age composition estimates within each genetic stock, estimates must sum to the corresponding aggregation of age class composition estimates within each genetic stock. Fish were added or subtracted from each total age and saltwater age group to match the corresponding aggregation of age classes, (e.g., saltwater age-2 CHMBLN must sum to the aggregated total estimate from age classes F1S2 and F2S2 for CHMBLN). After adjusting composition groups within each genetic stock, individual composition group estimates over all genetic stocks were summed to obtain aggregate estimates (e.g., male aggregate estimate is the sum of all male estimates from each genetic stock). All aggregate composition estimates must add up to the rear type estimate. In general, adjustments involved adding or subtracting less than five fish.

Reporting groups for each of the primary and secondary categories were defined based on criteria important for fishery management and monitoring and evaluation. Genetic stock encompassed the species specific reporting groups (ten for steelhead and seven for Chinook Salmon) described in the Genetics Tissue Processing and Analysis section above. Sex included a male and a female reporting group. Age class, brood year, and saltwater age reporting groups vary in number based on the freshwater and saltwater age structure observed from scale samples of trapped fish during the spawn year. Lastly, size included two length reporting groups (large, small); however, length cutoffs differ for each species. Large steelhead are greater than or equal to 78 cm FL, whereas small steelhead are less than 78 cm FL and correspond to lengths describing A-index and B-index steelhead. For Chinook Salmon, large fish are greater than or equal to 57 cm FL (24 inches total length) corresponding to adult sized fish, whereas small fish are less than 57 cm FL (24 inches total length) corresponding to jack sized fish. Fish length was recorded as a FL at the LGR adult trap. A linear regression equation for saltwater-caught Chinook Salmon in Southeast Alaska was used to convert the 24 inch (61 cm) total length cutoff to a FL equivalent of 57 cm (Conrad and Gutmann 1996).

Chinook Salmon Smolt-to-Adult Return Rate

To estimate the aggregate smolt-to-adult return (SAR) rate for wild Chinook Salmon, the age composition of adults at LGR was combined with estimates of emigrating wild Chinook Salmon smolts at LGR. Adult age composition from SY2017 was incorporated into the age proportion series last published in Camacho et al. (2017). Smolt production estimates were acquired from Camacho et al. (2018).

To calculate a SAR for a particular smolt migration year (MY), the sum of ocean returns from that cohort was divided by the estimate of wild smolts arriving at LGR:

$$SAR_k = \frac{\sum_{l-1}^{4} r_{k+l}}{S_k},$$

where SAR_k is the smolt-to-adult return rate of smolt migration year k; r_{k+l} is the return from that cohort in year $k+l$; l is saltwater age; and S_k is the estimate of smolts migrating in year k. The maximum value of l is four because that is the maximum saltwater age observed for Chinook Salmon at LGR (Copeland et al. 2004). Formulas from Fleiss (1981) were used to estimate the 95% confidence limits on SAR values. The lower limit is given by

$$\frac{\left(2np + t_{\propto/2}^2 - 1\right) - t_{\propto/2}\sqrt{t_{\propto/2}^2 - (2 + 1/n) + 4p(nq + 1)}}{2\left(n + t_{\propto/2}^2\right)},$$

and the upper limit by

$$\frac{\left(2np + t_{\propto/2}^2 + 1\right) + t_{\propto/2}\sqrt{t_{\propto/2}^2 + (2 + 1/n) + 4p(nq + 1)}}{2\left(n + t_{\propto/2}^2\right)},$$

where n is the number of smolts, p is the SAR value as a proportion, q is 1-SAR, and $t_{\propto/2}$ is 1.96.

RESULTS

Steelhead Escapement

The USACE window count of steelhead for SY2017 was 101,826 fish (Appendix A-5). The LGR trap captured 3,558 wild fish, of which 3,513 were considered valid samples. The estimated escapement of wild fish was 15,576 (15,171-15,991 90% CI) and comprised 15% of the window count (Table 2). The remaining 86,250 hatchery fish were 78,549 (78,064-79,030 90% CI) ad-clipped and 7,701 (7,382-8,017 90% CI) ad-intact. External marks, internal tags, and genetics were used to determine that 9% of the total hatchery fish and 8% of the run were ad-intact hatchery fish. For all ad-intact steelhead, 33% were hatchery fish.

Steelhead by Genetic Stock, Size, Sex, and Age

Abundance of wild steelhead by genetic stock varied greatly with the GRROND having the highest abundance and the LOSALM having the least (Appendix C-1). Escapement estimates for each genetic stock were 1,174 (1,047-1,296 90% CI) for the UPSALM; 1,021 (905-1,139 90% CI) for the MFSALM; 627 (536-720 90% CI) for the SFSALM; 157 (113-206 90% CI) for the LOSALM; 2,149 (1,980-2,322 90% CI) for the UPCLWR; 1,055 (935-1,174 90% CI) for the SFCLWR; 1,084 (962-1,202 90% CI) for the LOCLWR; 1,004 (890-1,121 90% CI) for the IMNAHA; 5,165 (4,903-5,421 90% CI) for the GGROND; and 2,140 (1,979-2,317 90% CI) for the LSNAKE.

Small fish (<78 cm FL) dominated wild and ad-clipped hatchery steelhead returns, whereas large fish (≥78 cm FL) dominated ad-intact hatchery returns (Table 2; Appendix C-2). Small ad-clipped hatchery steelhead were estimated at 52,825 (52,247-53,408 90% CI); small ad-intact hatchery at 3,556 (3,334-3,779 90% CI); and small wild at 12,575 (12,194-12,903 90% CI). Large ad-clipped hatchery steelhead were estimated at 25,724 (90% CI 25,226-26,225); large ad-intact hatchery at 4,145 (90% CI 3,909-4,384); and large wild at 3,001 (90% CI 2,841-3,145). Small fish accounted for the majority of steelhead returning to the UPSALM, MFSALM, LOCLWR, GRROND, LOSALM, IMNAHA, and LSNAKE wild genetic stocks, whereas large steelhead were as numerous as small steelhead in the SFCLWR and SFSALM.

The steelhead sex ratio was female-biased and females accounted for 75% of the wild return (Appendix C-2). Females were estimated at 11,694 (11,327-11,991 90% CI) and males at 3,882 (3,727-4,016 90% CI). Sex ratios for genetic stocks ranged from 61% females for LOSALM to 83% females for SFSALM. Sex ratios were statistically significant for all genetic stocks, except the LOSALM.

Sixteen different age classes were observed from 1,327 wild fish assigned an age (Appendix C-3). Age at spawning ranged from three to seven years with freshwater age ranging from one to four years and saltwater age ranging from one to three years; additional fish returned as repeat spawners. Age estimates were 103 (90% CI 86-123) age-3 fish from BY 2014; 1,497 (90% CI 1,409-1,575) age-4 fish from BY2013; 8,687 (90% CI 8,392-8,919) age-5 fish from BY2012; 4,890 (90% CI 4,695-5,066) age-6 fish from BY2011; and 399 (90% CI 358-440) age-7 fish from BY2010. Saltwater age estimates were 1,706 (90% CI 1,613-1,794) one-saltwater fish from MY2016; 13,499 (90% CI 13,102-13,839) two-saltwater fish from MY2015; 121 (90% CI 97-146) three-saltwater fish from MY2014; and 250 (90% CI 221-282) repeat spawning steelhead not assigned to a specific migratory year. The majority of the wild return or 60% emigrated to the ocean as freshwater age-2. For all genetic stocks, age-5 was the dominant age class, except for UPCLWR, MFSALM, and SFSALM where age-6 was the dominant age class. Furthermore, two-saltwater fish made up the vast majority of returning steelhead to all genetic stocks.

Repeat spawning fish made up <2% of all steelhead crossing LGR. Repeat spawners made up <3% of the fish with the UPSALM, SFSALM, UPCLWR, LOCLWR, IMNAHA, GRROND, and LSNAKE. Consecutive and skip year repeat spawners were observed. However, skip year repeat spawners were only observed in the GRROND.

Readers accurately determined the saltwater-age of 97.2% of the scale samples (n = 141) from known saltwater-age steelhead collected during SY2017 (Appendix B-1). The known saltwater-age sample was 5% one-saltwater, 94% two-saltwater, and 1% three-saltwater fish. There were no four-saltwater fish or repeat spawners in the known saltwater-age sample.

Steelhead Adult-to-Adult Productivity

Wild steelhead returning to LGR in SY2017 completed the BY2009 cohort necessary for an adult-to-adult productivity estimate. Brood year 2009 returned 22,964 adults from 23,875 parents resulting in an adult-to-adult productivity estimate of 0.96 recruits per spawner, which is below the 1.0 recruits per spawner necessary for replacement (Figure 4). For genetic stocks, adult-to-adult productivity estimates that were above replacement included LSNAKE at 1.26, UPSALM at 1.21, SFSALM at 1.20, GRROND at 1.04, and IMNAHA at 1.01; estimates that were below replacement included LOSALM at 0.98, LOCLWR at 0.94, MFSALM at 0.90, UPCLWR at 0.58, and SFCLWR at 0.55.

Chinook Salmon Escapement

The USACE window count of Chinook Salmon for SY2017 was 48,192 fish (Appendix A-6). The LGR trap captured 1,225 wild fish, all of which were considered valid samples. The estimated escapement of wild fish was 5,793 (5,537-6,043 90% CI) and comprised 12% of the window count (Table 3). The remaining 42,399 hatchery fish were 38,438 (38,129-38,749 90% CI) ad-clipped and 3,961 (3,746-4,173 90% CI) ad-intact. External marks, internal tags, and genetics were used to determine that 9% of the total hatchery fish and 8% of the run were ad-intact hatchery fish. For all ad-intact Chinook Salmon, 41% were hatchery fish.

Chinook Salmon by Genetic Stock, Size, Sex, and Age

Abundance of wild Chinook Salmon by genetic stock varied greatly with the HELLSC having the highest abundance and the TUCANO having the least (Appendix D-1). Escapement estimates for each genetic stock were 907 (801-1,019 90% CI) for the UPSALM; 137 (96-183 90% CI) for the CHMBLN, 789 (687-892 90% CI) for the MFSALM, 976 (864-1,088 90% CI) for the SFSALM; 2,259 (2,092-2,433 90% CI) for the HELLSC; 41 (21-66 90% CI) for the TUCANO; and 684 (599-774 90% CI) for the FALL.

Large fish (≥57 cm fork length) dominated wild, ad-clipped hatchery, and ad-intact hatchery Chinook Salmon returns (Appendix D-2). Large ad-clipped hatchery Chinook Salmon were estimated at 29,325 (90% CI 28,944-29,700); large ad-intact hatchery at 3,014 (90% CI 2,827-3,213); and large wild at 4,357 (90% CI 4,145-4,549). Small ad-clipped hatchery Chinook Salmon were estimated at 9,113 (90% CI 8,795-9,428); small ad-intact hatchery at 947 (90% CI 838-1,063); and small wild at 1,436 (90% CI 1,343-1,523). Large fish accounted for the majority of Chinook Salmon returning to all wild genetic stocks except the TUCANO.

The Chinook Salmon sex ratio was male-biased and males accounted for 57% of the wild return (Appendix D-2). Females were estimated at 2,490 (2,352-2,611 90% CI) and males at

3,303 (3,125-3,460 90% CI). Sex ratios for the MFSALM, SFSALM, and HELLSC genetic stocks resembled the overall wild Chinook Salmon return, ranging from 67% males for MFSALM to 59% males for HELLSC, whereas the UPSALM, CHMBLN, TUCANO, and FALL genetics stocks were not statistically biased to either sex.

Thirteen different age classes were observed from 1,120 wild fish assigned an age (Appendix D-3). Age at spawning ranged from two to six years with freshwater age ranging from zero to two years and saltwater age ranging from zero (mini-jacks) to four years. Age estimates were 95 (90% CI 79-113) age-2 fish from BY2015; 1,674 (90% CI 1,569-1,774) age-3 fish from BY2014; 2,716 (90% CI 2,564-2,845) age-4 fish from BY2013; 1,242 (90% CI 1,156-1,318) age-5 fish from BY2012; and 66 (90% CI 50-82) age-6 fish from BY2011. Saltwater age estimates were 34 (90% CI 24-46) zero-saltwater mini-jacks from MY2017; 1,651 (90% CI 1,543-1,749) one-saltwater jacks from MY2016; 2,817 (90% CI 2,665-2,950) two-saltwater fish from MY2015; 1,258 (90% CI 1,175-1,333) three-saltwater fish from MY2014; and 33 (90% CI 22-44) four-saltwater fish from MY2013. The majority of the wild return or 93% emigrated to the ocean as freshwater age-2.

For all genetic stocks, age-4 was the dominant age class, except for FALL where age-5 was the dominant age class. Furthermore, two-saltwater fish dominated HELLSC; one-saltwater jacks and two-saltwater fish dominated CHMBLN, MFSALM, SFSALM, and TUCANO; and two-saltwater and three-saltwater fish dominated UPSALM and FALL. All zero-saltwater mini-jacks assigned to the FALL genetic stock. Over 90% of the UPSALM, CHMBLN, MFSALM, SFSALM, HELLSC, and TUCANO fish emigrated at freshwater age-2; from 2 to 6% of the UPSALM, MFSALM, SFSALM, and HELLSC fish emigrated at freshwater age-1; and <1% of the HELLSC fish emigrated as freshwater age-3.

Readers accurately determined the saltwater-age of 93.0% of the scale samples (n = 43) from known saltwater-age PIT-tagged and coded-wire-tagged Chinook Salmon collected during SY2017 (Appendix B-2). The known saltwater-age sample was 44% one-saltwater, 37% two-saltwater, and 19% three-saltwater fish. There were no four-saltwater fish in the known saltwater-age sample.

Chinook Salmon Adult-to-Adult Productivity

Wild Chinook Salmon returning to LGR in SY2017 completed the BY2011 cohort necessary for an adult-to-adult productivity estimate. Brood year 2011 returned 28,536 adults from 26,583 parents resulting in an adult-to-adult productivity estimate of 1.07 recruits per spawner, which is above the 1.0 recruits per spawner necessary for replacement (Figure 5). For genetic stocks, adult-to-adult productivity estimates that were above replacement included UPSALM at 1.23, MFSALM at 1.21, and HELLSC at 1.01; estimates that were below replacement included CHMBLN at 0.80 and SFSALM at 0.77 (Figure 6). Adult-to-adult productivity was not calculated for the TUCANO and FALL genetic stocks.

Chinook Salmon Smolt-to-Adult Return Rate

Chinook Salmon returning to LGR in SY2017 completed their life cycle as smolts migrating in 2013. Migration year 2013 returned 28,372 fish from 1,006,960 emigrating yearlings resulting in a SAR estimate of 2.82% (2.79-2.85 95% CI; Table 4).

