

## WILD ADULT STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, SPAWN YEAR 2021

## ANNUAL PROGRESS REPORT



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## 2021 Annual Report

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## ABBREVIATIONS AND ACRONYMS

| BPA | Bonneville Power Administration |
| :--- | :--- |
| BY | Brood Year |
| CI | Confidence Interval |
| CHMBLN | Chamberlain Creek Genetic Stock |
| CLRWTR | Clearwater River Genetic Stock |
| CWT | Coded Wire Tag |
| DPS | Distinct Population Segment |
| EFGL | Eagle Fish Genetics Laboratory |
| 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 |
| SALMON | Salmon River Major Population Group |
| SAR | Smolt-to-adult return rate |
| SCOBI | Salmonid Compositional Bootstrap Intervals |


| SFCLWR | South Fork Clearwater River Genetic Stock |
| :--- | :--- |
| SFSALM | South Fork Salmon River Genetic Stock |
| SNP | Single Nucleotide Polymorphism |
| SY | Spawn Year |
| 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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[^0]
#### 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 2021. We used a combination of window counts, nighttime passage rates, fallback-reascension rates, and biological samples collected using a systematic random sample design from the fish trap at Lower Granite Dam to decompose each species by origin, body size, sex, age, and stock. The time series of abundance and composition was then used to calculate adult-to-adult productivity, expressed as recruits per spawner, and smolt-to-adult return rate for each species. The estimated total escapement for hatchery and wild steelhead was $61,315(60,515-62,21490 \% \mathrm{Cl})$. The estimated wild steelhead escapement was 15,478 fish ( $15,001-15,97390 \% \mathrm{CI}$ ), comprising $25 \%$ of the total estimate. The Grande Ronde River genetic stock was the most abundant followed by the Upper Salmon River. Small steelhead ( $<78 \mathrm{~cm}$ fork length [FL]) dominated the ad-clipped hatchery run and the total wild run; however, large steelhead ( $\geq 78 \mathrm{~cm}$ FL) were most abundant in the ad-intact hatchery run. The wild steelhead aggregate at Lower Granite Dam was female biased (78\%) with female percentages of genetic stocks that ranged from $71 \%$ for the South Fork Clearwater River to $82 \%$ for the Middle Fork Salmon River. We observed 20 different steelhead age classes. Total age for adults at Lower Granite Dam ranged from three to seven years, with freshwater ages that ranged from one to four years, and saltwater ages that ranged from zero to three years, and additional fish returning as repeat spawners. Adult-to-adult productivity was completed for brood year 2013 and was 0.34 returning recruits per spawner. Productivities for all genetic stocks were below replacement. The smolt-to-adult return rate for the aggregate wild steelhead run was $0.86 \%$ for smolts crossing Lower Granite Dam in migration year 2017. We noted overall declining trends in wild steelhead escapement, productivity, and smolt-to-adult return rates over the past five years. The estimated total escapement for hatchery and wild spring-summer Chinook Salmon was 46,429 (45,967$46,90390 \% \mathrm{Cl})$. The estimated wild Chinook Salmon escapement was 8,604 (8,318-8,929 90\% $\mathrm{Cl})$ fish, comprising $19 \%$ of the total estimate. The Hells Canyon genetic stock was the most abundant followed by the South Fork Salmon River. Large Chinook Salmon ( $\geq 57 \mathrm{~cm} \mathrm{FL}$ ) dominated the ad-clipped hatchery run, ad-intact hatchery run, and the wild run. Wild Chinook Salmon were male biased at $61 \%$. Sex ratios for each genetic stock mirrored the aggregate wild run and ranged from $58 \%$ male for Hells Canyon to $77 \%$ male for Chamberlain Creek, with the exception of the Tucannon River stock, which was female biased. We observed nine different Chinook Salmon age classes. Total age for adults at Lower Granite Dam ranged from two to six years, with freshwater ages ranged from one to two years, and saltwater ages that ranged from zero (mini-jacks) to four years. Adult-to-adult productivity was completed for brood year 2015 and was 0.18 returning recruits per spawner. Productivities for all genetic stocks were below replacement. The smolt-to-adult return rate for the aggregate wild Chinook Salmon run was $0.35 \%$ for smolts crossing Lower Granite Dam in migration year 2017. Although we noted a slight overall increasing 5 -year trend in wild Chinook Salmon escapement, abundance is still relatively low compared to previous years' data and we noted overall declining trends in overall Chinook Salmon abundance (hatchery included), productivity, and smolt-to-adult return rates 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. In total, 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. In total, 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 population in Washington, which is downstream of LGR. Some of the wild fish migrate 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; Baum et al. 2022). 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 2021). 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 wild adult steelhead and spring-summer Chinook Salmon returning to LGR during spawn year (SY) 2021. 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 described by Baum et al. (2022). The objectives of this report are to:

1. Describe LGR adult trap operations and data collection during 2020-2021, which is the timeframe encompassing all steelhead and Chinook Salmon passing LGR for SY2021.
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 ascending 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 captured 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 is determined based on sample size goals of the various projects using the adult trapping data combined with forecasted abundance of the targeted species, run, and rear type. Ideally, the
sample rate is apportioned equally across the entire sampling season. However, the trap did not operate during weekends from March 1 to August 17, and the trap rate was adjusted to continue achieving the sample rate goal by compensating for the two non-trapping weekend days. Inseason 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 $\left(\geq 21^{\circ} \mathrm{C}\right.$ 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 SY2021, the trap was closed November 13, 2020 through March 1, 2021 for the winter (Appendix A-1). Outside the winter and weekend closures, daily trapping rates varied from 18 to $80 \%$. For steelhead, $93.4 \%$ of the fish passed the window while the trap was open (Appendix A-2). The majority of the steelhead run crossed LGR in the fall of 2020, but a second small pulse occurred in mid-March and April 2021. For Chinook Salmon, $71.6 \%$ of the fish passed the window while the trap was open (Appendix A-3). More information about the trap logistics can be found in Harmon (2003), Steinhorst et al. (2010), and USACE $(2020,2021)$.

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). Number of fish processed each day at the LGR trap in SY2021 ranged from two fish to 726 fish. Each fish was directly handled for a minimum of 15 seconds to a maximum of 1 minute and 15 seconds.

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 or other external marks and tags. 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 fish; genotyping for parentage-based tagging (PBT) analysis was conducted post hoc to further classify ad-intact hatchery fish (Hargrove et al. 2020). In summary, final classification of hatchery fish was made using any of five marks or tags: adipose fin clip (complete removal or partial clip), CWT, ventral fin clip, dorsal or ventral fin erosion (steelhead only), or PBT. Information associated with previous PIT tagging events was not used to determine origin.

For all ad-intact fish, scale samples were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG Nampa Research Anadromous Ageing Laboratory (NRAAL). For all ad-intact fish, 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 Fish Genetics Laboratory (EFGL). All ad-intact fish captured were also PIT tagged (if not previously tagged) for abundance estimation at instream PIT detectors upstream of LGR (IPTDSW 2020; See et al. 2021). After processing, all fish were returned to the adult fish ladder to resume their upstream migration.

## Trap Data Management

All data were entered into a NMFS cloud-based database via touch-screen computer systems located in the trap work area. Initiated in 2012, 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 FL.

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. Every ad-intact steelhead and Chinook Salmon 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 fish were systematically subsampled if more than approximately 2,000 samples were available for each species. The result was a pool of samples collected systematically across the spawning run of each species and generally in constant proportion to their abundance. Hence, for either species, the sample pool can be considered a daily systematic sample (Steinhorst et al. 2017).

## Scale Processing, Analysis, and Age Validation

Technicians processed scale samples in the NRAAL according to protocols detailed in Wright et al. (2015). Ages were formatted using the European system where freshwater age was separated from saltwater 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 freshwater, saltwater, 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 fish saltwater age assignments with known saltwater ages from hatchery and wild fish PIT tagged as juveniles and hatchery fish with CWT. Accuracy of age assignments was estimated by percent agreement between saltwater age and known emigration date determined from juvenile PIT-tag detection in the hydrosystem. Known saltwater age fish were used to compute accuracy rates for steelhead and Chinook Salmon ages. Analysis of 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 were examined at a 343 SNP marker panel. 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 unique 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 the Program R package rubias (Moran and Anderson 2019). An individual's genetic stock was assigned as the stock with the maximum probability of membership.

Ten wild steelhead genetic stocks were used. The genetic stocks include: 1) UPSALM: upper Salmon River (including North Fork Salmon River and upstream); 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: Little Salmon River and tributaries of the lower Salmon River; 5) UPCLWR:
upper Clearwater River (Lochsa and Selway rivers); 6) SFCLWR: South Fork Clearwater River (including Clear Creek); 7) LOCLWR: lower Clearwater River; 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSNAKE: tributaries of the lower Snake River both 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

Total aggregate escapement of steelhead and Chinook Salmon in SY2021 were estimated using a new statistical model EASE (Estimating Adult Salmonid Escapement) developed by Thomas Delomas (GitHub - delomast/escapeLGD: Escapement Estimation at Lower Granite Dam; R Development Core Team 2021). The general process of EASE involves obtaining the total number of ascensions (nighttime and daytime ascensions combined), estimating the composition of ascensions (relative to stock groups; Figure 3), defining strata sets, then applying the stockspecific (upper or lower) fallback-reascension rates to the composition of ascensions to obtain the adjusted escapement estimates (hereafter referred to as total adjusted escapement). Uncertainty surrounding GSI is quantified between steps by bootstrapping. A more detailed description of EASE methods can be found in Appendix B-1.

