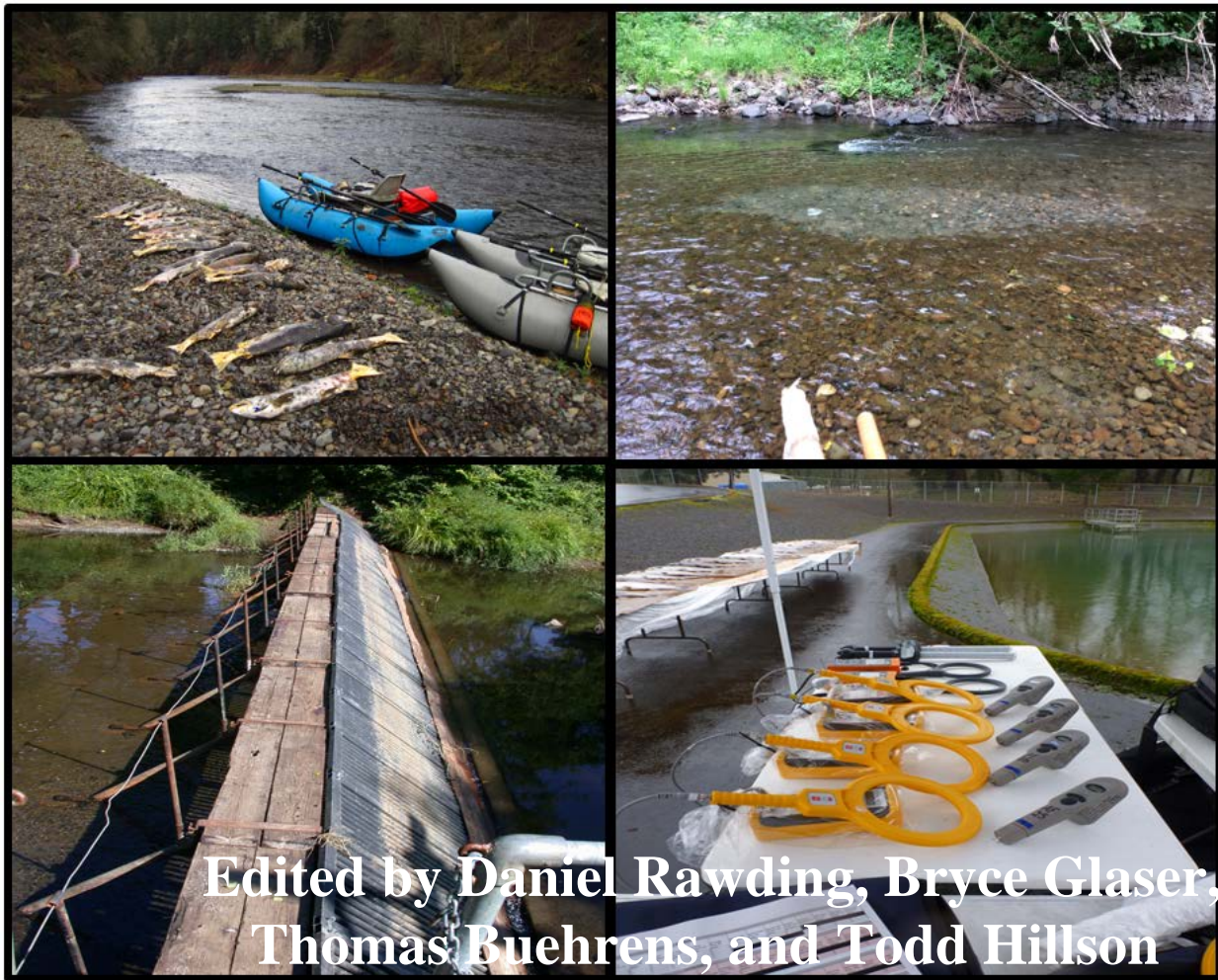


Lower Columbia River Fisheries and Escapement Evaluation in Southwest Washington, 2012



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Executive Summary

In 2010, The Washington Department of Fish and Wildlife (WDFW) began implementation of an expanded monitoring program for Chinook and coho salmon populations in the Lower Columbia River (LCR) region of Southwest Washington (WDFW's Region 5) and fishery monitoring in the lower mainstem of the Columbia River. The focus of this expanded monitoring was to 1) gather data on Viable Salmonid Population (VSP) parameters – spawner abundance, including proportion of hatchery origin spawners (pHOS), spatial distribution, diversity, and productivity and 2) to increase the Coded Wire Tag (CWT) recovery rate from spawning grounds to meet regional standards, and 3) to evaluate the use of PIT tags to develop harvest rates for salmon and steelhead populations by having fishery samplers recovery PIT tags from fish being sampled for CWT in existing fisheries monitoring programs. Monitoring protocols and analysis methods utilized were intended to produce unbiased estimates with measurements of precision in an effort to meet NOAA monitoring guidelines (Crawford and Rumsey 2011). These reports summarize the third year of the expanded monitoring program.

Funding for this program came from multiple sources: 1) the Bonneville Power Administration (BPA) through the Lower Columbia Coded Wire Tag (CWT) Recovery Project (BPA Project #: 2010-036-00) ; 2) the National Oceanic and Atmospheric Administration (NOAA) via Mitchell Act Monitoring, Evaluation and Reform (MA MER) funds; 3) NOAA via Pacific Coastal Salmon Recovery Funds (PCSRF) (administered thru the Washington State Recreation and Conservation Office (RCO)); 4) Washington State; 5) PacifiCorp (NF Lewis River Chinook salmon monitoring) and 6) Tacoma Power (Cowlitz River Basin).

This report is structured into three components:

1) Fall Chinook Salmon Escapement Estimates and Coded-Wire-Tag Recoveries in Washington's Lower Columbia River Tributaries in 2012

- Key Results
 - Adult fall Chinook abundance was estimated using weir counts, open and closed mark-recapture models, Area-Under-the-Curve (AUC), redd counts, and peak count expansion depending on resources and survey conditions.
 - We estimated 22,963 adult Tule, 99 adult Rogue River Bright hatchery, 8,849 adult Lewis and Cowlitz river Bright natural origin, and 1,624 adult Bonneville (BON) Pool Bright fall Chinook salmon in the Washington portion of the LCR ESU.
 - For Tules and BON Brights the proportion of marked adults was 68% and 46%, respectively. Age structure varied by population but most Tule Chinook salmon were age 3 or 4.
 - Most Tules populations were comprised primarily of hatchery fish except the Coweeman (89% unmarked), Lewis (82% unmarked), and the White Salmon (93% unmarked).
 - A total of 141 snouts were collected from the field and examined for CWT. CWT recoveries were uploaded to the regional coded-wire-tag database (RMIS). Unexpanded CWT recoveries indicate most Tule hatchery fish returned to the basin of release or an adjacent basin.
 - BON Brights are not native to this ESU and continue to successfully spawn in the Upper Gorge and White Salmon populations. Rogue River Brights, also not native to this ESU, continue to successfully spawn in the Grays River.

2) Coho Salmon Escapement Estimates and Coded-Wire-Tag Recoveries in Washington's Lower Columbia River Tributaries in 2012

- Key Results
 - The adult coho salmon population monitoring program used trap and haul census counts, mark-recapture, smolt expansion, and redd-based methods to monitor adult coho salmon.
 - We estimated a mean escapement of 34,174 (95% CI 24,720 – 51,680) adults and 7,656 jacks (95% CI 2,014 - 12,980) for the Washington portion of this ESU below Bonneville Dam excluding the mainstem Lower Cowlitz, and mainstem Toutle/ lower North Fork Toutle (below the Sediment Retention Structure) populations.
 - The total mean estimate of unmarked coho salmon adults for the Washington portion of this ESU below Bonneville Dam excluding the mainstem Lower Cowlitz, and mainstem Toutle/ lower North Fork Toutle (below the Sediment

- Retention Structure) populations was 21,083 (95% CI 12,870 – 36,580).
- As expected, it was generally true that populations with an operating coho salmon hatchery, including the Grays, Elochoman, Upper Cowlitz/Cispus, Kalama and NF Lewis populations, had high proportions of hatchery spawners (mean = 19%, 25 %, 75%, 81%, and 58%, respectively). The converse was also generally true for populations without hatcheries, such as the Mill-Abernathy-Germany, Coweeman, South Fork Toutle, and EF Lewis populations, where we observed low percentages of marked adults (mean = 3%, 2%, 13%, and 8% respectively).
 - From carcass recoveries on stream surveys, a total of nine CWTs were recovered from coho salmon in 2012.

3) Detection Probabilities for Passive Integrated Transponder (PIT) Tags in Adult Salmon and Steelhead with Hand Held Scanners, 2012

- Key Results
 - The objectives in 2012 were to measure the effects of PIT tag reader type, as well as fish characteristics, and sampling methods on detection rates.
 - Results suggest that the Destron Fearing FS2001F-ISO reader maintains near-perfect detection efficiency in the presence of minor deviations from scanning protocol. While the Biomark 601-3 reader maintains high but declining efficiency and the Agrident AWR100 stick reader has markedly reduced performance in the presence of minor deviations from protocol. We therefore recommend the use of the Destron Fearing reader in commercial fishery sampling applications where minor protocol violations are more likely to occur due to the high volume of fish sampled.
 - The study revealed that reader type, sampling method, and fish characteristics affect detection rates. The significant effect of girth and species on detection probabilities suggests that our results may be less applicable to fisheries sampling efforts encountering fish outside the range of girths tested in this study (e.g., very large chinook).

Relationship to the 2008 Federal Columbia River Power System Biological Opinion

Work conducted under the BPA Lower Columbia River CWT Recovery Project (#2010-036-00) supports the following Reasonable and Prudent Actions (RPA) as identified in the 2008 Federal Columbia River Power System Biological Opinion (FCRPS BiOp).

http://www.nwr.noaa.gov/hydropower/fcrps_opinion/federal_columbia_river_power_system.html

RPA:

50.4: Review/modify existing fish pop status monitoring projects

Review and modify existing Action Agencies fish population status monitoring projects to improve their compliance with regional standards and protocols, and ensure they are prioritized and effectively focused on critical performance measures and populations. (Initiate in FY 2008)

Relationship: Through increased monitoring conducted under this project, WDFW was able to develop comprehensive LCR ESU wide VSP monitoring estimates of NOR abundance, pHOS, spatial distribution, and data points for several abundance and productivity metrics (adult to adult recruitment, smolt to adult returns, and natural origin spawners) for Washington Chinook and coho populations; including estimates of precision for the LCR ESU and for individual populations in an effort to meet NOAA monitoring guidelines (Crawford and Rumsey 2011).

51.1: Report available information on population viability metrics in annual and comprehensive evaluation reports. (Initiate in FY 2008).

Relationship: Reported population viability metrics and indicators for Washington's portion of the LCR Chinook and coho salmon. These indicators are formatted to be entered into the Coordinated Assessments data exchange standard.

51.1: Synthesize fish population metrics thru Regional Data Repositories. Support the coordination, data management, and annual synthesis of fish population metrics through Regional Data Repositories and reports such as the CBFWA State of the Resource. (Annually).

Relationship: In 2010, WDFW began implementing standardized data collection and storage protocols for information collected at fish traps and weirs, and during spawning ground surveys. Data was stored in corporate databases including WDFW's Spawning Ground Survey (SGS) and Age & Scales (A&S) databases. Also, WDFW began development of a regional relational database, entitled Traps, Weirs, & Surveys (TWS), to store all monitoring data in a single

location and to further facilitate standardization of data collection, data entry, and quality assurance, in order to increase quality, efficiency, and improve analysis/reporting timeliness. This database will feed statewide corporate databases and regional reporting platforms as they are developed.

62.1: Evaluate the feasibility of obtaining PIT-tag recoveries between Bonneville and McNary dams (Zone 6) to determine whether recoveries can help refine estimates of in-river harvest rates and stray rates used to assess adult survival rates. For FY 2009, focus on a pilot to test the feasibility of PIT-tag recoveries of harvested fish in this reach (spring, summer, and fall Chinook salmon and summer steelhead). (Initiate in FY 2007-2009 Projects).

Relationship: In 2010 and 2011, this project developed PIT tag harvest rates by modifying the current mainstem lower Columbia River fisheries sampling program to include the collection of PIT tag information along with CWT recovery. Our PIT tag harvest rates provided harvest rates for fall Chinook and steelhead at a finer resolution than previously available. Using PIT tag methods we provided harvest rates for natural origin populations that are currently not available using CWT.

62.4: Support coded-wire tagging and coded-wire tag recovery operations that inform survival, straying, and harvest rates of hatchery fish by stock, rearing facility, release treatment, and location. (Initiate in FY 2007-2009 Projects)

Relationship: This project increased the frequency and intensity of spawning ground surveys in LCR tributaries for CWT recoveries. This led to additional CWT recoveries and more precise CWT expansion estimators to estimate survival, straying and harvest rates by release group.

