

## WILD ADULT STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, SPAWN YEAR 2020

## ANNUAL PROGRESS REPORT



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## 2020 Annual Report

## By

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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 |
| 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 |
| MPG | Major Population Group |
| MY | Smolt Migration Year |
| NMFS | National Marine Fisheries Service |
| NOAA | National Oceanic and Atmospheric Administration |
| NRAAL | Nampa Research Anadromous Ageing Laboratory |
| NWFSC | Northwest Fisheries Science Center |
| PBT | Parentage Based Tag |
| PIT | Passive Integrated Transponder |
| PSMFC | Pacific States Marine Fisheries Commission |
| QCI | Quantitative Consultants, Inc. |
| Salmon River Major Population Group |  |
| Smoltoadult 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 |
| TUCANO | Tucannon River Genetic Stock |
| UPCLWR | Upper Clearwater River Genetic Stock |
| UPSALM | Upper Salmon River Genetic Stock |
| USACE | U. S. Army Corps of Engineers |
| W | Wild |
| WDFW | Washington Department of Fish and Wildlife |

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#### Abstract

This report summarizes the abundance and composition of wild adult steelhead Oncorhynchus mykiss and spring-summer Chinook Salmon O. tshawytscha returning to Lower Granite Dam in spawn year 2020. We used a combination of window counts and biological samples collected using a systematic random sample design 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, and smolt-to-adult return rate for each species. For steelhead, the combined window count was 34,410 hatchery and wild fish. The estimated wild steelhead escapement was 9,634 fish (9,337-9,933 90\% CI), which comprised $28 \%$ of the window count. The Grande Ronde River genetic stock was the most abundant followed by the Lower Snake River. Small steelhead ( $<78 \mathrm{~cm}$, FL) dominated the total hatchery run, the total wild run, and all wild genetic stocks. The wild steelhead aggregate at Lower Granite Dam was female biased (65\%) with female percentages of genetic stocks that ranged from $53 \%$ for the Upper Clearwater River to $74 \%$ for the Lower Salmon River. We observed 19 different age classes for wild steelhead. Total age for adults at Lower Granite Dam ranged from three to eight years, with freshwater ages that ranged from one to five years, and saltwater ages that ranged from zero to three years with additional fish returning as repeat spawners. Adult-to-adult productivity was completed for brood year 2012 and was 0.56 returning recruits per spawner. Productivities for all wild steelhead genetic stocks were below replacement. The smolt-to-adult return rate for the aggregate wild steelhead run was $1.58 \%$ for smolts crossing Lower Granite Dam in migration year 2016. For spring-summer Chinook Salmon, the combined window count was 34,786 hatchery and wild fish. Few Chinook Salmon were trapped at the dam during spawn year 2020 due to COVID19 trap closures; therefore, Chinook Salmon decomposition estimates were generated using a combination of run reconstruction methods and previous years' data. The estimated wild Chinook Salmon escapement was 9,774 fish, which comprised $28 \%$ of the window count. The Hells Canyon genetic stock was the most abundant followed by the Upper Salmon River. Two-saltwater fish dominated the wild return, comprising $84 \%$ of wild Chinook Salmon. Adult-to-adult productivity was completed for brood year 2014 at 0.31 returning recruits per spawner. Productivities for all wild Chinook Salmon genetic stocks were below replacement. The smolt-to-adult return rate for the aggregate wild Chinook Salmon run was $0.64 \%$ for smolts crossing Lower Granite Dam in migration year 2016. We noted overall declining trends in escapement, productivity, and smolt-to-adult return rates for both species over the past five years.


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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 spring-summer Chinook Salmon (hereafter Chinook Salmon) were classified as threatened under the Endangered Species Act (ESA) in 1992 and Snake River steelhead trout (hereafter steelhead) were classified as threatened under the 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; ICBTRT 2003, 2005, 2009; Ford 2011, 2015; 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.

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; ICBTRT 2003, 2005, 2009; Ford 2011, 2015; NMFS 2016). 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 2019). 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; 2018a; 2018b; 2019a; 2019b; Lawry et al. 2020). 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 total length. Salmonids under 30 cm (12 inches) in length are not identified to species. Minijacks 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 LGR 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 fallrun Chinook Salmon. For steelhead, the run year at LGR is defined to be from July 1 of the previous year to June 30 of the current year. 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 (Joint Columbia River Management Staff 2020). Most steelhead pass LGR in the fall but are assigned to their spawn year the following spring.

The goal of this report is to summarize the abundance and composition of adult wild steelhead and spring-summer Chinook Salmon returning to LGR during spawn year (SY) 2020 as defined by the USACE calendar date designations. We also update the abundance trends for adult-to-adult productivity series for both species and the smolt-to-adult return (SAR) rate series for Chinook Salmon and steelhead last published by Lawry et al. 2020. The objectives of this report are to:

1. Describe LGR adult trap operations and data collection during 2019-2020, which is the timeframe encompassing all steelhead and Chinook Salmon passing LGR for SY2020.
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 SAR rate for the aggregate return of wild steelhead and Chinook Salmon.

## METHODS

## Adult Trap Operations at Lower Granite Dam

Systematic samples of adult steelhead and Chinook Salmon returning to LGR were collected during daily operation of the adult fish trap by National Marine Fisheries Service (NMFS). 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 computerized trap gate according to a predetermined sample rate. The trap gate was opened four times per hour for a length of time directed by the programmed sample rate; the trap was operational 24 hours per day. The sample rate was 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 did not operate during weekends from March 1 to August 17, and the trap rate was adjusted to still sample at the sample rate goal by compensating for the two non-trapping weekend days. In-season adjustments to the sample rate were sometimes needed to accommodate limitations at the trapping facility, changes to the forecast, or sample size goal modifications. Additionally, high ( $21^{\circ} \mathrm{C}$ or $\geq 70^{\circ} \mathrm{F}$ ) and low ( $\leq 0^{\circ} \mathrm{C}$ or $\leq 32^{\circ} \mathrm{F}$ ) water temperatures require the trapping facility to temporarily modify or cease operations.

During SY2020, the trap was closed September 7 through September 12, 2019 due to high water temperatures (Appendix A-1). It was also closed November 13, 2019 through March 1, 2020 for the winter. In addition to these closures, a unique situation occurred during SY2020 when the trap was shut down from March 25 through July 1, 2020 to comply with COVID-19 safety policies. Outside these closures, daily trapping rates varied from 20 to 100\%. The trapping rate was set at $100 \%$ from September 13 through September 16, 2019 to make up for fall Chinook Salmon broodstock sampling that was missed the week prior during the high water temperature closure. For steelhead, $88.7 \%$ of the run passed the window while the trap was open (Appendix A-2). The majority of the steelhead run crossed LGR in the fall of 2019, but a second small pulse occurred in March and April 2020. For Chinook Salmon, $8.2 \%$ of the run passed the window while the trap was open; this extremely low percentage was attributed mainly to the COVID-19 closure but also the weekend closures (Appendix A-3). Additional details on the trap can be found in Harmon (2003), Steinhorst et al. (2010), and USACE $(2019,2020)$.

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 a 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 marks and internal tags 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 were 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, or (for steelhead only) dorsal fin erosion were classified as ad-intact hatchery fish. The trap crew sampled fin tissue from all ad-intact steelhead (Chinook Salmon were excluded); genotyping for parentage-based tagging (PBT) analysis was conducted post hoc to further classify ad-intact hatchery steelhead (Hargrove et al. 2020). 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 (steelhead only). Information associated with previous PIT tagging events was not used to determine origin.

For all ad-intact steelhead, 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 (NRAAL). For all ad-intact steelhead, tissue samples for genetic analysis 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 (EFGL). All ad-intact steelhead 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 et al. 2016; Orme and Kinzer 2018; IPTDSW 2020). After processing, all fish were returned to the adult fish ladder to resume their upstream migration.

## Chinook Salmon Adjustments due to COVID-19 Closure

Chinook Salmon data collection and analysis in SY2020 faced unprecedented challenges associated with COVID-19, particularly the extended closure of the adult fish trap at LGR to follow safety policies. This trap closure occurred during the majority of the spring-summer Chinook Salmon run (Appendix A-3). Although USACE window counts for Chinook Salmon continued, estimates from limited numbers of trapped fish were deemed infeasible and, thus, we did not collect any biological samples; therefore, alternative analysis methods were developed to obtain SY2020 Chinook Salmon estimates (Appendix B-1).

## Trap Data Management

Since 2012, 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 needed 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. The IDFG LGR SQL server database also queries and combines all genetic data from the EFGL Progeny database and the ageing data from the NRAAL BioSamples database to the associated trap records.

## 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 was 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 objective was to age and genotype approximately 2,000 wild steelhead and 2,000 wild Chinook Salmon. In collaboration with our work, a second objective was to PIT tag, age, and genotype approximately 4,000 wild steelhead and 4,000 wild Chinook Salmon to estimate abundance at instream PIT detectors. We emphasize that both objectives were complimentary and not mutually exclusive, and that no wild Chinook Salmon were PIT tagged, aged, or genotyped for SY2020. While the trap was open, every ad-intact steelhead trapped at LGR was genotyped to simplify collaborative logistics and to increase accuracy and precision of abundance estimates using genetic stock identification (GSI) and PBT. All valid samples from wild steelhead were systematically subsampled if more than approximately 2,000 samples were available. The result was a pool of samples collected systematically across the spawning run and generally in constant proportion to its abundance. Hence, 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 NRAAL according to protocols detailed in Wright et al. (2015). Ages were 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 (see Copeland et al. 2018 for ageing repeat spawners). Age classes are defined as the unique combinations of SW, FW, and repeat spawning ages. Brood year (BY) is the spawn year minus the total age at spawning (total age = freshwater age + saltwater age +1 ). One year is added to scale age determinations for steelhead and Chinook Salmon where a visible annulus is not formed during growth but is assumed to have occurred. For steelhead, no visible annulus forms during the adult period of the lifecycle spent in freshwater over winter, when mineral deposits that form on scales are metabolized for gonadal and gamete growth (Persson et al. 1998; Witten and Huysseune 2009). For Chinook Salmon, no annulus forms during the first winter of juvenile development because they are still in the redd. Fish lacking either a freshwater or saltwater age were not used for analysis.