To obtain total number of ascensions, EASE began with the USACE daily window counts, or counts of salmonids over 30 cm in length identified to species as they swim past the viewing window during counting hours. Before SY2021, the 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. However, for EASE, the window counts were treated as a measure of the number of daytime ascensions (Appendix B-1, Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions section). Window count data were downloaded from the Fish Passage Center (FPC) website: Adult Daily Dam Counts - Data Query (fpc.org). The total number of daytime ascensions was estimated by expanding the window counts for the sampling rate (historically $\frac{5}{6}$, or 50 minutes out of every hour). The counts were only performed during the daytime, therefore the frequency of nighttime ascensions (nighttime passage) also needed to be estimated (Appendix B-1, Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions section). The proportion of ascensions occurring at night was estimated using PIT tag detections in the ladder and was used to estimate the total number of ascensions (Columbia River Data Access in Real Time [DART]; DART PIT Tag Adult Lower Granite Ladder Window Count Hour Summary and Detection Details | Columbia Basin Research [washington.edul). After incorporating sampling rate and nighttime passage, the resulting estimate represents the total number of ascensions.

To estimate the composition of ascensions, the total number of ascensions were then decomposed into escapement estimates for reporting groups of interest with $90 \%$ confidence intervals (CI) so the fallback-reascension rates (proportion of fish that fell back below the dam and later reascended) can be proportionally applied (Appendix B-1, Fallback Rates and Composition of Ascensions sections). The total number of ascensions initially includes repeat ascensions, so the fallback-reascension rates were applied to the total number of ascensions after decomposition, assuming every fish that fell back reascended. Fallback-reascension rate was calculated separately for upper (upstream of LGR) and lower (downstream of LGR) stocks to account for differences in rates between the stocks. Fallback-reascension rates were also calculated using PIT tag detections from DART (excluding fish tagged as adults at LGR). The basic methods for estimating the composition of ascensions were developed by Delomas and Hess (2021) and implemented in the EASE R package (GitHub - delomast/escapeLGD: Escapement Estimation at Lower Granite Dam; R Development Core Team 2021). The EASE model combined the number of ascensions 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. In addition to the defined strata for composition estimates, two other sets of strata were defined for fallback-reascension and nighttime passage estimates through time. Criteria for these strata sets can be found in the Stratification section of Appendix B-1. Escapement by stratum was estimated by applying the strata-specific nighttime passage and fallback-reascension rates to the ascensions and then multiplying the ascensions by the trap proportions. The total adjusted escapement to LGR for the spawn year was the sum of escapement estimates from each stratum. In essence, the stratum proportions were weighted by stratum run size of all fish from each species. We assumed 1) the total number of ascensions represents true abundance; 2) fish pass LGR only by the ladder; 3) counts by species are accurate; 4) PIT-tagged fish represent the behavior of untagged fish in regards to fallback-reascension and nighttime passage; and 5) proportions are constant within each stratum.

The composition of ascensions decomposes total adjusted escapement into rearing type, primary, and secondary categories (Figure 3; Appendix B-1, Composition of Ascensions section). These are hierarchical and each category is nested within the previous category, thus point estimates of nested categories must sum to equal the parent category. First, the total adjusted 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 (adclipped 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).

To obtain abundance estimates for each category of interest, the composition proportions were multiplied by the total number of ascensions. Escapement in each category was then calculated by multiplying the ascension estimates by $1-p_{f}$, where $p_{f}$ is the corresponding fallback rate for that category of interest. A small minority of hatchery steelhead groups are split between release sites and have ambiguous PBT groups, so PIT tag detections were used to split the composition estimate into separate release groups and assign the appropriate fallbackreascension rate (Appendix B-1, Non-specific PBT Groups section). To obtain estimates at higher levels (e.g., total number of wild fish), the estimates for the relevant categories are summed. A parametric bootstrap is used to find $90 \%$ Cls on the estimated abundance of wild (W), ad-clipped hatchery $(\mathrm{H})$, 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 $\mathrm{W}, \mathrm{H}$, 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 ascensions 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.

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.

Additional steps were developed to adjust point estimates due to rounding error in the final output of data. First, all rear types must sum to the total adjusted escapement (Figure 3). If rear types do not sum to the total adjusted escapement, 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., two-saltwater age 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 fewer 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 2021). 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 corresponding to jack-sized fish. 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. Smolt production estimates for both species were acquired from Ebel et al. (2022). For steelhead, we continue the SAR series that began with smolt migration year (MY) 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 downstream survival rates than smolts. For Chinook Salmon, we continue the SAR series that began with MY1996. No smolt estimates were available for MY2020 due to COVID-19 closures; however, IDFG and FPC personnel are currently collaborating to develop the best approach to address the data gap implications.

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

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

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 $l$ was four because that was the maximum saltwater age observed for steelhead and spring-summer Chinook Salmon at LGR (Copeland et al. 2004). Formulas from Fleiss (1981) were used to estimate the $95 \%$ confidence limits on SAR values. The lower limit is given by

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

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 total escapement estimate of steelhead for SY2021 was 61,315 fish (60,515-62,214 $90 \% \mathrm{Cl})$ based on a window count of 59,126 fish (Table 2). The fallback-reascension rate for upper stock groups (upstream of LGR) was 3.89\% (3.31-4.52 90\% CI) and was 21.60\% (15.95$27.4890 \% \mathrm{Cl}$ ) for lower stock groups (downstream of LGR). The overall nighttime passage rate for the entire run was $8.74 \%(7.79-9.7790 \% \mathrm{CI})$. Of the 61,315 fish, the LGR trap captured 11,996 of them, of which 3,195 were valid wild fish (Appendix A-5). Our estimate of wild escapement was 15,478 fish ( $15,001-15,97390 \% \mathrm{CI}$ ), which comprised approximately $25 \%$ of the total estimate (Table 2). The remaining 45,837 fish were of hatchery origin. We estimate adclipped hatchery escapement was 40,429 fish (39,754-41,154 90\% CI) and ad-intact hatchery escapement was 5,408 fish (5,117-5,720 90\% CI). External marks, internal tags, and genetics were used to determine that $12 \%$ of the total hatchery fish and $9 \%$ of the total steelhead run were ad-intact hatchery fish. Hatchery fish comprised $26 \%$ of the ad-intact steelhead.

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

Relative abundance of wild steelhead by genetic stock varied greatly in SY2021 with the Grande Ronde highest at 30\% and the Lower Salmon stock lowest at <3\% (Appendix D-1). Escapement estimates for each genetic stock were as follows (Appendix D-2): UPSALM 1,911 (1,675-2,122 90\% CI); MFSALM 950 (819-1,077 90\% CI); SFSALM 457 (365-546 90\% CI); LOSALM 401 (292-535 90\% CI); UPCLWR 1,665 (1,509-1,837 90\% CI); SFCLWR 1,526 (1,3541,706 90\% CI); LOCLWR 1,138 (946-1,356 90\% CI); IMNAHA 988 (825-1,151 90\% CI); GRROND 4,622 (4,281-4,982 90\% CI); and LSNAKE 1,820 (1,518-2,153 90\% CI).

Small steelhead dominated ad-clipped hatchery and wild runs for SY2021. Small wild steelhead escapement was 12,213 fish (11,744-12,620 90\% CI), small ad-clipped hatchery steelhead at 26,248 fish ( $25,483-27,12390 \% \mathrm{CI}$ ), and small ad-intact hatchery steelhead at 1,528 fish (1,366-1,691 90\% CI). However, large steelhead ( $\geq 78 \mathrm{~cm} \mathrm{FL}$ ) were most abundant among the ad-intact hatchery fish. Large wild steelhead escapement was 3,265 fish (3,052-3,548 90\% Cl ), large ad-clipped hatchery steelhead at 14,181 fish ( $13,467-14,85090 \% \mathrm{Cl}$ ), and large adintact hatchery steelhead at 3,880 fish ( $3,657-4,16190 \% \mathrm{CI}$ ). Stock-specific estimates for wild fish by size are reported in Appendix D-2.

Wild steelhead were female-biased, and females accounted for $78 \%$ of the overall wild aggregate return to LGR (Appendix D-3). Female escapement was estimated at 12,031 fish ( $11,609-12,44790 \% \mathrm{CI}$ ) and males at 3,447 fish (3,200-3,70190\% CI). Sex ratios for each genetic stock mirrored the aggregate wild run and ranged from $71 \%$ female for South Fork Clearwater River to 82\% female for Middle Fork Salmon River (Appendix D-2).

Twenty different age classes were observed from the 2,085 wild fish that were assigned a genetic stock and a total age (Appendix D-4). Total age at spawning ranged from three to seven years with freshwater age ranging from one to four years and saltwater age ranging from zero to three years. Some steelhead returned as repeat spawners. Repeat spawning fish made up 0.6\% of all wild steelhead crossing LGR. Repeat spawners were observed in most genetic stocks except for LOSALM, UPCLWR, and SFCLWR. 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 $0.4 \%$ (SFSALM) to up to $1.2 \%$ (MFSALM).

For most genetic stocks of steelhead, age-5 fish (hatched in BY2016) was the dominant total age cohort, with the exception of Middle Fork Salmon and South Fork Salmon where age-6 fish (BY2015) were the dominant total age cohort (Appendix D-4). We estimated that 53 (23-88 $90 \% \mathrm{Cl})$ of the returning adults were age-3 fish (BY2018); 1,582 (1,411-1,769 90\% CI) were age4 fish (BY2017); 9,631 (9,215-10,049 90\% CI) were age-5 fish (BY2016); 4,096 (3,822-4,387 90\% $\mathrm{Cl})$ were age-6 fish (BY2015); and 116 (69-179 90\% CI) were age-7 fish (BY2014).