DISCUSSION

Abundance of returning SY2017 wild steelhead and spring-summer Chinook Salmon was low across the Snake River basin as measured at Lower Granite Dam. Returning adults endured drought conditions and warm water temperatures during their juvenile freshwater life stages, and abnormally warm ocean temperatures during their saltwater life stage, especially in 2015. We conclude that a combination of low out-migrant abundance in 2015 for Chinook Salmon (Camacho et al. 2018) combined with poor smolt-to-adult survival for Chinook Salmon and steelhead resulted in the low escapements to the dam observed in SY2017.

For steelhead, escapement counted at the LGR window was the lowest since SY2000 and the wild fish escapement estimate was the lowest since SY2008. The extremely low abundance of one-saltwater wild steelhead is likely attributed to the poor conditions of 2015 (Appendix C-4). Two-saltwater steelhead returned in higher abundance compared to one-saltwater returns, but continued the declining trend mirroring the one-saltwater returns of the same cohort from the previous year. Genetic stocks exhibited similar decreasing abundance patterns as the aggregate wild run (Appendix C-5). However, the extremely low abundance of one-saltwater returns shifted the proportional stock composition of the aggregate wild fish. Stocks typically comprised of half or more one-saltwater fish drastically decreased in proportion, such as the UPSALM, which decreased from its 16% average (SY2009-2016) to 8% in SY2017 (Appendix C-1). Conversely, stocks consisting of mainly two-saltwater fish, such as the UPCLWR, increased in proportion from its average of 8% (SY2009-2016) to 14% in SY2017.

For spring-summer Chinook Salmon, escapement counted at the LGR window was the lowest since SY2007 and the wild fish escapement estimate was the lowest since SY1999. Two-saltwater Chinook Salmon, which make up the majority of returns in a given spawn year, had extremely low abundance (Appendix D-4). Similar to one-saltwater steelhead, these two-saltwater Chinook Salmon migrated to the ocean in 2015 enduring poor freshwater and ocean conditions. Genetic stocks exhibited similar decreasing abundance patterns as shown in the aggregate wild run (Appendix D-5). However, the extremely low abundance of spring-summer Chinook Salmon returns shifted the proportional stock composition of the aggregate wild fish. From SY2009-2015, FALL Chinook Salmon averaged 3% of the wild Chinook Salmon crossing LGR from March 1-August 17 (Appendix D-1). In SY2016-2017, FALL Chinook Salmon increased to 10% and 12%, respectively, even though escapement abundance during the window count spring-summer calendar time period has remained low in all years.

The wild Chinook Salmon SAR time series was last updated through smolt MY2016 by Camacho et al. (2017); here it is partially updated through the MY2017 cohort. The SAR for the MY2013 cohort, for which adult returns are now complete, exceeded the Northwest Power and Conservation Council (NPCC) fish and wildlife program minimum goal of 2% (NPCC 2009; Figure 7). However, the annual arithmetic mean SAR (1.78%), the 10-year geometric mean SAR (1.51%), and the 5-year geometric mean SAR (1.88%) for the 1996-2013 cohorts (n = 18) are all less than the NPCC minimum SAR goal. Further, only five cohorts or 28% fell within the NPCC goal range of 2-6%, and none exceeded 6%. Our estimated SAR rates in the past have been slightly higher but closely track the estimates provided by the Comparable Survival Study (CSS; McCann et al. 2015). It is unknown whether the observed SAR differences are the result of our methods based on abundances at LGR or the CSS methods based on PIT-tagged fish.

A combination of accurate and precise age and abundance estimates provided the foundation for estimating adult-to-adult productivity. For steelhead, returning fish were from BY2009-2014, and completed the BY2009 cohort. Productivity has declined since BY2007 and was below replacement for BY2009 indicating a decreasing trend in population growth for Snake River steelhead. This is the first cohort that was below replacement for BY2006-2009. Brood year 2009 was the first complete cohort for steelhead genetic stocks. Unlike the aggregate, productivity varied among the genetic stocks with all Clearwater genetic stocks, MFSALM, and LOSALM below replacement and the IMNAHA, GRROND, LSNAKE, UPSALM, and SFSALM above replacement. For Chinook Salmon, returning fish were from BY2011-2015 and completed the BY2011 cohort. That cohort's adult-to-adult productivity declined from BY2010, but was still above replacement. The completion of the BY2011 cohort was the third complete brood year for genetic stocks. Brood year 2011 productivity varied for each genetic stock when compared to BY2010, but all genetic stocks were above replacement.

Steelhead and Chinook Salmon exhibit multiple life history strategies through a diversity of age at maturation, which provides an added measure of resiliency when specific life stages or year classes endure abnormally high mortality (Quinn 2005; Copeland et al. 2017). Snake River steelhead have a range of age classes with one to six years in freshwater, one to three years in saltwater, and a variety of repeat spawners. However, most Snake River steelhead spend two years in freshwater and one to two years in saltwater before returning to spawn. Similarly, Chinook Salmon have a range of age classes spending zero to two years in freshwater and zero to four years in saltwater. However, the most common age class for Chinook Salmon spends one year in freshwater and two years in saltwater. Additionally, the sex of a fish can influence when a fish matures. Steelhead are typically dominated by anadromous females because some males residualize and are non-anadromous (Appendix C-6; Ohms et al. 2014; Sloat et al. 2014). Theory suggests females benefit from anadromy by attaining larger body size and higher fecundity, while males can successfully mature and reproductively compete in a non-anadromous form (Hendry et al. 2004). Similarly, Chinook Salmon males exhibit both anadromous and non-anadromous, precocial forms and tend to mature earlier than females (Johnson et al. 2012). For males, earlier maturation correlates to smaller body size, but is often offset by a higher probability of survival to reproduction resulting in male bias of returning fish (Appendix D-6; Olsen et al. 2006). By spreading the risk across multiple life histories, unfavorable conditions, such as those that occurred in 2015, can have a reduced impact on abundance and productivity.

Estimates for some genetics stocks reported in this document are not complete for the entirety of that stock. A genetic stock can have an incomplete estimate in two ways. The first way is that the genetic stock, wholly or partially, contains populations that originate below LGR. The LSNAKE (steelhead) and TUCANO (Chinook Salmon) contain the Tucannon River population located below LGR. Some returning adults born in the Tucannon River overshoot their natal stream and stray above LGR. Without abundance information from the Tucannon River for each species, estimates for the LSNAKE and TUCANO should be considered a minimum for the returns to the Snake River basin. The second way is that a genetic stock overlaps run designations defined by USACE calendar dates. The FALL (Chinook Salmon) genetic stock reported here only includes fall Chinook Salmon that cross LGR during the spring-summer Chinook Salmon run timing (March 1-August 17). The vast majority of the FALL genetic stock cross LGR after August 17. However, by accounting for FALL Chinook Salmon August 17 and earlier, we get a better estimate of the true spring-summer stocks returning to the Snake River. Additionally, preliminary evidence from pit tags suggests some spring-summer Chinook Salmon cross LGR after August 17. However, quantifying abundances during the USACE fall run timing designation is not within the scope of this report. Reporting estimates from the incomplete genetic stocks is mainly for accounting purposes and caution should be used when interpreting associated results. The inclusion of these stocks provides critical information for a more refined decomposition of the aggregate run at LGR into desired reporting groups.

Our wild (and hatchery) escapement estimates are based on unadjusted window counts, i.e. we treat the counts as a complete census. Unadjusted window counts were a critical component the ESA listing and have been used for decades to evaluate population performance in the hydrosystem. Therefore, our products are clearly and directly related to the common currency. However, there are a number of potential biases when estimating total adult escapement at LGR using unadjusted window counts. Some returning fish are known to fallback below LGR after successfully crossing above. A portion of these fallback fish re-ascend the LGR ladder again, essentially being counted twice at the window, while others stay below LGR. Furthermore, the window is not counted 24-hours a day throughout the season (USACE 2016, 2017). We recognize that it is possible that our wild escapement estimates at LGR are slightly biased. However, our estimates are likely more accurate than estimates based solely on window counts due to our accounting and removal of ad-intact hatchery fish from wild fish estimates using PBT, which began in SY2011 (Steele et al. 2011; Camacho et al. 2017). We will continue to refine our stock assessments for both species while clearly maintaining a transparent relationship with window count data.

This report continues the wild Snake River steelhead and Chinook Salmon comprehensive genetic stock time series and productivity assessments reported by Camacho et al. (2017), and the Chinook Salmon SAR time series last reported by Stiefel et al. (2015). The wild escapement and composition estimates reported here directly estimate adult abundance at LGR, as well as elements of diversity such as sex ratio and life history variations. We estimate abundance by brood year through the use of age data, and these estimates are necessary for productivity analyses. Productivity is the generational replacement rate defined as the number of progeny per parent. In this report, we used returning adults as progeny. In the future, estimates of wild adult abundance and composition will be combined with similar information for smolts from the LGR juvenile facility (e.g., Camacho et al. 2018) to estimate adult-to-juvenile and juvenile-to-adult productivity.

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TABLES

Table 1. Major population groups and independent populations within the Snake River steelhead distinct population segment (DPS) and spring-summer Chinook Salmon evolutionary significant unit (ESU; ICBTRT 2003, 2005, 2009; Ford et al. 2015; NMFS 2016).

Snake River steelhead DPS	
Major population group	**Population name**
Lower Snake River	1. Tucannon River 2. Asotin Creek
Grande Ronde River	3. Lower Grande Ronde River 4. Joseph Creek 5. Wallowa River 6. Upper Grande Ronde River
Imnaha River	7. Imnaha River
Clearwater River	8. Lower Clearwater River 9. North Fork Clearwater River (extirpated) 10. Lolo Creek 11. Lochsa River 12. Selway River 13. South Fork Clearwater River
Salmon River	14. Little Salmon River 15. Chamberlain Creek 16. South Fork Salmon River 17. Secesh River 18. Panther Creek 19. Lower Middle Fork Salmon River 20. Upper Middle Fork Salmon River 21. North Fork Salmon River 22. Lemhi River 23. Pahsimeroi River 24. East Fork Salmon River 25. Upper Salmon River
Hells Canyon Tributaries (extirpated)	

Table 1. Continued.

Snake River spring-summer Chinook Salmon ESU	
Major population group	**Population name**
Lower Snake River	1. Tucannon River 2. Asotin Creek (extirpated) [a]
Grande Ronde/Imnaha Rivers	3. Wenaha River 4. Lostine River 5. Minam River 6. Catherine Creek 7. Upper Grande Ronde River 8. Imnaha River 9. Big Sheep Creek (extirpated) [a] 10. Lookinglass Creek (extirpated) [a]
South Fork Salmon River	11. Little Salmon River 12. South Fork Salmon River 13. Secesh River 14. East Fork South Fork Salmon River
Middle Fork Salmon River	15. Chamberlain Creek 16. Lower Middle Fork Salmon River 17. Big Creek 18. Camas Creek 19. Loon Creek 20. Upper Middle Fork Salmon River 21. Sulphur Creek 22. Bear Valley Creek 23. Marsh Creek
Upper Salmon River	24. North Fork Salmon River 25. Lemhi River 26. Upper Salmon River Lower Mainstem 27. Pahsimeroi River 28. East Fork Salmon River 29. Yankee Fork Salmon River 30. Valley Creek 31. Upper Salmon River Upper Mainstem 32. Panther Creek (extirpated) [a]
Dry Clearwater River (extirpated) [a]	33. Potlatch River (extirpated) [a] 34. Lapwai Creek (extirpated) [a] 35. Lawyer Creek (extirpated) [a] 36. Upper South Fork Clearwater River (extirpated) [a]
Wet Clearwater River (extirpated) [a]	37. Lower North Fork Clearwater River (extirpated) 38. Upper North Fork Clearwater River (extirpated) 39. Lolo Creek (extirpated) [a] 40. Lochsa River (extirpated) [a] 41. Meadow Creek (extirpated) [a] 42. Moose Creek (extirpated) [a] 43. Upper Selway River (extirpated) [a]

[a] Reintroduced fish exist in extirpated areas except the North Fork Clearwater River.

Table 2. Estimated annual escapement, by fish size and origin, of steelhead, spawn years 1998-2017. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Ad-clipped and ad-intact refer to the adipose fin. Estimates were generated by IDFG and are the USACE window counts decomposed using adult trap data (Alan Byrne, IDFG, personal communication; Camacho et al. 2017; present study).

		Estimated number of steelhead at LGR that were:							
Spawn year[a]	**LGR window count**	**Large wild**[b]	**Large hatchery ad-clipped**	**Large hatchery ad-intact**[b]	**Small wild**[b]	**Small hatchery ad-clipped**	**Small hatchery ad-intact**[b]	**Total hatchery**	**Total wild**
1998	86,646	1,325	10,878	0	7,424	67,019	0	77,897	8,749
1999	70,662	2,301	17,455	0	7,074	43,832	0	61,287	9,375
2000	74,051	914	8,834	0	10,184	54,119	0	62,953	11,098
2001	117,302	2,886	17,128	0	17,689	79,589	10	96,727	20,575
2002	268,466	3,174	30,677	0	37,545	191,091	5,979	227,747	40,719
2003	222,176	13,623	51,358	6,618	28,308	110,535	11,734	180,245	41,931
2004	172,510	7,254	23,058	2,132	21,892	106,334	11,840	143,364	29,146
2005	151,646	4,774	23,179	2,005	18,297	94,225	9,166	128,575	23,071
2006	158,165	3,544	26,143	3,345	14,586	96,644	13,903	140,035	18,130
2007	149,166	1,633	33,332	5,880	7,877	85,210	15,234	139,656	9,510
2008	155,142	2,924	20,513	3,446	11,242	102,374	14,643	140,976	14,166
2009	178,870	5,659	40,713	6,998	18,216	94,205	13,079	154,995	23,875
2010	323,382	4,529	16,555	2,700	38,210	231,003	30,385	280,643	42,739
2011	208,296	9,584	31,574	4,118	34,549	110,750	17,721	164,163	44,133
2012	180,320	4,198	17,801	2,113	35,240	113,038	7,930	140,882	39,438
2013	109,186	3,337	13,695	3,970	19,806	63,611	4,767	86,043	23,143
2014	108,154	1,885	5,546	1,593	23,470	70,332	5,328	82,799	25,355
2015	165,591	6,928	21,067	3,639	38,861	89,341	5,755	119,802	45,789
2016	136,150	3,130	8,465	1,408	30,806	88,296	4,045	102,214	33,936
2017	101,826	3,001	25,724	4,145	12,575	52,825	3,556	86,250	15,576

[a] Steelhead at Lower Granite Dam are considered fish passing July 1 through June 30; most steelhead pass the dam in the fall but are assigned to their spawn year the following spring.
[b] Spawn year 2011 was the first year of adult PBT returns used to adjust wild and hatchery ad-intact fish estimates.