We validated wild steelhead 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 steelhead ages. Analysis of steelhead scales is sufficiently accurate to produce unbiased age compositions (Copeland et al. 2018; Reinhardt et al. 2022).

## Genetics Tissue Processing and Analysis

Detailed methods for extraction of genomic DNA from tissue samples, DNA amplification, and single nucleotide polymorphism (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) protocols at either the EFGL in Eagle, Idaho, or the Columbia River InterTribal Fish Commission's genetics laboratory in Hagerman, Idaho. Steelhead were examined at a 368 SNP marker panel and Chinook Salmon are normally examined at a 343 SNP marker panel, but no biological Chinook Salmon samples were taken in SY2020. Each panel contains SNPs for PBT, GSI, and sex-determination analysis.

Parentage-based tagging involves annual sampling and genotyping of hatchery broodstock that are used to create a database of parental genotypes. Subsequently, progeny of these genotyped parents (collected either as juveniles or adults) can be assigned back to their parents via parentage analysis. Parentage assignments were performed on all ad-intact adults returning to LGR to identify hatchery fish that were phenotypically wild (unclipped/unmarked) using the program SNPPIT (Anderson 2010, available at: https://github.com/eriqande/snppit). 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 (Delomas et al. 2020). 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 hatchery of origin and total age (Steele et al. 2013). Parentage Based Tagging is a critical tool to differentiate hatchery fish when no other physical tags (e.g., CWT and fin clips) are present and can significantly improve escapement estimates for wild Chinook Salmon and steelhead (Hargrove et al. 2021)

Genetic stock identification is a complimentary genetic technique to PBT that seeks to identify the source of origin of wild fish. Briefly, this technique involves genotyping wild fish sampled on the landscape and using these population-level allele frequencies to assign individual fish of unknown origin (adults sampled at LGR) to reporting groups (referred henceforth as genetic stocks). 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) and Powell et al. (2018) provide a detailed description of the Snake River genetic baselines used for both steelhead and Chinook Salmon GSI analyses (Figure 1; Figure 2). Genetic stocks were 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 algorithms implemented in rubias (Moran and Anderson 2019). 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: Iower Clearwater River; 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSNAKE: tributaries of the lower Snake River both upstream (e.g., Alpowa and Asotin creeks) and downstream (primarily Tucannon River) of LGR. Some Tucannon River steelhead ascend the 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 account for returning adults that originated from populations 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 springsummer 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 (Hargrove et al. 2020).

Phenotypic sex was not, and generally cannot, be reliably determined by personnel at the LGR trap, as most adult anadromous fish typically do not exhibit sexually dimorphic characteristics at LGR. A sex-determination assay 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 Fish Passage Center (FPC) website: http://www.fpc.org/environment/home.asp. Additional daily window count operation information was obtained from USACE annual fish passage reports (USACE 2019, 2020). For Chinook Salmon, the adult count was combined with the jack count to derive the total count on a daily basis.

For SY2020, we generated estimates of Chinook Salmon escapement by origin, genetic stock, and age using a combination of run reconstruction methods and previous years' data (Appendix B-1). Origin and genetic data from the past eleven years (SY2009-2019), and age data from the previous year (SY2019), were used to decompose the 2020 window counts. The age composition of the SY2019 wild adult PIT tag returns (fish tagged as juveniles) was used to break out the saltwater age-2 and -3 wild adults. To obtain brood year estimates, freshwater ages were reconstructed using the SY2014-2019 average freshwater age proportions within a saltwater age class and applying those proportions to the saltwater age estimates. We did not attempt to estimate escapement by size or sex, nor did we attempt to estimate precision ( $90 \%$ confidence intervals, CI).

For steelhead only, 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; R Development Core 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 ( $n \geq 100$ ) 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 is nested within the previous category (Figure 3). First, the total escapement is decomposed into rearing type (ad-intact hatchery, ad-clipped hatchery, and wild). Fish from each rearing type are then divided into primary categories. Hatchery-reared fish (ad-clipped and ad-intact) are divided into primary size categories (large and small). Wild-reared fish are divided into primary categories by genetic stock and Major Population Group. Wild fish genetic stocks are then 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 $90 \%$ Cls 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 (B-Index), whereas small steelhead are less than 78 cm FL (A-Index), for fisheries managed under the U.S. v. Oregon Management Agreement (Joint Columbia River Management Staff 2020). 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).

## Smolt-to-Adult Return Rate

To estimate the aggregate SAR rate for wild steelhead and Chinook Salmon, the age composition of adults at LGR was combined with estimates of emigrating wild smolt cohorts at LGR. For steelhead, we continue the SAR series that began with smolt migration year 2010. Repeat spawning steelhead were not included in the SAR estimates because they were already accounted for on their maiden spawning migration. Furthermore, repeat spawners likely have different survival rates than smolts. For Chinook Salmon, we continue the SAR series that began with smolt migration year 1996. Smolt production estimates for both species were acquired from Ebel et al. (2022).

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:

$$
S A R_{k}=\frac{\sum_{l-1}^{4} r_{k+l}}{S_{k}},
$$

where $S A R_{k}$ 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 spring-summer Chinook Salmon and steelhead 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

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

and the upper limit by

$$
\frac{\left(2 n p+t_{\alpha / 2}^{2}+1\right)+t_{\alpha / 2} \sqrt{t_{\alpha / 2}^{2}+(2+1 / n)+4 p(n q+1)}}{2\left(n+t_{\alpha / 2}^{2}\right)}
$$

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

## RESULTS

## Steelhead Escapement

The USACE total window count of steelhead for SY2020 was 34,410 fish (Table 2). The LGR trap captured 7,795 of them, of which 2,349 were valid wild fish (Appendix A-5). Our estimate of wild escapement is 9,634 fish ( $9,337-9,93390 \% \mathrm{CI}$ ), which comprises approximately $28 \%$ of the window count (Table 2). The remaining 24,776 fish were of hatchery origin. We estimate adclipped hatchery escapement was 22,453 fish ( $22,130-22,77490 \% \mathrm{CI}$ ) and ad-intact hatchery escapement was 2,323 fish ( $2,142-2,50790 \% \mathrm{CI}$ ). External marks, internal tags, and genetics were used to determine that $9 \%$ of the total hatchery fish and $7 \%$ of the total steelhead run were ad-intact hatchery fish. For all ad-intact steelhead, $19 \%$ were hatchery fish.

## Steelhead by Genetic Stock, Size, Sex, and Age

Relative abundance of wild steelhead by genetic stock varied greatly in SY2020, with the Grande Ronde highest at $34 \%$ and the South Fork Salmon stock lowest at 1\% (Appendix D-1). Escapement estimates for each genetic stock were as follows (Figure 4; Appendix D-2): UPSALM 1,779 fish (1,641-1,922 90\% CI); MFSALM 453 fish (385-521 90\% CI); SFSALM 99 fish (67-133 90\% CI); LOSALM 175 fish (131-223 90\% CI); UPCLWR 363 fish (292-437 90\% CI); SFCLWR 459 fish (379-546 90\% CI); LOCLWR 476 fish (399-555 90\% CI); IMNAHA 714 fish (621-810 90\% $\mathrm{CI})$; GRROND 3,285 fish (3,088-3,481 90\% CI); and LSNAKE 1,831 fish (1,685-1,987 90\% CI).

Small steelhead were most abundant across all origins (Table 2). Small wild steelhead were estimated at 9,234 fish ( $8,930-9,50090 \% \mathrm{CI}$ ), small ad-clipped hatchery steelhead at 20,259 fish (19,929-20,593 90\% CI), and small ad-intact hatchery steelhead at 1,452 fish (1,3051,602 90\% CI). Large wild steelhead were estimated at 400 fish ( $349-44290 \% \mathrm{CI}$ ), large adclipped hatchery steelhead at 2,194 fish ( $2,028-2,36390 \% \mathrm{Cl}$ ), and large ad-intact hatchery steelhead at 871 fish ( $757-99290 \% \mathrm{Cl}$ ). Stock-specific estimates for wild fish by size are in Appendix D-2.

Wild steelhead were female biased, and females accounted for $65 \%$ of the overall wild return (Appendix D-3). Female escapement was estimated at 6,213 fish (5,985-6,393 90\% CI) and males at 3,421 fish ( $3,260-3,54890 \% \mathrm{CI}$ ). Sex ratios for each genetic stock mirrored the aggregate wild run and ranged from 53\% female for Upper Clearwater River to 74\% female for Lower Salmon River (Appendix D-2).

Nineteen different age classes were observed from the 1,884 wild fish that we were able to assign both a genetic stock and a total age (Appendix D-4). Total age at LGR ranged from three to eight years with freshwater age ranging from one to five years and saltwater age ranging from zero to three years. Some steelhead returned as repeat spawners.