The majority of the wild return (62\%) emigrated to the ocean as two-freshwater fish and excluding repeat spawners, 90\% returned as two-saltwater fish (Appendix D-5). Saltwater age estimates were 15 (0-35 90\% CI) zero-saltwater fish (MY2020); 1,354 (1,201-1,528 90\% CI) onesaltwater fish (MY2019); 13,988 (13,540-14,460 90\% CI) two-saltwater fish (MY2018); 25 (0-53 $90 \% \mathrm{Cl})$ three-saltwater fish (MY2017); and 96 (51-151 90\% CI) repeat spawning steelhead regardless of migratory year. Furthermore, two-saltwater fish made up the majority of returning steelhead in all ten genetic stocks (Appendix D-6). The mean fork lengths of one-saltwater and two-saltwater fish were less than the 78 cm FL threshold for large steelhead (Appendix D-7).

Readers accurately determined the saltwater age of $100 \%$ of the scale samples ( $\mathrm{n}=69$ ) from known saltwater age steelhead collected during SY2021 (Appendix C-1). The known saltwater age sample was $12 \%$ one-saltwater and $88 \%$ 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 SY2021 completed the BY2013 cohort necessary for an adult-to-adult productivity estimate. Brood year 2013 returned 7,889 adults from 23,143 parents resulting in an adult-to-adult productivity estimate of 0.34 recruits per spawner, which is well below the 1.0 recruits per spawner necessary for replacement (Figure 5). A preliminary estimate of adult-to-adult productivity for the BY2014 cohort also placed it below replacement. Although unlikely to change significantly, the estimate for BY2014 is preliminary and will be completed with the SY2022 return.

None of the 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 0.20, MFSALM 0.28, SFSALM 0.35, LOSALM 0.21, UPCLWR 0.62, SFCLWR 0.21, LOCLWR 0.18, IMNAHA 0.30, and GRROND 0.48. 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 BY2014 placed all genetic stocks below replacement. The estimates for BY2014 are preliminary and will be completed with the SY2022 return.

## 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 SY2021, the SAR time series was completed for MY2010-2017. The most recently completed cohort, MY2017, returned 7,822 fish from 908,556 emigrants for a SAR estimate of $0.86 \%(0.84-0.8695 \% \mathrm{CI})$. The 5 -year geometric mean SAR was $1.62 \%$.

## Chinook Salmon Escapement

The total escapement estimate of Chinook Salmon for SY2021 was 46,429 fish (45,967$46,90390 \% \mathrm{Cl}$ ) based on a window count of 47,251 fish (Table 4). The overall fallbackreascension rate for the entire run was $3.49 \%(2.77-4.2890 \% \mathrm{CI})$ and the overall nighttime passage rate was $1.79 \%(1.32-2.3690 \% \mathrm{CI})$. Of the 46,429 fish, the LGR trap captured 10,104 of them, of which 1,995 were valid wild fish (Appendix A-6). Our estimate of wild escapement was $8,604$ fish ( $8,318-8,92990 \% \mathrm{CI})$, which comprised approximately $19 \%$ of the total estimate (Table 4). The remaining 37,825 fish were of hatchery origin. We estimate ad-clipped hatchery escapement was 34,655 fish ( $34,175-35,17190 \% \mathrm{CI}$ ) and ad-intact hatchery escapement was 3,170 fish ( $2,958-3,36190 \% \mathrm{Cl}$ ). External marks, internal tags, and genetics were used to determine that $8 \%$ of the total hatchery fish and $7 \%$ of the total Chinook Salmon run were adintact hatchery fish. Hatchery fish comprised $27 \%$ of the ad-intact Chinook Salmon.

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

Relative abundance of wild Chinook Salmon by genetic stock varied greatly in SY2021 with the Hells Canyon stock highest at $35 \%$ and the Tucannon River stock lowest at approximately $0.2 \%$ (Figure 8; Appendix E-1). Escapement estimates for each genetic stock were as follows (Appendix E-2): UPSALM 1,655 (1,490-1,825 90\% CI); CHMBLN 149 (100-198 90\% CI); MFSALM 1,060 (927-1,205 90\% CI); SFSALM 2,218 (2,014-2,427 90\% CI); HELLSC 3,008 (2,797-3,238 90\% CI); TUCANO 15 (0-39 90\% CI); and FALL 499 ( $432-575$ 90\% CI).

Large fish ( $\geq 57 \mathrm{~cm}$ FL) dominated wild, ad-clipped hatchery, and ad-intact hatchery Chinook Salmon returns. Large wild Chinook Salmon were estimated at 7,025 fish (6,730-7,329 $90 \% \mathrm{CI})$, large ad-clipped hatchery Chinook Salmon at 26,721 fish (26,284-27,182 90\% CI), and large ad-intact hatchery Chinook Salmon at 2,430 fish (2,233-2,588 90\% CI). Small wild Chinook Salmon were estimated at 1,579 fish (1,436-1,740 90\% CI), small ad-clipped hatchery Chinook Salmon at 7,934 fish ( $7,634-8,23190 \% \mathrm{Cl}$ ), and small ad-intact hatchery Chinook Salmon at 740 fish (647-842 90\% CI). Stock-specific estimates for wild fish by size are reported in Appendix E-2.

Wild Chinook Salmon were male-biased, and males accounted for $61 \%$ of the overall wild aggregate return at LGR (Appendix E-3). Male escapement was estimated at 5,220 fish (4,975$5,45690 \% \mathrm{CI}$ ) and females at 3,384 fish (3,190-3,588 90\% CI). Sex ratios for all but one genetic stock mirrored the aggregate wild run and ranged from 58\% male for Hells Canyon to $77 \%$ male for Chamberlain Creek (Appendix E-2). The exception was the Tucannon River stock, located downstream of LGR, with a sex ratio of $7 \%$ male to $93 \%$ female, based on a low sample size of four trapped Tucannon fish.

Nine different age classes were observed from the 1,832 wild fish that we assigned a genetic stock and a total age (Appendix E-4). Age at spawning ranged from two to six years with freshwater age ranging from one to two years and saltwater age ranging from zero (mini-jacks) to four years.

For all genetic stocks, age-4 fish (hatched in BY2017) was the dominant total age cohort (Appendix E-4). We estimated that $9(0-2190 \% \mathrm{CI})$ of the returning adults were age-2 fish (BY2019); 1,958 (1,807-2,103 90\% CI) were age-3 fish (BY2018); 5,568 (5,324-5,825 90\% CI) were age-4 fish (BY2017); 1,056 (941-1,172 90\% CI) were age-5 fish (BY2016); and 13 (0-26 $90 \% \mathrm{Cl}$ ) were age-6 fish (BY2015).

The majority of the wild return (97\%) emigrated to the ocean as one-freshwater fish and 65\% returned as two-saltwater fish (Appendix E-5). Saltwater age estimates were 32 (14-54 90\% $\mathrm{Cl})$ zero-saltwater mini-jacks (MY2021); 2,009 (1,847-2,157 90\% CI) one-saltwater jacks (MY2020); 5,629 (5,369-5,879 90\% CI) two-saltwater fish (MY2019); 929 (825-1,046 90\% CI) three-saltwater fish (MY2018); and 5 (0-14 90\% CI) four-saltwater fish (MY2017). Furthermore, two-saltwater fish made up the majority of returning Chinook Salmon in all seven genetic stocks (Appendix E-6). The mean FL of two-saltwater fish was greater than the $57-\mathrm{cm}$ FL threshold for large Chinook Salmon (Appendix E-7).

Readers accurately determined the saltwater age of $94.6 \%$ of the scale samples ( $n=56$ ) from known saltwater age Chinook Salmon collected during SY2021 (Appendix C-2). The known saltwater age sample was $32 \%$ one-saltwater, $61 \%$ two-saltwater, and $7 \%$ three-saltwater. There were no four-saltwater fish in the known saltwater age sample.

## Chinook Salmon Adult-to-Adult Productivity

Wild Chinook Salmon returning to LGR in SY2021 completed the BY2015 cohort necessary for an adult-to-adult productivity estimate. Brood year 2015 returned 4,134 adults from 23,409 parents resulting in an adult-to-adult productivity estimate of 0.18 recruits per spawner, which is well below the 1.0 recruits per spawner necessary for replacement (Figure 9). A preliminary estimate of adult-to-adult productivity for the BY2016 cohort also placed it below replacement. Although unlikely to change significantly, the estimate for BY2016 is preliminary and will be completed with the SY2022 return.

Adult-to-adult productivity estimates were below replacement for all genetic stocks. Recruits per spawner of each genetic stock were as follows: UPSALM 0.12; CHMBLN 0.10; MFSALM 0.09; SFSALM 0.27; and HELLSC 0.18 (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 the entire stock. Preliminary estimates of adult-to-adult productivity by genetic stock for BY2016 also placed all genetic stocks below replacement. The estimates for BY2016 are preliminary and will be completed with the SY2022 return.

## 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 SY2021, the SAR time series was completed for MY19962017. The most recently completed cohort, MY2017, returned 4,113 fish from 1,171,926 yearling emigrants for a SAR estimate of 0.35 ( $0.34-0.6695 \% \mathrm{CI})$. The 10-year geometric mean SAR was $1.32 \%$ and the 5 -year geometric mean SAR was $0.85 \%$.