Table 3. Estimated annual escapement, by origin and saltwater age, of Chinook Salmon, spawn years 1998-2017. Jacks are saltwater age-1 and include saltwater age-0 mini-jacks; adults are saltwater age-2 and older. Estimates were generated by IDFG and are the USACE window counts decomposed using adult trap data (Camacho et al. 2017; present study).

		Estimated number of Chinook Salmon at Lower Granite Dam that were:							
Spawn year[a]	**Window count**	**Wild adults**[b]	**Wild jacks**[b]	**Total wild**	**Hatchery adults**[b]	**Hatchery jacks**[b]	**Total hatchery**	**Total adults**[b]	**Total jacks**[b]
1998	14,646	5,378	122	5,500	8,831	315	9,146	14,209	437
1999	10,647	2,695	236	2,931	3,861	3,855	7,716	6,556	4,091
2000	51,835	7,347	1,500	8,847	30,414	12,574	42,988	37,761	14,074
2001	192,632	37,063	1,621	38,684	148,630	5,318	153,948	185,693	6,939
2002	101,226	27,743	340	28,083	69,441	3,702	73,143	97,184	4,042
2003	99,463	29,270	2,349	31,619	57,761	10,083	67,844	87,031	12,432
2004	86,501	16,808	982	17,790	62,701	6,010	68,711	79,509	6,992
2005	35,100	8,691	386	9,077	25,118	905	26,023	33,809	1,291
2006	31,223	8,775	292	9,067	21,312	844	22,156	30,087	1,136
2007	42,551	7,694	1,114	8,808	21,034	12,709	33,743	28,728	13,823
2008	88,776	14,046	2,333	16,379	53,027	19,370	72,397	67,073	21,703
2009	111,580	12,963	3,454	16,417	45,477	49,686	95,163	58,440	53,140
2010	134,684	26,281	1,368	27,649	97,273	9,762	107,035	123,554	11,130
2011	134,594	22,407	4,176	26,583	69,636	38,375	108,011	92,043	42,551
2012	84,771	20,298	1,242	21,540	59,221	4,010	63,231	79,519	5,252
2013	70,966	12,407	6,856	19,263	30,556	21,147	51,703	42,963	28,003
2014	114,673	26,351	3,987	30,338	65,415	18,920	84,335	91,766	22,907
2015	132,432	21,499	1,910	23,409	96,163	12,860	109,023	117,662	14,770
2016	81,753	15,939	813	16,752	58,187	6,814	65,001	74,126	7,627
2017	48,192	4,108	1,685	5,793	30,179	12,220	42,399	34,287	13,905

[a] Spring-summer Chinook Salmon at Lower Granite Dam are considered fish passing March 1 through August 17.

[b] For spawn years 2005-2017 (unshaded), the wild vs. hatchery and adults vs. jacks splits were estimated using scale samples, other biological data, and starting in 2011 parentage based tagging (PBT) samples collected at the LGR adult trap. For spawn years 1998-2004 (shaded gray), the splits were estimated using fin ray samples collected on the spawning grounds and biological samples collected at the adult trap.

Table 4. Estimated number of wild Chinook Salmon smolts, number of returning adults by saltwater age, and percent smolt-to-adult return (%SAR) rate at Lower Granite Dam. Fin ray samples were used to estimate age composition for adults returning from smolt migration years 1996-2004 (above the dashed line) whereas scale samples were used for smolt migration years 2005-2017 (below the dashed line). SAR 95% confidence intervals are given in parentheses.

Smolt Migration Year	Smolts[a]	Adults Returning to Lower Granite Dam Saltwater Age 0[b]	1	2	3	4	%SAR (95% CI)
1996	419,826	n/a	n/a[c]	628	451	0	0.26 (0.24-0.27)
1997	161,157	n/a	122	2,162	409	23	1.69 (1.62-1.75)
1998	599,159	n/a	236	6,938	1,056	281	1.42 (1.39-1.45)
1999	1,560,298	n/a	1,500	35,984	12,455	481	3.23 (3.20-3.26)
2000	1,344,382	n/a	1,621	15,007	22,724	43	2.93 (2.90-2.96)
2001	490,534	n/a	340	6,065	1,799	53	1.68 (1.65-1.72)
2002	1,128,582	n/a	2,349	14,966	2,739	24	1.78 (1.75-1.80)
2003	1,455,786	n/a	982	5,899	1,886	10	0.60 (0.59-0.62)
2004	1,517,951	n/a	351	6,865	3,903	27	0.73 (0.72-0.75)
2005	1,734,464	35	280	3,781	2,703	22	0.39 (0.38-0.40)
2006	1,227,474	12	1,104	11,316	2,937	0	1.25 (1.23-1.27)
2007	787,150	10	2,306	10,004	1,368	0	1.74 (1.71-1.77)
2008	856,556	27	3,431	24,914	7,658	59	4.21 (4.17-4.26)
2009	894,629	23	1,344	14,751	6,258	14	2.50 (2.47-2.54)
2010	1,268,659	23	3,985	13,980	4,523	0	1.77 (1.75-1.80)
2011	1,184,839	189	1,194	7,870	1,408	0	0.90 (0.88-0.92)
2012	1,674,268	49	6,780	24,942	2,866	27	2.07 (2.05-2.09)
2013	1,006,960	76	3,921	18,633	5,709	33	2.82 (2.79-2.85)
2014[d]	1,406,596	67	1,894	10,203	1258	-	0.95 (0.94-0.97)
2015[e]	525,743	16	766	2817	-	-	0.68 (0.66-0.71)
2016[f]	1,424,036	47	1651	-	-	-	0.12 (0.11-0.13)
2017[g]	1,171,926	34	-	-	-	-	0.00 (0.00-0.00)

[a] Smolt abundance for 2010-2017 derived from SCRAPI program (Camacho et al. 2018).

[b] Mini-jack (saltwater age-0) samples were not sampled on the spawning grounds, thus mini-jack fin rays are not available (n/a) for smolt migration years 1996-2004; only mini-jacks ≥30 cm, FL, were sampled for scales at Lower Granite Dam for smolt migration years 2005-2017.

[c] Jack (saltwater age-1) fin ray samples were not collected on the spawning grounds and are not available (n/a) for smolt migration year 1996.

[d] Preliminary SAR until saltwater age-4 is added (SY2018).

[e] Preliminary SAR until saltwater ages 3 through 4 are added (SY2019).

[f] Preliminary SAR until saltwater ages 2 through 4 are added (SY2020).

[g] Preliminary SAR until saltwater ages 1 through 4 are added (SY2021).

FIGURES

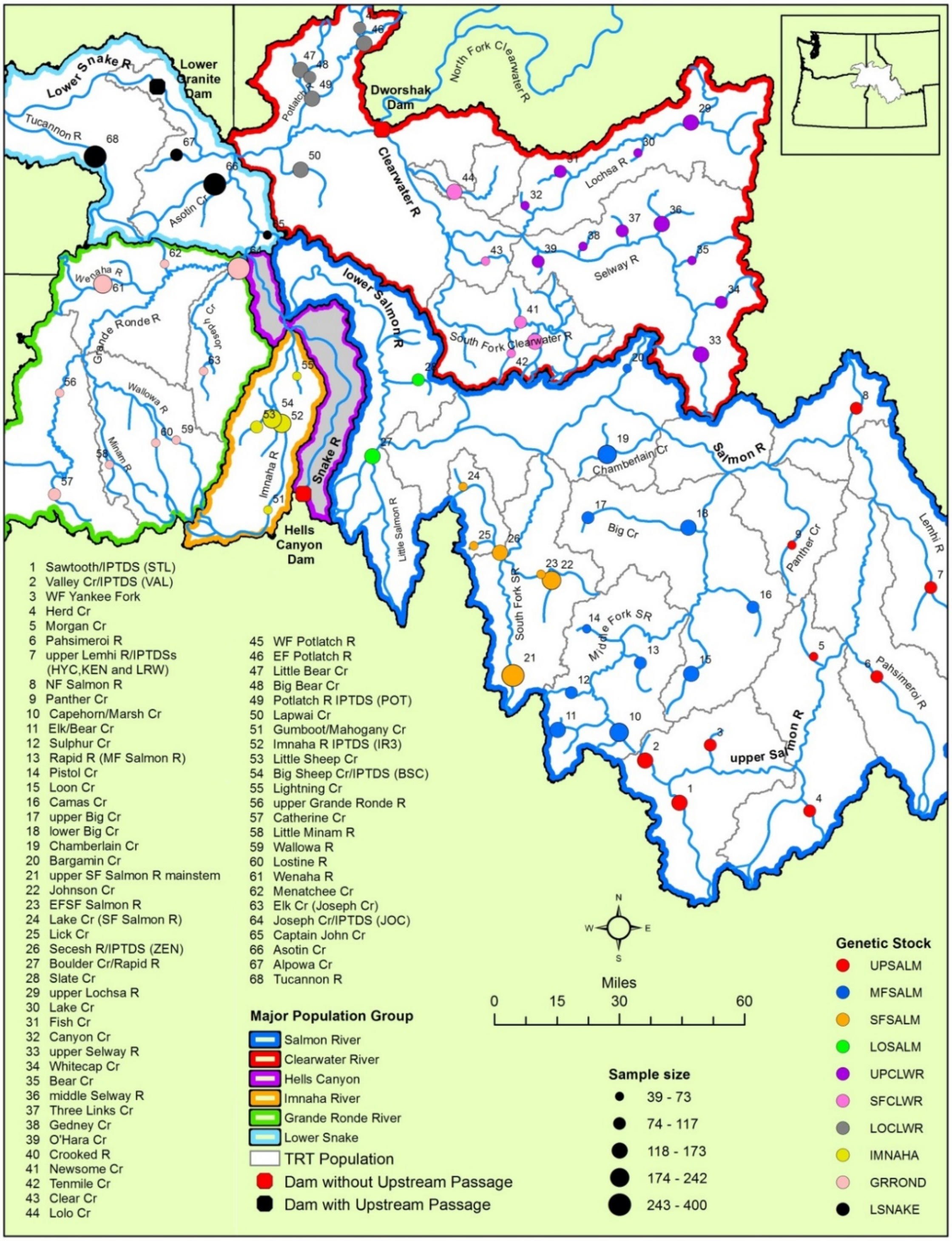


Figure 1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn years 2009-2016 (Vu et al. 2015). The Hells Canyon Tributaries major population group (shaded gray) does not support independent populations and is considered extirpated (NMFS 2016). See text for genetic stock abbreviations.

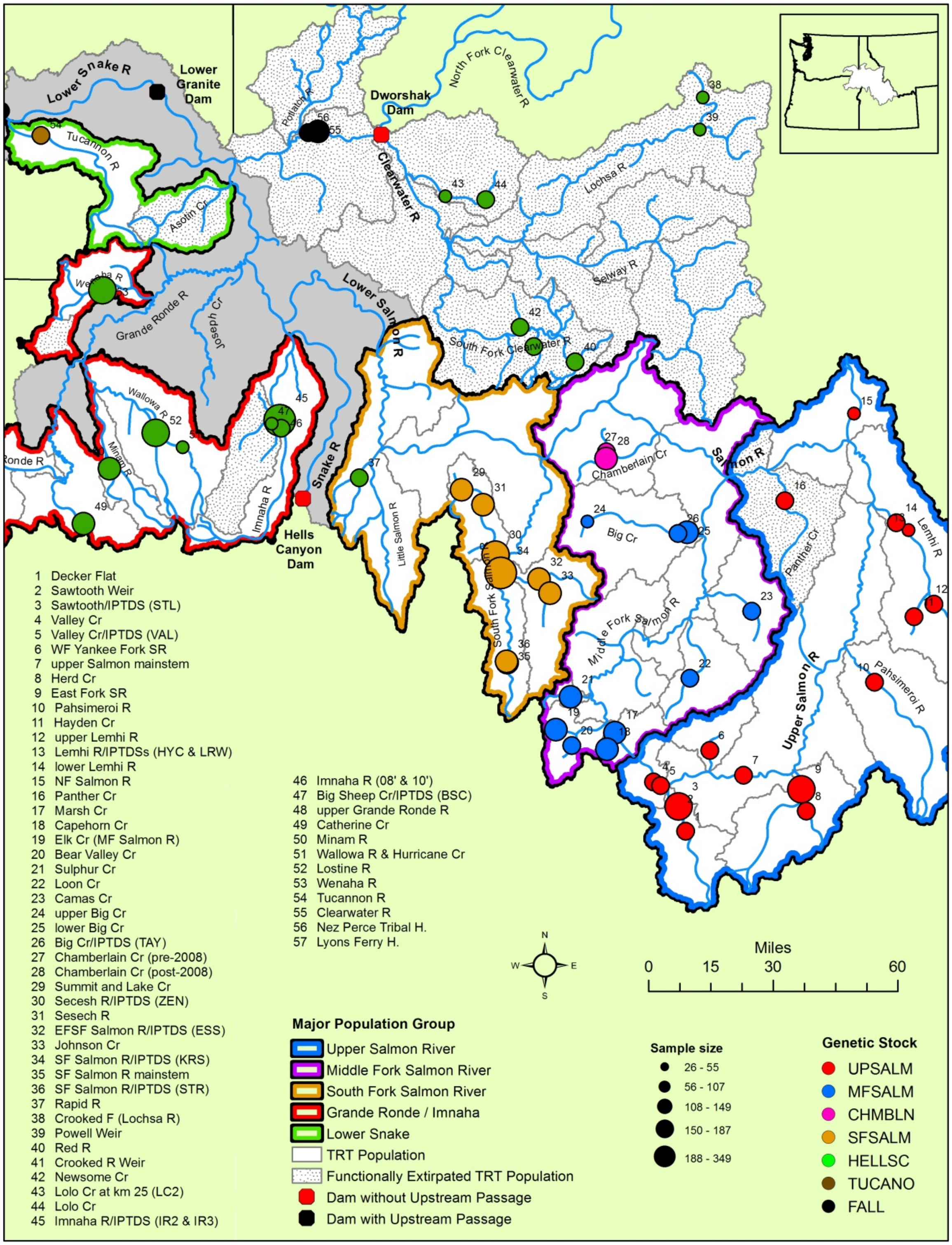


Figure 2. Genetic stocks and baseline collections used for Chinook Salmon mixed stock analysis at Lower Granite Dam, spawn years 2009-2016 (Vu et al. 2015). Reintroduced fish exist in functionally extirpated TRT populations as mapped. See text for genetic stock abbreviations.