Repeat spawning fish made up $0.5 \%$ of all wild steelhead crossing LGR. Repeat spawners were observed in most genetic stocks except for IMNAHA, SFCLWR, SFSALM, and UPCLWR. The proportions of repeat spawners slightly varied across the other genetic stocks. Repeat spawners as a proportion of the run for each genetic stock ranged from $0.2 \%$ (UPSALM) to up to 1.7\% (LOSALM).

For all genetic stocks, age-5 (fish that hatched in BY2015) was the dominant total age cohort, with the exception of Lower Clearwater where age-4 (BY2016) was the dominant age cohort. We estimated that $174(141-20790 \% \mathrm{CI})$ of the returning adults were hatched in brood year (BY) 2017 and were age-3; 3,667 (3,507-3,799 90\% CI) were from BY2016 and were age-4; 4,429 (4,251-4,578 90\% CI) were from BY2015 and were age-5; 1,268 (1,188-1,339 90\% CI) were from BY2014 and were age-6; 91 ( $72-10790 \% \mathrm{Cl}$ ) were from BY2013 and were age-7; and 5 (1-9 90\% CI) were from BY2012 and were age-8.

The majority of the wild return, or 59\%, emigrated to the ocean as freshwater age-2 and, excluding repeat spawners, $57 \%$ returned as saltwater age-1 (Appendix D-5). Saltwater age estimates were 29 (19-40 90\% CI) zero-saltwater from MY2019; 5,511 (5,297-5,685 90\% CI) one-saltwater from MY2018; 3,993 (3,823-4,134 90\% CI) two-saltwater from MY2017; 53 (38-67 $90 \% \mathrm{Cl})$ three-saltwater from MY2016; and 48 (35-59 90\% CI) repeat spawning steelhead regardless of migratory year. Furthermore, one-saltwater fish made up the vast majority of returning steelhead for six of the ten genetic stocks; the remaining four stocks (LOCLWR, SFCLWR, SFSALM, and UPCLWR) consisted mostly of two-saltwater fish (Appendix D-6). The mean fork lengths of one-saltwater and two-saltwater fish were below the 78 cm FL threshold for large steelhead (Appendix D-7).

Readers accurately determined the saltwater-age of $98 \%$ of the scale samples ( $\mathrm{n}=63$ ) from known saltwater-age steelhead collected during SY2020 (Appendix C-1). The known saltwater-age sample was $48 \%$ one-saltwater and $52 \%$ two-saltwater. There were no threesaltwater fish, four-saltwater fish, or repeat spawners in the known saltwater-age sample.

## Steelhead Adult-to-Adult Productivity

Wild steelhead returning to LGR in SY2020 completed the BY2012 cohort necessary for an adult-to-adult productivity estimate. Brood year 2012 returned 22,240 adults from 39,438 parents resulting in an adult-to-adult productivity estimate of 0.56 recruits per spawner, which is below the 1.0 recruits per spawner necessary for replacement (Figure 5). A preliminary estimate of adult-to-adult productivity for the BY2013 cohort also placed it below replacement. Although unlikely to change significantly, the estimate for BY2013 is preliminary and will be completed in SY2021.

None of the ten genetic stocks had adult-to-adult productivity estimates that were above replacement (Figure 6). The recruits per spawner estimates for each stock were as follows: UPSALM 0.54, MFSALM 0.29, SFSALM 0.25, LOSALM 0.39, UPCLWR 0.60, SFCLWR 0.42, LOCLWR 0.65, IMNAHA 0.44, and GRROND 0.73. Estimates for LSNAKE were not included because the fish from this stock recorded at LGR were only a proportion of the total returning adults; therefore, productivity estimates for LSNAKE were not representative of the entire stock. Preliminary estimates of adult-to-adult productivity by genetic stock for BY2013 placed all genetic stocks below replacement. The estimates for BY2013 are preliminary and will be completed in SY2021.

## Steelhead Smolt-to-Adult Return Rate

This report continued the SAR series that began with smolt MY2010 (Table 3; Figure 7). With adult returns from SY2020, the SAR time series was complete for MY2010-2016. The most recent completed cohort, MY2016, returned 12,720 fish from 805,433 emigrants for a SAR estimate of 1.58 ( $1.55-1.6195 \% \mathrm{CI}$ ). The 5 -year geometric mean SAR was $2.32 \%$.

SARs ranged from a high of 5.33 (5.29-5.38 95\% CI) in MY2012 to a low of 0.56 (0.55$0.5895 \% \mathrm{CI}$ ) in MY2015. Four of the seven completed MY cohorts were above the Northwest Power and Conservation Council (NPCC) fish and wildlife program minimum of 2\% (NPCC 2009). However, the 5-year geometric mean SAR (2.32\%) for the 2012-2016 cohorts ( $n=5$ ) was less than the target geometric mean of $4 \%$.

The SAR estimate for the MY2016 cohort was well below the NPCC fish and wildlife program mean of $4 \%$ and minimum of $2 \%$; however, the 5 -year geometric mean just barely reached the minimum (NPCC 2009; Figure 7). Our estimated SAR rates in the past have been slightly higher but closely track the estimates provided by the Comparative Survival Study (CSS; McCann et al. 2015).

## Chinook Salmon Escapement

The USACE total window count of Chinook Salmon for SY2020 was 34,786 fish (Table 4). Few Chinook Salmon were captured in the LGR trap due to COVID-19 safety closures, and these trap data were not suitable to use for any SY2020 estimates because they only represented a small proportion of the total run (Appendix A-3). Our estimate of wild escapement using run reconstruction was 9,774 fish ( 8,565 adults plus 1,209 jacks), which comprised approximately $28 \%$ of the window count (Table 4). The remaining 25,012 fish ( 21,564 adults plus 3,448 jacks) were of hatchery origin. We estimated ad-clipped hatchery escapement was 22,418 fish and adintact hatchery escapement was 2,594 fish. Ten percent of the total hatchery fish and $8 \%$ of the total Chinook Salmon run were ad-intact hatchery fish. For all ad-intact Chinook Salmon, 21\% were hatchery fish. Calculations for SY2020 estimates can be found in Appendix B-1.

## Chinook Salmon by Genetic Stock and Age

Relative abundance of wild Chinook Salmon by genetic stock in SY2020 using run reconstruction varied greatly with HELLSC having the highest percentage of the total wild adults at $35 \%$ and TUCANO having the least at $0.5 \%$ (Appendix E-1). Of the 8,565 wild adults, escapement estimates for each genetic stock were UPSALM 1,725; MFSALM 1,486; CHMBLN 214; SFSALM 1,193; HELLSC 3,438; TUCANO 50; and FALL 459 fish (Figure 8; Appendix E-2).

Saltwater age estimates of wild Chinook Salmon were estimated to be 1,209 one-saltwater jacks from MY2019; 8,172 two-saltwater fish from MY2018; and 393 three-saltwater fish from MY2017 (Appendix E-3). The majority of the wild return (84\%) returned as saltwater age-2.

## Chinook Salmon by Size and Sex

Abundance of wild Chinook Salmon by size and sex was not possible for SY2020 due to the COVID-19 trap closure and lack of trap samples.

## Chinook Salmon Adult-to-Adult Productivity

Wild Chinook Salmon returning to LGR in SY2020 completed the BY2014 cohort necessary for an adult-to-adult productivity estimate. Brood year 2014 returned 9,294 adults from 30,338 parents resulting in an adult-to-adult productivity estimate of 0.31 recruits per spawner, which is below the 1.0 recruits per spawner necessary for replacement (Figure 9). A preliminary estimate of adult-to-adult productivity for the BY2015 cohort also placed it below replacement (Figure 9). Although unlikely to change significantly, the estimate for BY2015 is preliminary and will be completed in SY2021.

Adult-to-adult productivity estimates were below replacement for all genetic stocks. Recruits per spawner of each genetic stock are as follows: UPSALM at 0.24; MFSALM at 0.24; CHMBLN at 0.25 ; SFSALM at 0.39 ; and HELLSC at 0.33 (Figure 10). Estimates for TUCANO and FALL stocks were not included because the fish from these stocks recorded at LGR were only a proportion of the total returning adults; therefore, productivity estimates for these two stocks were not representative of their entire stock. Preliminary estimates of adult-to-adult productivity by genetic stock for BY2015 also placed all genetic stocks below replacement (Figure 10). The estimates for BY2015 are preliminary and will be completed in SY2021.

## Chinook Salmon Smolt-to-Adult Return Rate

This report continued the SAR series that began with smolt migration year 1996 (Table 5; Figure 11). With adult returns from SY2020, the SAR time series was complete for MY1996-2016. The most recent completed cohort, MY2016, returned 9,184 fish from 1,424,036 yearling emigrants for a SAR estimate of 0.64 ( $0.63-0.6695 \% \mathrm{CI}$ ). The 10-year geometric mean SAR was $1.55 \%$ and the 5 -year geometric mean SAR was $1.22 \%$.

SARs for the MY2016 cohort and both geometric means were below the NPCC fish and wildlife program mean of $4 \%$ and minimum of $2 \%$ (NPCC 2009; Figure 11). Our estimated SAR rates in the past have been slightly higher but closely track the estimates provided by the Comparative Survival Study (CSS; McCann et al. 2015).