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Fall Chinook Salmon Abundance Estimates and Coded-Wire-Tag Recoveries in Washington's Lower Columbia River Tributaries in 2012

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Abstract

The Lower Columbia River (LCR) Chinook Salmon Evolutionarily Significant Unit (ESU) is composed of spring and fall Chinook salmon populations split between the states of Washington and Oregon. Washington has been estimating abundance and age structure for all its fall Chinook salmon populations for decades but often fell short of the accuracy and precision guidance recommended for salmon recovery monitoring and there was no standardized reporting of important management and salmon recovery indicators. In 2010, the Washington Department of Fish and Wildlife initiated an integrated and comprehensive monitoring program to estimate Chinook salmon abundance, the proportion of hatchery-origin spawners, age structure, percent females, spawn timing, and to recover Coded Wire Tags (CWT). This report presents results from the third year of this monitoring program. Due to challenges in recovering sufficient numbers of jack Chinook salmon, we reported only adult Chinook salmon (≥ 60 cm) estimates. Adults were estimated using weir counts, closed mark-recapture models, Area-Under-the-Curve, redd counts, and PCE depending on resources and survey conditions. We estimated 22,963 adult Tule, 99 adult Rogue River Bright hatchery, 8,849 adult Bright natural-origin in the Lewis and Cowlitz rivers, and 1,624 adult Bonneville (BON) Pool Bright fall Chinook salmon in the Washington portion of the LCR ESU. The marked (adipose-clipped) proportion was adjusted for hatchery juvenile mass mark rates to account for hatchery production that was released unmarked (~2%). For Tules and BON Brights, the proportion of hatchery-origin adults was 67.5% and 45.7%, respectively. Operation of weirs successfully reduced the proportion of hatchery-origin spawners for some populations. Most Tule populations were comprised of predominately hatchery fish except the White Salmon (6.5% hatchery-origin), Coweeman (11.0% hatchery-origin), and Lewis (17.9% hatchery-origin). Age structure varied by population, but most Tule Chinook salmon were age-3 or age-4. A total of 141 snouts were collected from the field and examined for CWT. CWT recoveries were uploaded to the regional coded-wire-tag database (Regional Mark Information System; RMIS) and unexpanded CWT recoveries indicate most Tule hatchery fish returned to the basin of release or an adjacent basin. BON Brights, not native to this ESU, are successfully spawning in the Upper Gorge and White Salmon populations. Rogue River Brights are successfully spawning in the Grays River. Assumption testing indicated our abundance and proportion estimates were relatively unbiased. This Chinook salmon monitoring program is currently the only Washington program to estimate multiple high level indicators and the associated uncertainty in these indicators at the population and ESU scales.

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Introduction

Chinook salmon (*Oncorhynchus tshawytscha*) in the Lower Columbia River (LCR) Evolutionarily Significant Unit (ESU) were listed for protection under the Endangered Species Act (ESA) in 1998. In a recent five-year review, the National Oceanic and Atmospheric Administration (NOAA) Fisheries concluded that these fish should remain listed as threatened under the ESA (NOAA 2016). The LCR Chinook Salmon ESU is composed of spring and fall populations split between the states of Washington and Oregon (Myers et al. 2006). The Washington Department of Fish and Wildlife (WDFW) has monitored these populations for decades (WDFW 2011) focused primarily on providing an abundance estimate. However, the need for monitoring of additional indicators and more accurate and precise estimates of these indicators, especially for the fall Chinook populations, has been identified as a high priority for salmon management and recovery (LCFRB 2004, Rawding and Rodgers 2013, Crawford and Rumsey 2011).

The coast-wide Coded-Wire-Tag (CWT) program was developed in the 1970s to evaluate the contribution of different salmonid populations and hatchery programs to various fisheries and to estimate salmon fishery harvest rates, along with evaluation of hatchery rearing practices. The initial protocols for the CWT program included the insertion of a CWT into the snout of a juvenile hatchery salmon, which was accompanied by an adipose fin clip. A proportion of hatchery fish released from selected facilities had a CWT inserted. When salmon were recovered from fisheries and spawning areas, the snout of fish with missing adipose fins were taken to fisheries agency labs for decoding. Later the purpose of the CWT program was expanded to include forecasting run sizes to meet conservation and harvest objectives. For conservation purposes, the vast majority of Chinook salmon released from hatcheries are now adipose fin clipped (sometimes referred to as mass marked and from here on referred to as marked) and WDFW has implemented selective fisheries, which require the release of all adipose-intact (natural-origin and unclipped hatchery-origin; from here on referred to as unmarked) fish. CWTs are now detected electronically by scanning fish with handheld or stationary detectors, rather than using the adipose fin clip as an indicator of CWT presence.

In 2010, the WDFW updated and modified its program to sample LCR spawning grounds for Chinook salmon (Rawding et al. 2014). This program had dual objectives: 1) to estimate Viable Salmonid Population (VSP) indicators (McElhaney et al. 2000) and measure specific indicators to assess Chinook salmon viability (Rawding and Rodgers 2013) including abundance, the proportion of hatchery-origin spawners, spatial distribution, and sex ratio including the proportion of jacks; and 2) to recover CWTs from spawning fish to provide complete accounting of CWTs, so that harvest rates could accurately be determined and to more comprehensively implement hatchery effectiveness monitoring. The first objective addressed a salmon recovery monitoring gap while the second objective addressed a gap identified from the CWT expert panel (Hankin et al. 2005) and Hatchery Scientific Reform Group (HSRG 2014). This report summarizes population monitoring of VSP indicators for LCR Chinook salmon returns and CWT recoveries in 2011 including overall abundance, abundance by sex, abundance by age and origin, the proportion of hatchery-origin and natural-origin adults, the proportion of marked and unmarked adults, and the proportion of each age class by origin.

Methods

Study area

The LCR Chinook salmon ESU extends from the mouth of the Columbia River up to and including the Big White Salmon River in Washington and Hood River in Oregon, and includes the Willamette River to Willamette Falls, Oregon. Within this ESU, there are a total of 13 Washington populations, 8 Oregon populations, and 2 populations (Lower and Upper Gorge) that are split between the states (Figure 1). In this document, we report on 11 populations in Washington. The Salmon Creek population is believed to have been extirpated, and it is unclear if the Lower Gorge historically supported a Chinook salmon population, but if it did this population is likely extirpated. The Lower Cowlitz and North Fork Lewis populations are surveyed using funds provided by hydropower companies and their results have a separate reporting structure. In addition, we report on Rogue River and Bonneville Pool Brights populations, which have established themselves in the Grays/Chinook population (Roegner et al. 2010) and in the Lower Gorge, Upper Gorge, and White Salmon populations, respectively.

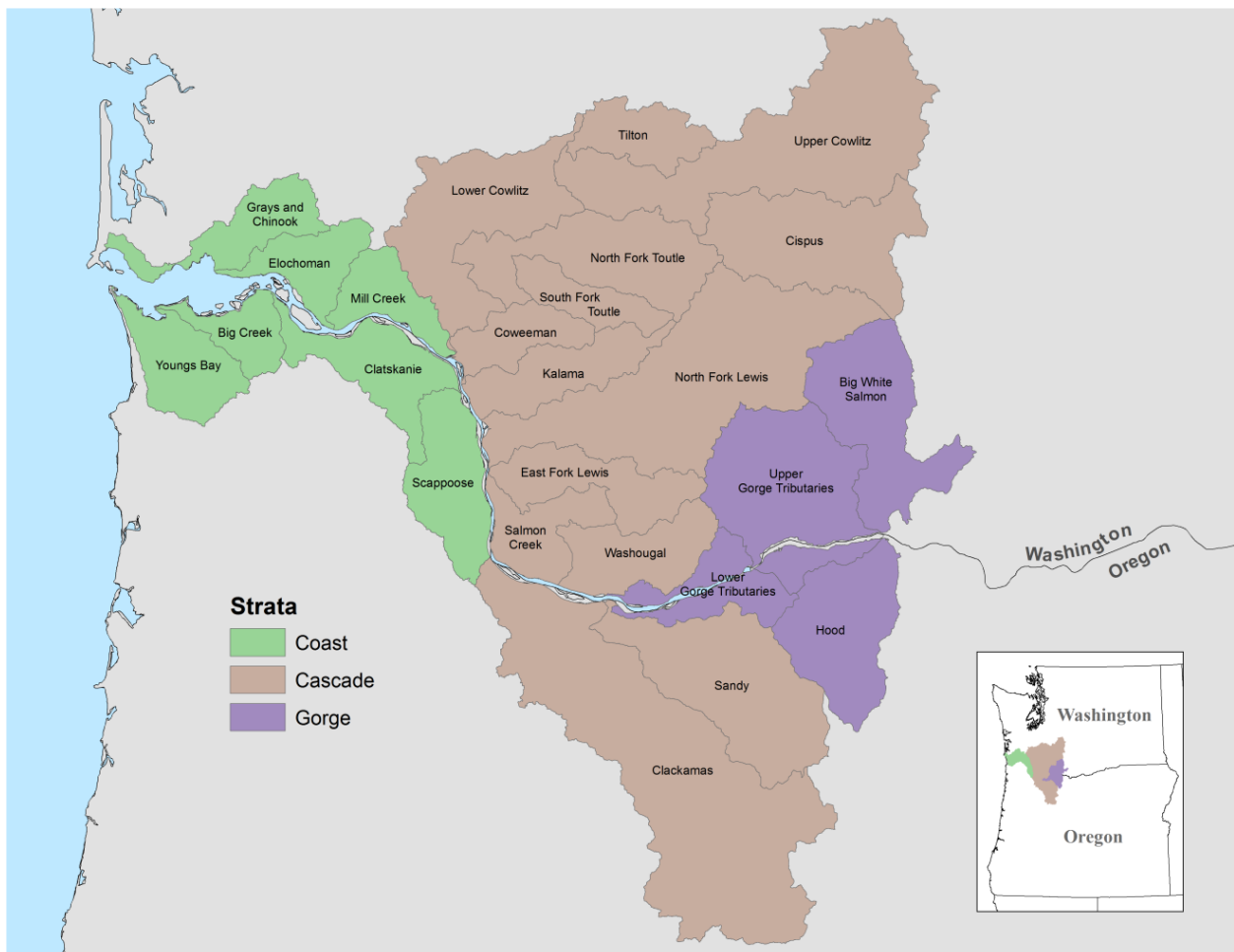


Figure 1. Lower Columbia River Chinook salmon populations and the regional groupings (i.e. strata) in which they occur within the LCR subunit recovery domain.

Monitoring Design

The Chinook salmon monitoring design for the study area used a variety of methods including weir counts, mark-recapture estimates based on live and carcass tagging, redd counts, and periodic counts of live spawners to estimate abundance (Schwarz and Taylor 1998; Sykes and Botsford 1986; Gallagher and Gallagher 2005; Parken et al. 2003, Parsons and Skalski 2010) (Figure 2). When facilities existed, we used census weir counts because these provide the most accurate measure of escapement (Cousens et al. 1982). A permanent dam (Barrier Dam) and the adjacent sorting facility on the Cowlitz River (rkm 82.08) provided census counts of Chinook salmon trapped and hauled to the upper basin (Tilton, Upper Cowlitz, and Cispus rivers). Seasonal fall Chinook salmon monitoring weirs are located on the Grays River (rkm 16.50), Elochoman River (rkm 4.39), Green River (rkm 0.64), Coweeman River (rkm 10.94), and the Washougal River (rkm 19.15). However, none of the seasonal weirs provided census counts because a portion of Chinook salmon by-passed the weirs during high flow events. We anticipated that the weirs would not provide a census, so all weir operations simultaneously implemented a mark-recapture design (Schwarz and Taylor 1998), where fish were tagged at the weir and recovered on spawning ground surveys (Grays, Elochoman, Green, Coweeman, and Washougal rivers). We implemented carcass tagging mark-recapture studies (Sykes and Botsford 1986) in Grays, Skamokawa, Elochoman, Mill, Germany, Abernathy, Lower Green, South Fork Toutle, Coweeman, and Washougal basins. We tracked individual, unique redds on spawning ground surveys in Grays, Coweeman, South Fork Toutle, and East Fork Lewis basins. In all basins, we counted lives and deads, as well as redds, which allowed us to use Area-Under-the Curve (AUC) using live counts of Chinook salmon identified as “spawners” (Parken et al. 2003; English et al. 1992; Hilborn et al. 1999; Rawding et al. 2014) or peak count expansion (PCE) based on historic PCE factors from Jolly-Seber carcass tagging projects in the 1960’s and 1980’s (Tracy et al. 1967; Stockley 1965; Hymer 1991) when census, mark-recapture, or redd-based estimates were not feasible. As mentioned above, estimates for the Lower Cowlitz and North Fork Lewis populations were conducted in conjunction with hydropower companies and are not reported here.