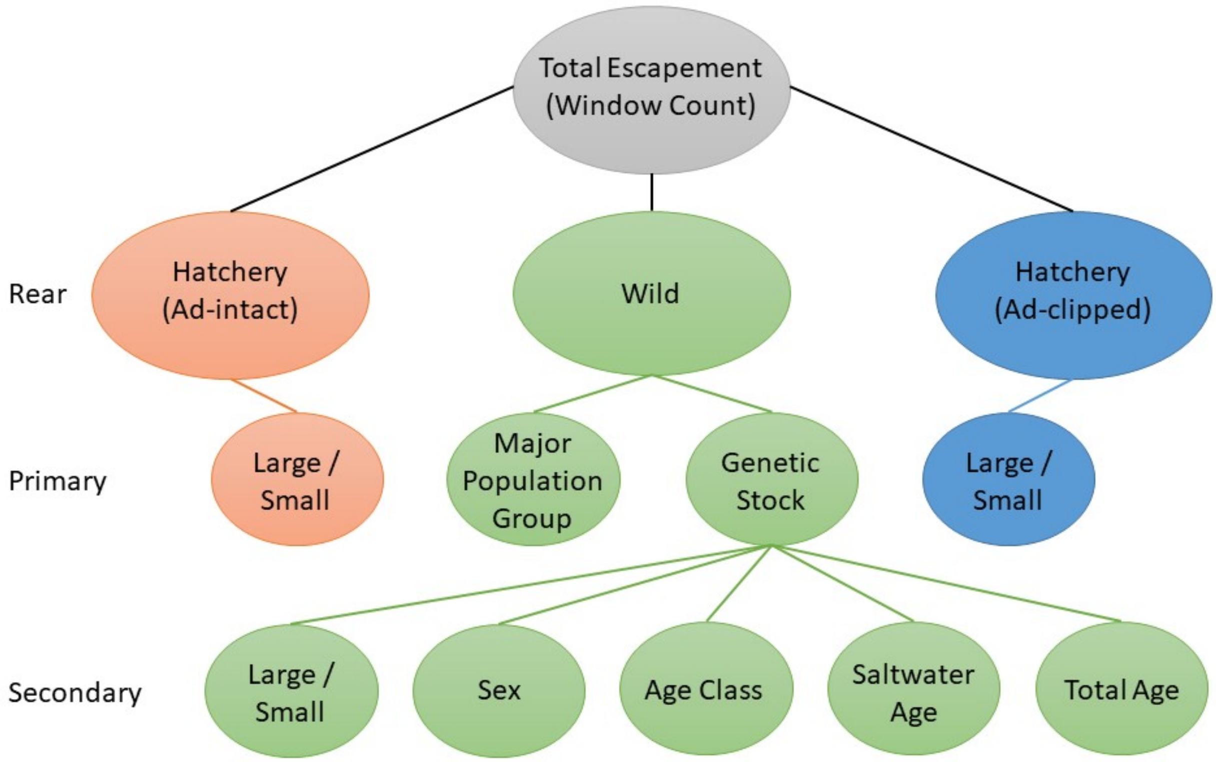


Figure 3. Schematic of the Salmonid Compositional Bootstrap Intervals (SCOBI) Lower Granite Dam decomposition model. Large/Small refer the fork length designations for Chinook Salmon large (≥57 cm) and small (<57 cm) and steelhead large (≥78 cm) and small (<78 cm). Fish less than 30 cm (FL) are not designated to species and are ignored.

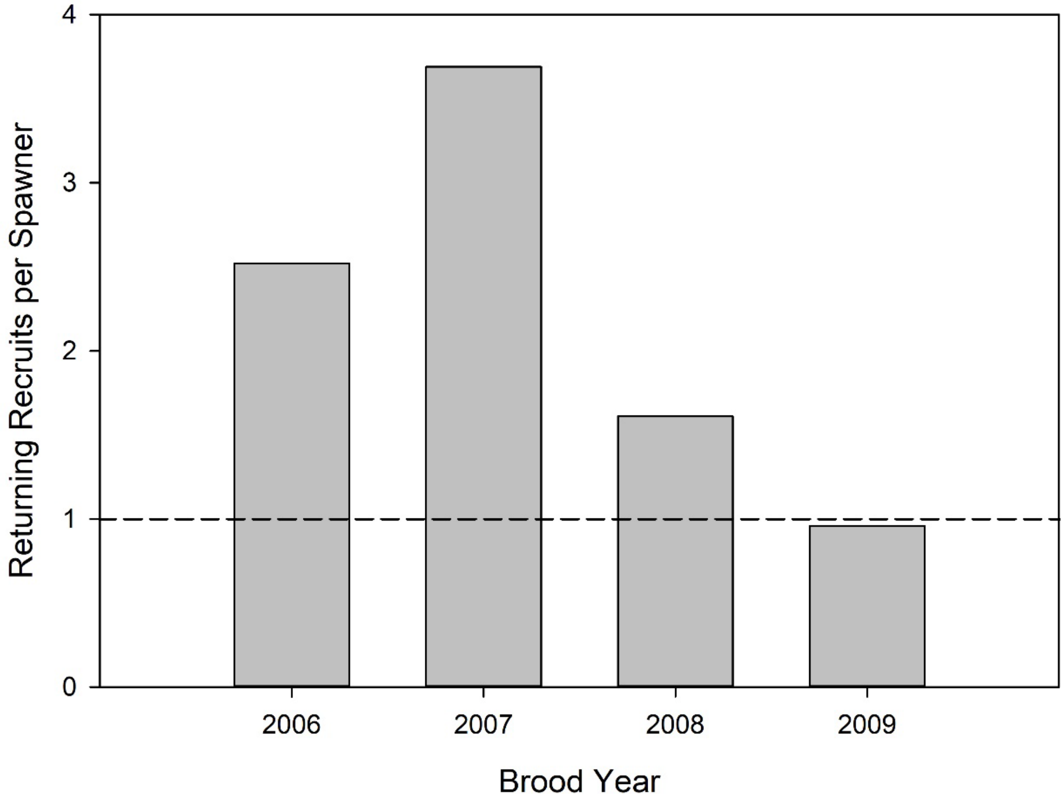


Figure 4. Adult-to-adult productivity (returning recruits/parent spawner) of wild steelhead at Lower Granite Dam. The dashed line at 1.0 recruit/spawner represents replacement.

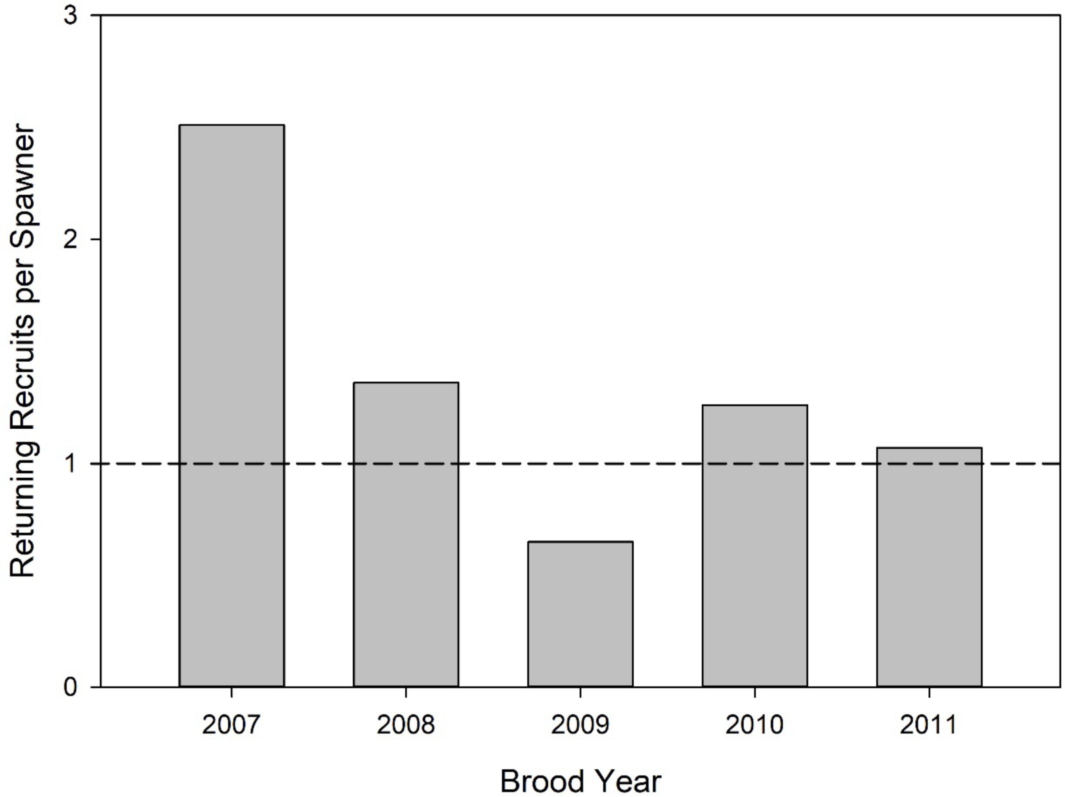


Figure 5. Adult-to-adult productivity (returning recruits/parent spawner) of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruit/spawner represents replacement.

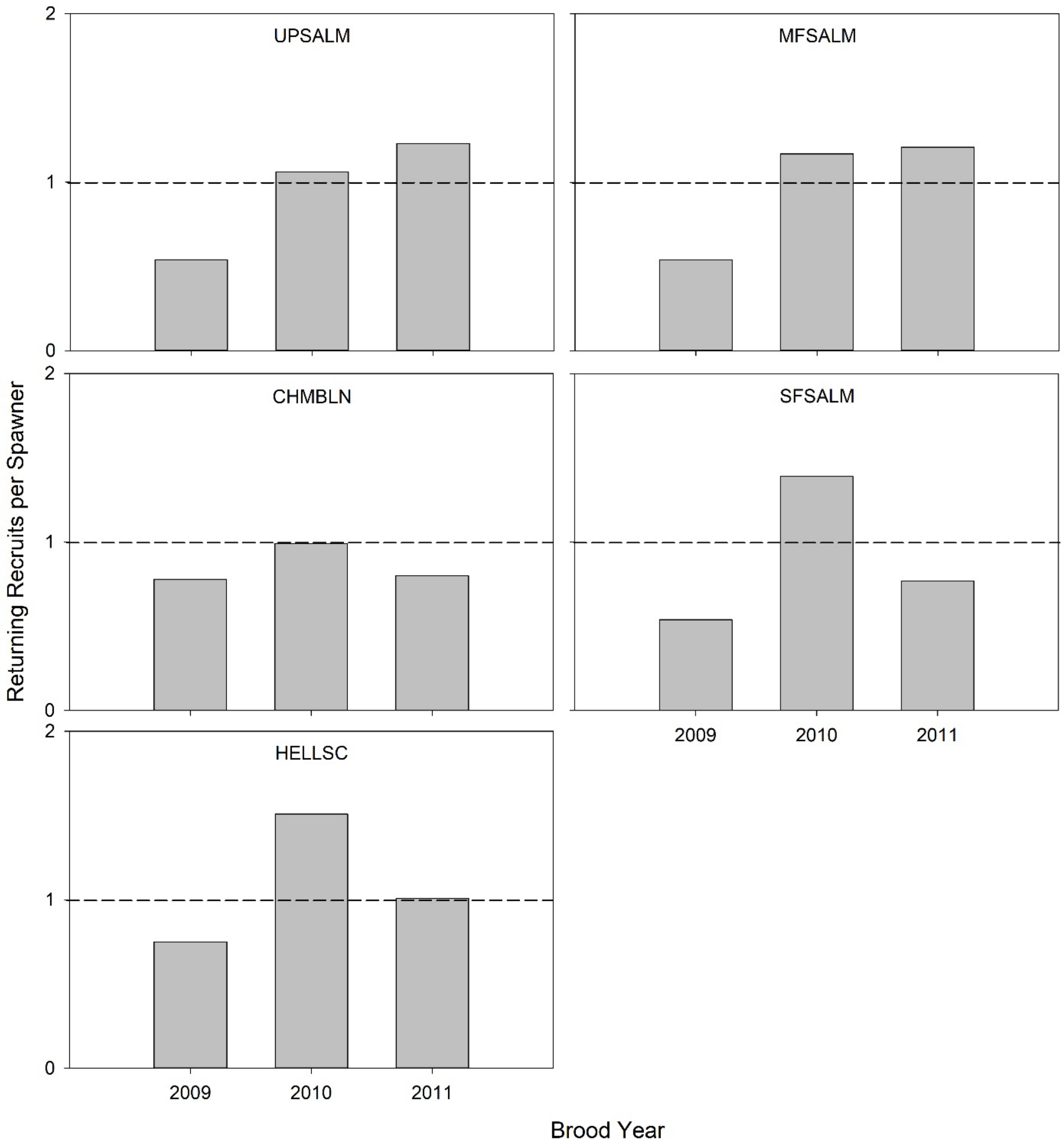


Figure 6. Adult-to-adult productivity (returning recruits/parent spawner) for each genetic stock of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruit/spawner represents replacement. TUCANO and FALL are not shown here because estimates at Lower Granite are incomplete.

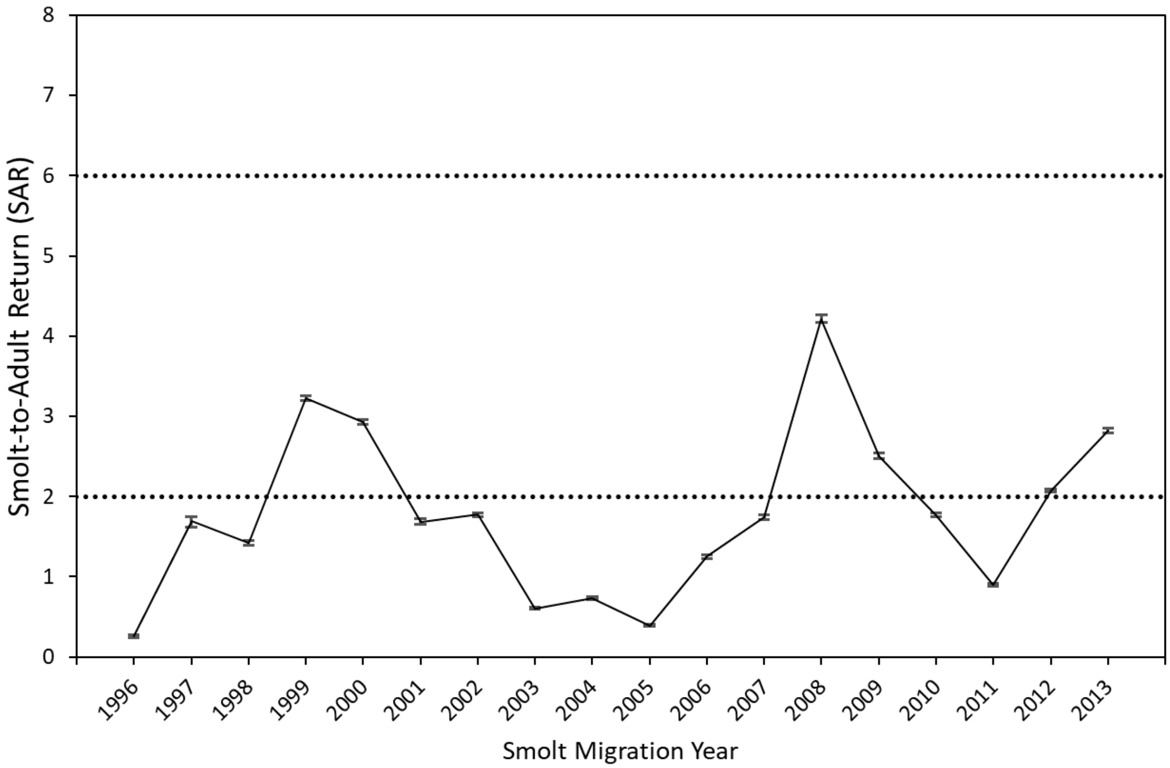


Figure 7. Estimated smolt-to-adult return (SAR) rate of smolts emigrating and adult returning to Lower Granite Dam. Confidence intervals are at 95%. The dashed lines represent the lower and upper range SAR objectives for wild Chinook Salmon established by the Northwest Power and Conservation Council (NPCC 2009). See Table 4 for numbers.