## DISCUSSION

Abundance of returning SY2020 wild summer steelhead and spring-summer Chinook Salmon measured at Lower Granite Dam was low. For steelhead, overall escapement (all rear types combined) counted at the LGR window in SY2020 was the lowest on record going back to at least SY1998 (Table 2). Hatchery steelhead escapement was also the lowest on record, and wild steelhead escapement was below 10,000 fish, the fifth lowest on record. Abundance of wild, natural-origin steelhead was well below IDFG's "healthy and harvestable" escapement goals and NMFS' minimum abundance thresholds (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). Wild steelhead escapement was less than one-tenth of the proposed escapement goal of 104,500 fish, and less than half of NMFS' minimum abundance threshold of 21,000 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). The stock-specific wild escapement estimate for the Lower Snake and Upper Salmon stocks increased significantly, whereas South Fork Salmon and Upper Clearwater stocks decreased significantly compared to SY2019, as evidenced by non-overlapping 90\% CIs (Figure 4). The remaining genetic stocks did not change significantly from last year. Despite the presence or absence of statistical significance, the 5-year trend in point estimates suggests a continued decline for all stocks.

Unfortunately, large wild, large hatchery ad-clipped, and large hatchery ad-intact steelhead escapement all decreased significantly from SY2019 to SY2020 (Table 2). Additionally, the mean length-at-age for two-saltwater steelhead was below the length cutoff for the B-run size classification. Steelhead and fall Chinook Salmon fisheries in the Columbia and Snake rivers are partially constrained by the abundance of large steelhead, often called B-run steelhead in fisheries regulations, counted at Bonneville and Lower Granite dams. B-run steelhead are defined as fish $\geq 78 \mathrm{~cm}$ in fork length and are often associated with a two-saltwater age. A-run steelhead can also have two-saltwater fish returning, but are typically smaller in size than the B-run dominated stocks. In SY2020, two-saltwater returns were on average 2.8 cm smaller than SY2019 two-saltwater fish and 7.5 cm smaller than the 78 cm length requirement (Appendix D-7). The reduced length-atage is not novel or restricted to this spawn year, but a continuation of a developing trend, and poor growth and survival in the ocean may be a contributing factor (Bowersox et al. 2019). The depressed returns of populations that typically produce larger two- and three-saltwater fish, particularly, the Upper Clearwater, South Fork Clearwater, Middle Fork Salmon, and South Fork Salmon river wild populations and the Dworshak hatchery stock, contributed to the apparent return of smaller steelhead. Total two-saltwater wild steelhead returns in SY2020 were also the second lowest on record going back to at least SY2009. Idaho fisheries were restricted during the fall of 2019 in attempt to ensure adequate broodstock to Dworshak National Fish Hatchery and to keep impacts on wild fish within limits. The declining average length of two-saltwater steelhead poses a challenge to fisheries managers because it has impacted fishing regulations and public perception of fewer returning B-run steelhead (Copeland et al. 2017; Bowersox et al. 2019).

We observed some changes in the sex composition in the SY2020 steelhead run compared to previous years. Wild steelhead stocks continue to be female biased, and historically the Upper Clearwater stock was the most female biased; however, this year it is the lowest percentage female among all stocks. Sex composition is likely driven by relative saltwater age composition of one-saltwater and two-saltwater fish, creating a cohort effect. Generally, returning one-saltwater fish tend to be mostly males; females benefit from remaining in the ocean longer by growing larger to increase their fecundity (Hendry et al. 2004). In previous years, whenever the Upper Clearwater stock showed an increase in the percentage of one-saltwater fish, there appeared to also be a slight increase in the percentage of males. The Upper Clearwater stock in SY2020 followed the same trend with a relative increase in both one-saltwater fish and males, which could explain the lower relative abundance of females. Although the sex and age composition of steelhead cohorts may vary from year to year, the overall abundance of steelhead stocks in SY2020 was low.

Chinook Salmon returns in SY2020 were also low. Although overall escapement counted at the LGR window in SY2020 was higher than SY2019, it was the fifth lowest escapement recorded going back to at least SY1998 (Table 4). Hatchery Chinook Salmon escapement was also the fifth lowest on record, and wild Chinook Salmon escapement was below 10,000 fish. Abundance of wild- and natural-origin Chinook Salmon was well below IDFG's "healthy and harvestable" escapement goals and NMFS' minimum abundance thresholds. Wild Chinook Salmon escapement was less than one-twelfth of the proposed escapement goal of 127,000 fish, and less than one-third of NMFS' minimum abundance threshold of 31,500 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). The stockspecific wild escapement estimate for all stocks (except FALL) increased compared to SY2019 (Figure 8). There was an also improvement in two-saltwater returns in SY2020, likely due to the increased number of returning wild jacks and hatchery jacks in SY2019 (Lawry et al. 2020). Despite the increases in abundance among stocks and two-saltwater returns, the 5-year trend in point estimates suggests a continued decline for all stocks.

Considering the challenges of SY2020 Chinook Salmon data analyses associated with COVID-19 closures, our reported estimates reflect averages of previous years and we need to exercise caution when interpreting these data. Decomposition estimates were needed for the purposes of forecasting for fisheries planning and to continue the productivity and SAR time series. We are confident these data are adequate for those purposes; however, we do not want to further speculate or overanalyze fine-scale stock-specific trends based on these estimates.

In this report, we omitted the productivity estimates for three genetic stocks that 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 from downstream of LGR. The LSNAKE (steelhead) and TUCANO (Chinook Salmon) stocks contain the Tucannon River population located downstream of LGR. Some returning adults born in the Tucannon River overshoot their natal stream and stray upstream of 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-run Chinook Salmon that cross LGR during the spring-summer Chinook Salmon run timing (March 1-August 17). The majority of the FALL genetic stock cross LGR after August 17. However, by accounting for FALL Chinook Salmon trapped on August 17 and earlier, we get a better estimate of the true springsummer stocks returning to the Snake River. Additionally, preliminary evidence from PIT tags suggests a small amount (<30 PIT-tagged fish in any given year) of spring-summer Chinook Salmon cross LGR after August 17. However, quantifying abundances of spring-summer Chinook Salmon 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 inferences should not be made using the 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 of 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 downstream of LGR after successfully crossing to the upstream side. A portion of these fallback fish re-ascend the LGR ladder, essentially being counted twice at the window, while others stay downstream of LGR. Furthermore, the window is not counted 24 hours a day throughout the season (USACE 2019, 2020). 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, 2018a, 2019a). Currently a different method for adult escapement estimates at LGR is under development to continue to refine our stock assessments for both species by accounting for fallback with reascension and nighttime passage. While some technical and conceptual concerns have been addressed, others need to be resolved while clearly maintaining a transparent relationship with window count data. Accounting for these issues will increase the value of the series to address multiple management and assessment needs.

This report summarized the abundance and composition of wild adult steelhead and spring-summer Chinook Salmon returning to LGR during spawn year 2020 as defined by the USACE calendar date designations. We estimated wild steelhead and Chinook Salmon escapement and age, sex, and size composition in aggregate and by genetic stock. We also updated the adult-to-adult productivity series for both species and the smolt-to-adult return (SAR) rate series for steelhead and Chinook Salmon. We noted overall declining trends in escapement, productivity, and smolt-to-adult return rates for both species over the past five years.

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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 2011, 2015; NMFS 2016). Extirpated populations are shaded.

| Snake River steelhead DPS |  |
| :---: | :---: |
| Major population group | Population name |
| Lower Snake River | 1. Tucannon River <br> 2. Asotin Creek |
| Grande Ronde River | 3. Lower Grande Ronde River <br> 4. Joseph Creek <br> 5. Wallowa River <br> 6. Upper Grande Ronde River |
| Imnaha River | 7. Imnaha River |
|  | 8. Lower Clearwater River |
|  | 9. North Fork Clearwater River (extirpated) |
| Clearwater River | 10. Lolo Creek <br> 11. Lochsa River <br> 12. Selway River <br> 13. South Fork Clearwater River |
| Salmon River | 14. Little Salmon River <br> 15. Chamberlain Creek <br> 16. South Fork Salmon River <br> 17. Secesh River <br> 18. Panther Creek <br> 19. Lower Middle Fork Salmon River <br> 20. Upper Middle Fork Salmon River <br> 21. North Fork Salmon River <br> 22. Lemhi River <br> 23. Pahsimeroi River <br> 24. East Fork Salmon River <br> 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) ${ }^{\text {a }}$ |
| 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) ${ }^{\text {a }}$ |
|  | 10. Lookinglass Creek (extirpated) ${ }^{\text {a }}$ |
| 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) ${ }^{\text {a }}$ |
| Dry Clearwater River (extirpated) ${ }^{\text {a }}$ | 33. Potlatch River (extirpated) ${ }^{\text {a }}$ |
|  | 34. Lapwai Creek (extirpated) ${ }^{\text {a }}$ |
|  | 35. Lawyer Creek (extirpated) ${ }^{\text {a }}$ |
|  | 36. Upper South Fork Clearwater River (extirpated) ${ }^{\text {a }}$ |
| Wet Clearwater River (extirpated) ${ }^{\text {a }}$ | 37. Lower North Fork Clearwater River (extirpated) |
|  | 38. Upper North Fork Clearwater River (extirpated) |
|  | 39. Lolo Creek (extirpated) a ${ }^{\text {a }}$ |
|  | 40. Lochsa River (extirpated) ${ }^{\text {a }}$ |
|  | 41. Meadow Creek (extirpated) ${ }^{\text {a }}$ |
|  | 42. Moose Creek (extirpated) ${ }^{\text {a }}$ |
|  | 43. Upper Selway River (extirpated) ${ }^{\text {a }}$ |

a Reintroduced fish exist in extirpated areas except the North Fork Clearwater River basin upstream of Dworshak Dam.