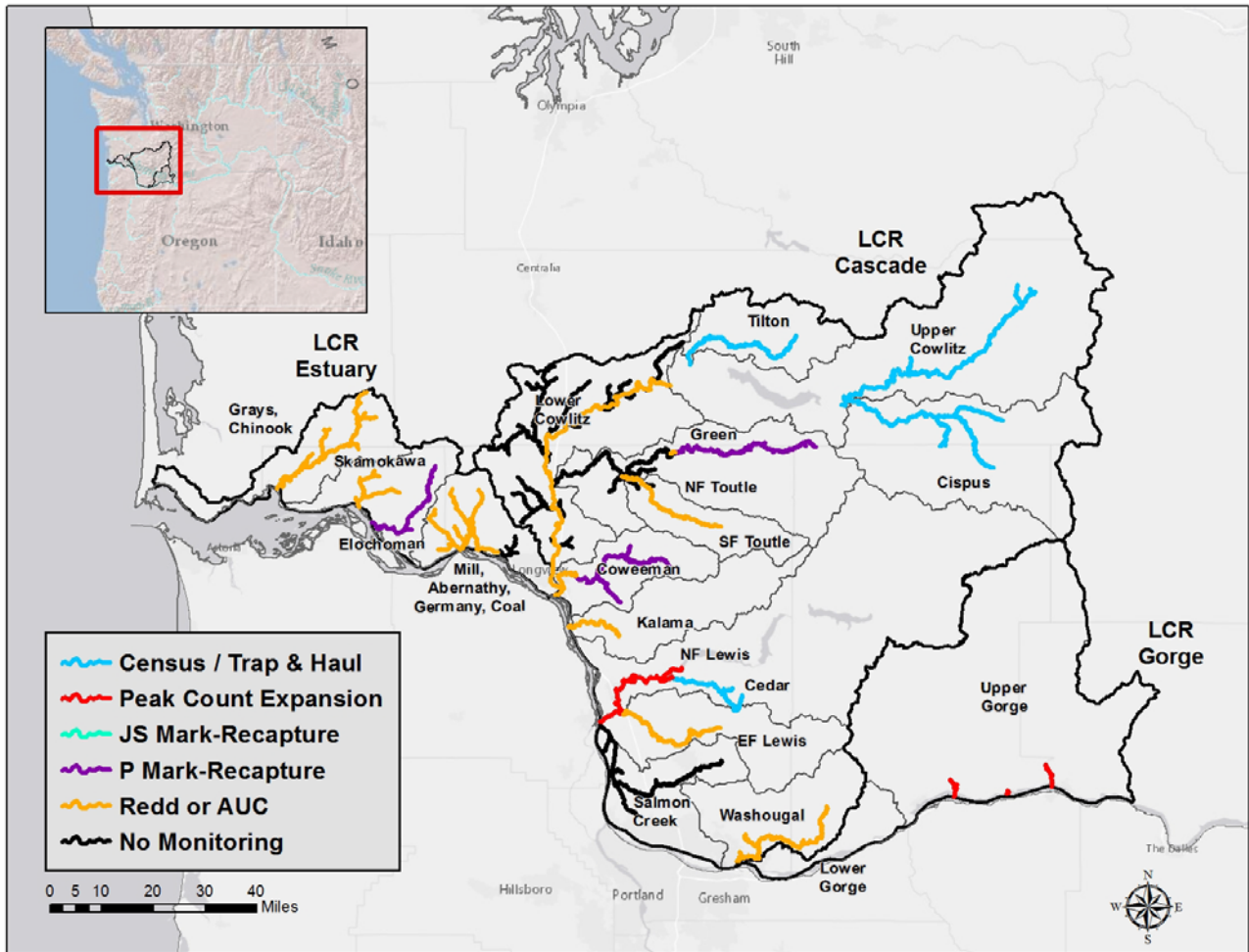


Figure 2. Watersheds comprising the Washington populations of the Lower Columbia River Chinook salmon ESU and the methods WDFW used to estimate their abundance, 2012.

Weirs

Temporary weirs were operated to estimate escapement and obtain biological data in the Grays River (rkm 16.50), Elochoman River (rkm 4.39), Green River (rkm 0.64), Coweeman River (rkm 10.94), and Washougal River (rkm 19.15). The Barrier Dam on the Cowlitz River (rkm 82.08) and the Toutle Fish Collection Facility (TFCF) on the North Fork Toutle River (rkm 19.31) were also operated. No Chinook salmon were transported into the North Fork Toutle River because there are no mainstem release sites above the Sediment Retention Structure (SRS) for Chinook salmon trapped at the TFCF. As a result, any Chinook salmon trapped were released downstream into the North Fork Toutle River. In Cedar Creek, a tributary to the North Fork Lewis River, a ladder trap was operated in a fishway adjacent to a natural falls (rkm 3.22).

Depending on management objectives, Chinook salmon collected at these facilities were used for hatchery broodstock, donated to food banks, used for nutrient enhancement, or transported and released above or below the facility. We made the following key assumptions for the weir programs: 1) the count of all transported fish was without error, 2) all unmarked fish released survived to spawn except on the Green, Elochoman, and Coweeman rivers where we had

estimates of pre-spawning mortality, 3) transported fish spawned in the watershed they were released in, 4) when fisheries in the Elochoman, Green, Upper Cowlitz, Cispus, and Tilton rivers occurred only marked fish were harvested in accordance with regulations, 5) there was no illegal harvest of salmon, 6) survival of all unmarked caught and released fish was 100%, and 6) the WDFW methodology to expand catch record card (CRC) reported catch to total harvest and variance are correct.

Closed Population Models

To measure the success of weir operation in the Grays, Elochoman, Green, Coweeman, and Washougal rivers, we implemented mark-recapture studies. Chinook salmon captured at these sites were tagged with uniquely numbered Floy tags and secondary mark prior to release upstream of the weir with recaptures occurring at either upstream traps or during spawning ground surveys. This allowed us to use the Darroch estimator, which was developed for time stratified Petersen mark-recapture abundance estimates (Darroch 1961, Seber 1982). Schwarz and Taylor (1998) indicate that the following assumptions must be met to provide an unbiased estimate of abundance using the Petersen estimator: 1) no tag loss, 2) no handling mortality, 3) all tagged and untagged fish are correctly reported, 4) the population is closed, and 5) equal capture probability during the tagging or recapture events, or tagged fish mix uniformly with untagged fish.

Open Population Models

The Jolly-Seber (JS) model estimates abundance in mark-recapture studies where the population is open (Jolly 1965; Seber 1965), and has been widely used in estimating Pacific salmon spawning escapement using both live fish (Schwarz et al. 1993; Jones and McPherson 1997; Rawding and Hillson 2003) and salmon carcasses (Parker 1968; Stauffer 1970; Sykes and Botsford 1986). The carcass-tagging model has been used extensively in LCR tributaries to estimate Chinook salmon abundance (McIssac 1977; Rawding et al. 2006; Rawding et al. 2014; Rawding et al. 2019). We implemented carcass-tagging studies in the Grays, Skamokawa, Mill, Abernathy, Germany, and Washougal basins as well as Lower Cedar Creek. Seber (1982) and Pollock et al. (1990) provide details of study design, assumptions, and analysis of mark-recapture experiments using the JS model. The five assumptions of the JS model that must be met in order to obtain unbiased population estimates from the model (Seber 1982) are: 1) equal catchability, 2) equal survival of tagged and untagged individuals between sampling events, 3) no handling mortality, 4) no tag loss, and 5) instantaneous sampling.

Peak Count Expansion

We used historic JS estimates to develop peak count expansion (PCE) factors for the Wind, Little White Salmon, and Big White Salmon basins. For Cedar Creek, we used JS estimates from 2010 and 2011 (Rawding et al. 2014; Rawding et al. 2019) to develop a PCE for the area below the ladder. There are a number of ways to estimate the PCE factor including the mean of the ratios (Parken et al. 2003), calibrated regression, and inverse prediction (Parsons and Skalski 2009). Using a Bayesian framework (detailed in Methods-Data Analysis section below), we divided the posterior distribution of the abundance estimate by the highest single weekly count (or peak count) of live fish plus carcasses or the peak count of carcasses only, depending on the basin, to obtain a PCE factor. Rawding and Rogers (2013) list the following critical assumptions for the PCE method: 1) the peak day of abundance is known and the survey takes place on the peak, 2)

if the entire spawning distribution is not surveyed, the proportion of fish in the index or indices sections is similar to that of the year(s) used to develop the PCE factor, 3) observer efficiency is similar in all years, and 4) the proportion of fish observed on the peak day is similar over all years.

Spawning Ground Surveys

The purpose of spawning ground surveys was to collect data required to estimate abundance and to collect biological information from sampled fish. Surveys were scheduled weekly from the beginning of fish entry (August to September) until completion of spawning (October to December), depending on the population, and over the entire spawning distribution as developed by Rawding et al. (2010). Exceptions were areas where the PCE method was used to estimate abundance. For those areas, three weekly surveys were scheduled around the historical peak spawning week in the index area to capture the actual peak week. In cases where census or mark-recapture estimates were not successful, we needed alternate methods to estimate abundance. We used previous JS estimates in conjunction with surveys designed to provide the number of unique redds to develop estimates of apparent females per redd (AFpR) on the Coweeman and East Fork Lewis rivers from 2003-2012, where the AFpR is the mark-recapture estimate of females divided by the number of unique redds counted during the season. These females per redd estimates were applied to redd counts to estimate abundance in the Elochoman and Coweeman river below each of their respective weir sites and in the Grays River. Similarly, we used the 2011 mark-recapture data to develop estimates of apparent residence time (ART) from the Grays, Abernathy, Germany, and Washougal basins, where ART is the estimate of Area-Under-the-Curve (in fish days) divided by the mark-recapture adult abundance estimate. ART estimates were applied to live fish counts to estimate abundance in the Skamokawa, Mill, Abernathy, Germany, South Fork Toutle, Kalama, East Fork Lewis, and Washougal basins and below the weir site on the Green River. Rawding and Rodgers (2013) listed the critical assumptions for redd surveys used to estimate abundance: 1) representative spatial and temporal sampling throughout the spawning period, 2) estimates of apparent females-per-redd which are from adjacent populations, or from the same population in previous years, are consistent between the study population (one used to derive the females per redd estimate) and the treatment population and the methods used to identify and enumerate redds follow a standard redd survey protocol, and 3) the apparent females-per-redd and sex ratio from other streams, or years, accurately represent the females-per-redd and sex ratio of the treatment population. For the AUC method, Rawding and Rodgers (2013) identified the first assumption is that representative spatial and temporal sampling occurs throughout the spawning period. If concurrent observer efficiency and residence time estimates are made, the second critical assumption for AUC is that these estimates are spatially and temporally representative of the survey area and occur throughout the spawning period. Finally, survey frequency should occur every 7 to 10 days and surveys should not be missed during peak spawning time (Hill 1997). The methods used to estimate abundance for each monitoring unit are found in Table 1.

Table 1. Methods used to estimate fall Chinook salmon escapement in 2012.

Subpopulation	Abundance Method
Grays	Redds with mean AFpR and population specific sex ratio
Skamokawa	AUC with mean ART from 2011
Elochoman	Above weir: Petersen estimate minus prespawm mortality and CRC harvest; Below weir: redds with mean AFpR and population sex ratio
Mill	AUC with mean ART from 2011
Abernathy	AUC with mean ART from 2011
Germany	AUC with mean ART from 2011
Tilton	Trap and haul census count minus CRC harvest
Upper Cowlitz/Cispus	Trap and haul census count minus CRC harvest
Green	Above weir: Petersen estimate minus prespawm mortality and CRC harvest; Below weir: AUC with mean ART from 2011
South Fork Toutle	AUC with mean ART from 2011
Coweeman	Above weir: Petersen estimate minus prespawm mortality and CRC harvest; Below weir: redds with mean AFpR and population sex ratio
Kalama	AUC with mean ART from 2011
Cedar	PCE based on 2010 and 2011 estimates (Above ladder: census count at ladder; Below ladder: JS model based on carcass tagging adjusted for ladder fallbacks)
East Fork Lewis	AUC with mean ART from 2011
Washougal	AUC with mean ART from 2011
Wind	PCE based on 1964 JS Tule carcass tagging model
Little White Salmon	PCE of carcasses based on 1966 JS Tule carcass tagging model
Big White Salmon	PCE based on 1989 JS Bright carcass tagging model
Grays (Rogue)	Redds with mean AFpR and population specific sex ratio and the percent Rogue River Bright based on left ventral clip
Wind (Brights)	PCE based on 1964 Tule JS carcass tagging model
L. White Salmon(Bright)	PCE of carcasses based on 1966 JS Tule carcass tagging model
B. White Salmon (Brights)	PCE based on 1989 JS Bright carcass tagging model

Data Collection

Traps and Weirs

Data collection at weirs was similar to the standardized methods for collecting salmon data at weirs described in Zimmerman and Zubkar (2007). Chinook salmon populations originating above dams in the Cowlitz watershed were trapped at the Barrier Dam and hauled into the Tilton and Upper Cowlitz /Cispus rivers allowing for their enumeration and the collection of biological data. Cowlitz River Chinook salmon captured at the Barrier Dam were anesthetized using electro-anesthesia and sampled for sex and origin. In addition, male Chinook salmon were classified as jacks or adults based on size. Adult salmon captured at the Barrier Dam were released to their natal watersheds based upon differential marking they received as smolts when they were transported downstream of the Cowlitz dams; since out-migrants caught at the Mayfield trap were tagged with blank CWT and not adipose fin clipped, these fish were released in the Tilton River which empties into Mayfield Lake, whereas non-CWT positive unmarked fish

were transported to the Upper Cowlitz and Cispus Rivers where they presumably originated. In addition, adipose-clipped hatchery Chinook salmon were also trucked and released in the Tilton, Upper Cowlitz and Cispus rivers to provide recreational fishing opportunity and spawners to seed the available habitat.