## DISCUSSION

Abundance of returning SY2021 summer steelhead and Chinook Salmon estimated at Lower Granite Dam were relatively low compared to previous years' estimates. For steelhead, overall escapement (all rear types combined) in SY2021 was the third lowest on record going back to at least SY1998 and shows a declining 5-year trend (Table 2). Hatchery steelhead escapement was also the third lowest on record, and wild steelhead escapement was below 20,000 fish. Abundance of wild steelhead was 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 $17 \%$ of the proposed escapement goal of 104,500 fish, and about $75 \%$ of NMFS' minimum abundance threshold of 21,000 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). Fortunately, overall steelhead abundance increased compared to SY2020, and for eight of the ten of wild stocks, escapement estimates increased significantly, as evidenced by non-overlapping 90\% Cls (Figure 4). The remaining two genetic stocks, Upper Salmon and Lower Snake, did not change statistically from last year. Despite recent increases in abundance, the 5-year trend in point estimates still shows a continued decline for the majority of wild steelhead stocks. For Chinook Salmon, overall escapement (all rear types combined) in SY2021 was the ninth lowest on record going back to at least SY1998 and shows a declining 5year trend (4). Hatchery Chinook Salmon escapement was also the ninth lowest on record, and wild Chinook Salmon escapement was below 10,000 fish. Abundance of wild Chinook Salmon was below IDFG's "healthy and harvestable" escapement goals and NMFS' minimum abundance thresholds (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). Wild Chinook Salmon escapement was less than $8 \%$ of the proposed escapement goal of 127,000 fish, and less than 33\% of NMFS' minimum abundance threshold of 31,500 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). Fortunately, overall Chinook Salmon abundance increased compared to SY2020; however, this trend was mostly attributed to an increase in hatchery fish because wild escapement estimates decreased for five of the seven stocks (Figure 8). Despite recent decreases in wild abundance, the 5-year trend in point estimates actually showed a slight increase for the majority of wild Chinook Salmon stocks.

Regardless of abundance, low adult-to-adult productivity estimates are a major cause for concern because steelhead and Chinook Salmon populations with productivities far below one recruit per spawner (replacement) are at risk of severe population declines or extirpation. In both species, overall adult-to-adult productivities have shown a steady declining trend below replacement in the recently completed brood year cohorts (Figure 5; Figure 9). Additionally, stockspecific adult-to-adult productivities have been declining below replacement since BY2011 (Figure 6; Figure 10). In the most recently completed brood year cohorts, all genetic stocks of both species (except Upper Clearwater steelhead) showed productivities below 0.5 recruits per spawner. Small stocks with dwindling productivities are particularly the most vulnerable to extirpation, and their extinction would be a big loss for the overall genetic diversity of both species in the Snake River basin.

Adult-to-adult productivity is directly linked to smolt-to-adult return rates, which have also remained below recovery goals. For both steelhead and Chinook Salmon, SARs of the most recently completed brood year cohorts as well as the 5 - and 10- year geometric means were all below the NPCC fish and wildlife program objective to achieve a range of 2-6\% (minimum of 2\%; mean of 4\%; NPCC 2014, 2020; Figure 7; Figure 11). Estimated Chinook Salmon SARs in the
past using our analysis have been slightly higher but closely track the estimates provided by the Comparative Survival Study (CSS; McCann et al. 2015). Smolt-to-adult returns rates are affected by environmental conditions, predation, and other factors that vary across years, but are also directly influenced by the marine environment and passage conditions at hydropower dams during smolt outmigration (Petrosky et al. 2020). Although ocean conditions are becoming increasingly variable and unfeasible to regulate, managers may be able to improve SARs by altering passage conditions at hydropower dams. For example, managers have designed flex-spill operations at LGR that may prove beneficial for outmigrating smolts.

Continuous monitoring of population metrics, such as size and age, is essential for adaptive management and tracking trends over time. Steelhead 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 $\geq 78 \mathrm{~cm}$ FL and are often associated with a two-saltwater age. A-run steelhead ( $<78 \mathrm{~cm} \mathrm{FL}$ ) can also have two-saltwater fish returning, but are typically smaller in size than the B-run dominated stocks. Large steelhead ( $\geq 78 \mathrm{~cm} \mathrm{FL}$ ) abundance increased significantly from SY2020 to SY2021 for hatchery, hatchery ad-clipped, and wild runs (Table 2). Interestingly, total two-saltwater wild steelhead returns in SY2021 were also the highest they have been in the past five years (Appendix D-5). However, the mean length-at-age for two-saltwater steelhead was below the length cutoff for the B-run size classification. In SY2021, two-saltwater returns were on average 1.5 cm larger than SY2020 two-saltwater fish, but still 6 cm smaller than the 78 cm length requirement for large fish (Appendix D-7). The reduced FL-at-age 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, may have contributed to the apparent return of smaller steelhead. The declining average FL 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). It is also important to recognize that size and age trends likely behave differently between A-run dominant and B-run dominant stocks; therefore, fisheries managers must be cautious in their data interpretation and instead look at stock-specific trends to better inform their conclusions.

We observed some changes in Chinook Salmon age composition in SY2021 compared to previous years. The number of returning wild jacks and hatchery jacks in SY2021 increased compared to last year. This is encouraging, as it suggests an improvement in two-saltwater returns is on the horizon for next year. We also observed a slight increasing trend in wild jacks over the past five years (Table 4).

In this report, we omitted the productivity estimates for three genetic stocks that are not complete for the entirety of that stock. In other words, the estimates represented only a portion of the stock population that could be accounted for at LGR. 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 downstream of LGR. The LSNAKE (steelhead) and TUCANO (Chinook Salmon) stocks contain the Tucannon River population which are downstream of LGR. Some returning adults that are born in the Tucannon River overshoot their natal stream and stray upstream of LGR (Boggs et al. 2004; Richins and Skalski 2018). Without abundance information from the Tucannon River for each species, estimates for the LSNAKE and TUCANO should be considered minimum 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 vast 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 spring-summer 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.

The newly developed EASE model estimated escapement of steelhead and Chinook Salmon at LGR by utilizing the same basic principles of previous methods, but combining their strengths and addressing biases (steelhead run reconstruction [Stark et al. 2021], fall Chinook run reconstruction [Steinhorst et al. 2010], SCOBI [Steinhorst et al. 2017], STADEM [See et al. 2021]). Prior to this report, wild (and hatchery) escapement estimates were previously based on unadjusted window counts (i.e. the counts were treated as a complete census). However, there were a couple of potential biases when estimating total adult escapement at LGR using unadjusted window counts. First, some returning fish were known to fallback downstream of LGR after successfully crossing to the upstream side. The fallback fish that re-ascend the LGR ladder were essentially counted twice at the window. Second, the window was not counted 24 hours a day throughout the season; therefore, the daily counts did not include nighttime passage (USACE 2020, 2021). The EASE model is fundamentally similar to the previously implemented SCOBI R package; however, it incorporates fallback/reascension with group-specific rates and estimates nighttime passage rates to inform the total daily counts. Window counts are a critical component of the ESA listing and have been used for decades to evaluate population performance in the hydrosystem; therefore, the adjusted EASE escapement estimates are still directly related to and maintain a transparent relationship with window count data. Window counts at LGR are still reported in Table 2. EASE also provides a measure of GSI uncertainty when assigning stocks and does not utilize the number of trapped fish to inform the total number of fish that ascended the ladder. Accounting for all the aforementioned issues increases the value of the series to address multiple management and assessment needs.

This report provides valuable basin-wide escapement information for assessing the status of Snake River summer steelhead and spring-summer Chinook Salmon. We summarized the abundance and composition of wild adult steelhead and Chinook Salmon returning to LGR during SY2021. 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 and the SAR series for both species. We noted an overall declining trend in wild steelhead abundance and a slight increasing trend in wild Chinook Salmon abundance over the past five years. We also observed overall declining trends in productivity and smolt-to-adult return rates for both species over the past five years.

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

Table 1. Continued.

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 1998-2021. 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 from 1998-2020 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; Baum et al. 2022). Spawn year 2021 estimates were generated by IDFG using the USACE window counts and adult trap data in EASE (present study).

| Spawn year ${ }^{(a)}$ | EASE escapement estimate | LGR <br> window count | Estimated number of steelhead at LGR that were: |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Large wild | Large hatchery adclipped | Large hatchery ad-intact | Small wild | Small hatchery ad-clipped | Small hatchery adintact | 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 ${ }^{\text {(b) }}$ | $34,549^{(b)}$ | 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 |
| $2021{ }^{\text {(c) }}$ | 61,315 | 59,126 | 3,265 | 14,181 | 3,880 | 12,213 | 26,248 | 1,528 | 45,837 | 15,478 |

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 Parentage Based Tagging returns used to adjust wild and hatchery ad-intact fish estimates.
c Escapement estimates using EASE model began in SY2021. EASE estimate does not exactly match the LGR window counts. Decomposition estimates add up to EASE escapement estimate, not the LGR window count

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 ${ }^{(\mathrm{a})}$ | 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 | $\mathrm{n} / \mathrm{a}$ | n/a | 12,129 | 869 | 270 | $\mathrm{n} / \mathrm{a}$ |
| 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 | 908,556 | 3,804 | 3,993 | 25 | 96 | 0.86 (0.84-0.88) |
| $2018{ }^{(b)}$ | 949,098 | 5,511 | 13,988 | - | - | 2.05 (2.03-2.08) |
| 2019 ${ }^{(c)}$ | 845,815 | 1,354 | - | - | - | 0.16 (0.15-0.17) |

a Smolt abundance for 2010-2019 derived from SCRAPI program (Camacho et al. 2018b, 2019b; Ebel et al. 2022).
b Preliminary SAR until saltwater age-3 is added (SY2022).
c Preliminary SAR until saltwater age-2 and age-3 are added (SY2023).