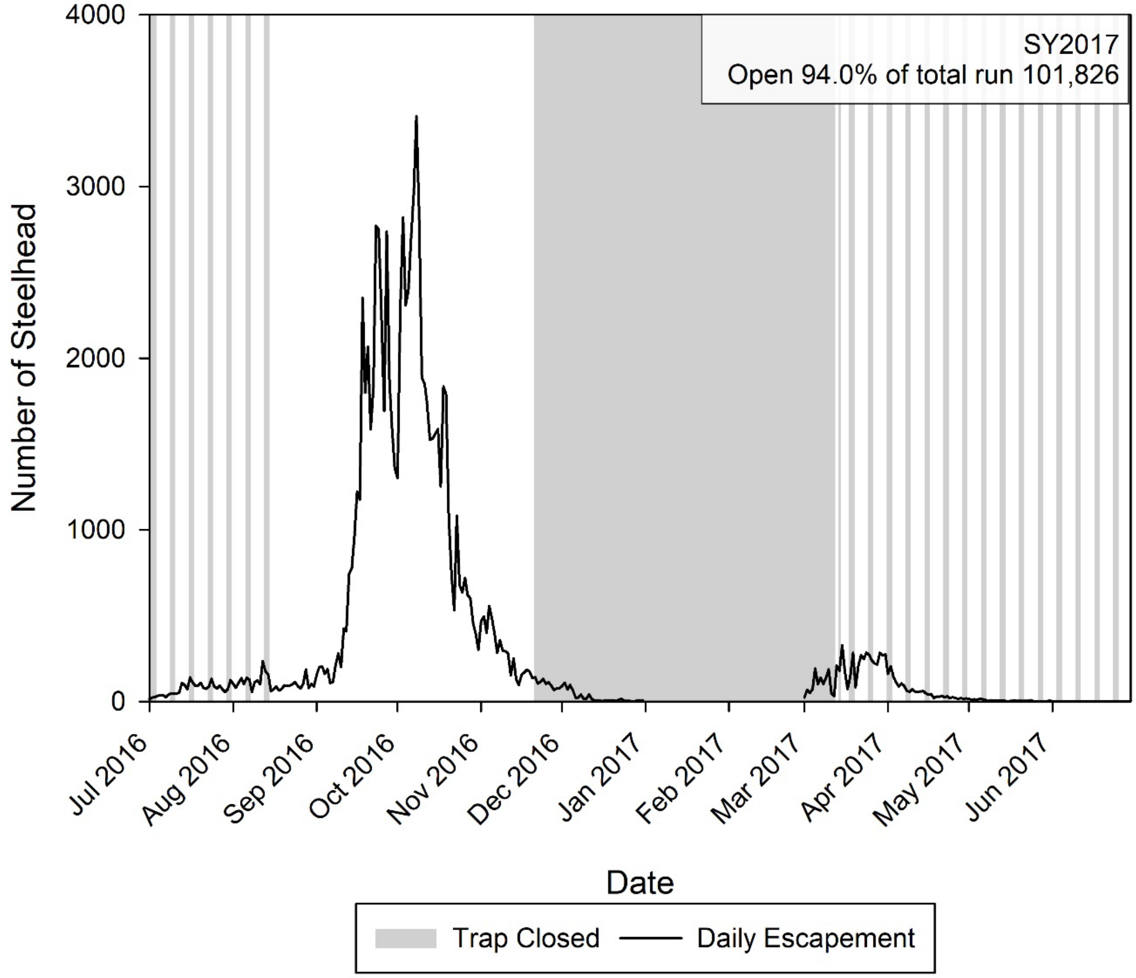
APPENDICES

Appendix A: Annual Lower Granite Dam trapping operations, 2016-2017.

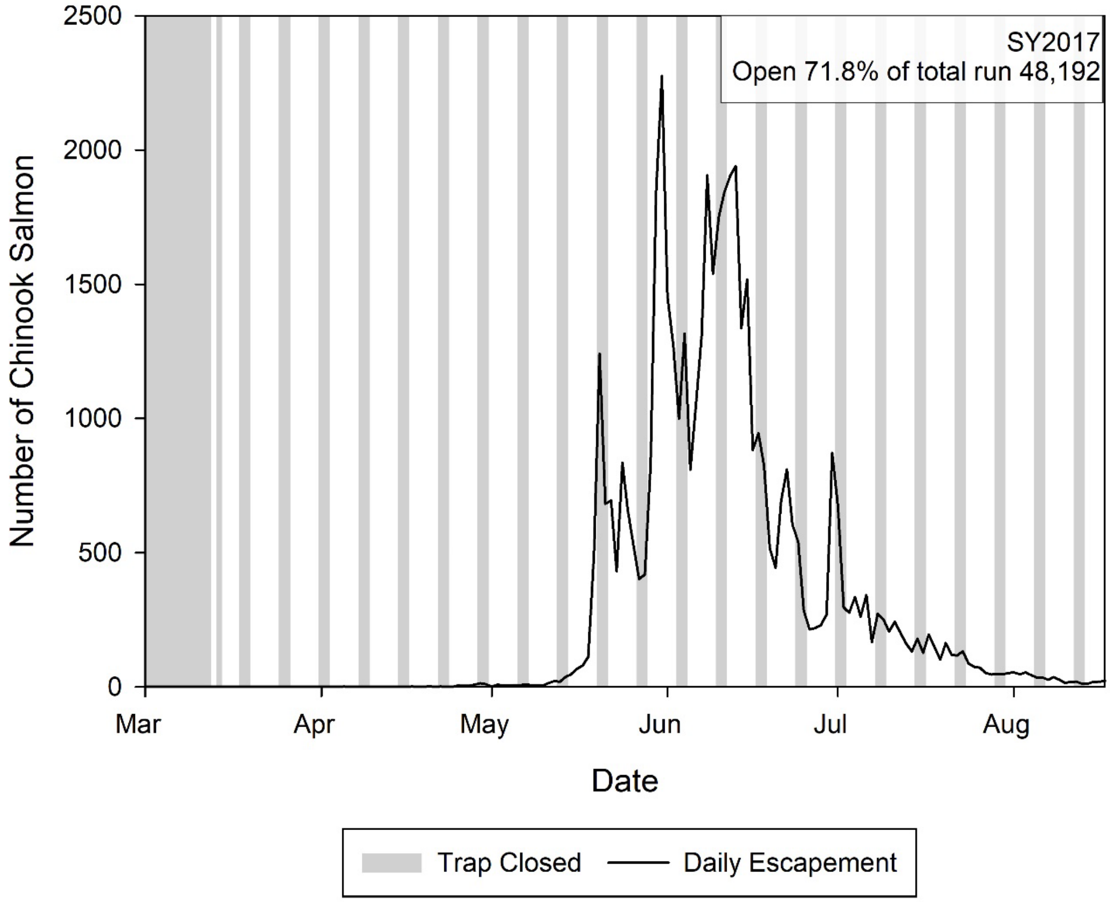
Appendix A-1. Annual Lower Granite Dam trapping operations, 2016-2017 (USACE 2016; Ogden 2016).

Date	Trap Operation	Comments
2016		
January 1-March 2	Closed	Freezing water temperature
March 3-April 14	5 d/week, 17% Rate	
April 15-May 9	5 d/week, 27% Rate	
May 10-13	5 d/week, 21% Rate	
May 14-August 17	5 d/week, 27% Rate	
August 18-November 20	7 d/week, 19% Rate	
November 21-December 31	Closed	Freezing water temperature
2017		
January 1-March 13	Closed	Freezing water temperature
March 14-April 16	5 d/week, 26% Rate	
August 18-September 12	7 d/week, 19% Rate	
September 13-September 21	7 d/week, 33% Rate	
September 22-November 19	7 d/week, 20% Rate	
November 20-December 31	Closed	Freezing water temperature

Appendix A-2. Daily number of steelhead counted at the Lower Granite Dam window, spawn year 2017. Vertical gray bars indicate when the trap was closed.



Appendix A-3. Daily number of Chinook Salmon counted at the Lower Granite Dam window, spawn year 2017. Vertical gray bars indicate when the trap was closed.



Appendix A-4. A hierarchical (top to bottom) key of external marks and internal tags used to determine hatchery origin steelhead and Chinook Salmon at Lower Granite Dam (LGR), spawn years 2009-2017. Only fish failing to meet criteria are considered wild.

If the LGR mark or tag is:	Then the origin at window is:	Then the origin at trap is:	And the final origin is:
Adipose fin clip	Hatchery	Hatchery	Hatchery
Coded wire tag (CWT)	N/A[a]	Hatchery	Hatchery
Ventral fin clip	N/A	Hatchery	Hatchery
Dorsal/ventral fin erosion (steelhead only)	N/A	Hatchery	Hatchery
Parentage based tag (PBT)	N/A	N/A	Hatchery[b]
Passive integrated transponder (PIT)	N/A	N/A	N/A[c]

[a] N/A = not applicable.
[b] Started in SY2011 with complete coverage by SY2013.
[c] Minor discrepancies occur between the PIT-tag database (PTAGIS) and LGR trap databases (LGTrappingDB, Biosamples, and Progeny) that prevent the use of PIT-tags to determine origin at this time.

Appendix A-5. Weekly window counts and adult valid trap samples of steelhead at Lower Granite Dam, spawn year 2017.

SCOBI Strata	Statistical Week[a]	Sampling Period	Number of Days	Days Trap Open[b]	Window Count	Total Valid Fish Trapped	Valid Wild Fish Trapped	Number of Valid Wild Fish Samples Used In SCOBI Analysis			
								Genetic Stock	Size	Sex	Age
						Fall 2016					
1	27A - 34[c]	7/1 - 8/21	52	38	4,469	898	395	392	392	391	172
2	35 – 37	8/22 - 9/11	21	21	3,269	618	180	180	180	180	79
3	38	9/12 - 9/18	7	7	7,636	1,398	251	249	249	248	110
4	39	9/19 - 9/25	7	7	15,045	3,115	464	463	463	460	196
5	40	9/26 - 10/2	7	7	12,809	2,610	284	283	283	283	138
6	41	10/3 - 10/9	7	7	19,439	4,032	429	425	425	410	187
7	42	10/10 - 10/16	7	7	11,669	2,629	283	281	281	251	125
8	43	10/17 - 10/23	7	7	8,303	1,786	208	208	208	199	96
9	44 - 53[c]	10/24 - 12/31	69	28	11,870	2,009	271	270	270	264	123
						Spring 2017					
10	10 - 27B[c]	3/1 - 6/30	124	79	7,317	1,235	297	296	296	293	101
Total:			308	208	101,826	20,330	3,062	3,047	3,047	2,979	1,327

[a] Statistical weeks are grouped to try to provide a minimum sample size of 100 valid fish with a genotype and age.

[b] See Appendix A-1 for trapping operation details.

[c] Includes a partial week.

Appendix A-6. Weekly window counts and adult valid trap samples of Chinook Salmon at Lower Granite Dam, spawn year 2017.

SCOBI Strata	Statistical Week[a]	Sampling Period	Number of Days	Days Trap Open[b]	Window Count	Total Valid Fish Trapped	Valid Wild Fish Trapped	Number of Valid Wild Fish Samples Used In SCOBI Analysis			
								Genetic Stock	Size	Sex	Age
1	12 - 23[c]	3/1 - 6/4	96	59	16,883	3,274	186	183	183	183	168
2	24	6/5 - 6/11	7	5	10,205	1,822	165	164	164	164	155
3	25	6/12 - 6/18	7	5	9,348	2,335	308	307	307	307	275
4	26	6/19 - 6/25	7	5	3,889	1,023	173	172	172	171	160
5	27 – 28	6/26 - 7/9	14	10	4,677	751	171	171	171	171	160
6	29 – 30	7/10 - 7/23	14	10	2,224	503	135	134	134	134	121
7	31 - 34[c]	7/24 - 8/17	25	19	966	235	87	87	87	87	81
Total:			170	113	48,192	9,943	1,225	1,218	1,218	1,217	1,120

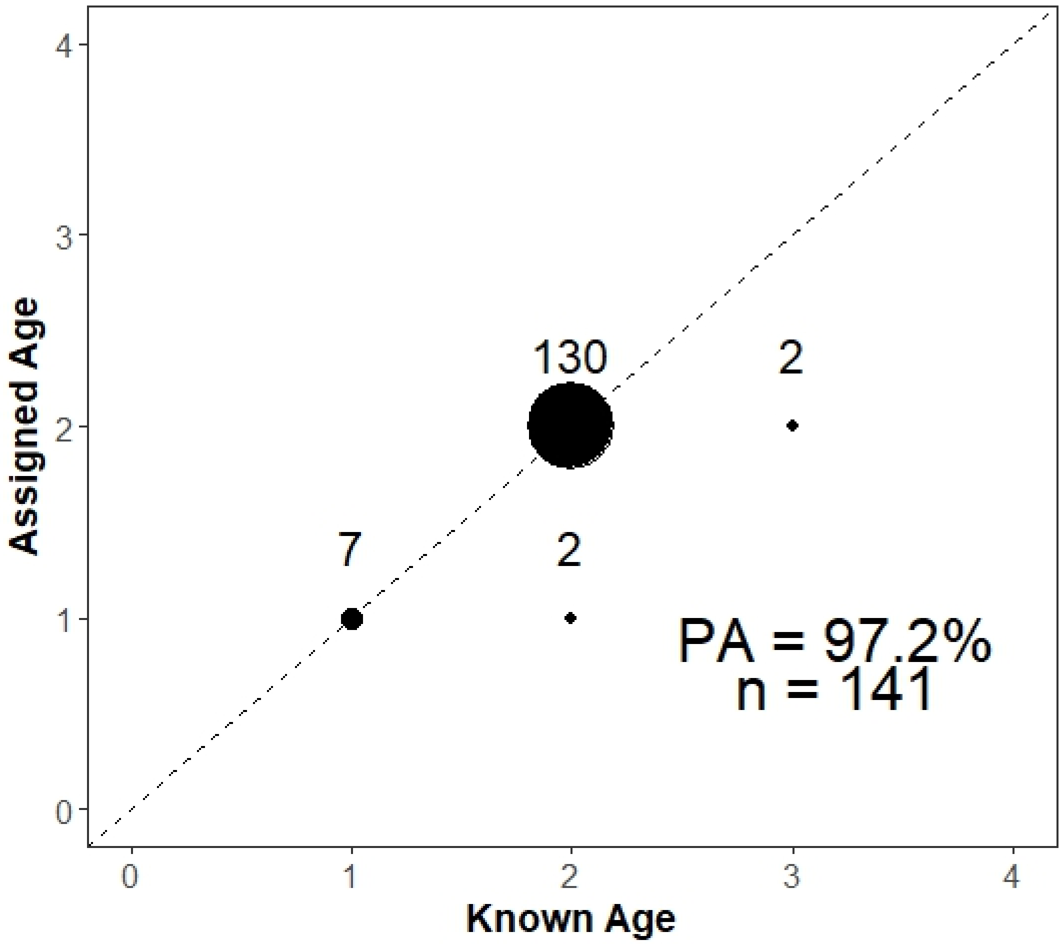
[a] Statistical weeks are grouped to try to provide a minimum sample size of 100 valid fish with a genotype and age.