Temporary weirs were installed on the Grays, Elochoman, Green, Coweeman, and Washougal rivers on August 3, August 17, August 27, August 28, and September 5, respectively. The Grays River Weir was removed on October 25. The Elochoman River Weir was removed on October 26. The Green River Weir operated until November 15 for a coho salmon study. However, weir effectiveness was compromised after October 25 due to scour along the substrate rail. The Coweeman River Weir was removed on October 25. The Washougal River Weir was removed on October 22. Because of the possibility of weir failure due to high water events, we tagged fish to implement a mark-recapture study at each of the locations. All fish passed upstream at the weirs were double tagged with uniquely numbered Floy™ (hereafter Floy) tags (FD 68BC T-bar Anchor tags; Floy™ Tag & Mfg., Inc. Seattle, WA). Floy tags were placed adjacent to the posterior edge of the dorsal fin, with one tag on each side of the fish. An operculum punch was applied as a secondary mark, and punch shapes were rotated weekly, allowing assessment of Floy tag loss and assignment of a recovered fish back to the weekly release group if both Floy tags were lost. Additionally, all fish were sampled for biological data (e.g. fork length, gender, mass mark status), tissue samples for genetics analysis, and scales for aging.

A ladder trap was installed in the fishway at the Grist Mill Falls on Cedar Creek. It was operational on September 14 and was operated continuously throughout the entire Chinook salmon migration period. Due to variability in ladder efficiency (some fish likely jump the falls at certain flows), a mark-recapture study was implemented. All Chinook salmon passed were tagged with a single, uniquely numbered operculum tag and sampled for biological data. Biological data consisted of collecting scale samples, sex determination, measuring the fork length, and recording fin clips to determine mass mark status (hatchery- or natural-origin).

Except for the trap at the Barrier Dam on the Cowlitz River, scales were taken from live fish in the preferred area, as described in Crawford et al. (2007b). Scales were also collected from carcasses (see Spawning Ground Survey section below). Biological sampling included the following: fork length, which was taken by running the tape measure from the tip of the snout to the fork in the tail, gender, which was determined based on morphometric differences between males and females, and mass mark status, which was determined by the presence or absence of the adipose fin.

Spawning Ground Surveys.

Data collection during scheduled weekly spawning ground surveys was similar to the standardized methods for collecting salmon data from carcass counts, redd surveys, and foot-based visual counts described in Crawford et al. (2007a and 2007b) and Gallagher et al. (2007). Data were collected at the reach scale, which often were based on historical WDFW section breaks but in some cases were collected at finer scale (Grays, Mill, Abernathy, Germany, and Coweeman). The start and end of each survey reach was geo-referenced and its coordinates were recorded on a Garmin Oregon 550 global position system (GPS) unit set in NAD 83.

All live adult and jack salmonids were identified to species based on physical characteristics unique to each species and recorded by species (Crawford et al. 2007a). Live salmon were classified as adults or jacks although this can be difficult to accurately determine on live fish during visual surveys. Live salmon were also classified as either a “spawner” or a “holder”. Salmon were classified as a spawner if they were on redds or observed in spawning habitat (in, on, or around tailouts, riffles, and glides with spawnable substrate). A fish was classified as a holder if it was observed in an area not considered spawning habitat, such as pools or observed in areas of large cobble, bedrock or in boulder riffles (Parken et al. 2003).

Redd surveys in the Grays, Coweeman, South Fork Toutle, and the East Fork Lewis followed the protocols of Gallagher et al. (2007). Surveys were scheduled weekly and followed methods described in Rawding et al. (2006a and 2006b). All identifiable redds were flagged, and their location (latitudinal and longitudinal coordinates) was recorded. Prior to recording a redd’s location, GPS units were allowed to acquire satellites until an accuracy of ± 100 feet or less was obtained. In subsequent surveys, previously flagged redds were inspected to determine if they should be classified as “still visible” or “not visible”. A redd was classified as “still visible” if it would have been observed and identified without the flagging present, and was recorded as “not visible” if it did not meet these criteria. These data were collected to generate an estimate of the time period redds were visible to surveyors, or apparent redd life.

All carcasses that were not totally decomposed were sampled for external tags (Floy T-bar or carcass tags), secondary marks (e.g., operculum punches), and biologically sampled for fork length, sex, adipose fin presence, and condition (extent of decomposition). Sex was determined based on morphometric differences between males and females. If necessary, the abdominal cavity was cut open to confirm sex and determine spawning success. Spawning success was approximated based on visual inspection, ranging from 100% to 0% success. A fish with <25% spawning success (>75% egg retention) was considered a pre-spawning mortality. Carcass condition and gill color were recorded to assess carcass freshness (Sykes and Botsford 1986). Scale samples were collected from preferred area and in the methods described in Crawford et al. (2007b). Scales were removed using forceps with special care to select scales that were of good quality (round shape, non-regenerated) and not adjacent to one another (to minimize the effects of regeneration) as described in a WDFW technical report (Cooper et al. 2011). Scales were placed on the gummed portion of WDFW scale cards with their exterior surfaces facing up. Due to a high number of carcasses on the Washougal and Kalama rivers, these carcasses were systematically sampled for biological data and scales.

For analysis and reporting purposes, Chinook salmon carcasses were grouped into the following categories: unmarked, marked, and unknown. Unmarked fish had an intact adipose fin and an intact snout, marked fish have an intact snout but were missing their adipose fin, and unknown fish either damaged caudal peduncle (e.g., adipose fin area unexaminable unknown) or missing portions of the snout. All unmarked and marked fish were sampled for CWT following standard protocols (NWMT 2001). The surface of the CWT wand with radiating arrows was placed in contact with the snout and moved from the right to the left eye, and then up and over the snout area. The wand was also inserted into the mouth with the radiating arrows rubbed against the roof of the mouth in vertical strokes. If a CWT was detected, the wand’s red LED light illuminated and the wand emitted a beeping sound. When a CWT was detected, the snout was

collected by cutting across the head straight down behind the eyes (Crawford et al. 2007b). The snout was placed in a plastic bag with a numbered tag to link the snout to biological data (length, sex, fin clips, spawning success for females, and scale sample number) recorded on the scale card or other datasheet. Snouts were stored in a freezer and periodically delivered to WDFW's CWT lab in Olympia for CWT recovery and decoding.

All carcasses were inspected for carcass tags (a uniquely numbered small square plastic tag). Untagged carcasses in the Grays, Skamokawa, Elochoman, Mill, Germany, Abernathy, Lower Green, South Fork Toutle, Coweeman, and Washougal basins were then tagged on the inside of both opercula with a carcass tag (McIssac 1977). Carcass tags were placed on the inside of the operculum to limit predation and potential bias in recovery rates due to observation of brightly colored tags. Carcass tagged carcasses were then placed/released into moving water to facilitate mixing with untagged carcasses (Sykes and Botsford 1986). When carcass tagged carcasses were recovered, surveyors recorded the tag numbers, the tags were removed, and the carcass was mutilated by removing the tail to prevent re-sampling/tagging (a loss on re-capture event in the JS model).

Sample Processing

Scale Analysis

Scale preparation and analysis followed WDFW protocols (Cooper et al. 2011). Acetate impressions were made of the scale samples using a scale card press. Samples were covered with strip of clear acetate (0.5mm thickness) and pressed under 1200-1300 PSI @ 100 degrees C for 30 seconds to 1 minute. The acetate impressions of the scales were aged using a modified Gilbert/Rich ageing notation (Groot and Margolis 1991), where annuli were counted along with the scale edge to produce a total age in years. Annuli were defined as an area of narrowly spaced circuli that represent winter/early spring growth. Age was recorded as the total age in years followed by the age at outmigration. For example, a typical fall Chinook salmon adult is age 4₁. This notation indicates a total age of 4 and that as a juvenile this individual only spent one winter in freshwater and migrated to the ocean as a fry or sub-yearling. After being aged in Olympia by an ageing specialist, scale samples were returned and entered into the Region 5 Traps, Weirs, & Surveys database.

CWT Lab Analysis

The recovery of CWT tags at the WDFW lab follows the procedures outlined in the tag recovery chapter (Blankenship and Hiezer 1978) of the Pacific Coast Coded Wire Tag Manual and is briefly repeated here. Each snout is passed through a magnetic detector to determine "tagged" or "untagged" status. Untagged snouts are set aside and rechecked after following protocols to re-magnetizing the tag. Large heads are often dissected to maximize tag detections. Snouts determined to have no CWT after re-magnetization attempts have been made are saved and an x-ray machine is periodically used to determine tag presence in these "no tag" snouts. After determining a tag is present, the snout is dissected, and the tag located by process of elimination. After recovering the tag, the binary code is determined using a microscope. Recovered CWT data is then entered into the WDFW CWT database and provided to managers as needed and uploaded into the Regional Mark Information System (RMIS).

Data Analysis

Overview

Chinook salmon abundance estimation was relatively straightforward for mark-recapture, trap and haul, and peak count expansion areas, but required combining multiple sources of information for AUC and redd survey areas. Briefly, a spawning habitat model was developed for the ESU to predict the extent of spawning habitat (i.e. the spawning habitat sampling frame) (Rawding et al. 2010). Either the entire sampling frame was surveyed weekly or an index reach was surveyed weekly with the entire sampling frame surveyed near peak abundance. The estimate for the remainder of the frame was based on the ratio of the total count within the index compared to the count within the index on the day the entire sampling frame was surveyed. For the purpose of reporting metrics in the document, we classified adult Chinook salmon as ≥ 60 cm.

Modeling Approach

Data analysis was conducted using a Bayesian framework. Bayes rule states the posterior distribution, $p(\theta|y)$, is the product of the prior distribution, $p(\theta)$, and the probability of the data given the model or likelihood, $p(y|\theta)$, which is expressed by

$$p(\theta | y) = \frac{p(\theta)p(y | \theta)}{p(y)} \quad (1)$$

where y are the data, θ are the parameters, and $p(y) = \sum_{\theta} p(\theta)p(y|\theta)$ for all discrete values or $p(y) = \int p(\theta)p(y|\theta)d\theta$ for continuous data (Gelman et al. 2004). The formula of the posterior distribution may be complex and difficult to directly calculate. Samples from the posterior distribution can often be obtained using Markov chain Monte Carlo (MCMC) simulations (Gilks et al. 1996). WinBUGS is a software package that implements MCMC simulations using a Metropolis within Gibbs sampling algorithm (Spiegelhalter et al. 2003) and has been used to estimate fish abundance (Rivot and Prevost 2002, Link and Barker 2010). For the Bayesian methods we tested the sensitivity of the prior and convergence based on the Brook-Gelman-Rubin statistic (Su et al. 2001, Appendix 1).

We chose to specify vague priors for parameters because there was little prior information and we wanted an objective analysis to “let the data speak for themselves”. Currently, there are not consensus reference priors for objective Bayesian analysis, although there has been much work in this area (Tuyl et al. 2009). For the binomial or multinomial distributions, we chose to evaluate the Beta and Dirichlet priors parameterized with $\alpha = \beta = 1$ or 0.5, which are the Bayes-LaPlace uniform prior and the Jefferies prior, respectively. We adopted the Bayes/LaPlace prior for our analysis but conducted a sensitivity analysis by comparing the results of the two priors in select cases. For abundance estimates in mark-recapture, we chose a uniform prior, so that the minimum and maximum bounds did not truncate the posterior distribution.

We used a generalized linear model (GLM) assuming a binomial distribution and using a logit link function for both open and closed mark recapture estimates to determine whether abundance estimates could be pooled or needed to be stratified. Covariates included sex, categorical size (≥ 80 cm or < 80 cm), and all subsets of main effects models. Results of the GLM tests were compared and ranked using AICc (Burnham and Anderson 2002). When the null model, indicating homogeneous recovery probabilities, was supported (ΔAIC value of < 2), we pooled

all fish. When the null model, indicating homogeneous recovery probabilities, was not supported, we stratified by either sex or size, depending which was the best model based on the AICc ranking for a particular dataset. When stratifying by size, we used an 80cm cutoff as described in Rawding et al. (2014) to classify fish into two groups, large and small. If stratifying was needed, we conducted the same series of tests described above with two independent datasets to ensure that the null model was the best model for each of the groups.

If estimates for a particular subpopulation were stratified by sex or categorical size, as described above, we summed the stratified estimates to develop an overall estimate. Next, we looked at what if we had assumed the null model was the best model and did not stratify by sex or categorical size and looked to see if credible intervals between the null estimate and two combined stratified overlapped.

Abundance Estimates

Weirs

A census count of Chinook salmon occurred in the Cowlitz River at the Barrier Dam. At the Green, Elochoman, and Coweeman weirs, a portion of the trapped fish were released above the weir, depending on WDFW management objectives for that basin. In some cases, not all fish released above a weir successfully spawned. To estimate the proportion of successful spawners (p_{Suc}) female carcasses are inspected for spawning success (Table 2). In some cases, a fishery may occur above the weir, and harvest is estimated through a statistical expansion of catch record card (CRC) returns (Kraig 2014). The number of spawners above the weir ($WeirSpawners$) is the weir count ($count$) times the proportion of successful spawners minus the estimated harvest (Table 3).