Table 2. Estimated annual escapement, by fish size and origin, of steelhead, spawn years 1998-2020. Large fish were greater than or equal to 78 cm fork length (FL) and small fish were 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, 2018a, 2019a; Lawry et al. 2020; present study).

|  |  | Estimated number of steelhead at LGR that were: |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Spawn year ${ }^{(a)}$ | LGR window count | Large wild | Large hatchery ad-clipped | Large hatchery ad-intact | Small wild | Small hatchery ad-clipped | Small hatchery ad-intact | 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 ${ }^{\text {(b) }}$ | 31,574 | 4,118 ${ }^{\text {(b) }}$ | 34,549 ${ }^{\text {(b) }}$ | 110,750 | 17,721 ${ }^{\text {(b) }}$ | 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 |
| 2018 | 74,097 | 263 | 3,845 | 539 | 10,454 | 56,738 | 2,258 | 63,380 | 10,717 |
| 2019 | 51,818 | 1,232 | 13,119 | 2,223 | 7,055 | 26,776 | 1,413 | 43,531 | 8,287 |
| 2020 | 34,410 | 400 | 2,194 | 871 | 9,234 | 20,259 | 1,452 | 24,776 | 9,634 |

[^0]Table 3. Estimated number of wild steelhead smolts, number of returning adults by saltwater age, and percent smolt-to-adult return (\% SAR) rate at Lower Granite Dam. Scale samples were used for all smolt migration years. Repeat spawners (shaded) were not used to estimate SARs. Included in parentheses are 95\% confidence intervals for SARs.

| Smolt migration year | Estimated number of smolts ${ }^{(a)}$ | Adults returning to Lower Granite Dam by saltwater age |  |  |  | \%SAR (95\% CI) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 1 | 2 | 3 | Repeat spawners |  |
| 2005 | n/a | n/a | n/a | 902 | n/a | n/a |
| 2006 | n/a | n/a | 12,129 | 869 | 270 | n/a |
| 2007 | n/a | 10,844 | 16,404 | 252 | 441 | n/a |
| 2008 | n/a | 25,175 | 32,096 | 345 | 643 | n/a |
| 2009 | n/a | 11,360 | 24,538 | 157 | 555 | n/a |
| 2010 | 851,481 | 14,051 | 14,596 | 317 | 386 | 3.40 (3.36-3.44) |
| 2011 | 911,602 | 7,785 | 7,750 | 364 | 278 | 1.74 (1.72-1.77) |
| 2012 | 890,665 | 16,936 | 30,450 | 124 | 484 | 5.33 (5.29-5.38) |
| 2013 | 792,037 | 14,482 | 21,839 | 121 | 222 | 4.60 (4.56-4.65) |
| 2014 | 816,219 | 11,598 | 13,499 | 71 | 124 | 3.08 (3.05-3.12) |
| 2015 | 669,442 | 1,706 | 2,040 | 30 | 257 | 0.56 (0.54-0.58) |
| 2016 | 805,433 | 8,498 | 4,169 | 53 | 48 | 1.58 (1.55-1.61) |
| $2017{ }^{(b)}$ | 908,556 | 3,804 | 3,993 | - | - | 0.86 (0.84-0.88) |
| 2018 ${ }^{\text {c }}$ ) | 949,098 | 5,511 | - | - | - | 0.58 (0.57-0.60) |

a Smolt abundance for 2010-2018 derived from SCRAPI program (Camacho et al. 2018b, 2019b).
b Preliminary SAR until saltwater age-3 is added (SY2021).
c Preliminary SAR until saltwater age-2 and age-3 are added (SY2022).

Table 4. Estimated annual escapement, by origin and saltwater age, of Chinook Salmon, spawn years 1998-2020. Jacks were saltwater age-1 and include saltwater age-0 mini-jacks; adults were 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, 2018a, 2019a; Lawry et al. 2020; present study). Spawn year 2020 estimates were generated using LGR window count data and run reconstruction methods.

|  |  | Estimated number of Chinook Salmon at Lower Granite Dam that were: |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Spawn year ${ }^{(a)}$ | Window count | $\begin{gathered} \text { Wild } \\ \text { adults }^{(b)} \end{gathered}$ | $\begin{aligned} & \text { Wild } \\ & \text { jacks }^{(b)} \end{aligned}$ | Total wild | Hatchery adults ${ }^{(b)}$ | Hatchery jacks ${ }^{(b)}$ | Total hatchery | Total adults ${ }^{\left({ }^{\text {b }}\right.}$ | Total jacks ${ }^{(\mathbf{b})}$ |
| 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 | 30,180 | 12,219 | 42,399 | 34,288 | 13,904 |
| 2018 | 42,232 | 6,863 | 519 | 7,382 | 31,820 | 3,030 | 34,850 | 38,683 | 3,549 |
| 2019 | 29,617 | 4,152 | 1,010 | 5,162 | 19,528 | 4,927 | 24,455 | 23,680 | 5,937 |
| $2020{ }^{(c)}$ | 34,786 | 8,565 | 1,209 | 9,774 | 21,564 | 3,448 | 25,012 | 30,129 | 4,657 |

a Spring-summer Chinook Salmon at Lower Granite Dam are considered fish passing March 1 through August 17.
b For spawn years 2005-2019 (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. No scale samples were taken during SY2020 due to COVID19 trap closures, therefore adults and jacks were estimated using length at the LGR counting window (adult $\geq 57 \mathrm{~cm}, \mathrm{FL}$; jack $<57 \mathrm{~cm}, \mathrm{FL}$ ). 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.
c Window count, total adult, and total jack numbers for SY2020 are from actual LGR window count data. All other SY2020 estimates were calculated using run reconstruction methods.

Table 5. 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 2005-2019 (below the dashed line). SAR 95\% confidence intervals are in parentheses.

| Smolt migration year | Estimated number of smolts ${ }^{(a)}$ | Adults returning to Lower Granite Dam by saltwater age |  |  |  |  | \%SAR (95\% CI) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | $0{ }^{(b)}$ | 1 | 2 | 3 | 4 |  |
| 1996 | 419,826 | n/a | $\mathrm{n} / \mathrm{a}^{(\mathrm{c})}$ | 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 | 1,406,596 | 67 | 1,894 | 10,203 | 1,258 | 0 | 0.95 (0.94-0.97) |
| 2015 | 525,743 | 16 | 766 | 2,817 | 333 | 5 | 0.75 (0.73-0.77) |
| 2016 | 1,424,036 | 47 | 1,651 | 6,530 | 956 | 0 | 0.64 (0.63-0.66) |
| $2017{ }^{(d)}$ | 1,171,926 | 34 | 490 | 3,191 | 393 | - | 0.35 (0.34-0.36) |
| 2018 ${ }^{(\text {e }}$ | 1,437,312 | 29 | 992 | 8,172 | - | - | 0.64 (0.62-0.66) |
| $2019{ }^{(f)}$ | 794,695 | 18 | 1,209 | - | - | - | 0.15 (0.14-0.17) |
| 2020(g) | $\mathrm{n} / \mathrm{a}^{(\mathrm{h})}$ | 0 | - | - | - | - | - |
| a Smolt abundance for 2010-2019 derived from SCRAPI program (Camacho et al. 2018b, 2019b; Ebel et al. 2022). |  |  |  |  |  |  |  |
| b Mini-jack (saltwater age-0) samples were not sampled on the spawning grounds, thus mini-jack fin rays are not available ( $\mathrm{n} / \mathrm{a}$ ) for smolt migration years 1996-2004; only mini-jacks $\geq 30 \mathrm{~cm}$, FL, were sampled for scales at Lower Granite Dam for smolt migration years 2005-2019. |  |  |  |  |  |  |  |
| c Jack (saltwater age-1) fin ray samples were not collected on the spawning grounds and are not available ( $\mathrm{n} / \mathrm{a}$ ) for smolt migration year 1996. |  |  |  |  |  |  |  |
| ry |  |  |  |  |  |  |  |
| e Preliminary SAR until saltwater age-3 and age-4 are added (SY2022). |  |  |  |  |  |  |  |
| $f$ Preliminary SAR until saltwater age-2 through age-4 are added (SY2023). |  |  |  |  |  |  |  |
| $g$ Preliminary SAR until saltwater age-1 through age-4 are added (SY2024). |  |  |  |  |  |  |  |
| h MY2020 smolt estimate not available (n/a) due to COVID-19 safety closures. |  |  |  |  |  |  |  |

FIGURES


Figure 1. Map of steelhead genetic stocks and sample collections included in the Snake River basin SNP baseline version 3.1 (Powell et al. 2018) used for genetic stock identification at Lower Granite Dam. A detailed description of collections can be found in Hargrove et al. (2021). The Hells Canyon Tributaries major population group does not support independent populations and is considered extirpated (NMFS 2016). See Genetic Tissue Processing and Analysis section for genetic stock abbreviations.