[b] See Appendix A-1 for trapping operation details.

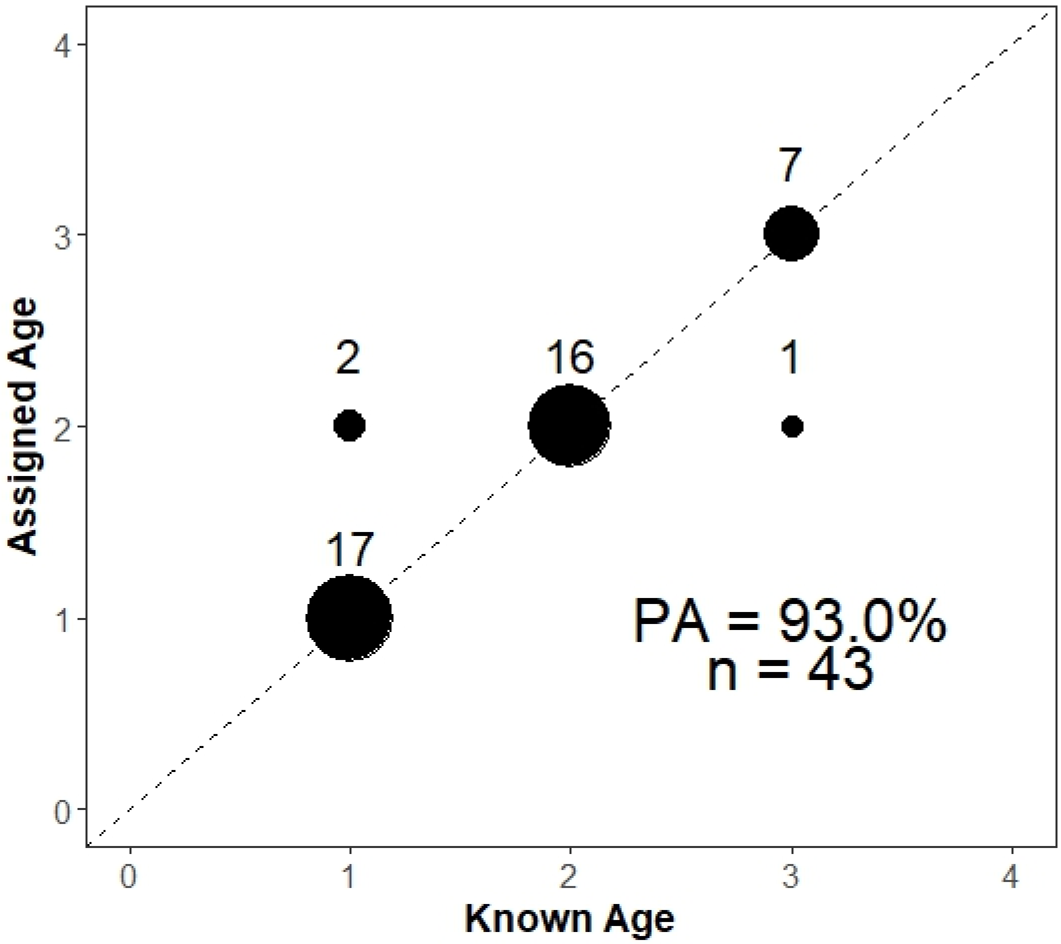
[c] Includes a partial week.

Appendix B: Steelhead and Chinook Salmon age validation.

Appendix B-1. Age bias plot illustrating pairwise comparisons of scale assigned saltwater-age with known age for steelhead at Lower Granite Dam, SY2017 (Micah Davison, IDFG, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. PA = percent agreement.

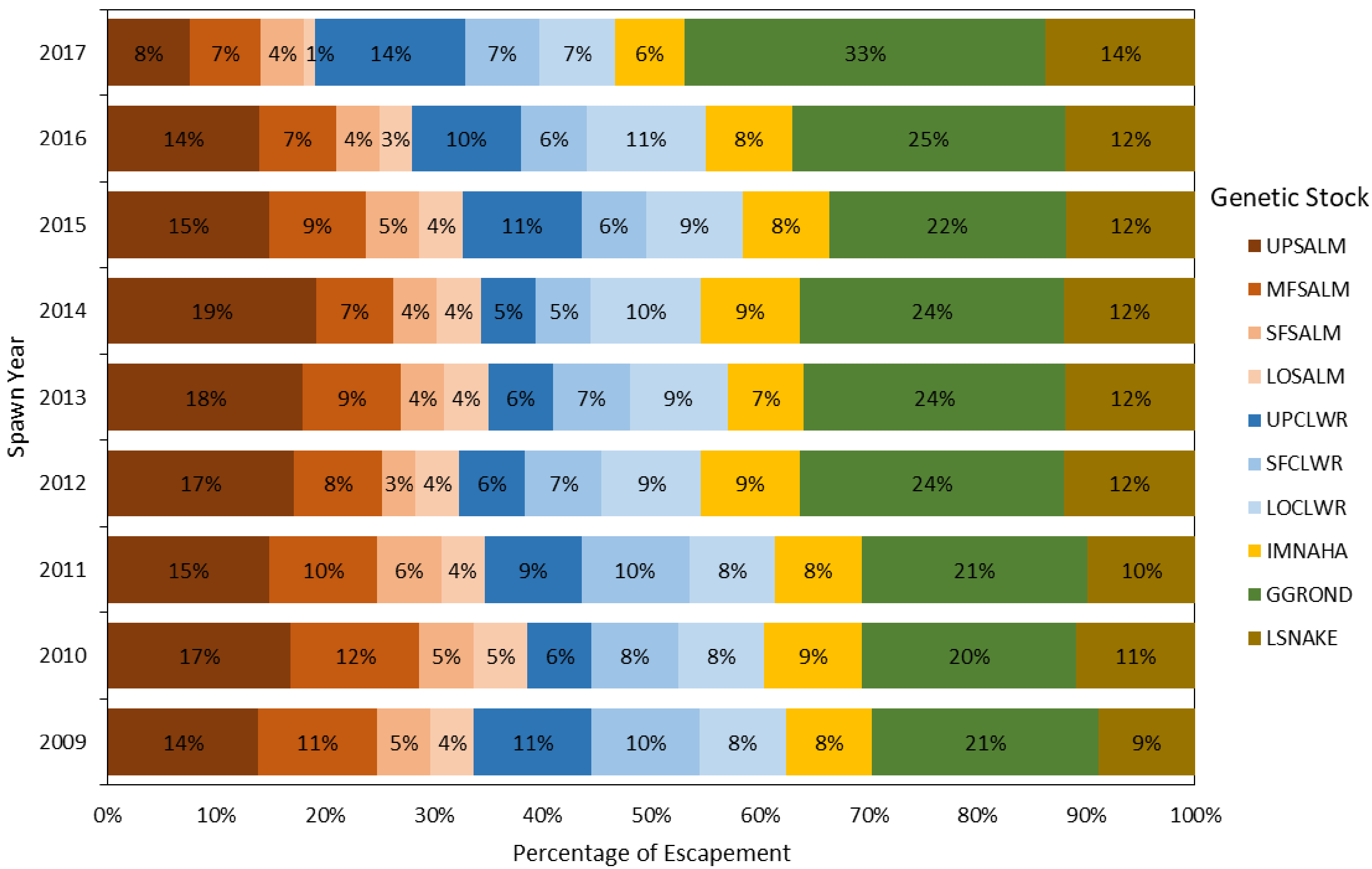


Appendix B-2. Age bias plot illustrating pairwise comparisons of scale assigned saltwater-age with known age for Chinook Salmon at Lower Granite Dam, SY2017 (Micah Davison, IDFG, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. PA = percent agreement.



Appendix C: Wild steelhead at Lower Granite Dam, spawn year 2017.

Appendix C-1. Percentage of the estimated escapement of wild steelhead by genetic stock to the overall estimated wild escapement at Lower Granite Dam, spawn years 2009 - 2017. See text for stock abbreviations.



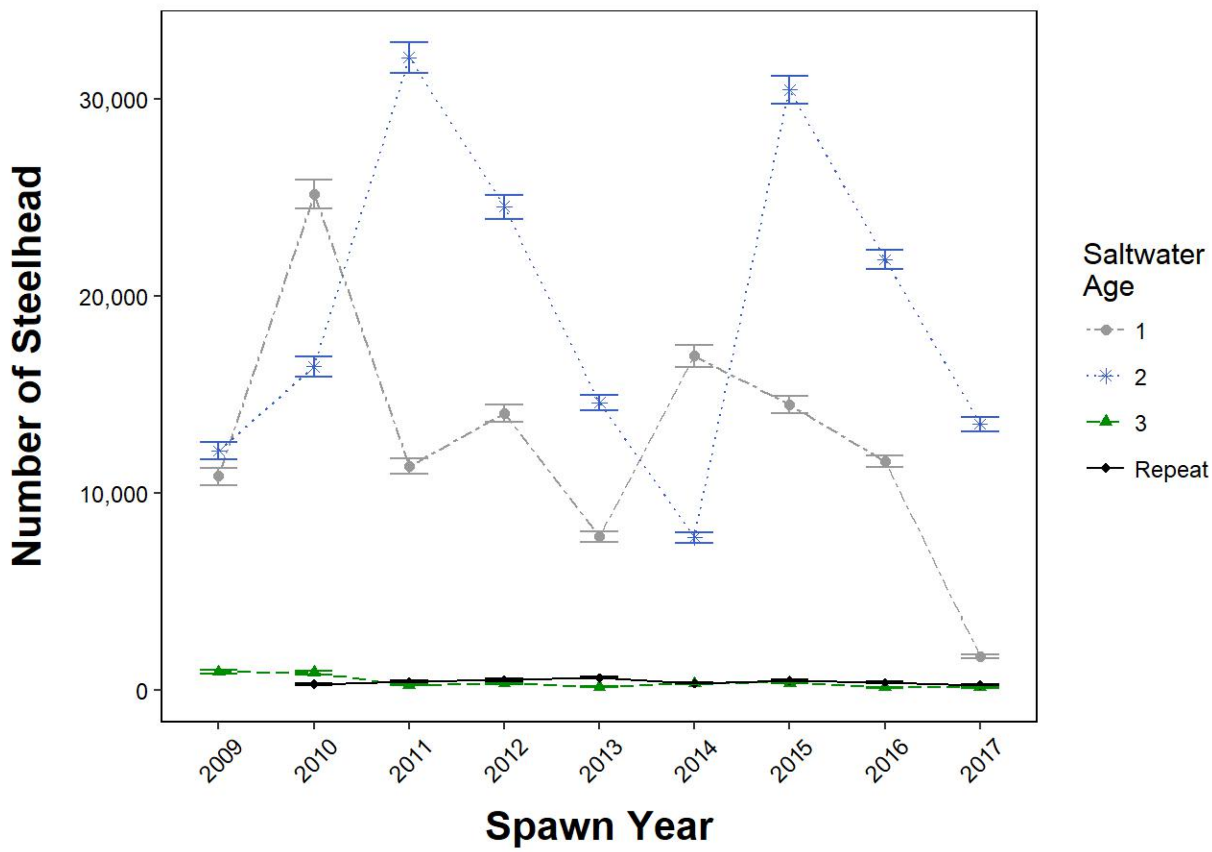
Appendix C-2. Estimated escapement of wild steelhead at Lower Granite Dam by sex and size for each genetic stock, spawn year 2017. L = lower bound and U = upper bound of 90% confidence intervals. See text for stock abbreviations.