Table 4. Estimated annual escapement, by origin and saltwater age, of Chinook Salmon, spawn years 1998-2021. Jacks were one-saltwater age and include zero-saltwater age mini-jacks; adults were two-saltwater age and older. Estimates from 1998-2020 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; Baum et al. 2022). Spawn year 2021 estimates were generated by IDFG using adult trap data in EASE (present study).

| Estimated number of Chinook Salmon at Lower Granite Dam that were: |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Spawn year ${ }^{(a)}$ | escapement estimate | window count | Wild adults ${ }^{(b)}$ | Wild jacks ${ }^{(b)}$ | Total wild | Hatchery adults ${ }^{(b)}$ | Hatchery jacks ${ }^{(b)}$ | Total hatchery | Total adults ${ }^{(b)}$ | Total jacks ${ }^{(b)}$ |
| 1998 | - | 14,646 | 5,378 | 122 | 5,500 | 8,831 | 315 | 9,146 | 14,209 | 437 |
| 1999 | - | 10,647 | 2,695 | 236 | 2,931 | 3,861 | 3,855 | 7,716 | 6,556 | 4,091 |
| 2000 | - | 51,835 | 7,347 | 1,500 | 8,847 | 30,414 | 12,574 | 42,988 | 37,761 | 14,074 |
| 2001 | - | 192,632 | 37,063 | 1,621 | 38,684 | 148,630 | 5,318 | 153,948 | 185,693 | 6,939 |
| 2002 | - | 101,226 | 27,743 | 340 | 28,083 | 69,441 | 3,702 | 73,143 | 97,184 | 4,042 |
| 2003 | - | 99,463 | 29,270 | 2,349 | 31,619 | 57,761 | 10,083 | 67,844 | 87,031 | 12,432 |
| 2004 | - | 86,501 | 16,808 | 982 | 17,790 | 62,701 | 6,010 | 68,711 | 79,509 | 6,992 |
| 2005 | - | 35,100 | 8,691 | 386 | 9,077 | 25,118 | 905 | 26,023 | 33,809 | 1,291 |
| 2006 | - | 31,223 | 8,775 | 292 | 9,067 | 21,312 | 844 | 22,156 | 30,087 | 1,136 |
| 2007 | - | 42,551 | 7,694 | 1,114 | 8,808 | 21,034 | 12,709 | 33,743 | 28,728 | 13,823 |
| 2008 | - | 88,776 | 14,046 | 2,333 | 16,379 | 53,027 | 19,370 | 72,397 | 67,073 | 21,703 |
| 2009 | - | 111,580 | 12,963 | 3,454 | 16,417 | 45,477 | 49,686 | 95,163 | 58,440 | 53,140 |
| 2010 | - | 134,684 | 26,281 | 1,368 | 27,649 | 97,273 | 9,762 | 107,035 | 123,554 | 11,130 |
| 2011 | - | 134,594 | 22,407 | 4,176 | 26,583 | 69,636 | 38,375 | 108,011 | 92,043 | 42,551 |
| 2012 | - | 84,771 | 20,298 | 1,242 | 21,540 | 59,221 | 4,010 | 63,231 | 79,519 | 5,252 |
| 2013 | - | 70,966 | 12,407 | 6,856 | 19,263 | 30,556 | 21,147 | 51,703 | 42,963 | 28,003 |
| 2014 | - | 114,673 | 26,351 | 3,987 | 30,338 | 65,415 | 18,920 | 84,335 | 91,766 | 22,907 |
| 2015 | - | 132,432 | 21,499 | 1,910 | 23,409 | 96,163 | 12,860 | 109,023 | 117,662 | 14,770 |
| 2016 | - | 81,753 | 15,939 | 813 | 16,752 | 58,187 | 6,814 | 65,001 | 74,126 | 7,627 |
| 2017 | - | 48,192 | 4,108 | 1,685 | 5,793 | 30,180 | 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 ${ }^{\text {c }}$ | - | 34,786 | 8,565 | 1,209 | 9,774 | 21,564 | 3,448 | 25,012 | 30,129 | 4,657 |
| $2021{ }^{\text {(d) }}$ | 46,429 | 47,251 | 6,563 | 2,041 | 8,604 | 29,252 | 8,573 | 37,825 | 35,815 | 10,614 |

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. Due to COVID-19 trap closures in SY2020, few scale samples were taken, so adults and jacks were estimated using length at the LGR counting window (adult $\geq 57 \mathrm{~cm}$ 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 described in Baum et al. (2022).
d Escapement estimates using EASE model began in SY2021. EASE estimate does not exactly match the LGR window counts. Decomposition estimates add up to EASE escapement estimate, not the LGR window count.

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 in smolt migration year 2005 and after (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 | $\mathrm{n} / \mathrm{a}$ | 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 | $\mathrm{n} / \mathrm{a}$ | 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 | 1,171,926 | 34 | 490 | 3,191 | 393 | 5 | 0.35 (0.34-0.36) |
| $2018{ }^{\text {(d) }}$ | 1,437,312 | 29 | 992 | 8,172 | 929 | - | 0.70 (0.68-0.73) |
| 2019(e) | 794,695 | 18 | 1,209 | 5,629 | - | - | 0.86 (0.83-0.89) |
| 2020 | $n / a^{(f)}$ | 0 | 2,009 | - | - | - | - |
| 2021 | $\mathrm{n} / \mathrm{a}^{(\mathrm{g})}$ | 32 | - | - | - | - | - |

a Smolt abundance for 2010-2019 derived from SCRAPI program (Camacho et al. 2018b, 2019b; Ebel et al. 2022).
b Mini-jack (zero-saltwater age) samples were not sampled on the spawning grounds, thus mini-jack fin rays are not available 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.
d Preliminary SAR until saltwater age-4 is added (SY2022).
e Preliminary SAR until saltwater age-3 and age-4 are added (SY2023).
f MY2020 smolt estimate not available due to COVID-19 closures.
g MY2021 smolt estimate not yet analyzed.

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 Lower Granite Dam Estimating Adult Salmonid Escapement (EASE) decomposition model. Total adjusted escapement refers to the LGR window counts with nighttime passage and fallback-reascension rates incorporated. Large/Small refer the fork length (FL) designations for Chinook Salmon large ( $\geq 57 \mathrm{~cm} \mathrm{FL}$ ) and small ( $<57 \mathrm{~cm} \mathrm{FL}$ ) and steelhead large ( $\geq 78 \mathrm{~cm} \mathrm{FL}$ ) and small ( $<78 \mathrm{~cm}$ 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 2009-2021. 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 2021 completed brood year 2013. Note brood year 2014 was shown for reference, but represents a preliminary result that will be completed in SY2022.


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 2021 completed brood year 2013. Note brood year 2014 was shown for reference, but represents a preliminary result that will be completed in SY2022.


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 2010-2017. 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 2014, 2020). See Table 3 for numbers.


Figure 8. Estimated escapement by genetic stock of wild Chinook Salmon at Lower Granite Dam during March 1 to August 17 of spawn years 2009-2021. Confidence intervals are at $90 \%$. Spawn year 2020 stock-specific estimates were generated using run reconstruction and do not include jacks or have confidence intervals. Hells Canyon stock is an aggregate genetic stock that includes the Clearwater, Little Salmon, Lower Salmon, Grande Ronde, Imnaha, and Lower Snake rivers.


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 2021 completed brood year 2015. Note brood year 2016 was shown for reference, but represents a preliminary result that will be completed in SY2022.


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 2021 completed brood year 2015. Note brood year 2016 was shown for reference, but represents a preliminary result that will be completed in SY2022.


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 2014, 2020). See Table 5 for numbers.

## APPENDICES

Appendix A: Annual Lower Granite Dam trapping operations, 2020-2021.

Appendix A-1. Annual Lower Granite Dam trapping operations, 2020-2021. Shaded areas were outside the 2021 spawn year (July 1, 2020 to June 30, 2021 for steelhead and March 1 to August 17, 2021 for Chinook Salmon).

| Calendar date | Trap operation | Comments |
| :---: | :---: | :---: |
| Calendar year 2020 |  |  |
| January 1-March 1 <br> March 2-24 <br> March 25-July 1 | Closed <br> 5 days/week, 28\% Daily Rate Closed ${ }^{(a)}$ | Winter closure 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 ${ }^{(\mathrm{b})}$ |  |
| September 2-November 12 | 7 days/week, 18\% Daily Rate |  |
| November 13-December 31 | Closed | Winter closure |
|  | Calendar year 2021 |  |
| January 1-March 1 | Closed | Winter closure |
| March 2-April 9 | 5 days/week, 25\% Daily Rate |  |
| April 10-August 17 | 5 days/week, 28\% Daily Rate |  |
| August 18-September 1 | 7 days/week, 70\% Daily Rate ${ }^{(b)}$ |  |
| September 2-November 18 | 7 days/week, 18\% Daily Rate |  |
| November 19-December 31 | Closed | Winter closure |

${ }^{\text {a }}$ Trap operations were shut down due to COVID-19 safety policies.
b 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.