Table 2. Summary statistics used to estimate spawners above weirs.

Statistic	Definition/Equation
count	Number of fish released and passed above the weir
Fcarc	Number of females examined above the weir for spawning success
Fsuc	Number of females examined that had spawned (i.e., egg retention < 25%)

Table 3. Likelihoods and derived parameters to estimate abundance above weirs.

Description	Likelihood/Derived Estimates
Mu	μ is the mean catch from CRC harvest estimates
Prec	$prec = 1/\text{variance}$ from the CRC harvest estimates
Pr (catch)	$catch \sim \text{Normal}(\mu, prec)$ estimated from CRC returns
Pr (spawn success)	$F_{suc} \sim \text{Binomial}(p_{Suc}, F_{carc})$
WeirSpawners	$WeirSpawners$ is the number of fish above the weir that attempted to spawn, $WeirSpawners = count * p_{Suc} - catch$

Closed Population Abundance Estimates

Our study design was developed based on stratified Petersen or Darroch, closed population mark-recapture, models because they are relatively robust to heterogeneity in capture and movement probabilities (Seber 1982).

First, we tested for equal mixing of Floy tagged and untagged carcasses spatially above each of the weir sites by creating a matrix of Floy tagged and untagged carcass recoveries from spawning ground surveys by pre-established reach as well as weir wash-ups (carcasses that wash up onto the weir structure and are sampled daily rather than on weekly spawning ground surveys). We logically grouped reaches together to ensure we had a minimum of three tagged and untagged per spatial location (reach) then conducted a series of chi-square tests to ensure there was equal mixing spatially.

Second, we created an matrix of the number of fish Floy tagged at the weir site, the number of carcasses recoveries that were Floy tagged, and the total number of carcasses examined for Floy tags from spawning ground surveys and weir wash-ups (if pooling weir-ups and spawning ground surveys carcass recoveries was supported) by statistical week. This is typically known as a “DARR table” or temporally stratified mark recapture summary.

Third, we tested the null hypothesis of complete mixing and equal proportion (Schwarz and Taylor 1998) to determine if pooling periods was appropriate. We used the package DARR for R (Bjorkstedt 2010) to take advantage of its built-in algorithms for initial pooling of periods. Then, took the newly created periods and conducted two separate chi-square tests: 1.) to determine whether the tagged proportion was constant by recovery period and 2.) to determine whether the recapture rate was constant by period. Based on the results of these two tests, we manually pooled periods further in the DARR for R program. The results of these tests supported pooled Petersen estimates for all of our closed population datasets in 2012. Summary statistics were generated from outputs of the DARR program, which included the number of marks (M), recaptures (R), and captures (C). These were used as inputs to each individual population-level R file (Table 4).

Table 4. Summary statistics used to estimate abundance using the Darroch (1961) model.

Statistic	Definition/Equation
d_{m_i}	Number of fish marked and released at sample time i .
$d_{r_{ij}}$	Number of marked fish recaptured at sample time ij , $i = 1, \dots, s, j = 1, \dots, s$.
$d_{m_i} - d_{r_i}$	Number of marked fish not recaptured
d_{u_j}	Number of fish captured at sample time j that were not previously marked.

The fundamental parameters include the probability of capture, probability of movement between strata, probability a fish is caught in a stratum, and the population estimate at the time of tagging (Table 5) are estimates based on the likelihoods presented in Table 6.

Table 5. Fundamental and derived parameters for the Darroch (1961) model.

Parameter	Definition/Equation
d_s	Number of sample times
d_{p_j}	Probability of capture at sample time j , $j = 1, \dots, s$.
$d_{\theta_{ij}}$	Probability that a fish from m_i moves to stratum j , $i = 1, \dots, s, j = 1, \dots, s$. Since the population is closed & no mortality the $\sum \theta_{ij} = 1$, $i = 1, \dots, s$.
$d_{\psi_{ij}}$	Probability that a fish from m_i is caught at time j , $i = 1, \dots, s, j = 1, \dots, s$. $\psi_{ij} = \theta_{ij} p_j$.
	Probability of not being captured, $\psi_{ij} = (1 - \sum \psi_{ij})$, $i = 1, \dots, s, j = s + 1$.
d_{U_j}	Number of fish at sample time j . $N = \sum U_j$, which is the population estimate

Table 6. The likelihoods for the Darroch (1961) model.

Description	Likelihood/Derived Estimates
Pr (capture)	$d_{uj} \sim \text{Binomial}(d_{pj}, d_{Uj}), j = 1, \dots, s.$
Pr (capture at time _j)	$d_{rij} \sim \text{Binomial}(d_{\psi_{ij}}, d_{mi}), i = 1, \dots, s, j = 1, \dots, s.$

When there is an equal probability of capture during the tagging event, or an equal probability of capture during the second tagging event, or there is complete mixing of tagged and untagged fish between events, all releases, recoveries and captures may be combined into a “pooled” Petersen estimator (Schwarz and Taylor 1998). The summary statistics include the number of marks (Floy tagged), recaptures, and captures (Table 7). The fundamental parameter is the population size estimated from the summary statistics and hypergeometric distribution (Table 8). The hypergeometric distribution is appropriate to use when there is sampling without replacement as salmon carcasses captured in the second event were mutilated (tail-chopped) and not available for recapture in future sampling events.

Table 7. Summary statistics used in the hypergeometric Petersen model where Chinook salmon were live tagged and recovered as carcasses.

Statistic	Definition/Equation
m_h	Number of fish marked in the first sample ($n1$) for the hypergeometric model
r_h	Number of marked fish recaptured in the 2 nd sample ($m2$) for the hypergeometric model
c_h	Number of fish captured in the second sample ($n2$) for the hypergeometric model

Table 8. The fundamental parameters and likelihoods for the hypergeometric Petersen model.

Description	Definition/Likelihood
N_h	The population size Nh
Pr (Recapture)	$r_h \sim \text{Hypergeometric}(m_h, c_h, N_h)$

Open Population Abundance Estimates

We parameterized the Schwarz et al. (1993) “super population” JS model into a Bayesian framework. Rather than using individual capture histories, we used summary statistics to increase the computational speed (Table 9). It is important to note that in the more popular Schwarz and Arnason (1996) model the super population and other fundamental parameters are based on births while in the Schwarz et al. (1993) model the super population is the total of gross births or abundance (Table 10). This model allows salmon abundance estimates to be hierarchically modeled (Rivot and Prevost 2002) and the probability of entry to be modeled based on various distributions (Hilborn et al. 1999).

Derived parameter estimates in Table 11 are based on Schwarz et al. (1993) and Manske and Schwarz (2000). We included the later author’s derived estimates for cases when the mark-recapture study ends early, as they proposed a method to estimate abundance based on the residence time estimated from the mark-recapture data and AUC method, which is a plot of the population size at each sampling period. The JS likelihood is the product of three likelihoods: 1) the probability of first capture based on a super population (N) that enter the population (b^*_i) following a multinomial distribution, 2) the probability of release on capture (v_i) from a binomial distribution using total fish sampled (n_i) and number of n_i that are released (R_i), and 3) the

probability of recapture which is the product of two binomial distributions to estimate the probability of capture (p_i) and survival (ϕ_i) (Burnham 1991) (Table 12).

Table 9. Summary statistics used in the Jolly-Seber model.

Statistic	Definition/Equation
m_i	Number of fish captured at sample time i that were previously marked.
u_i	Number of fish captured at sample time i that were unmarked.
n_i	Number of fish captured at sample time i . $n_i = m_i + u_i$.
l_i	Number of fish lost on capture at time i .
R_i	Number of fish that were released after the i th sample. R_i need not equal n_i if there were losses on capture or injections of new fish at sample time i .
r_i	Number of R_i fish released at sample time i that were recaptured at one or more future sample times.
z_i	Number of fish captured before time i , not captured at time i , and captured after time i .
T_i	Number of fish captured at or before time i and captured at or after time i . $T_i = m_i + z_i$.

Table 10. Fundamental parameters for the Jolly-Seber model under the salmon escapement super population model (Schwarz et al. 1993).

Parameter	Definition/Equation
s, tm	Number of sample times and length of interval between samples
p_i	Probability of capture at sample time i , $i = 1, \dots, s$.
ϕ_i	Probability of a fish surviving and remaining in the population between sample time i and sample time $i + 1$, given it was alive and in the population at sample time i , $i = 1, \dots, s-1$.
b^*_i	Probability that a fish enters the population between sample times i and $i + 1$, $i = 0, \dots, s-1$ under the constraint that $\sum b^*_i = 1$. These are referred to as entry probabilities.
v_i	Probability that a fish captured at time i will be released, $i = 1, \dots, s-1$.
N	Total number of fish that enter the system before the last sample time or the abundance. This is referred to as the super population.

Table 11. Derived parameters for the Jolly-Seber model under the salmon abundance super population model (Schwarz et al. 1993) and the stream residence time model (Manske and Schwarz 2000).

Parameter	Definition/Equation
λ_i	Probability that a fish is seen again after sample time i , $i = 1, \dots, s$. $\lambda_i = \phi_i p_{i+1} + \phi_i (1 - p_{i+1}) \lambda_{i+1}$, $i = 1, \dots, s-1$; $\lambda_s = 0$.
τ_i	Conditional probability that a fish is seen at sample time i given that it was seen at or after sample time i , $i = 1, \dots, s$. $\tau_i = p_i / (p_i + (1-p_{i+1}) \lambda_i)$.
ψ_i	Probability that a fish enters the population between sample time $i-1$ and i and survives to the next sampling occasion. $\psi_i = b^*_i$, $\psi_{i+1} = \psi_i (1 - p_i) \phi_i + b^*_i (\phi_i - 1) / \log(\phi_i)$
B_i	Number of fish that enter after sample time i and survive to sample time $i+1$, $i = 0, \dots, s-1$. These are referred to as net births. $B_0 = B^*_0$, $B_i = B^*_i (\phi_i - 1) / \log(\phi_i)$.
B^*_i	Number of fish that enter between sampling occasion $i-1$ and i , $i = 0, \dots, s-1$. These are referred to as gross births. $B^*_i = N(b^*_i)$
N_i	Population size at time i , $i = 1, \dots, s$. $N_1 = B_0$, $N_{i+1} = (N_i - n_i + R_i) \phi_i + B_i$
N^-_i	Number of fish alive immediately before sample time i , $i = 1, \dots, s$. $N^-_1 = B_0$; $N^-_{i+1} = N^+_i \phi_i + B_i$
N^+_i	Number of fish alive immediately after sampling time i , $i = 1, \dots, s$. $N^+_i = (N^-_i - n_i + R_i)$. N^+_i may differ from N^-_i if there were losses on capture or injections of new fish.
RT	Average residence time; for $i = 1, \dots, s-1$. $RT = 0.5 \sum t m_i N^+_i (\phi_i + 1) + 0.5 t m_s N^+_s + 0.5 t m_0 B_0 + \sum B_i t m_i (\phi_i / \phi_{i-1} - 1 / \log(\phi_i))$
AUC	Aggregate residence time over all spawners. This is referred to as the total fish days or Area-Under-the-Curve. $AUC = 0.5 t m_0 N^-_1 + \sum 0.5 t m_i (N^+_i + N^-_i) + 0.5 t m_s N^+_s$.
ESC	Escapement. $ESC = AUC/RT$. This is slightly greater than N , which is also a measure of escapement due to accounting for fish before and after sampling.

Table 12. The likelihoods for the Schwarz et al. (1993) model.

Description	Likelihood
Pr (first capture part a)	$u_i \sim \text{Binomial}(\sum \psi_i p_i, N)$, $i = 0, \dots, s-1$. $u_i = \sum u_i$
Pr (first capture part b)	$u_i \sim \text{Multinomial}(\psi_i p_i / \sum \psi_i p_i, u_i)$, $i = 0, \dots, s-1$.
Pr (release on capture)	$R_i \sim \text{Binomial}(v_i, n_i)$, $i = 1, \dots, s-1$.
Pr (recapture part a)	$m_i \sim \text{Binomial}(\tau_i, T_i)$, $i = 2, \dots, s-1$.
Pr (recapture part b)	$r_i \sim \text{Binomial}(\lambda_i, R_i)$, $i = 1, \dots, s-1$.

Due to computational challenges, it is difficult to estimate Bayes factors when using MCMC approaches (Ntzoufras et al. 2009, Lunn et al. 2012) and this occurred in JS mark-recapture model selection. As a practical solution, we limited the number of JS models to four (Table 13), and used the Deviance Information Criteria (DIC) developed by Spiegelhalter et al. (2002) for model selection:

$$DIC = \text{Dev}(\theta_m) + pv \quad (2)$$

where $D(\theta_m)$ is the posterior mean deviance for the model and $pv = \text{Var}(D(\theta|Y))/2$ and is a measure of the number of effective terms in the model. We choose pv over the more commonly used pD for an estimate of effective parameters, because pv performs well when there is weak prior information and is invariant to parameterization (Gelman et al. 2004). DIC is a Bayesian analog of Akaike Information Criteria (AIC) but based on MCMC outputs (Burnham and Anderson 2002). Similar to the model support scale developed by Burnham and Anderson (2002), Spiegelhalter et al. (2002) suggested that models ΔDIC of less than two have considerable support, models with ΔDIC having three-seven have less support, and models with $\Delta\text{DIC} > 10$ have negligible support.