Figure 2. Map of Chinook Salmon genetic stocks and sample collections included in the Snake River basin SNP baseline version 3.1 (Powell et al. 2018) used for genetic stock identification at Lower Granite Dam. A detailed description of collections can be found in Hargrove et al. (2022). Reintroduced fish exist in functionally extirpated TRT populations as mapped. See Genetic Tissue Processing and Analysis section 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 ( $\geq 57 \mathrm{~cm}$, fork length [FL]) and small ( $<57 \mathrm{~cm}, \mathrm{FL}$ ) and steelhead large ( $\geq 78 \mathrm{~cm}, \mathrm{FL}$ ) and small ( $<78 \mathrm{~cm}, \mathrm{FL}$ ). Fish less than 30 cm (FL) are not designated to species and are ignored.


Figure 4. Estimated escapement by genetic stock of wild steelhead at Lower Granite Dam for spawn years 2009-2020. Confidence intervals are at 90\%.


Figure 5. Adult-to-adult productivity (returning recruits per parent spawner) of wild steelhead at Lower Granite Dam. The dashed line at 1.0 recruits per spawner represents replacement. Spawn year 2020 completed brood year 2012. Note brood year 2013 was shown for reference, but represents a preliminary result that will be completed in SY2021.


Figure 6. Adult-to-adult productivity (returning recruits per parent spawner) for each genetic stock of wild steelhead at Lower Granite Dam. The dashed line at 1.0 recruits per spawner represents replacement. Spawn year 2020 completed brood year 2012. Note brood year 2013 was shown for reference, but represents a preliminary result that will be completed in SY2021.


Figure 7. Estimated wild steelhead smolt-to-adult return (\%SAR) rate of emigrant smolts and adult returns to Lower Granite Dam for smolt migration years 2010-2016. Confidence intervals are at 95\%. The dashed lines represent the lower and upper range SAR objectives for wild steelhead established by the Northwest Power and Conservation Council (NPCC 2009). See Table 3 for numbers.


## Spawn year

Figure 8. Estimated escapement by genetic stock of wild Chinook Salmon at Lower Granite Dam for spawn years 2009-2020. Confidence intervals, when shown, are at 90\%. Spawn year 2020 estimates were generated using run reconstruction and does not include jacks or have confidence intervals.


Figure 9. Adult-to-adult productivity (returning recruits per parent spawner) of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruits per spawner represents replacement. Spawn year 2020 completed brood year 2014. Note brood year 2015 was shown for reference, but represents a preliminary result that will be completed in SY2021.


## Brood year

Figure 10. Adult-to-adult productivity (returning recruits per parent spawner) for each genetic stock of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruits per spawner replacement. Spawn year 2020 completed brood year 2014. Note brood year 2015 was shown for reference, but represents a preliminary result that will be completed in SY2021.


Figure 11. Estimated wild Chinook Salmon smolt-to-adult return (SAR) rate of emigrant smolts and adult returns 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 5 for numbers.

## APPENDICES

Appendix A: Annual Lower Granite Dam trapping operations, 2019-2020.

Appendix A-1. Annual Lower Granite Dam trapping operations, 2019-2020. Shaded areas were outside the 2020 spawn year (July 1, 2019 to June 30, 2020 for steelhead and March 1 to August 17, 2020 for Chinook Salmon).

| Calendar date | Trap operation | Comments |
| :---: | :---: | :---: |
| Calendar year 2019 |  |  |
| January 1-April 4 | Closed | Winter closure; anesthesia disposal and water supply problems |
| April 5-August 17 | 5 days/week, 28\% Daily Rate |  |
| August 18-September 6 | 7 days/week, 70\% Daily Rate ${ }^{(a)}$ |  |
| September 7-12 | Closed | Hot water closure |
| September 13-16 | 7 days/week, 100\% Daily Rate ${ }^{(a)}$ |  |
| September 17-November 12 | 7 days/week, 20\% Daily Rate |  |
| November 13-December 31 | Closed | Winter closure |
| Calendar year 2020 |  |  |
| January 1-March 1 | Closed | Winter closure |
| March 2-24 | 5 days/week, 28\% Daily Rate |  |
| March 25-July 1 | Closed ${ }^{(b)}$ | COVID-19 closure |
| July 2-August 2 | 5 days/week, 28\% Daily Rate |  |
| August 3-17 | 5 days/week, 25\% Daily Rate |  |
| August 18-September 1 | 7 days/week, 80\% Daily Rate ${ }^{(a)}$ |  |
| September 2-November 12 | 7 days/week, 18\% Daily Rate |  |
| November 13-December 31 | Closed | Winter closure |
| a Trap rate exceeded co-manager agreement for a trap rate maximum of 20\% (7 days/week) to accommodate fall-run Chinook Salmon broodstock collection at the LGR trap. <br> b Trap operations were shut down due to COVID-19 safety policies. |  |  |

Appendix A-2. Daily number of steelhead counted at the Lower Granite Dam window, spawn year 2020. Vertical gray bars indicate when the trap was open and daily trapping rate. $88.7 \%$ of the steelhead passed LGR when the trap was open. See Appendix A-1 and text for explanation of various trap closures.


Appendix A-3. Daily number of Chinook Salmon counted at the Lower Granite Dam window, spawn year 2020. Vertical gray bars indicate when the trap was open and daily trapping rate. 8.2\% of the Chinook Salmon passed LGR when the trap was open. See Appendix A-1 and text for explanation of various trap closures.


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 2009-2020. Only fish failing to meet criteria were considered wild.

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

${ }^{\text {a }} \quad$ Started in SY2011 with complete coverage by SY2013.
b Minor discrepancies occurred 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 valid adult trap samples of steelhead at Lower Granite Dam, spawn year 2020. Data were summarized by weekly strata for analysis using the Salmonid Composition Bootstrap Intervals (SCOBI) method.

|  |  |  |  | Days |  | Total | Valid | Numb | valid SCO | sh sam alysis | used in |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Time strata | Statistical week ${ }^{(a)}$ | Sampling period | Number of days | $\begin{gathered} \operatorname{trap}^{(b)} \\ \text { open }^{(b)} \end{gathered}$ | Window count | valid fish trapped | wild fish trapped | Genetic stock | Size | Sex | Age |
| Fall 2019 |  |  |  |  |  |  |  |  |  |  |  |
| 1 | 27A-36 | 7/1-9/8 | 70 | 55 | 2,283 | 805 | 486 | 482 | 482 | 482 | 367 |
| 2 | 37-38 | 9/9-9/22 | 14 | 10 | 3,021 | 1,179 | 426 | 425 | 425 | 425 | 355 |
| 3 | 39 | 9/23-9/29 | 7 | 7 | 5,730 | 1,235 | 371 | 371 | 371 | 371 | 301 |
| 4 | 40 | 9/30-10/6 | 7 | 7 | 5,772 | 1,265 | 302 | 302 | 302 | 302 | 256 |
| 5 | 41 | 10/7-10/13 | 7 | 7 | 4,979 | 1,046 | 233 | 233 | 233 | 233 | 189 |
| 6 | 42 | 10/14-10/20 | 7 | 7 | 3,426 | 742 | 162 | 162 | 162 | 162 | 121 |
| 7 | 43 | 10/21-10/27 | 7 | 7 | 2,839 | 661 | 157 | 156 | 156 | 156 | 130 |
| 8 | 44 | 10/28-11/3 | 7 | 7 | 1,852 | 407 | 107 | 106 | 106 | 106 | 91 |
| 9 | 45-53 ${ }^{(c)}$ | 11/4-12/31 | 58 | 9 | 2,294 | 204 | 48 | 47 | 47 | 47 | 40 |
|  |  |  |  |  | Sprin | $g 2020$ |  |  |  |  |  |
| 10 | 9-27B ${ }^{(c)}$ | 3/1-6/30 | 122 | 17 | 2,214 | 251 | 57 | 54 | 54 | 54 | 34 |
| Total: |  |  | 306 | 133 | 34,410 | 7,795 | 2,349 | 2,338 | 2,338 | 2,338 | 1,884 |

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: Run reconstruction methods used for spring-summer Chinook Salmon estimates, spawn year 2020.

Appendix B-1. Methodology for spring-summer Chinook Salmon run reconstruction at Lower Granite Dam, spawn year 2020.

Unprecedented changes and interruptions to normal workflows occurred during 2020 due to COVID-19. The adult fish trap at Lower Granite Dam (LGR) was not operated during the majority of the spring-summer Chinook Salmon run and therefore biological sampling of returning fish did not occur. With a lack of sampling and genetic data, we employed the following alternative methodologies to reconstruct the spring-summer Chinook Salmon return at Lower Granite Dam for spawn year 2020. The results from this analysis are shown in Table B-1.

Window counts were obtained from the U.S. Army Corps of Engineers (USACE) for the spring and summer management periods at Lower Granite Dam. Available data included adclipped and ad-intact counts for adults and an aggregate count for jacks that was not separated by adipose fin status. We parsed out the window counts into finer-scale estimates using a combination of methods (Figure B-1) which are described below.

ADULTS

## Ad-Clipped Hatchery Adults

We estimated age-specific returns of ad-clipped hatchery $(\mathrm{H})$ adults using traditional run reconstruction which is the summation of harvest + hatchery trap returns + below/above weir escapement. For hatchery trap returns, we assumed fish $<83 \mathrm{~cm}$ FL were two-saltwater adults and fish $\geq 83 \mathrm{~cm}$ FL were three-saltwater adults. We applied the age composition of the hatchery trap returns to the harvest and escapement estimates for the same release group. We determined the composition of the entire pool of H adults using traditional run reconstruction, then applied that composition to the total ad-clipped adult window count to obtain final age- and release sitespecific estimates of H adults.