Appendix A-2. Daily number of steelhead counted at the Lower Granite Dam window, spawn year 2021. Vertical gray bars indicate when the trap was open and daily trapping rate. $93.4 \%$ 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 2021. Vertical gray bars indicate when the trap was open and daily trapping rate. $71.6 \%$ 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 2009-2021. Only fish failing to meet criteria were considered wild.

| If the LGR mark or tag is: | Then the origin <br> at window is: | Then the origin <br> at trap is: | And the final <br> origin is: |
| :--- | :---: | :---: | :---: |
| Adipose fin clip | Hatchery | Hatchery | Hatchery |
| Coded wire tag (CWT) | N/A ${ }^{(a)}$ | Hatchery | Hatchery |
| Ventral fin clip | N/A | Hatchery | Hatchery |
| Parentage based tag (PBT) | N/A | N/A | Hatchery(a) |
| Passive integrated transponder (PIT) | N/A | N/A | N/A ${ }^{(\mathrm{b})}$ |

${ }^{\text {a }}$ 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 2021. Data were summarized by weekly strata for analysis using the Estimating Adult Salmonid Escapement (EASE) model.

|  |  |  |  | Days |  | Total | Valid | Number | f valid w EAS | fish sam nalysis | used in |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Time strata | Statistical week ${ }^{(\mathrm{a})}$ | Sampling period | Number of days | $\begin{gathered} \text { trap }^{\text {open }^{(b)}} \\ \hline \end{gathered}$ | Window count | valid fish trapped | wild fish trapped | Genetic stock | Size | Sex | Age |
| Fall 2020 |  |  |  |  |  |  |  |  |  |  |  |
| 1 | 27A-33 ${ }^{(c)}$ | 7/1-8/16 | 47 | 32 | 2,610 | 462 | 291 | 285 | 285 | 285 | 185 |
| 2 | 34-36 | 8/17-9/6 | 21 | 21 | 1,926 | 1,107 | 473 | 444 | 444 | 444 | 277 |
| 3 | 37 | 9/7-9/13 | 7 | 7 | 2,211 | 426 | 162 | 161 | 161 | 161 | 106 |
| 4 | 38 | 9/14-9/20 | 7 | 7 | 5,261 | 881 | 229 | 218 | 218 | 218 | 149 |
| 5 | 39 | 9/21-9/27 | 7 | 7 | 9,961 | 1,901 | 458 | 446 | 446 | 446 | 294 |
| 6 | 40 | 9/28-10/4 | 7 | 7 | 10,205 | 2,101 | 361 | 359 | 359 | 358 | 252 |
| 7 | 41 | 10/5-10/11 | 7 | 7 | 9,490 | 1,852 | 345 | 345 | 345 | 345 | 242 |
| 8 | 42 | 10/12-10/18 | 7 | 7 | 5,820 | 1,235 | 216 | 214 | 214 | 214 | 161 |
| 9 | 43 | 10/19-10/25 | 7 | 7 | 3,758 | 787 | 193 | 187 | 187 | 187 | 143 |
| 10 | $44-53^{(c)}$ | 10/26-12/31 | 67 | 18 | 5,301 | 640 | 163 | 161 | 161 | 161 | 130 |
|  |  |  |  |  | Sprin | $g 2021$ |  |  |  |  |  |
| 11 | 10-27B ${ }^{\text {c }}$ ( | 3/1-6/30 | 122 | 122 | 2,583 | 604 | 304 | 285 | 285 | 285 | 146 |
| Total: |  |  | 306 | 242 | 59,126 | 11,996 | 3,195 | 3,105 ${ }^{\text {(d) }}$ | 3,105 ${ }^{\text {(d) }}$ | $3,104{ }^{(d)}$ | 2,085 |

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.
d One hundred-six additional fish without ages were removed from the genetic stock, size, and sex sample due to analytical complications in EASE, reducing the sample size to 2,999, 2,999, and 2998 fish, respectively.

Appendix A-6. Weekly window counts and valid adult trap samples of Chinook Salmon at Lower Granite Dam, spawn year 2021. Data were summarized by weekly strata for analysis using the Estimating Adult Salmonid Escapement (EASE) model.

| Time strata | Statistical week ${ }^{(\mathrm{a})}$ | Sampling period | Number of days | Days trap open ${ }^{(b)}$ | Window count | Total valid fish trapped | Valid wild fish trapped | Number of valid wild fish samples used in EASE analysis |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  |  |  | Genetic stock | Size | Sex | Age |
| 1 | 10-20 | 3/1-5/16 | 77 | 77 | 12,510 | 2,043 | 163 | 161 | 161 | 161 | 148 |
| 2 | 21 | 5/17-5/23 | 7 | 7 | 9,987 | 2,168 | 243 | 241 | 241 | 241 | 227 |
| 3 | 22 | 5/24-5/30 | 7 | 7 | 5,359 | 1,376 | 217 | 216 | 216 | 216 | 202 |
| 4 | 23 | 5/31-6/6 | 7 | 7 | 4,514 | 913 | 171 | 171 | 171 | 171 | 159 |
| 5 | 24 | 6/7-6/13 | 7 | 7 | 2,568 | 579 | 132 | 132 | 132 | 132 | 123 |
| 6 | 25 | 6/14-6/20 | 7 | 7 | 3,146 | 773 | 217 | 217 | 217 | 217 | 199 |
| 7 | 26 | 6/21-6/27 | 7 | 7 | 2,971 | 575 | 188 | 188 | 188 | 188 | 175 |
| 8 | 27 | 6/28-7/4 | 7 | 7 | 2,441 | 551 | 213 | 211 | 211 | 211 | 199 |
| 9 | 28-29 | 7/5-7/18 | 14 | 14 | 2,319 | 742 | 290 | 287 | 287 | 287 | 262 |
| 10 | 30-34 ${ }^{\text {(c) }}$ | 7/19-8/17 | 30 | 30 | 1,436 | 384 | 161 | 158 | 158 | 158 | 138 |
| Total: |  |  | 170 | 170 | 47,251 | 10,104 | 1,995 | 1,982 ${ }^{\text {(d) }}$ | 1,982 ${ }^{\text {(d) }}$ | 1,982 ${ }^{\text {(d) }}$ | 1,832 |

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.
d Seven additional fish without ages were removed from the genetic stock, size, and sex sample due to analytical complications in EASE, reducing the sample size to 1,975 fish for all three categories.

Appendix B. Methods description of Estimating Adult Salmonid Escapement (EASE) model used for all steelhead and spring-summer Chinook Salmon estimates, spawn year 2021.

Appendix B-1. Methods description of Estimating Adult Salmonid Escapement (EASE) model used for all steelhead and spring-summer Chinook Salmon estimates, spawn year 2021.

The following methods provide detailed information about the newly developed Estimating Adult Salmonid Escapement model (EASE) used for all escapement estimates of steelhead and spring-summer Chinook Salmon at Lower Granite Dam in SY2021.

Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions
For daytime ascensions, the window count, $w$, is considered a binomial random variable

$$
\begin{equation*}
w \sim \operatorname{bin}\left(r, a_{d}\right), \tag{1}
\end{equation*}
$$

where $r$ is the proportion of time counting was performed and $a_{d}$ is the number of daytime ascensions. The point estimate of $a_{d}$ is therefore $\frac{w}{r}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of $r$ and number of trials of $a_{d}$. These random binomials are then divided by $r$ to yield bootstrap estimates of $a_{d}$.

For nighttime passage, the probability a given ascension occurs at night is estimated using PIT tag detections in the ladder. The number of PIT ascensions at night, $d_{n}$, is treated as a binomial random variable

$$
\begin{equation*}
d_{n} \sim \operatorname{bin}\left(p_{n}, d_{a}\right) \tag{2}
\end{equation*}
$$

where $p_{n}$ is the probability a given ascension occurs at night and $d_{a}$ is the total number of PIT ascensions. The maximum likelihood estimate of $p_{n}$ is therefore $\frac{d_{n}}{d_{a}}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of the maximum likelihood estimate of $p_{n}$ and number of trials of $d_{a}$. These random binomials are then divided by $d_{a}$ to yield bootstrap estimates of $p_{n}$.

Using the estimates of $a_{d}$ and $p_{n}$, the total number of ascensions, $a_{t}$, is calculated as

$$
\begin{equation*}
a_{t}=a_{d} /\left(1-p_{n}\right) \tag{3}
\end{equation*}
$$

To generate $d_{n}$ for input to the model, a user must categorize PIT ascensions as occurring during the day or night. This is currently performed by Columbia River DART. Detection histories are broken into ascensions with each ascension beginning with a detection at the viewing window array and ending with a detection at the ladder exit array. We then exclude any fish that were PIT tagged as adults in the Lower Granite trap. Ascensions whose first detection at the viewing window is outside of counting hours are assigned to the night. Detection efficiency of PIT tags in the ladder is assumed to be $100 \%$, and if any fish are not detected at the viewing window and subsequently at the ladder exit, they are excluded.

## Fallback Rates

Fallback rates have previously been observed to vary between groups of steelhead stocks, specifically between stocks upstream and downstream of LGR. To estimate escapement
to the level of these stocks, fallback rates must be estimated separately for each group. The method described here is applied separately to each group to yield group-specific estimates of fallback rates.

The probability that a given ascension results in fallback (e.g., the fish that ascended later fell back below the dam) is estimated using PIT tag detections. The number of PIT ascensions that later reascended, $d_{f}$, is treated as a binomial random variable

$$
\begin{equation*}
d_{f} \sim \operatorname{bin}\left(p_{f}, d_{a s}\right) \tag{4}
\end{equation*}
$$

where $p_{f}$ is the probability that a given ascension results in fallback and $d_{a s}$ is the total number of ascensions from the given stock group. The maximum likelihood estimate of $p_{f}$ is therefore $\frac{d_{f}}{d_{a s}}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of the maximum likelihood estimate of $p_{f}$ and number of trials of $d_{a s}$. These random binomials are then divided by $d_{a s}$ to yield bootstrap estimates of $p_{f}$.

It is important to realize that because fish are only detected as having fallen back if they later reascend, this assumes that the rate of fallback without reascension is 0 .

To generate $d_{f}$ for input to the model, a user must categorize PIT ascensions as being first ascensions or reascensions. This is currently performed by Columbia River DART by breaking detection histories into unique ascensions as described in the previous section. We then exclude any fish that were PIT tagged as adults in the Lower Granite trap. By only using fish PIT tagged prior to arrival at the dam, we ensure that sampling is not biased with respect to whether a fish is trapped or not.

## Composition of Ascensions

The trap provides a sample of all fish ascending the ladder as it traps fish 24 hours a day during the days it is operational. We used this sample to estimate the composition of fish ascending the ladder by adipose fin status (ad-clipped or ad-intact), origin (hatchery or wild), and one or two additional categorical variables (e.g. PBT, GSI, genetic sex). Composition is estimated using the methods developed by Delomas and Hess (2021) and implementing the approach discussed therein for integrating GSI uncertainty into the estimates. Inputs required for this step are the attributes recorded for trapped fish and parentage-based tagging (PBT) tag rates.