Table 13. Model notation used for JS carcass tagging (from Lebreton et al. 1992). Model names indicate whether capture, survival, or entrance probabilities were allowed to vary over time (“t”) or were held constant (“s”).

Model	Probability of capture (p)	Probability of survival (ϕ)	Probability of entry (b^*)
t t t	varies over periods	varies over periods	varies over periods
s t t	equal over periods	varies over periods	varies over periods
t s t	varies over periods	equal over periods	varies over periods
s s t	equal over periods	equal over periods	varies over periods

The purpose of a goodness-of-fit (GOF) test is to identify potential inadequacies in the fit of the model to the observed data. One Bayesian approach used for GOF testing is posterior predictive checking, which is a comparison of the posterior predictive distribution of replicated data from the model with the data analyzed by the model (Gelman et al. 2004). In other words, the predictive data ($y.rep_i$) is the expected observation after replicating the study having observed the data (y_i) and assuming the model is true. When using MCMC simulations, a measure of discrepancy (D) is computed for the actual and replicated datasets for each iteration. An assessment of the posterior distributions of $D(y^{rep}, \theta)$ and $D(y, \theta|y)$ provides individual and overall GOF measures. With the posterior or Bayesian p -value = $\Pr(D(y^{rep}, \theta) > D(y, \theta|y))$. The interpretation of the Bayesian p -value is the proportion of the times the discrepancy measure of the replicated data is more extreme than the observed data. If there is a good fit of the model to the data, we would expect the observed data to be similar to the replicated data, resulting in a Bayesian p -value of 0.50, while values near 0 or 1 indicate that the model does not fit the data.

There are many possible types of discrepancy measures including the Freeman-Tukey, standardized Pearson residual, chi-square, and deviance statistics (Brooks et al. 2000, Lunn et al. 2012). Since mark recapture counts consist of many zeros and this test statistic does not require the pooling of bins with small or zero values, we used the Freeman-Tukey statistic (Brooks et al. 2000), which is expressed as

$$d_i(\theta) = \sqrt{y_i} - \sqrt{E(y_i | \theta)} \quad (3)$$

where d_i is an individual discrepancy, y_i is an individual data point, and $E(y_i|\theta)$ is the fitted value of y_i based on the function to determine the parameter θ . When estimating independent values such as the proportion of hatchery fish or the age of hatchery fish in a single population, Bayesian p -values are typically near 0.5. Although Bayesian p -values are commonly used for model checking, there have been criticisms of this approach. First, it uses the data twice to build and check the model, which may not be as robust as other methods for testing model adequacy

(Carlin et al. 2009, Kery 2010). Second, it is unclear what cut off values to use for the interval (5% to 95%) to indicate lack of model fit. Third, the posterior distribution is influenced by the prior distribution, thus a Bayesian p -value is influenced by the prior distribution (Brooks et al. 2000). These concerns have been addressed (Gelman et al. 2004, Carlin et al. 2009, and Brooks et al. 2000) but are beyond the scope of this paper. Due to these concerns, we used posterior predictive model checking as a qualitative measure of model adequacy and if a Bayesian p -value indicated the model did not fit the data, we considered this to indicate significant lack of model fit (Link and Barker 2010). We primarily used GOF to test the recapture portion of the JS model, which is similar to the RELEASE GOF test or parametric bootstrapping in the program MARK (White and Burnham 1999), and to test the recapture portion of the Darroch model.

There is extrinsic non-identifiability in Bayesian models when the posterior distribution is dominated by the prior due to sparse data (Kery and Schaub 2012). In these cases, the parameter estimates are considered sensitive to the prior. One method of testing for extrinsic non-identifiability in a Cormack-Jolly-Seber (CJS) model is a sensitivity analysis based on different priors (Brooks et al. 2000). Since it can be time consuming to re-run models with different priors, Gimenez et al. (2009) proposed to test for extrinsic non-identifiability in mark-recapture models by comparing the overlap between a flat prior and the resulting posterior distribution. They proposed that parameters are considered weakly identifiable, thus sensitive to the prior, if the overlap between the prior and posterior is greater than 35%, which was the standard we used in our analysis. For our CJS models, we specified priors using the beta distribution where $\rho \sim \text{Beta}(1,1)$ and $\phi \sim \text{Beta}(1,1)$, which was used as an objective prior and its role in assessing weak identifiability (Brooks et al. 2002, Tuyl et al. 2009, Gimenez et al. 2009).

Spawning Ground Survey Abundance Estimates

Three types of abundance estimates may be obtained from weir or mark-recapture estimates when counts of redds, fish, or peak counts are collected concurrently (Table 14). Using the summary statistics, we estimated AFpR, ART, and PCE factors (Tables 15 and 16) (Gallagher et al. 2007, Parken et al. 2003).

Table 14. Summary statistics used from spawning ground surveys.

Statistic	Definition
<i>Redd_tot</i>	Total number of new redds observed during the spawning period
<i>Spawners_i</i>	Number of fish classified as spawners on day <i>i</i>
<i>PC</i>	The greatest number of live fish and/or carcasses observed on a single day during the spawning period

Table 15. Derived parameters for spawning ground abundance methods.

Parameter	Definition/Equation
F	Number of females in the population, $F = pF * N$
AFpR	Apparent females per redd, $AFpR = F / Redd_tot$
AUCsp	The total number of fish days for spawners or Area-Under-the-Curve. $AUCsp = 0.5 t_0 Spawner_1 + \sum 0.5 t_i (Spawner_i + Spawner_{i+1}) + 0.5 t_s Spawner_{s+1}$. For days $i = 1, \dots, s+1$.
ART	The apparent residence time, which is the average number of days a fish remains in the survey area, $ART = AUCsp / N$
PCEF	Peak count expansion factor, $PCEF = N/PC$

Table 16. Derived parameters for spawning ground abundance methods.

Parameter	Definition/Equation
Nredds	Redd-based abundance estimate, $Nredds = (Redd_tot * AFpR) / pF$
Nauc	AUC-based abundance estimate, $Nauc = AUCsp / ART$
Npc	Peak count-based abundance estimate, $Npc = PC * PCEF$

Proportions

Important indicators for salmon populations include the number of females and hatchery-origin fish (Rawding and Rodgers 2013). In addition, ages are a measure of diversity and are needed to reconstruct salmon runs for forecasting and spawner-recruit analysis (Rawding and Rodgers 2013, Hilborn and Walters 1992). When the data allow for only two possibilities, such as the sex being male or female, the binomial distribution is an appropriate model for analysis, but when there are more than two possibilities, such as adult ages, the multinomial model is appropriate.

Adipose fin excision as a mass mark for hatchery-origin salmonids is highly successful and 97-99% of juveniles examined post marking typically display acceptable marks (mass mark rate). However, the small proportion of hatchery fish that remain unmarked may lead to significant bias when attempting to enumerate natural-origin salmon abundance in small populations with large hatchery programs where substantial proportions of returning hatchery-origin adults spawn in the wild. We accounted for this source of bias by adjusting the estimate of marked and unmarked fish for each subpopulation by the hatchery specific mass mark rate for each age class. We examined CWT recoveries from both spawning ground surveys and weir removals to determine which hatchery mass rate to use for each subpopulation. Failure to adjust natural-origin abundance estimates for unmarked hatchery fish could lead to positively biased natural-origin abundance estimates.

The summary statistics and likelihoods for the proportions of males, females, marked, unmarked, hatchery-origin, natural-origin, age by origin, and marked juveniles by age are found in Tables 17 and 18. The total number of marked and unmarked adults, adult males and females, and subtotals of marked and unmarked fish by age were estimated by multiplying these proportions by the total abundance estimates.

Table 17. Summary statistics from spawning ground surveys to estimate proportions.

Statistic	Definition/Equation
Females	Number of adults that were females
Males	Number of adults that were males
Adults	Number of adults examined for sex and origin
HOS	Number of hatchery-origin adults that were mass marked (adipose fin clipped) and adjusted for unmarked hatchery releases
NOS	Number of natural-origin adults that were not mass marked (adipose fin clipped) and adjusted for unmarked hatchery releases
Marked	Number of adults that were mass marked (adipose fin clipped)
Unmarked	Number of adults that were not mass marked (adipose fin intact)
HOS_Age _i	Number of hatchery-origin adults that are age i , $i=3,4,5$
NOS_Age _i	Number of natural-origin adults that are age i , $i=3,4,5$
M_Age _i	Number of marked adults that are age i , $i=3,4,5$
U_Age _i	Number of unmarked adults that are age i , $i=3,4,5$
pF	Proportion of adults that are females
pM	Proportion of adults that are males
pHOS	Proportion of adults that are hatchery-origin
pNOS	Proportion of adults that are natural-origin
pMS	Proportion of adults that are mass marked
pUS	Proportion of adults that are not mass marked
pHOS_Age _i	Proportion of hatchery-origin adults that are age i , $i=3,4,5$
pNOS_Age _i	Proportion of natural-origin adults that are age i , $i=3,4,5$
pM_Age _i	Proportion of adults that are marked adults that are age i , $i=3,4,5$
pU_Age _i	Proportion of adults that are unmarked adults that are age i , $i=3,4,5$
pCH_Age _i	Proportion of juv. hatchery releases that are marked by brood year/age i , $i=3,4,5$

Table 18. The likelihoods and derived parameters for sex, origin, and age and their proportions.

Description	Likelihood
Pr (Females)	Females ~Binomial (pF, Adults)
Pr (Males)	Males ~Binomial (pM, Adults)
Pr (HOS)	$HOS = \sum HOS_age_i$
Pr (NOS)	$NOS = \sum NOS_age_i$
Pr (Marked)	Marked ~Binomial (pMS, Adults)
Pr (Unmarked)	Unmarked ~Binomial (pUS, Adults)
Pr (HOS_age _i)	$HOS_age_i = MS_Age_i / pCH_Age_i$
Pr (NOS_age _i)	$NOS_age_i = US_Age_i - HOS_Age_i + MS_Age_i$
Pr (pHOS_age _i)	$pHOS_age_i = HOS_Age_i / (HOS_Age_i + NOS_Age_i)$
Pr (pNOS_age _i)	$pNOS_age_i = NOS_Age_i / (HOS_Age_i + NOS_Age_i)$
Pr (M_age _i)	M_age _i ~Multinomial (pM_Age _i , Adults)
Pr (U_age _i)	U_age _i ~Multinomial (pU_Age _i , Adults)

ESU abundance

The ESU estimates by reporting group are the sum of the population estimates fitted to a normal distribution.

Timing

We used period (weekly) counts of spawners and divided these counts by the total count of spawners to estimate the cumulative timing of spawning for each Tule fall Chinook salmon population.

Results

Model Convergence and Diagnostics

We ran two chains with 10,000 iterations for a burn-in, followed by 50,000 iterations, in which every fifth iteration was saved using the Gibbs sampler in WinBUGS. We saved a total of 20,000 iterations for the posterior distribution of each of the parameters monitored. Chains were thinned to save space given the large number of parameters that were monitored. Visual inspection of the trace and history plots suggested the chains mixed and converged. The Brooks-Gelman-Rubin (BGR) diagnostic test for convergence yielded values of less than 1.05 for each parameter, which is less than the recommended value of 1.2. While it is impossible to conclusively demonstrate a simulation has converged, the above diagnostic tests did not detect that the simulations did not converge. The MCMC error rate was less than 5% of the standard deviation of the parameter estimates, which suggests our posterior distributions were accurate. Our population abundance estimates were similar for the different vague priors and the proportion results were not sensitive to the priors except when we had few observations. The results reported here used the LaPlace/Bayes prior (Tuyl et al. 2009).

Apparent Residence Time and Females per Redd

We did not have any successful mark-recapture estimates or census counts in any subpopulations that we could derive a year-specific estimate of ART in 2012. Therefore, we used the mean ART value derived in 2011 of ~ 5.06 days (95% CI 4.45-5.67) (Rawding et al. 2019) to develop AUC-based abundance estimates for 2012.

Similarly, for AFpR, we did not have any successful mark-recapture estimates or census counts in subpopulations where we had concurrent census counts of unique redds. All 2012 redd-based abundance estimates were derived using the mean AFpR of ~1.13 that was used in our 2011 analysis (Rawding et al. 2019).