## Ad-Intact Hatchery Adults

Ad-intact adults were separated into wild (W) and ad-intact hatchery (HNC) adults using historic data. The composition of the total adult hatchery ( $\mathrm{H}+\mathrm{HNC}$ ) has remained consistent from 2014-2019, so we used that information to estimate the adult HNC Chinook Salmon for SY2020. Window counts identified total number of H adults that passed LGR in 2020. The mean proportion (2014-2019) of all HNC adults ( $9.96 \%$; Table B-2) was applied to the H adult count in 2020. The total number of HNC adults were estimated using the following formula:

$$
\begin{gathered}
\text { HNC adults }=\frac{H \text { adult window count }}{1-\% \text { of total } H N C \text { adults }}-H \text { adult window count } \\
\text { HNC adults }=\frac{19,417}{1-0.0996}-19,417 \\
\text { HNC adults }=2,147
\end{gathered}
$$

## Wild Adults

We estimated the W adult estimate by subtracting the HNC adult estimate (see above) from the total ad-intact adult window count:

$$
\begin{aligned}
& W \text { adults }=\text { total ad intact adult window count }-H N C \text { adults } \\
& \qquad W \text { adults }=10,712-2,147 \\
& W \text { adults }=8,565
\end{aligned}
$$

The W adult estimate was parsed out to the genetic stock-level using genetic data from samples collected from 2009-2019 at LGR. We estimated stock-level escapement to LGR by multiplying the W adult estimate by the average proportion of each genetic stock from 2009-2019 (Table B-3). We separated the W adult estimate into two- and three-saltwater fish using PIT tag detections of wild adults that were PIT tagged as juveniles and were detected as adults at LGR in 2020.

## JACKS

Jacks represented the most complex group to reconstruct because the USACE window counts for jacks were not separated by adipose fin status. We applied the adult ad-clipped rate observed in 2020 based on the window count (64.4\%) to the aggregate jack window count to separate ad-clipped and ad-intact jacks. Data from 2014-2019 show that the adult and jack adclipped rates were similar among years (Table B-2).

## Ad-Clipped Hatchery Jacks

We applied the adult ad-clipped rate based on the window count (64.4\%) to the aggregate jack window count to estimate the number of ad-clipped hatchery $(\mathrm{H})$ jacks using the following formula:

$$
\begin{gathered}
H \text { jacks }=\text { jack window count } x \text { adult clip rate } \\
\text { H jacks }=4,657 \times 0.644 \\
H \text { jacks }=3,001
\end{gathered}
$$

## Ad-Intact Jacks

The total number of ad-intact jacks was calculated by subtracting the number of H jacks estimated above from the total jack window count:

$$
\begin{gathered}
\text { total ad intact jacks }=\text { jack window count }-H \text { jacks } \\
\text { total ad intact jacks }=4,657-3,001 \\
\text { total ad intact jacks }=1,656
\end{gathered}
$$

The total ad-intact jacks were separated into W and HNC jacks using previous years' data. Similar to adults, the composition of the total hatchery jacks ( $\mathrm{H}+\mathrm{HNC}$ ) has remained consistent from 2014-2019 (Table B-2), so we used that information to estimate the number of HNC jack Chinook Salmon. We applied the proportion of all HNC jacks (12.96\%) to the H jack estimate, to estimate the total number of HNC jacks using the following formula:

$$
\begin{gathered}
\text { HNC jacks }=\frac{H \text { jacks }}{1-\% \text { of total HNC jacks }}-H \text { jacks } \\
\text { HNC jacks }=\frac{3,001}{1-0.1296}-3,001
\end{gathered}
$$

$H N C$ jacks $=447$

## Wild Jacks

We calculated the W jack estimate by subtracting the HNC jack estimate (see above) from the total ad-intact jack estimate:

$$
\begin{gathered}
W \text { jacks }=\text { total ad intact jacks }- \text { HNC jacks } \\
\text { W jacks }=1,656-447 \\
W \text { jacks }=1,209
\end{gathered}
$$

Table B-1. Summary of escapement estimates of spring-summer Chinook Salmon at Lower Granite Dam in spawn year 2020.

| Saltwater <br> age | Hatchery <br> ad-clipped | Hatchery <br> ad-intact ${ }^{1}$ | Total <br> hatchery | Wild $^{2}$ | All returns |
| :--- | ---: | ---: | ---: | ---: | ---: |
| 0-saltwater | 0 | 0 | 0 | 0 | 0 |
| 1-saltwater | 3,001 | 447 | 3,448 | 1,209 | 4,657 |
| 2-saltwater | 18,924 | 2,092 | 21,016 | 8,172 | 29,189 |
| 3-saltwater | 493 | 55 | 548 | 393 | 941 |
| 4-saltwater | 0 | 0 | 0 | 0 | 0 |
|  |  |  |  |  |  |
| Total | 22,418 | 2,594 | 25,012 | 9,774 | 34,786 |

1 Used age composition of ad-clipped adults to parse out age of ad-intact hatchery adults.
2 Used age composition from wild PIT tag detections @ LGR to parse out age of wild adults.

Table B-2. Escapement estimates of Chinook Salmon at Lower Granite Dam from spawn year 2014-2019.

| Spawn year | Origin | Escapement at LGR ${ }^{(a)}$ |  |  |  | \% of HNC Chinook Salmon |  |  | Percent of total that are adclipped | Adult clip rate | Jack clip rate |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Total Chinook | Adults | Jacks ${ }^{(b)}$ | Unassigned | All <br> Chinook | Adults | Jacks |  |  |  |
| 2019 | H | 22,339 | 17,542 | 4,666 | 131 | 8.7\% | 9.6\% | 4.7\% | 75.4\% | 74.4\% | 79.2\% |
| 2019 | HNC | 2,116 | 1,869 | 231 | 16 |  |  |  |  |  |  |
| 2019 | W | 5,162 | 4,152 | 992 |  |  |  |  |  |  |  |
| 2018 | H | 31,040 | 27,689 | 2,506 | 845 | 10.9\% | 10.8\% | 15.3\% | 73.5\% | 73.1\% | 72.7\% |
| 2018 | HNC | 3,810 | 3,337 | 451 | 22 |  |  |  |  |  |  |
| 2018 | W | 7,382 | 6,863 | 490 |  |  |  |  |  |  |  |
| 2017 | H | 38,438 | 27,545 | 10,774 | 119 | 9.3\% | 8.5\% | 11.6\% | 79.8\% | 80.5\% | 77.9\% |
| 2017 | HNC | 3,961 | 2,545 | 1,410 | 6 |  |  |  |  |  |  |
| 2017 | W | 5,793 | 4,108 | 1,651 |  |  |  |  |  |  |  |
| 2016 | H | 57,187 | 50,738 | 5,959 | 490 | 12.0\% | 11.9\% | 11.6\% | 70.0\% | 69.0\% | 79.4\% |
| 2016 | HNC | 7,814 | 6,840 | 783 | 191 |  |  |  |  |  |  |
| 2016 | W | 16,752 | 15,939 | 766 |  |  |  |  |  |  |  |
| 2015 | H | 98,864 | 87,309 | 10,855 | 700 | 9.3\% | 8.6\% | 15.0\% | 74.7\% | 74.6\% | 74.0\% |
| 2015 | HNC | 10,159 | 8,228 | 1,922 |  |  |  |  |  |  |  |
| 2015 | W | 23,409 | 21,499 | 1,894 |  |  |  |  |  |  |  |
| 2014 | H | 74,153 | 56,800 | 14,745 | 2,608 | 12.1\% | 10.4\% | 19.6\% | 64.7\% | 63.3\% | 66.3\% |
| 2014 | HNC | 10,182 | 6,592 | 3,590 |  |  |  |  |  |  |  |
| 2014 | W | 30,338 | 26,351 | 3,921 |  |  |  |  |  |  |  |
| Average |  |  |  |  |  |  | 9.96\% | 12.96\% |  | 72.5\% | 74.9\% |

a See Lawry et al. 2020 for methodology used to derive these estimates.
b Jack count does not include saltwater age-0 minijacks.

Table B-3. Genetic stock proportions of entire adult Chinook Salmon wild run at Lower Granite Dam, spawn years 2009-2019. Average stock proportions were used to decompose stock-specific estimates for adult Chinook Salmon in SY2020; jacks were not included in these data.

|  | Proportion of each genetic stock in entire adult Chinook Salmon wild run per spawn year |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Stock | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | Average |
| UPSALM | 0.28 | 0.24 | 0.20 | 0.19 | 0.22 | 0.20 | 0.22 | 0.20 | 0.16 | 0.16 | 0.14 | 0.20 |
| CHMBLN | 0.03 | 0.04 | 0.02 | 0.03 | 0.04 | 0.03 | 0.02 | 0.02 | 0.02 | 0.02 | 0.01 | 0.03 |
| MFSALM | 0.19 | 0.24 | 0.17 | 0.18 | 0.17 | 0.20 | 0.22 | 0.15 | 0.12 | 0.16 | 0.12 | 0.17 |
| SFSALM | 0.16 | 0.14 | 0.14 | 0.13 | 0.14 | 0.15 | 0.09 | 0.11 | 0.14 | 0.17 | 0.16 | 0.14 |
| HELLSC | 0.31 | 0.31 | 0.42 | 0.43 | 0.40 | 0.39 | 0.42 | 0.43 | 0.40 | 0.44 | 0.44 | 0.40 |
| TUCANO | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | 0.01 | 0.00 | 0.01 | 0.00 | 0.01 | 0.01 |
| FALL | 0.02 | 0.02 | 0.04 | 0.03 | 0.02 | 0.03 | 0.02 | 0.09 | 0.15 | 0.05 | 0.12 | 0.05 |



Figure B-1. Schematic describing the calculations for spring-summer Chinook Salmon run reconstruction at Lower Granite Dam in spawn year 2020.