Composition is estimated in a hierarchical, step-wise manner (Steinhorst et al. 2017) to accommodate the desire for marginal totals for some variables to be the same regardless of the other variables being estimated in a given run of the model. For example, the number of ad-intact hatchery fish estimated should be the same regardless of whether the wild component is being estimated by genetic stock and sex or by genetic stock and size. The proportions of ad-clipped and ad-intact fish are first estimated using clip information recorded at the trap. The proportion of fish that are ad-clipped, $p_{A D}$, is estimated as $\frac{\text { Number of ad-clipped fish }}{\text { Total number of fish }}$. The ad-intact portion is then split further into fish with physical tags denoting them of hatchery origin (e.g. CWT, ventral fin clips) and fish without such physical tags. The proportion of ad-intact fish with physical tags, $p_{\text {phys }}$, is estimated as $\frac{\text { Number of physically tagged ad-intact fish }}{\text { Total number of ad-intact fish }}$. The unmarked (ad-intact, no physical tags), genotyped fish are then used to estimate the proportion of unmarked fish that are hatchery origin, $p_{P B T}$, and wild using PBT assignments and tag rates. This is done using a maximum
likelihood method (Delomas and Hess 2021). The proportions of fish that are ad-clipped hatcheryorigin $(H)$, ad-intact hatchery-origin ( $H N C$ ), and wild-origin $(W)$ can then be calculated as

$$
\begin{align*}
& H=p_{A D},  \tag{5}\\
& H N C=\left(1-p_{A D}\right)\left(p_{\text {phys }}+\left(1-p_{p h y s}\right) p_{P B T}\right),  \tag{6}\\
& W=\left(1-p_{A D}\right)\left(1-p_{\text {phys }}\right)\left(1-p_{P B T}\right) . \tag{7}
\end{align*}
$$

Composition within each group ( $H, H N C, W$ ) is then estimated for one or two additional variables.
For the H group, composition of the first variable is estimated using all ad-clipped fish with data for the first variable. Composition of a second variable (if included) within the categories of the first variable is then estimated using all ad-clipped fish with data for both the first and second variables and with marginal proportions for the first variable constrained to their estimated values. The composition of the PBT grouping variable (groups for which PBT tag rates are defined) and the composition of the second variable if the first variable is the PBT grouping variable are estimated using the maximum likelihood method described by Delomas and Hess (2021). Other variables are treated as multinomial random variables and maximum likelihood estimates (observed proportions in the sample) are calculated (ex: size category).

For the HNC group, composition is estimated using the maximum likelihood method described by Delomas and Hess (2021) applied separately to the ad-intact, physically tagged fish and the unmarked fish and then summed together. If the variable of interest is not the PBT grouping variable, the estimates for the ad-intact, physically tagged fish are simply the observed proportions in the sample. For the unmarked fish, the proportions of the PBT grouping variable are constrained to the values estimated during the previous estimation of $p_{P B T}$.

For the W group, composition for the first variable is estimated using the maximum likelihood method described by Delomas and Hess (2021) and using data from all ad-intact, genotyped samples with data for the first variable. The W group is a mixture of different genetic stocks and so the first variable should always be genetic stock. Composition of a second variable (if included) within the categories of the first variable is then estimated using all ad-intact, genotyped fish with data for both the first and second variables and with marginal proportions for the first variable constrained to their estimated values. Secondary variables for this analysis include size, sex, age class, saltwater age, and brood year (Figure 3). The proportions of the PBT grouping variable within the ad-intact, unmarked fish are constrained to the values estimated during the previous estimation of $p_{P B T}$. It is important that the variables of interest for the W group (e.g. GSI) are recorded for ad-intact, unmarked samples regardless of PBT assignment. This is because the composition of the ad-intact, unmarked, PBT assigned samples contributes to the likelihood used to calculate composition of the W group. For estimating composition of the second variable, it is assumed that within the PBT groups of the unmarked HNC fish, the first and second variables are independent. This is expected to be the case as one variable is typically GSI assignment, and within an HNC PBT group, variation in GSI assignment is not expected to reflect meaningful genetic structure.

The uncertainty in GSI assignments is incorporated into the composition point estimates by estimating composition iteratively while replacing GSI assignments with draws from the joint posterior distribution of all GSI assignments in the dataset (Delomas and Hess 2021). Point estimates are then calculated as the means across iterations. Bootstrap estimates are obtained
by non-parametric bootstrapping and simultaneously replacing GSI assignments with draws from the posterior of GSI assignments.

## Stratification

When estimating escapement over an extended time period, a stratified approach has been previously demonstrated to be superior to a pooled approach as many parameters change over time and the trap (sampling) rate can also change during the run (Steinhorst et al. 2017). As such, this model is implemented using a stratified approach and estimates are obtained by summing results across strata. Confidence intervals are then calculated as the quantiles $\left(\frac{\alpha}{2}\right.$ and $1-\frac{\alpha}{2}$ ) of the bootstrap estimates.

As multiple datasets are used to estimate different parameters, several sets of strata are defined. One set is defined for nighttime passage estimates. Separate sets of strata are defined for fallback rates for each stock group. This allows strata to be shorter in duration for stock groups with more PIT tag detections. Finally, a set of strata is defined for the composition estimates. The one interdependency between strata is that every composition estimate stratum must correspond to one and only one fallback stratum for each stock group. When defining strata, several criteria are kept in mind. The model must be able to estimate parameters in each time step, so there must be at least one sample informing each parameter. The parameters being estimated should be approximately constant in each stratum, so strata should not span changes in environmental conditions that could affect the underlying parameters (e.g., for estimating steelhead escapement, fall and spring time periods should not be combined). Additionally, while a minimum of one sample is required for each stratum, it is recommended that there be sufficient samples to provide a reasonable estimate of the underlying parameters. For example, if composition of the W portion of the run is being estimated by genetic stock, approximately 45 genotyped, unmarked, untagged samples per stratum (Given more than three possible categories, a sample size of 45 indicates a maximum error of any estimated multinomial proportion within that stratum of 0.15 with $\alpha=0.10$ ) for the composition estimates can be recommended (Thompson 1987).

Based on data for previous years, for the bulk of the run, a stratum corresponds to a week, but for the tails of the run several weeks may be combined into one stratum. The exception to this may be the fallback estimates for steelhead released below Lower Granite Dam. Since there are fewer PIT tagged fish in this group, combining weeks into a single stratum may be a more frequent occurrence.

## Non-specific PBT Groups

For a small minority of hatchery releases, PBT assignments do not definitively indicate which stock group (upper or lower) a fish belongs to for application of fallback rates. This occurs when fish from the same family are split (and not differentially marked) between two release groups. In these scenarios, the release groups are typically PIT tagged separately, and so PIT tag detections can be used to split the composition estimate for the PBT group into separate release groups. Consider a PBT group that is composed of two release groups (release $A$ and $B$ ), and the PIT tagging rates at release are $t_{A}$ and $t_{B}$. The number of detections of PIT tags from each group, $d_{A}$ and $d_{B}$, can be considered binomial random variables

$$
\begin{align*}
& d_{A} \sim \operatorname{bin}\left(t_{A}, N_{A}\right),  \tag{8}\\
& d_{B} \sim \operatorname{bin}\left(t_{B}, N_{B}\right), \tag{9}
\end{align*}
$$

where $N_{A}$ and $N_{B}$ are the total numbers of fish in each release. An estimate of $N_{A}$ is simply $\frac{d_{A}}{t_{A}}$, and similarly for $N_{B}$. The proportion of fish in the PBT group that belong to each release group is then calculated and used to split the PBT group composition estimate. Bootstrap estimates of $N_{A}$ and $N_{B}$ are obtained by parametric bootstrapping. Random binomials are generated using a probability of success of $t_{A}$ and $t_{B}$ and number of trials of $N_{A}$ and $N_{B}$. These random binomials are then divided by the tag rates to yield bootstrap estimates of $N_{A}$ and $N_{B}$. This procedure is extendable to PBT groups containing more than two separately PIT tagged release groups.

Appendix C: Steelhead and Chinook Salmon 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 2021 (Micah Davison, IDFG, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. PA = percent agreement.


Appendix C-2. Age bias plot illustrating pairwise comparisons of scale assigned saltwater age with known age for Chinook Salmon at Lower Granite Dam, spawn year 2021 (Micah Davison, IDFG, 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 2021.

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 2010-2021. 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 2021. $L=$ 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 | 1,477 | 1,280 | 1,668 | 434 | 333 | 534 | 90 | 43 | 144 | 1,821 | 1,590 | 2,021 | 1,911 | 1,675 | 2,122 |
| MFSALM | 783 | 662 | 895 | 167 | 116 | 221 | 255 | 196 | 322 | 695 | 579 | 797 | 950 | 819 | 1,077 |
| SFSALM | 361 | 278 | 438 | 96 | 56 | 135 | 266 | 207 | 333 | 191 | 127 | 253 | 457 | 365 | 546 |
| LOSALM | 325 | 233 | 446 | 76 | 40 | 131 | 22 | 2 | 51 | 379 | 276 | 508 | 401 | 292 | 535 |
| UPCLWR | 1,336 | 1,194 | 1,495 | 329 | 257 | 417 | 1,120 | 988 | 1,257 | 545 | 449 | 645 | 1,665 | 1,509 | 1,837 |
| SFCLWR | 1,080 | 938 | 1,225 | 446 | 360 | 547 | 1,033 | 892 | 1,176 | 493 | 394 | 597 | 1,526 | 1,354 | 1,706 |
| LOCLWR | 888 | 720 | 1,064 | 250 | 167 | 336 | 162 | 103 | 231 | 976 | 792 | 1,179 | 1,138 | 946 | 1,356 |
| IMNAHA | 804 | 656 | 944 | 184 | 119 | 257 | 30 | 7 | 59 | 958 | 793 | 1,114 | 988 | 825 | 1,151 |
| GRROND | 3,584 | 3,282 | 3,907 | 1,038 | 884 | 1,192 | 179 | 130 | 298 | 4,443 | 4,084 | 4,768 | 4,622 | 4,281 | 4,982 |
| LSNAKE | 1,393 | 1,148 | 1,642 | 427 | 318 | 550 | 108 | 60 | 170 | 1,712 | 1,414 | 2,026 | 1,820 | 1,518 | 2,153 |
| Total | 12,031 | 11,609 | 12,447 | 3,447 | 3,200 | 3,701 | 3,265 | 3,052 | 3,548 | 12,213 | 11,744 | 12,620 | 15,478 | 15,001 | 15,973 |

Appendix D-3. Estimated escapement by sex of wild steelhead at Lower Granite Dam, spawn years 2009-2021. Confidence intervals are at 90\%.