Grays/Chinook Population

The Grays/Chinook fall Chinook population consists of the Chinook and Grays subpopulations. Historical monitoring of the Chinook subpopulation indicates it is at extremely low abundance levels or may be extirpated. Additionally, tide gates are used for flood control in the Lower Chinook River, which can restrict access for anadromous fish. No monitoring for Chinook salmon was done in the Chinook River basin in 2012. The Grays subpopulation is comprised primarily of three stocks; hatchery-origin Tules, Rogue River Brights, and natural-origin Chinook salmon which are comprised of Tules, naturalized Rogue River Brights, and their hybrids (Roegner et al. 2010). Abundance estimates include the historic distribution below the Grays River canyon and spawning above areas altered to allow passage (e.g. above the canyon). Our study was designed to use to estimate escapement for Chinook salmon using up to five independent methods. However, due to low abundance and a lack of recaptures with our mark-recapture work, only two methods were viable options in 2012, AUC based on counts of live adults classified as spawners and redd expansion. The two estimates were not significantly

different from one another. We chose to report the redd-based estimate for consistency with prior years' estimates. This yielded an abundance estimate of 205 adult Chinook salmon (95% CI 111-318). Based on left ventral clips and adjusting for unmarked hatchery fish from the South Fork Klaskanine (an Oregon Department of Fish and Wildlife (ODFW) facility), we estimated 82 (95% CI 38-142) Rogue River Bright adult spawners. To estimate the hatchery-origin Tule component, we used Deep River net pen mass mark rates and estimated 80 (95% CI 37-138) adult spawners. The estimated proportion of hatchery-origin (adipose and/or left ventral clipped) adults was 79.2%. Most adults were age-3. Population abundance, origin, sex, and age estimates are reported in Tables 19-21.

Table 19. Estimates of abundance, including sex-, origin-, and stock-specific estimates, for the adult Grays/Chinook fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	205	53	111	201	318
Males	102	66	5	95	244
Females	103	66	5	96	243
HOS Rogue River Bright	82	27	38	79	142
HOS Tule	80	26	37	77	138
NOS	43	18	16	40	84
LV-marked	80	26	37	77	138
AD-Marked	80	26	37	77	138
Unmarked	45	18	18	43	87

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 20. Estimates of abundance by age and stock for the adult Grays/Chinook fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Rogue River Bright Age-3	75	25	34	72	132
HOS Rogue River Bright Age-4	6	6	0	4	22
HOS Rogue River Bright Age-5	1	2	0	0	5
HOS Rogue River Bright Age-6	1	2	0	0	5
HOS Tule Age-3	36	16	12	34	75
HOS Tule Age-4	42	18	16	40	84
HOS Tule Age-5	1	2	0	0	6
HOS Tule Age-6	1	2	0	0	6
NOS Age-3	23	13	5	21	54
NOS Age-4	19	11	4	16	46
NOS Age-5	1	2	0	0	6
NOS Age-6	1	2	0	0	6

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 21. Estimates of proportions of the adult Grays/Chinook fall Chinook population by sex, origin, and stock and proportions of each stock by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose or ventral fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.497	0.287	0.023	0.495	0.971
pFemale	0.503	0.287	0.029	0.505	0.977
pHOS (includes Rogue River Bright HOS & Tule HOS)	0.792	0.065	0.653	0.796	0.902
pNOS (includes Rogue River Bright HOS & Tule HOS)	0.208	0.065	0.098	0.204	0.347
pMark (includes Rogue River Bright HOS & Tule HOS)	0.780	0.064	0.643	0.784	0.889
pUnmark (includes Rogue River Bright HOS & Tule HOS)	0.220	0.064	0.111	0.216	0.357
p Age-3 HOS Rogue River Bright	0.917	0.068	0.741	0.934	0.995
p Age-4 HOS Rogue River Bright	0.071	0.064	0.003	0.053	0.237
p Age-5 HOS Rogue River Bright	0.006	0.019	0.000	0.000	0.062
p Age-6 HOS Rogue River Bright	0.006	0.019	0.000	0.000	0.060
p Age-3 HOS Tule	0.454	0.131	0.211	0.451	0.711
p Age-4 HOS Tule	0.531	0.132	0.275	0.533	0.780
p Age-5 HOS Tule	0.007	0.023	0.000	0.000	0.076
p Age-6 HOS Tule	0.007	0.022	0.000	0.000	0.073
p Age-3 NOS	0.536	0.184	0.172	0.544	0.868
p Age-4 NOS	0.435	0.183	0.114	0.427	0.805
p Age-5 NOS	0.014	0.043	0.000	0.000	0.144
p Age-6 NOS	0.014	0.041	0.000	0.000	0.139

Elochoman/Skamokawa Population

The Elochoman/Skamokawa fall Chinook population consists of the Elochoman and Skamokawa subpopulations. Additionally, the Elochoman and Skamokawa fall Chinook subpopulations are comprised primarily of three stocks: hatchery-origin Tules, hatchery-origin Rogue River Brights, and natural-origin.

Abundance estimates were based on a combination of three different methods. For the Elochoman River above the weir site, we used Petersen mark-recapture based on live tagging at the weir in conjunction with carcasses recovered on spawning ground surveys above the weir and carcasses recovered on the weir structure. For the Elochoman River below the weir site, we used redd expansion. AUC was used to estimate abundance in the Skamokawa subpopulation.

Both the Elochoman and Skamokawa subpopulation estimates were summed to obtain an estimate for the Elochoman/Skamokawa population.

The weir on the Lower Elochoman River operated over the entire spawning run and 30 natural-origin adults were tagged and released above the weir. We used generalized linear models (GLM) assuming a binomial distribution and using a logit link function to estimate the probability of recovery for Floy tagged individuals during spawning ground surveys to determine whether a pooled Petersen abundance estimates was appropriate. Covariates included sex, origin, and categorical size (≥ 80 cm or < 80 cm), and all subsets of main effects models were compared and ranked using AICc (Burnham and Anderson 2002). The best model of recovery probability included a single main effect of categorical size, where recovery probability was significantly greater for large fish (27%) than for small fish (16%). The null model, indicating homogeneous recovery probabilities, was equally supported ($\Delta AICc = 0.7$) therefore we used a pooled Petersen estimate. To estimate the number of spawners upstream of the weir, we subtracted sport harvest (zero reported via CRC) then multiplied the run size estimate by the proportion of successful spawners.

The total Elochoman/Skamokawa fall Chinook population abundance estimate was 233 (95% CI 164-354). The proportion of hatchery-origin Chinook salmon was 72.3% and most fish were age-4. Population abundance, origin, sex, and age estimates are reported in Tables 22-24.

The Elochoman River spawner abundance estimate above the lower river weir was 87 adults (95% CI 43-177) and the redd-based estimate below the weir was 54 (95% CI 20-153). Combining the estimate of spawners above and below the weirs yielded a spawner abundance estimate of 141 adults (95% CI 75-260). Adjusting for unmarked hatchery-origin fish using ODFW's Big Creek Hatchery's mass mark rates, the proportion of hatchery-origin spawners for the Elochoman subpopulation was estimated to be 59.3%. Most adults were age-4. Population abundance, origin, sex, and age estimates are reported in Tables 25-27.

For the Skamokawa subpopulation, the AUC-based abundance estimate was 92 (95% CI 75-116). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using ODFW's Big Creek Hatchery's mass mark rates, the proportion of hatchery-origin spawners was 90.8%. Most adults were age-3 and age-4. Subpopulation abundance, origin, sex, and age estimates are reported in Tables 28-30.

Table 22. Estimates of abundance, including sex-, origin-, and stock-specific estimates, for the adult Elochoman/Skamokawa fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	233	55	164	222	354
Males	127	47	71	118	235
Females	106	25	67	102	167
HOS Rogue River Bright	17	15	1	13	58
HOS Tule	151	44	102	142	252
NOS	65	29	24	59	138
LV-Marked	17	15	1	12	57
AD-Marked	148	43	100	139	248
Unmarked	68	29	27	62	141

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 23. Estimates of abundance by age and stock for the adult Elochoman/Skamokawa fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Rogue River Bright Age-3	13	13	0	8	48
HOS Rogue River Bright Age-4	1	4	0	0	13
HOS Rogue River Bright Age-5	2	4	0	0	13
HOS Rogue River Bright Age-6	2	4	0	0	14
HOS Tule Age-3	52	17	27	49	94
HOS Tule Age-4	79	33	43	72	154
HOS Tule Age-5	18	16	2	14	57
HOS Tule Age-6	3	6	0	1	17
NOS Age-3	31	16	9	28	70
NOS Age-4	32	16	11	29	72
NOS Age-5	1	2	0	0	6
NOS Age-6	1	2	0	0	7

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 24. Estimates of proportions of the adult Elochoman/Skamokawa fall Chinook population by sex, origin, and stock and proportions of each stock by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and fin clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose or ventral fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.539	0.089	0.369	0.538	0.717
pFemale	0.461	0.089	0.283	0.462	0.631
pHOS	0.723	0.095	0.521	0.730	0.892
pNOS	0.277	0.095	0.108	0.270	0.479
pMark	0.711	0.094	0.512	0.717	0.877
pUnmark	0.289	0.094	0.123	0.283	0.488
p Age-3 HOS Rogue River Bright	0.726	0.277	0.090	0.830	1.000
p Age-4 HOS Rogue River Bright	0.089	0.172	0.000	0.008	0.656
p Age-5 HOS Rogue River Bright	0.091	0.176	0.000	0.007	0.682
p Age-6 HOS Rogue River Bright	0.095	0.181	0.000	0.008	0.690
p Age-3 HOS Tule	0.351	0.098	0.168	0.347	0.552
p Age-4 HOS Tule	0.519	0.104	0.318	0.518	0.721
p Age-5 HOS Tule	0.114	0.075	0.017	0.098	0.299
p Age-6 HOS Tule	0.016	0.031	0.000	0.004	0.108
p Age-3 NOS	0.478	0.098	0.285	0.479	0.667
p Age-4 NOS	0.495	0.098	0.306	0.495	0.686
p Age-5 NOS	0.012	0.033	0.000	0.000	0.100
p Age-6 NOS	0.015	0.036	0.000	0.002	0.110

Table 25. Estimates of abundance, including sex-, origin-, and stock-specific estimates, for the adult Elochoman fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	141	54	75	129	260
Males	76	46	25	66	182
Females	65	24	32	60	124
HOS Rogue River Bright	17	15	1	12	58
HOS Tule	67	43	25	58	168
NOS	56	29	17	50	128
LV-Marked	16	15	1	12	57
AD-Marked	66	42	25	56	166
Unmarked	58	29	19	52	130

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 26. Estimates of abundance by age and stock for the adult Elochoman fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Rogue River Bright Age-3	12	13	0	8	47
HOS Rogue River Bright Age-4	1	4	0	0	13
HOS Rogue River Bright Age-5	1	4	0	0	13
HOS Rogue River Bright Age-6	2	4	0	0	13
HOS Tule Age-3	14	14	0	10	52
HOS Tule Age-4	37	31	9	30	111
HOS Tule Age-5	14	16	1	10	53
HOS Tule Age-6	2	6	0	0	17
NOS Age-3	27	15	7	24	65
NOS Age-4	28	15	8	25	68
NOS Age-5	0	2	0	0	4
NOS Age-6	1	2	0	0	4

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 27. Estimates of proportions of the adult Elochoman fall Chinook subpopulation by sex, origin, and stock and proportions of each stock by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and fin clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose or ventral fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.518	0.135	0.256	0.520	0.775
pFemale	0.482	0.135	0.225	0.480	0.744
pHOS	0.593	0.148	0.304	0.594	0.872
pNOS	0.407	0.148	0.129	0.406	0.696
pMark	0.581	0.145	0.299	0.582	0.855
pUnmark	0.419	0.145	0.145	0.418	0.701
p Age-3 HOS Rogue River Bright	0.741	0.278	0.092	0.854	1.000
p Age-4 HOS Rogue River Bright	0.084	0.172	0.000	0.004	0.663
p Age-5 HOS Rogue River Bright	0.086	0.176	0.000	0.004	0.683
p Age-6 HOS Rogue River Bright	0.089	0.181	0.000	0.004	0.694
p Age-3 HOS Tule	0.207	0.163	0.007	0.169	0.597
p Age-4 HOS Tule	0.551	0.194	0.173	0.557	0.897
p Age-5 HOS Tule	0.208	0.155	0.012	0.176	0.581
p Age-6 HOS Tule	0.034	0.068	0.000	0.004	0.246
p Age-3 NOS	0.478	0.097	0.289	0.479	0.662
p Age-4 NOS	0.506	0.097	0.319	0.505	0.692
p Age-5 NOS	0.007	0.029	0.000	0.000	0.071
p Age-6 NOS	0.009	0.032	0.000	0.000	0.078

Table 28. Estimates of abundance, including sex- and origin-specific estimates, for the adult Skamokawa fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	92	10	75	91	116
Males	52	10	34	51	72
Females	41	9	25	40	60
HOS	83	11	64	83	107
NOS	9	5	1	8	21
Marked	82	11	63	81	106
Unmarked	10	5	2	9	23

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 29. Estimates of abundance by age and origin for the adult Skamokawa fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	38	10	21	37	58
HOS Age-4	42	10	24	41	63
HOS Age-5	4	3	0	3	13
HOS Age-6	0	1	0	0	3
NOS Age-3	4	4	0	3	14
NOS Age-4	4	4	0	3	14
NOS Age-5	0	1	0	0	4
NOS Age-6	0	1	0	0	4

The sum of abundance by mark status, sex, and age may not equal the total abundance estimate due to rounding errors.