Appendix C: Steelhead age validation.

Appendix C-1. Age bias plot illustrating pairwise comparisons of scale assigned saltwater-age with known age for steelhead at Lower Granite Dam, spawn year 2020 (NRAAL, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. PA = percent agreement.


Appendix D: Wild steelhead at Lower Granite Dam, spawn year 2020.

Appendix D-1. Percentage of the estimated escapement of wild steelhead by genetic stock to the overall estimated wild escapement at Lower Granite Dam, spawn years 2010-2020. See Genetic Tissue Processing and Analysis section for stock abbreviations.


Appendix D-2. Estimated escapement of wild steelhead at Lower Granite Dam by sex and by size for each genetic stock, spawn year 2020. $L=$ lower bound and $U=$ upper bound of $90 \%$ confidence intervals. See Genetic Tissue Processing and Analysis section for stock abbreviations.

| Genetic stock | Estimated number of steelhead at Lower Granite Dam that were: |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Female |  |  | Male |  |  | Large |  |  | Small |  |  | Total wild |  |  |
|  | Estimate | L | U | Estimate | L | U | Estimate | L | U | Estimate | L | U | Estimate | L | U |
| UPSALM | 1,105 | 1,009 | 1,198 | 674 | 608 | 738 | 49 | 36 | 64 | 1,730 | 1,589 | 1,868 | 1,779 | 1,641 | 1,922 |
| MFSALM | 328 | 274 | 380 | 125 | 99 | 150 | 5 | 1 | 9 | 448 | 381 | 517 | 453 | 385 | 521 |
| SFSALM | 72 | 46 | 98 | 27 | 13 | 40 | 28 | 14 | 42 | 71 | 45 | 96 | 99 | 67 | 133 |
| LOSALM | 129 | 92 | 167 | 46 | 29 | 63 | 9 | 3 | 16 | 166 | 122 | 210 | 175 | 131 | 223 |
| UPCLWR | 192 | 151 | 233 | 171 | 125 | 218 | 84 | 62 | 106 | 279 | 215 | 341 | 363 | 292 | 437 |
| SFCLWR | 254 | 205 | 302 | 205 | 157 | 253 | 115 | 86 | 145 | 344 | 279 | 408 | 459 | 379 | 546 |
| LOCLWR | 336 | 274 | 394 | 140 | 110 | 170 | 28 | 15 | 42 | 448 | 374 | 524 | 476 | 399 | 555 |
| IMNAHA | 463 | 395 | 528 | 251 | 207 | 293 | 9 | 4 | 15 | 705 | 612 | 797 | 714 | 621 | 810 |
| GRROND | 2,104 | 1,971 | 2,231 | 1,181 | 1,093 | 1,267 | 40 | 29 | 51 | 3,245 | 3,046 | 3,435 | 3,285 | 3,088 | 3,481 |
| LSNAKE | 1,230 | 1,126 | 1,332 | 601 | 535 | 668 | 33 | 23 | 43 | 1,798 | 1,653 | 1,945 | 1,831 | 1,685 | 1,987 |
| Total | 6,213 | 5,985 | 6,393 | 3,421 | 3,260 | 3,548 | 400 | 349 | 442 | 9,234 | 8,930 | 9,500 | 9,634 | 9,337 | 9,933 |

Appendix D-3. Estimated escapement by sex of wild steelhead at Lower Granite Dam, spawn years 2009-2020. Confidence intervals are at 90\%.


Appendix D-4. Estimated escapement of wild steelhead at Lower Granite Dam by smolt migration year (MY), brood year (BY), and age class for each genetic stock, spawn year 2020. Only individual fish that had both a total age and an assigned stock were used ( $n=1,884$ ). Age class format is European: freshwater age.saltwater age. $R$ represents consecutive year repeat spawners who spawned two years in a row, and R1 represents skip spawners who spent one year in saltwater between spawning years. See Genetic Tissue Processing and Analysis section for stock abbreviations.

| Smolt migration year (MY), brood year (BY), and age class |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | MY16 |  |  |  |  |  | MY17 |  |  |  |  |  |  | MY18 |  |  |  | MY19 |  |  |
| $\begin{aligned} & \text { Genetic } \\ & \text { stock } \end{aligned}$ | $\frac{\mathrm{BY} 13}{3.1 \mathrm{R} 1}$ | $\frac{\mathrm{BY} 13}{3.3}$ | $\frac{\mathrm{BY} 14}{2.1 \mathrm{R} 1}$ | $\frac{\mathrm{BY} 14}{2.2 R}$ | $\frac{\text { BY14 }}{2.3}$ | $\frac{\text { BY15 }}{1.3}$ | $\frac{\text { BY12 }}{5.2}$ | $\frac{\mathrm{BY} 13}{4.1 \mathrm{R}}$ | $\frac{\text { BY13 }}{4.2}$ | $\frac{\text { BY14 }}{3.1 R}$ | $\frac{\text { BY14 }}{3.2}$ | $\frac{\text { BY15 }}{2.2}$ | $\frac{\text { BY16 }}{1.2}$ | $\frac{\text { BY14 }}{4.1}$ | $\frac{\text { BY15 }}{3.1}$ | $\frac{\text { BY16 }}{2.1}$ | $\frac{\text { BY17 }}{1.1}$ | $\frac{\text { BY16 }}{3.0}$ | $\frac{\text { BY17 }}{2.0}$ | Total wild |
| UPSALM | 4 | 0 | 0 | 0 | 5 | 0 | 0 | 0 | 9 | 0 | 126 | 418 | 71 | 19 | 413 | 690 | 24 | 0 | 0 | 1,779 |
| MFSALM | 0 | 0 | 0 | 3 | 0 | 0 | 5 | 0 | 13 | 0 | 124 | 48 | 0 | 8 | 217 | 35 | 0 | 0 | 0 | 453 |
| SFSALM | 0 | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 27 | 20 | 0 | 0 | 30 | 13 | 0 | 0 | 0 | 99 |
| LOSALM | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 | 0 | 3 | 14 | 40 | 5 | 4 | 38 | 66 | 0 | 0 | 0 | 175 |
| UPCLWR | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 5 | 0 | 40 | 113 | 25 | 0 | 120 | 54 | 0 | 0 | 0 | 363 |
| SFCLWR | 0 | 5 | 0 | 0 | 16 | 6 | 0 | 0 | 0 | 0 | 91 | 154 | 34 | 0 | 23 | 105 | 25 | 0 | 0 | 459 |
| LOCLWR | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 0 | 21 | 177 | 42 | 4 | 41 | 187 | 0 | 0 | 0 | 476 |
| IMNAHA | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11 | 0 | 72 | 155 | 16 | 9 | 152 | 283 | 16 | 0 | 0 | 714 |
| GRROND | 19 | 0 | 0 | 9 | 5 | 0 | 0 | 0 | 6 | 0 | 366 | 773 | 158 | 70 | 636 | 1,194 | 40 | 5 | 4 | 3,285 |
| LSNAKE | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 205 | 532 | 67 | 10 | 323 | 597 | 65 | 20 | 0 | 1,831 |
| Total | 23 | 10 | 6 | 12 | 37 | 6 | 5 | 4 | 54 | 3 | 1,086 | 2,430 | 418 | 124 | 1,993 | 3,224 | 170 | 25 | 4 | 9,634 |

Appendix D-5. Estimated escapement by saltwater age of wild steelhead at Lower Granite Dam, spawn years 2009-2020. Confidence intervals are at $90 \%$. Repeat refers to steelhead showing evidence of previous spawning events.


Appendix D-6. Estimated escapement by genetic stock and saltwater age of wild steelhead at Lower Granite Dam, spawn years 2009-2020. Confidence intervals are at 90\%. Repeat refers to steelhead showing evidence of previous spawning events.


Spawn year

Appendix D-7. Length frequency distribution by saltwater age of wild steelhead trapped at Lower Granite Dam, spawn year 2020. Solid black vertical line represents mean fork length (FL) at saltwater age. Dashed vertical red line represents the 780 mm (FL) cutoff for determining large-sized steelhead.


Appendix E: Wild Chinook Salmon at Lower Granite Dam, spawn year 2020.

Appendix E-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 2010-2020. Spawn year 2020 stock-specific estimates were generated using run reconstruction methods and do not include jacks in the total wild count. See Genetic Tissue Processing and Analysis section for stock abbreviations.


Appendix E-2. Estimated escapement of wild adult Chinook Salmon at Lower Granite Dam using run reconstruction and historic data, spawn year 2020. Stock-specific estimates do not include jacks. See Genetic Tissue Processing and Analysis section for stock abbreviations.

| Genetic stock | Wild adult estimate |
| :--- | ---: |
| UPSALM | 1,725 |
| CHMBLN | 214 |
| MFSALM | 1,486 |
| SFSALM | 1,193 |
| HELLSC | 3,438 |
| TUCANO | 50 |
| FALL | 459 |
| Total | 8,565 |

Appendix E-3. Estimated escapement by saltwater age of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2020. Confidence intervals, when present, are at $90 \%$. Spawn year 2020 saltwater age estimates were generated using run reconstruction methods and do not have confidence intervals.


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[^0]:    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.