Spawn Year & Genetic Stock	Estimated number of steelhead at Lower Granite Dam														
	Female			Male			Large			Small			Total Wild		
	Estimate	**L**	**U**	**Estimate**	**L**	**U**	**Estimate**	**L**	**U**	**Estimate**	**L**	**U**	**Estimate**	**L**	**U**
UPSALM	804	709	890	370	320	416	41	29	53	1,133	1,012	1,255	1,174	1,047	1,296
MFSALM	837	734	937	184	152	215	266	223	309	755	661	846	1,021	905	1,139
SFSALM	519	439	598	108	82	134	304	252	354	323	269	375	627	536	720
LOSALM	96	64	128	61	37	85	21	9	35	136	96	179	157	113	206
UPCLWR	1,709	1,572	1,847	440	392	487	1,290	1,176	1,398	859	778	936	2,149	1,980	2,322
SFCLWR	778	686	868	277	235	317	575	501	645	480	416	541	1,055	935	1,174
LOCLWR	815	715	906	269	228	306	165	136	193	919	806	1,020	1,084	962	1,202
IMNAHA	759	668	846	245	208	282	20	12	29	984	871	1,098	1,004	890	1,121
GGROND	3,895	3,685	4,088	1,270	1,186	1,354	218	192	246	4,947	4,702	5,194	5,165	4,903	5,421
LSNAKE	1,482	1,355	1,609	658	593	723	101	83	121	2,039	1,874	2,195	2,140	1,979	2,317
Total	**11,694**	**11,327**	**11,991**	**3,882**	**3,727**	**4,016**	**3,001**	**2,841**	**3,145**	**12,575**	**12,194**	**12,903**	**15,576**	**15,171**	**15,991**

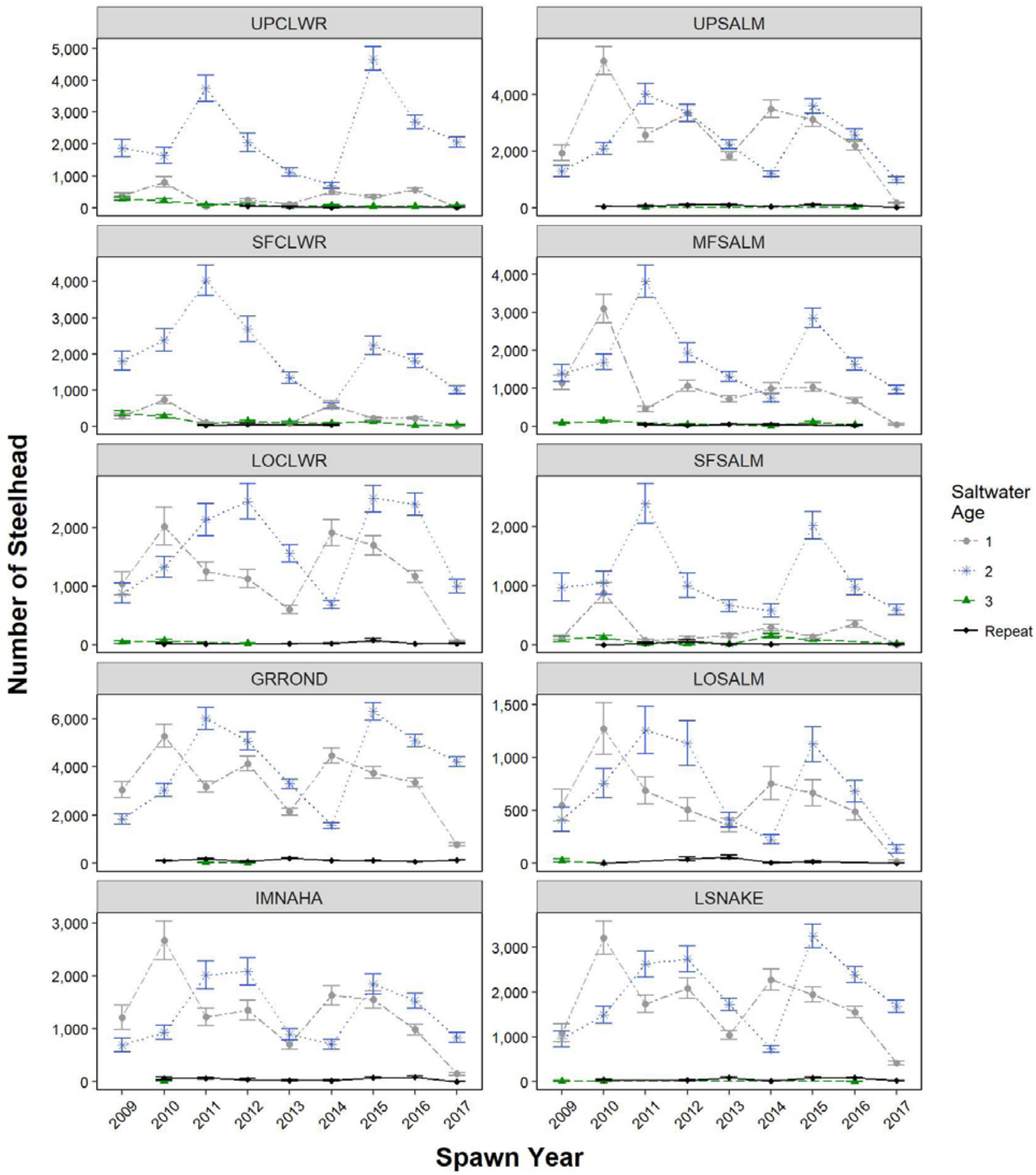
Appendix C-3. Estimated escapement of wild steelhead at Lower Granite Dam by age class, brood year, and migration year for each genetic stock, spawn year 2017. Only individual fish that had both a total age and an assigned stock were used (n = 1,327). See text for stock abbreviations.

	Smolt migration year (MY), brood year (BY), and age class																	
	MY2012	MY2013						MY2014						MY2015				
Genetic Stock	BY10 2.2R1	BY10 3.2R	BY10 3.3	BY11 2.2R	BY11 2.3	BY12 1.2R	BY12 1.3	BY10 4.2	BY11 3.2	BY12 2.1R	BY12 2.2	BY13 1.2	BY11 4.1	BY12 3.1	BY13 2.1	BY14 1.1	Total Abundance
UPSALM	0	0	0	0	0	13	0	18	185	0	752	37	0	61	84	24	1,174
MFSALM	0	0	0	0	0	0	0	44	566	0	355	0	12	24	20	0	1,021
SFSALM	0	12	0	0	21	0	0	78	403	0	109	1	0	1	2	0	627
LOSALM	0	0	0	0	0	0	0	0	31	0	96	10	0	10	10	0	157
UPCLWR	0	15	49	0	0	0	10	62	1,142	0	829	23	0	0	19	0	2,149
SFCLWR	0	0	9	0	32	0	0	9	343	0	614	37	0	11	0	0	1,055
LOCLWR	0	0	0	11	0	11	0	10	259	0	665	70	0	20	38	0	1,084
IMNAHA	0	0	0	10	0	0	0	11	303	0	526	0	0	67	77	10	1,004
GRROND	12	13	0	45	0	12	0	45	1,102	66	2,881	196	38	263	461	31	5,165
LSNAKE	0	0	0	30	0	0	0	12	357	0	1,225	93	0	66	319	38	2,140
Total	**12**	**40**	**58**	**96**	**53**	**36**	**10**	**289**	**4,691**	**66**	**8,052**	**467**	**50**	**523**	**1,030**	**103**	**15,576**

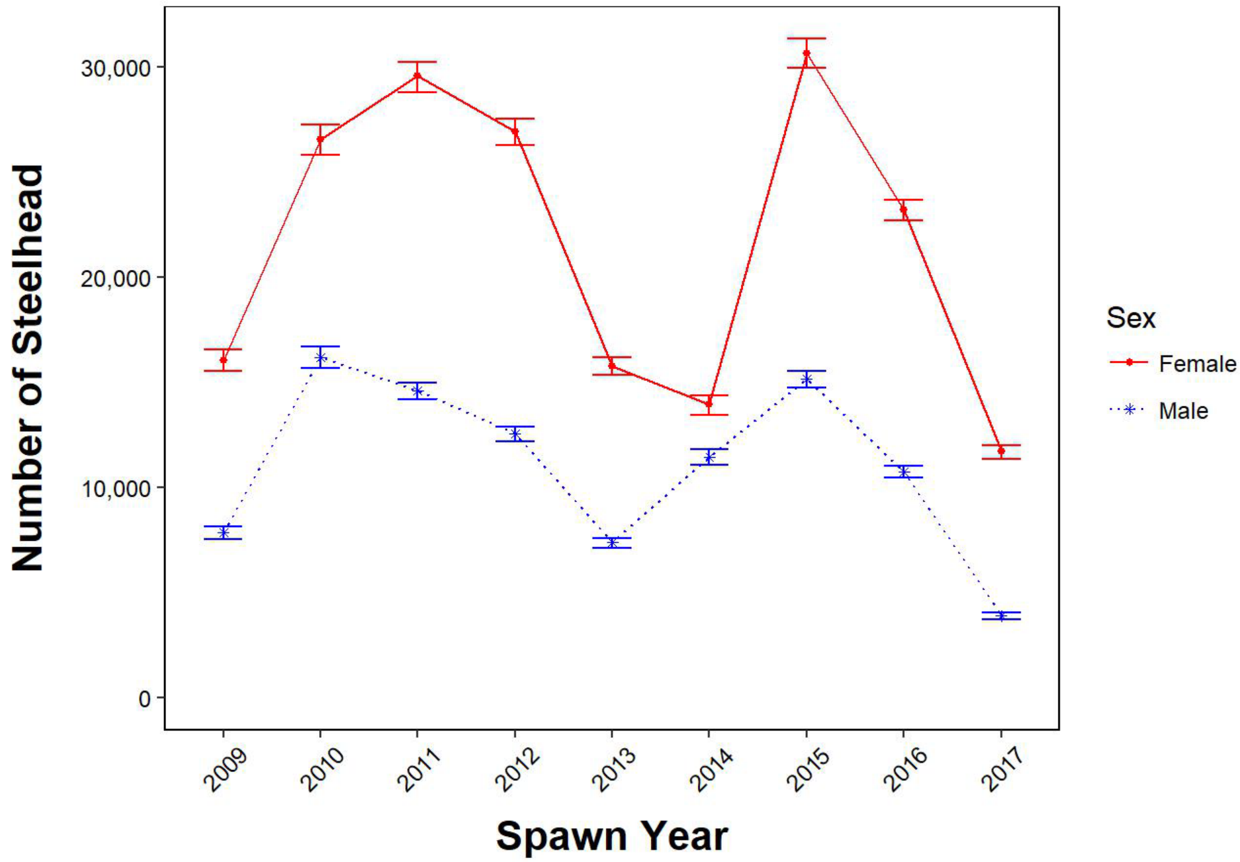
Appendix C-4. Estimated escapement by saltwater age of wild steelhead at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%. Repeat refers to steelhead showing evidence of participating in multiple spawning years.



Appendix C-5. Estimated escapement by genetic stock and saltwater age of wild steelhead at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%. Repeat refers to steelhead showing evidence of participating in multiple spawning years. See text for stock abbreviations.

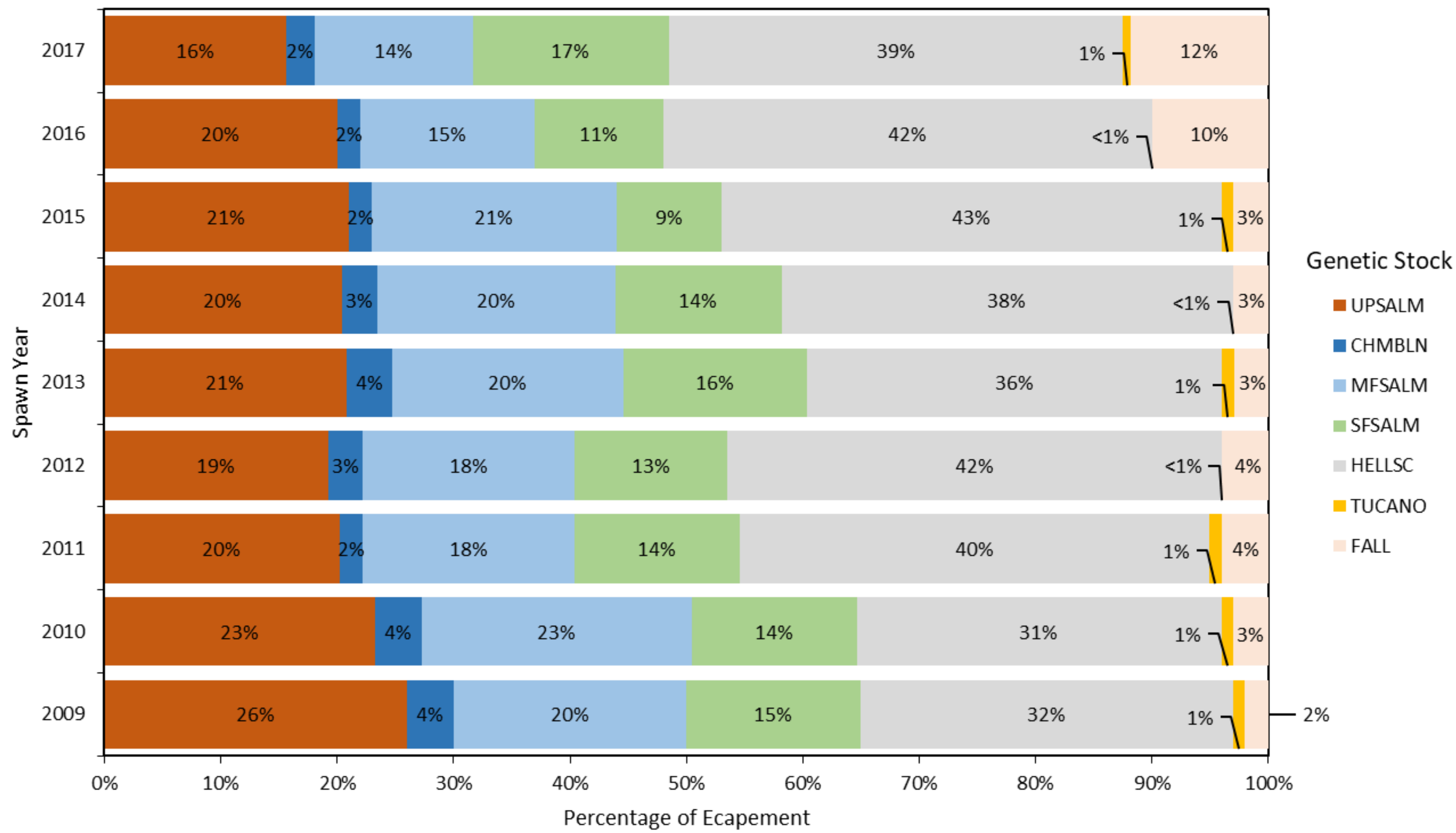


Appendix C-6. Estimated escapement by sex of wild steelhead at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%.



Appendix D: Wild Chinook Salmon at Lower Granite Dam, spawn year 2017.

Appendix D-1. Percentage of the estimated escapement of wild Chinook Salmon by genetic stock to the overall estimated wild escapement at Lower Granite Dam, spawn years 2009-2017. See text for stock abbreviations.