Appendix D-4. Estimated escapement of wild steelhead at Lower Granite Dam by smolt migration year, brood year, and age class for each genetic stock, spawn year 2021. Only individual fish that had both a total age and an assigned stock were used ( $n$ $=2,085)$. 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 |  |  |  | MY20 |  |  |
|  | BY14 | BY14 | BY14 | BY15 | BY15 | BY15 | BY16 | BY14 | BY14 | BY15 | BY15 | BY16 | BY16 | BY17 | BY15 | BY16 | BY17 | BY18 | BY17 | BY18 |  |
| Genetic stock | 2.2R1 | 3.1R1 | 3.3 | 2.1R1 | 2.2.R | 2.3 | 1.1R1 | 4.1R | 4.2 | 3.1R | 3.2 | 2.1R | 2.2 | 1.2 | 4.1 | 3.1 | 2.1 | 1.1 | 3.0 | 2.0 | Total wild |
| UPSALM | 0 | 7 | 0 | 0 | 0 | 0 | 4 | 0 | 8 | 0 | 374 | 0 | 1,137 | 136 | 24 | 80 | 121 | 17 | 0 | 3 | 1,911 |
| MFSALM | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 9 | 10 | 562 | 1 | 240 | 3 | 12 | 95 | 16 | 1 | 0 | 0 | 950 |
| SFSALM | 2 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 14 | 0 | 295 | 0 | 119 | 0 | 2 | 10 | 7 | 0 | 0 | 0 | 457 |
| LOSALM | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 114 | 0 | 212 | 7 | 2 | 28 | 32 | 2 | 0 | 0 | 401 |
| UPCLWR | 0 | 0 | 3 | 0 | 0 | 7 | 0 | 0 | 8 | 0 | 717 | 0 | 822 | 55 | 11 | 39 | 3 | 0 | 0 | 0 | 1,665 |
| SFCLWR | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 273 | 0 | 1,009 | 178 | 0 | 33 | 23 | 0 | 0 | 0 | 1,526 |
| LOCLWR | 1 | 0 | 0 | 0 | 0 | 0 | 2 | 6 | 3 | 0 | 165 | 0 | 764 | 101 | 2 | 29 | 58 | 4 | 0 | 3 | 1,138 |
| IMNAHA | 0 | 0 | 0 | 0 | 6 | 0 | 4 | 0 | 2 | 0 | 174 | 0 | 633 | 37 | 1 | 55 | 67 | 3 | 6 | 0 | 988 |
| GRROND | 11 | 1 | 0 | 5 | 7 | 0 | 6 | 0 | 12 | 0 | 990 | 5 | 2,938 | 280 | 7 | 160 | 190 | 8 | 2 | 0 | 4,622 |
| LSNAKE | 6 | 4 | 0 | 3 | 0 | 0 | 2 | 2 | 3 | 0 | 321 | 1 | 1,100 | 165 | 3 | 103 | 95 | 11 | 0 | 1 | 1,820 |
| Total | 20 | 12 | 9 | 8 | 13 | 16 | 18 | 8 | 67 | 10 | 3,985 | 7 | 8,974 | 962 | 64 | 632 | 612 | 46 | 8 | 7 | 15,478 |

Appendix D-5. Estimated escapement by saltwater age of wild steelhead at Lower Granite Dam, spawn years 2009-2021. 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 2009-2021. Confidence intervals are at 90\%. Repeat refers to steelhead showing evidence of previous spawning events.


Appendix D-7. Length frequency distribution by saltwater age of wild steelhead trapped at Lower Granite Dam, spawn year 2021. Solid black vertical line represents the mean fork length (FL) for each 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 2021.

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 2010-2021. 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 Chinook Salmon at Lower Granite Dam by sex and by size for each genetic stock, spawn year 2021. $L=$ 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 Chinook Salmon 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 | 652 | 556 | 753 | 1,003 | 873 | 1,121 | 1,405 | 1,245 | 1,552 | 250 | 191 | 329 | 1,655 | 1,490 | 1,825 |
| CHMBLN | 35 | 14 | 59 | 114 | 72 | 158 | 95 | 60 | 137 | 54 | 26 | 83 | 149 | 100 | 198 |
| MFSALM | 385 | 303 | 466 | 675 | 567 | 785 | 850 | 718 | 977 | 210 | 154 | 283 | 1,060 | 927 | 1,205 |
| SFSALM | 821 | 706 | 931 | 1,397 | 1,247 | 1,552 | 1,764 | 1,581 | 1,941 | 454 | 381 | 541 | 2,218 | 2,014 | 2,427 |
| HELLSC | 1,271 | 1,143 | 1,418 | 1,737 | 1,587 | 1,904 | 2,487 | 2,306 | 2,715 | 521 | 419 | 604 | 3,008 | 2,797 | 3,238 |
| TUCANO | 14 | 0 | 35 | 1 | 0 | 8 | 15 | 0 | 38 | 0 | 0 | 4 | 15 | 0 | 39 |
| FALL | 206 | 160 | 254 | 293 | 239 | 350 | 409 | 348 | 477 | 90 | 61 | 122 | 499 | 432 | 575 |
| Total | 3,384 | 3,190 | 3,588 | 5,220 | 4,975 | 5,456 | 7,025 | 6,730 | 7,329 | 1,579 | 1,436 | 1,740 | 8,604 | 8,318 | 8,929 |

Appendix E-3. Estimated escapement by sex of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2021. Spawn year 2020 sex estimates are not available because the trap was closed due to COVID-19 restrictions.


Appendix E-4. Estimated escapement of wild Chinook Salmon at Lower Granite Dam by smolt migration year, brood year, and age class for each genetic stock, spawn year 2021. Only individual fish that had both a total age and an assigned stock were used (n $=1,832$ ). See Genetic Tissue Processing and Analysis section for stock abbreviations.

| $\begin{gathered} \text { Genetic } \\ \text { stock } \end{gathered}$ | Smolt migration year (MY), brood year (BY), and age class |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | MY2017 | MY2018 |  | MY2019 |  | MY2020 |  | MY2021 |  | Total wild |
|  | $\frac{\text { BY15 }}{1.4}$ | $\frac{\text { BY15 }}{2.3}$ | $\frac{\text { BY16 }}{1.3}$ | $\frac{\text { BY16 }}{2.2}$ | $\begin{array}{r} \text { BY17 } \\ 1.2 \end{array}$ | $\frac{\text { BY17 }}{2.1}$ | $\frac{\text { BY18 }}{1.1}$ | $\begin{gathered} \text { BY18 } \\ 2.0 \end{gathered}$ | $\frac{\text { BY19 }}{1.0}$ |  |
| UPSALM | 0 | 0 | 236 | 8 | 1,108 | 8 | 295 | 0 | 0 | 1,655 |
| CHMBLN | 0 | 0 | 5 | 0 | 78 | 0 | 66 | 0 | 0 | 149 |
| MFSALM | 0 | 3 | 166 | 4 | 632 | 2 | 253 | 0 | 0 | 1,060 |
| SFSALM | 0 | 0 | 184 | 9 | 1,430 | 9 | 586 | 0 | 0 | 2,218 |
| HELLSC | 0 | 1 | 259 | 12 | 2,030 | 21 | 685 | 0 | 0 | 3,008 |
| TUCANO | 0 | 0 | 0 | 0 | 14 | 0 | 1 | 0 | 0 | 15 |
| FALL | 5 | 4 | 71 | 102 | 202 | 34 | 49 | 23 | 9 | 499 |
| Total | 5 | 8 | 921 | 135 | 5,494 | 74 | 1,935 | 23 | 9 | 8,604 |

Appendix E-5. Estimated escapement by saltwater age of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2021. Confidence intervals are at 90\%. Spawn year 2020 saltwater age estimates were generated using run reconstruction and do not have confidence intervals. Saltwater age-0 refers to mini-jacks.


Appendix E-6. Estimated escapement by genetic stock and saltwater age of wild Chinook Salmon at Lower Granite Dam, spawn years 2009-2021. Spawn year 2020 saltwater age estimates were not available at the stock level because the trap was closed due to COVID-19 restrictions. Confidence intervals are at 90\%. Saltwater age-0 refers to mini-jacks.


## Spawn year

Appendix E-7. Length frequency distribution by saltwater age of wild Chinook Salmon trapped at Lower Granite Dam, spawn year 2021. Solid black vertical line represents the mean length for each saltwater age. Dashed vertical red line represents the 570 mm FL cutoff for determining large-sized Chinook Salmon.


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[^0]:    Appendix E-7. Length frequency distribution by saltwater age of wild Chinook Salmon trapped at Lower Granite Dam, spawn year 2021. Solid black vertical line represents the mean length for each saltwater age. Dashed vertical red line represents the 570 mm FL cutoff for determining large-sized Chinook Salmon.