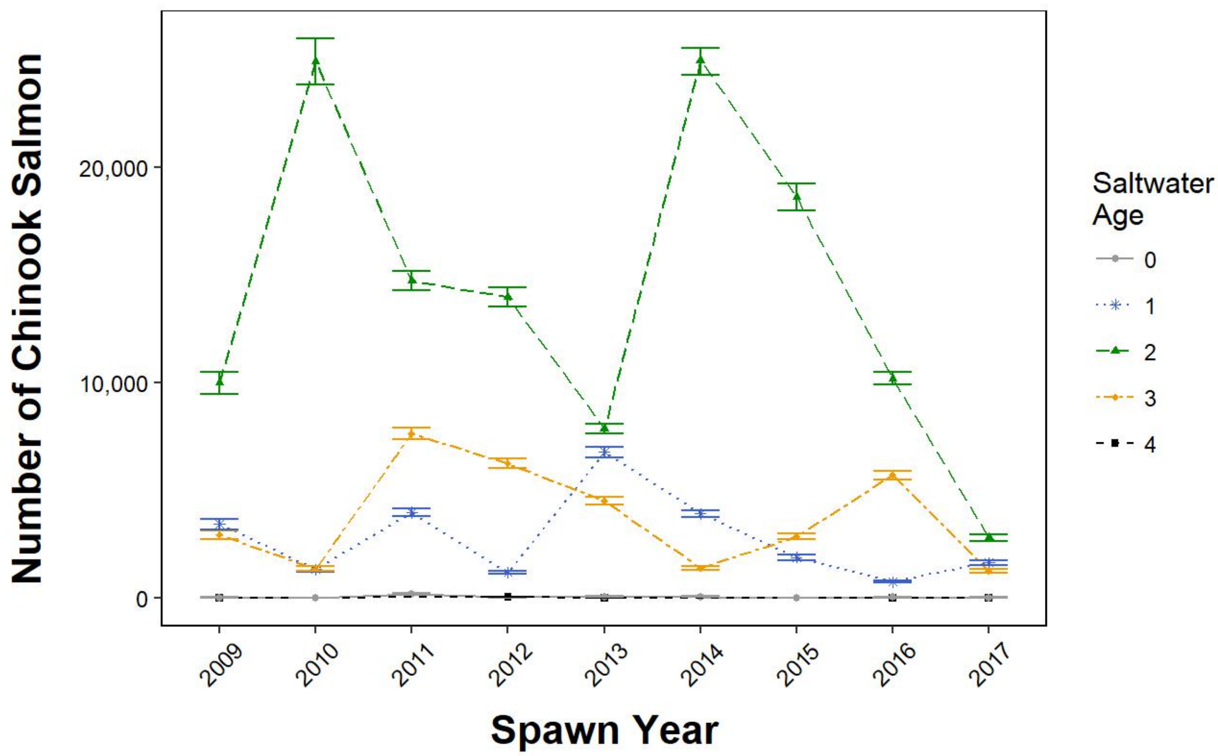
Appendix D-2. Estimated escapement of wild Chinook Salmon at Lower Granite Dam by sex and by size for each genetic stock, spawn years 2017. L = lower bound and U = upper bound of 90% confidence intervals. See text for stock abbreviations.

Spawn Year & Genetic Stock	Estimated number of Chinook Salmon at Lower Granite Dam														
	Female			Males			Large			Small			Total Wild		
	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U
UPSALM	485	419	548	422	364	479	714	626	801	193	161	225	907	801	1,019
CHMBLN	60	38	82	77	49	107	98	65	131	39	20	59	137	96	183
MFSALM	259	217	300	530	455	604	508	438	578	281	238	324	789	687	892
SFSALM	371	321	420	605	527	679	675	591	755	301	255	348	976	864	1,088
HELLSC	926	846	1,007	1,333	1,222	1,442	1,715	1,583	1,844	544	490	599	2,259	2,092	2,433
TUCANO	8	2	15	33	14	54	23	9	37	18	7	31	41	21	66
FALL	381	327	437	303	258	350	624	543	707	60	45	75	684	599	774
Total	**2,490**	**2,352**	**2,611**	**3,303**	**3,125**	**3,460**	**4,357**	**4,145**	**4,549**	**1,436**	**1343**	**1,523**	**5,793**	**5,537**	**6,043**

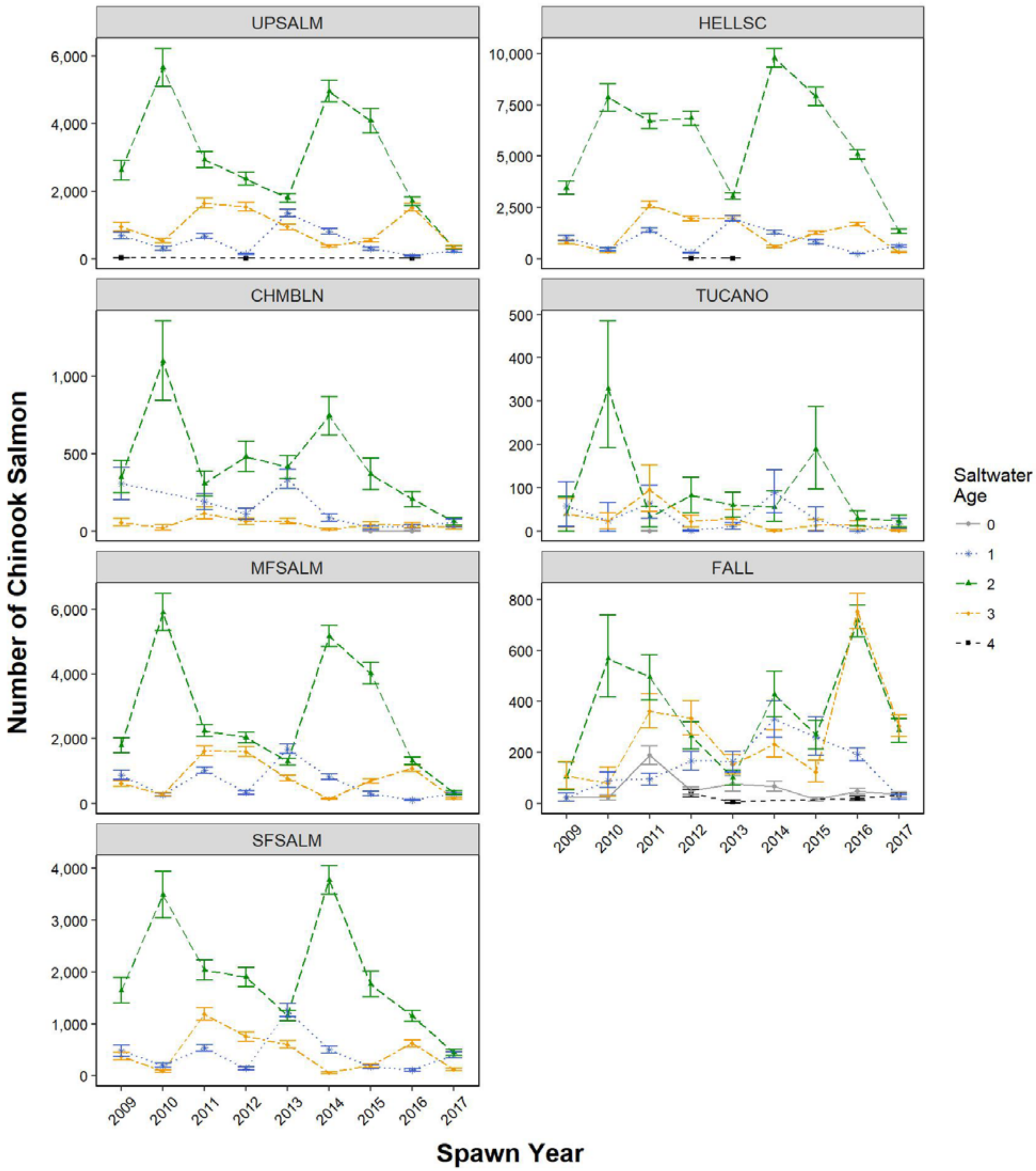
Appendix D-3. Estimated escapement of wild Chinook Salmon at Lower Granite Dam by age class for each genetic stock, spawn year 2017. Only individual fish that had both a total age and an assigned stock were used (n = 1,120). See text for stock abbreviations.

	Smolt migration year (MY), brood year (BY), and age class																	
	MY2013			MY2014				MY2015				MY2016				MY2017		
	BY11	BY12		BY11	BY12	BY13		BY12	BY13	BY14		BY13	BY14	BY15		BY14	BY15	Total
Genetic Stock	**1.4**	**0.4**		**2.3**	**1.3**	**0.3**		**2.2**	**1.2**	**0.2**		**2.1**	**1.1**	**0.1**		**2.0**	**1.0**	**Abundance**
UPSALM	0	0		0	331	13		0	325	4		0	223	11		0	0	907
CHMBLN	0	0		0	21	0		0	63	0		0	53	0		0	0	137
MFSALM	0	0		0	147	7		0	328	9		0	298	0		0	0	789
SFSALM	0	0		0	111	14		0	428	20		0	378	25		0	0	976
HELLSC	0	0		0	310	0		4	1,316	9		4	587	29		0	0	2,259
TUCANO	0	0		0	1	0		0	23	0		0	17	0		0	0	41
FALL	5	28		61	205	37		84	158	46		0	26	0		4	30	684
Total:	**5**	**28**	**0**	**61**	**1,126**	**71**	**0**	**88**	**2,641**	**88**	**0**	**4**	**1,582**	**65**	**0**	**4**	**30**	**5,793**

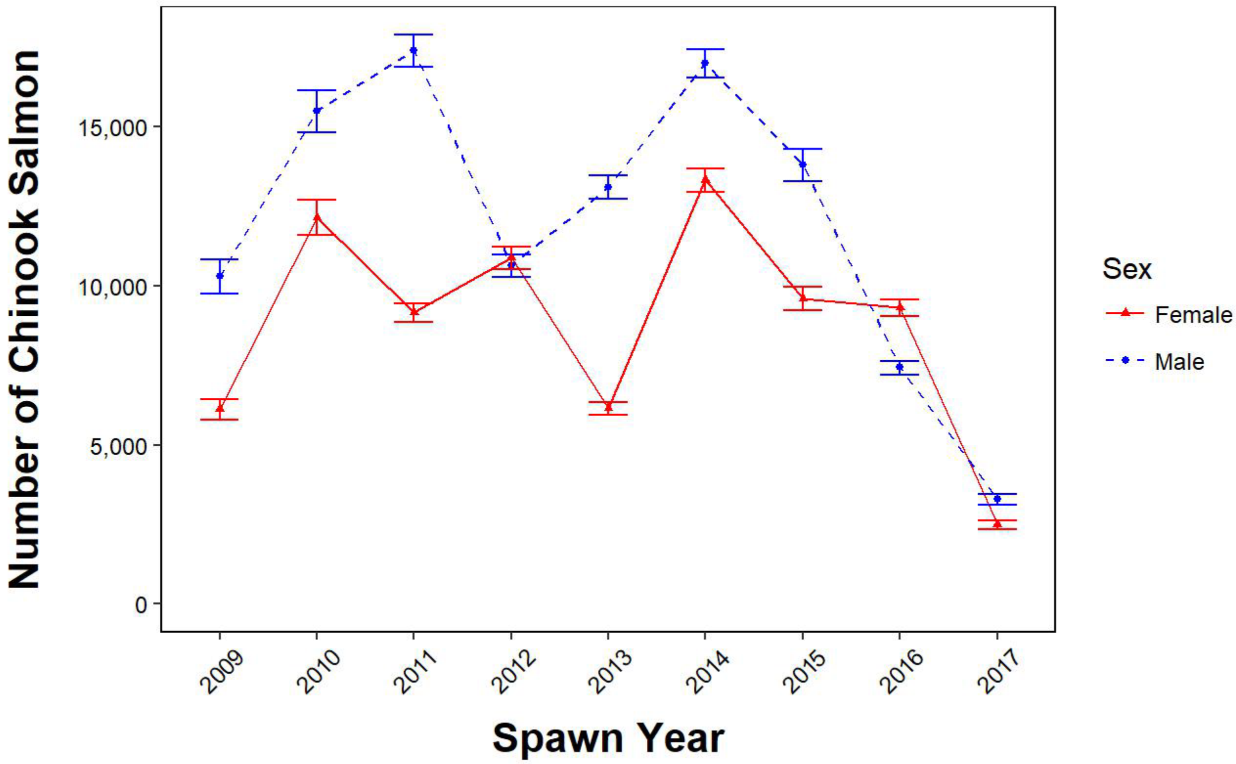
Appendix D-4. Estimated escapement by saltwater age of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%. Saltwater age-0 refers to mini-jacks.



Appendix D-5. Estimated escapement by genetic stock and saltwater age of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%. Saltwater age-0 refers to mini-jacks. See text for stock abbreviations.



Appendix D-6. Estimated escapement by sex of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2017. Confidence intervals are at 90%.



Appendix E: Comparison of visual and genetic identification of Fall Chinook at Lower Granite Dam.

INTRODUCTION

An increasing number of fall Chinook Salmon have been observed crossing LGR during the USACE spring-summer run period (on or before August 17th, Camacho et al. 2017, Powell et al. 2018). LGR trap personnel have noted a difference in appearance of spring-summer Chinook Salmon compared to fall Chinook Salmon and have used this difference to distinguish between the run types. Trap personnel determined that late in the spring-summer sampling period, spring-summer Chinook Salmon tend to be darker in color and the fall Chinook Salmon tend to be brighter in color.

The objective of this study was to determine the accuracy of visual identification at LGR of fall Chinook compared to genetic identification.

METHODS

Adult fish facility staff were asked to identify fall Chinook salmon crossing LGR during the spring-summer sample period in SY2017 to investigate the accuracy of visual identification of fall Chinook Salmon during this trapping period. We compared the visual identification to genetic identification using PBT and GSI analyses.

RESULTS

There were a total of 33 genotyped fish (1.6%, Table 1) identified as a fall Chinook salmon during the spring and summer sampling periods of the SY2017. One fish (0.0%, Table 1), or the 2,055 genotyped, was incorrectly identified as a fall Chinook (Type I error). In addition, there were 127 (6.2%, Table 1) genetically identified fall Chinook that were not visually identified by the adult fish facility (Type II error).

DISCUSSION

Visual identification of fall Chinook Salmon during the spring-summer sampling periods was highly accurate (97.0%) if an identification was made. The Type II error rate of 6.2% is likely an upper bound estimate of the true false negative rate. The cause of this potential Type II error rate inflation is that there are two ways an individual was not identified as a fall Chinook Salmon. First, staff may not have been able to visually distinguish a fish (true Type II error). Second, an identification may not have been attempted. Due to the type II error, it is recommended to use genetic identification to distinguish fall Chinook Salmon from spring-summer Chinook. Further investigation should occur during the fall run period to determine if error rates are similar.

Table 1. Visual and genetic identification to lineage of genotyped adult Chinook salmon trapped crossing Lower Granite Dam in SY2017.

	PBT/GSI Identification		
Visual Identification	Spring/Summer Chinook	Fall Chinook	*Total*
Spring/Summer Chinook	1,895 (92.2%)	127 (6.2%)	*2,022 (98.4%)*
Fall Chinook	1 (0.0%)	32 (1.6%)	*33 (1.6%)*
Total	*1,896 (92.3%)*	*159 (7.7%)*	*2,055 (100.0%)*

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