Table 30. Estimates of proportions of the adult Skamokawa fall Chinook subpopulation by sex and origin and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.559	0.084	0.392	0.560	0.720
pFemale	0.441	0.084	0.280	0.440	0.608
pHOS	0.908	0.056	0.773	0.917	0.989
pNOS	0.092	0.056	0.011	0.083	0.227
pMark	0.894	0.056	0.761	0.904	0.977
pUnmark	0.106	0.056	0.024	0.097	0.239
p Age-3 HOS Tule	0.454	0.099	0.264	0.453	0.649
p Age-4 HOS Tule	0.497	0.099	0.307	0.496	0.694
p Age-5 HOS Tule	0.045	0.041	0.002	0.033	0.152
p Age-6 HOS Tule	0.004	0.012	0.000	0.000	0.039
p Age-3 NOS	0.479	0.319	0.000	0.468	1.000
p Age-4 NOS	0.426	0.317	0.000	0.405	0.998
p Age-5 NOS	0.041	0.124	0.000	0.000	0.448
p Age-6 NOS	0.054	0.142	0.000	0.000	0.522

Mill (MAG) Population

The Mill (MAG) fall Chinook population consists of three subpopulations: Mill, Abernathy, and Germany. These three creeks enter the Columbia River within two miles of each other. We continue to report on the combined population as well as separately for each subpopulation to be consistent with historic reporting and because the subpopulations are part of Washington State’s Intensively Monitored Watershed (IMW) program (Zimmerman et al. 2015), which requires reporting at this scale.

Our study was designed to use open population mark-recapture (JS) via carcass tagging as the primary method of estimating abundance. However, due to low abundance and the lack of recaptures of previously tagged carcasses, we were unable to use this estimator. Instead, a secondary method, AUC based on counts of adults classified as spawners, was used for all three subpopulations.

Total abundance for the Mill fall Chinook population was estimated to be 185 adults (95% CI 151-234). The estimated proportion of hatchery-origin fish was high (87.1%) and age-3 hatchery-origin fish comprised over half of the adult return for this population. Total estimated abundance for the Mill fall Chinook subpopulation was 106 adults (95% CI 86-134). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using ODFW’s Big Creek Hatchery’s mass mark rates, the proportion hatchery-origin spawners was estimated to be 85.8% and almost 65% of the marked adults were age-3. Total abundance for the Abernathy fall Chinook subpopulation was estimated to be 60 adults (95% CI 49-75). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using ODFW’s Big Creek Hatchery’s mass

mark rates, the proportion hatchery-origin spawners was approximately 90% and 75% of the hatchery-origin adults were age-3. Total estimated abundance for the Germany fall Chinook subpopulation was 19 adults (95% CI 16-24). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using ODFW's Big Creek Hatchery's mass mark rates, the proportion hatchery-origin spawners was approximately 85% and age-3 hatchery-origin fish were the dominant age class. Mill (MAG) fall Chinook population abundance estimates and proportions by origin, sex, and age estimates can be found in Tables 31-33. Mill fall Chinook subpopulation abundance estimates and proportions by origin, sex, and age estimates are found in Tables 34-36. Abernathy fall Chinook subpopulation abundance estimates and proportions by origin, sex, and age estimates are found in Tables 37-39. Germany fall Chinook subpopulation abundance estimates and proportions by origin, sex, and age estimates are reported in Tables 40-42.

Table 31. Estimates of abundance, including sex- and origin-specific estimates, for the adult Mill (MAG) fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	185	21	151	183	234
Males	103	16	76	102	138
Females	82	14	58	81	114
HOS	162	20	127	160	207
NOS	24	9	9	23	43
Marked	154	19	122	152	197
Unmarked	31	9	16	30	51

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 32. Estimates of abundance by age and origin for the adult Mill (MAG) fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	115	17	85	113	153
HOS Age-4	37	10	20	36	59
HOS Age-5	9	5	2	8	20
HOS Age-6	1	2	0	0	6
NOS Age-3	20	8	6	19	38
NOS Age-4	1	2	0	0	8
NOS Age-5	1	2	0	0	8
NOS Age-6	1	2	0	0	8

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 33. Estimates of proportions of the adult Mill (MAG) fall Chinook population by sex and origin and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.557	0.056	0.446	0.558	0.664
pFemale	0.443	0.056	0.336	0.442	0.554
pHOS	0.871	0.045	0.775	0.874	0.949
pNOS	0.129	0.045	0.051	0.126	0.225
pMark	0.832	0.044	0.739	0.835	0.908
pUnmark	0.168	0.044	0.092	0.165	0.261
p Age-3 HOS	0.824	0.139	0.490	0.855	0.996
p Age-4 HOS	0.056	0.089	0.000	0.013	0.316
p Age-5 HOS	0.058	0.089	0.000	0.015	0.316
p Age-6 HOS	0.062	0.091	0.000	0.022	0.330
p Age-3 NOS	0.710	0.058	0.593	0.712	0.817
p Age-4 NOS	0.229	0.054	0.133	0.226	0.342
p Age-5 NOS	0.055	0.028	0.013	0.051	0.120
p Age-6 NOS	0.006	0.010	0.000	0.001	0.037

Table 34. Estimates of abundance, including sex- and origin-specific estimates, for the adult Mill fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	106	12	86	105	134
Males	54	10	37	54	76
Females	52	10	35	51	74
HOS	91	12	70	90	118
NOS	15	7	4	15	30
Marked	87	12	67	86	113
Unmarked	19	7	9	19	34

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 35. Estimates of abundance by age and origin for the adult Mill fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	59	11	39	58	83
HOS Age-4	24	7	11	23	40
HOS Age-5	8	4	2	7	19
HOS Age-6	0	1	0	0	2
NOS Age-3	14	7	4	14	29
NOS Age-4	0	1	0	0	2
NOS Age-5	0	1	0	0	2
NOS Age-6	0	1	0	0	3

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 36. Estimates of proportions of the adult Mill fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.510	0.072	0.368	0.511	0.651
pFemale	0.490	0.072	0.349	0.489	0.632
pHOS	0.858	0.060	0.727	0.863	0.961
pNOS	0.142	0.060	0.039	0.137	0.273
pMark	0.818	0.058	0.694	0.823	0.916
pUnmark	0.182	0.058	0.084	0.177	0.306
p Age-3 HOS	0.646	0.081	0.482	0.649	0.796
p Age-4 HOS	0.261	0.074	0.131	0.257	0.417
p Age-5 HOS	0.090	0.048	0.019	0.083	0.200
p Age-6 HOS	0.003	0.009	0.000	0.000	0.027
p Age-3 NOS	0.951	0.103	0.646	0.997	1.000
p Age-4 NOS	0.014	0.057	0.000	0.000	0.178
p Age-5 NOS	0.014	0.056	0.000	0.000	0.168
p Age-6 NOS	0.021	0.067	0.000	0.000	0.208

Table 37. Estimates of abundance, including sex- and origin-specific estimates, for the adult Abernathy fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	60	7	49	59	75
Males	35	7	22	35	51
Females	25	7	13	24	39
HOS	54	8	40	54	70
NOS	6	5	0	5	17
Marked	51	7	38	51	67
Unmarked	9	5	2	8	20

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 38. Estimates of abundance by age and origin for the adult Abernathy fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	41	8	25	40	57
HOS Age-4	13	6	4	12	26
HOS Age-5	0	1	0	0	3
HOS Age-6	0	1	0	0	3
NOS Age-3	5	4	0	4	16
NOS Age-4	0	1	0	0	3
NOS Age-5	0	1	0	0	3
NOS Age-6	0	1	0	0	3

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 39. Estimates of proportions of the 2012 adult Abernathy fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.590	0.103	0.385	0.593	0.783
pFemale	0.410	0.103	0.217	0.407	0.615
pHOS	0.902	0.077	0.717	0.916	1.000
pNOS	0.098	0.077	0.000	0.084	0.283
pMark	0.857	0.076	0.681	0.869	0.968
pUnmark	0.143	0.076	0.032	0.131	0.319
p Age-3 HOS	0.750	0.102	0.524	0.760	0.917
p Age-4 HOS	0.239	0.101	0.075	0.228	0.464
p Age-5 HOS	0.006	0.017	0.000	0.000	0.056
p Age-6 HOS	0.006	0.018	0.000	0.000	0.058
p Age-3 NOS	0.735	0.355	0.000	0.928	1.000
p Age-4 NOS	0.061	0.184	0.000	0.000	0.789
p Age-5 NOS	0.091	0.223	0.000	0.000	0.983
p Age-6 NOS	0.113	0.257	0.000	0.001	1.000

Table 40. Estimates of abundance, including sex- and origin-specific estimates, for the adult Germany fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	19	2	16	19	24
Males	14	3	7	14	20
Females	5	3	1	5	13
HOS	16	3	9	17	22
NOS	3	3	0	2	10
Marked	16	3	9	16	22
Unmarked	3	3	0	2	10

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 41. Estimates of abundance by age and origin for the adult Germany fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	15	4	7	15	22
HOS Age-4	0	1	0	0	4
HOS Age-5	0	1	0	0	4
HOS Age-6	0	1	0	0	4
NOS Age-3	0	1	0	0	5
NOS Age-4	1	2	0	0	6
NOS Age-5	1	2	0	0	6
NOS Age-6	1	2	0	0	6

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 42. Estimates of proportions of the adult Germany fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.715	0.159	0.362	0.735	0.956
pFemale	0.285	0.159	0.045	0.265	0.638
pHOS	0.850	0.141	0.488	0.891	1.000
pNOS	0.150	0.141	0.000	0.109	0.512
pMark	0.833	0.142	0.475	0.871	0.995
pUnmark	0.167	0.142	0.005	0.129	0.525
p Age-3 HOS	0.932	0.107	0.606	0.981	1.000
p Age-4 HOS	0.023	0.064	0.000	0.000	0.224
p Age-5 HOS	0.023	0.064	0.000	0.000	0.232
p Age-6 HOS	0.022	0.062	0.000	0.000	0.215
p Age-3 NOS	0.139	0.312	0.000	0.000	0.999
p Age-4 NOS	0.282	0.392	0.000	0.014	1.000
p Age-5 NOS	0.281	0.392	0.000	0.011	1.000
p Age-6 NOS	0.299	0.399	0.000	0.022	1.000

Toutle Population

The Toutle fall Chinook population consists of the Green and the South Fork Toutle subpopulations. A third subpopulation may exist in the North Fork Toutle River but this area was not surveyed due to high sediment loads resulting from the eruption of Mt. Saint Helens, which cause poor survey conditions, and have historically resulted in zero or negligible use by Chinook salmon.

Abundance estimates were generated using three different methods. For the Green subpopulation above the weir site at the North Toutle Hatchery, we used Petersen mark-recapture based on live tagging at the weir in conjunction with spawning ground surveys above the weir and carcasses that were recovered on the weir structure. For the Green subpopulation below the weir site, and on the South Fork Toutle River, we used AUC based on counts of adults classified as spawners. On the South Fork Toutle, a redd-based estimate was also generated. Both the Green and South Fork Toutle subpopulation estimates were summed to obtain an estimate for the Toutle population.

The weir at North Toutle Hatchery on the Green River operated over the entire spawning run and 612 adults were tagged and released above the weir. We used generalized linear models (GLM) assuming a binomial distribution and using a logit link function to estimate the probability of recovery for Floy tagged Chinook salmon during spawning ground surveys to determine if a pooled Petersen abundance estimates was appropriate. Covariates included sex, origin, and categorical size (≥ 80 cm or < 80 cm), and all subsets of main effects models were compared and ranked using AICc (Burnham and Anderson 2002). The null model, indicating homogeneous recovery probabilities, was not supported ($\Delta\text{AICc} = 7.7$). The best recovery probability model included a single main effect of categorical size where recovery probability was significantly greater for large fish (27%) than for small fish (16%). We stratified to estimate abundance of large fish and small fish separately then combined those estimates for an overall estimate of fish passing the weir site. This estimate was not significantly different from the pooled Petersen estimate, so we have chosen to report the pooled Petersen estimate. To estimate the number of spawners upstream of the weir, we subtracted sport harvest (two) then multiplied the run size estimate by the proportion of successful spawners.

The total Toutle fall Chinook population estimate was 949 (95% CI 854-1,053). The proportion of hatchery-origin Chinook salmon was 73.0% and most fish were age-4. Population abundance, origin, sex, and age estimates are reported in Tables 43-45.

The Green fall Chinook subpopulation estimate above the North Toutle Hatchery weir was 648 adults (95% CI 575-720) and the estimate below the weir was 35 (95% CI 28-44). Combining the estimates of spawners above and below the weir yielded an estimate of 684 (95% CI 610-757). Based on adipose fin clips and adjusting for unmarked hatchery fish using North Toutle Hatchery's mass mark rates, the proportion of hatchery-origin spawners for the Green subpopulation was 71.9%. Most fish were age-3. Subpopulation abundance, origin, sex, and age estimates are reported in Tables 46-48.

The redd-based estimate for the South Fork Toutle fall Chinook subpopulation was 442 (95% CI 233-702) compared to the AUC based estimate of 265 (95% CI 215-333). We chose to use the AUC-based estimate due to a two factors: 1) staff identified a high proportion of test digs and/or small redds in the basin, which may have resulted in an overestimate of redds; 2) a small number of carcass recoveries and a higher than average proportion of males also suggested positive bias in the redd-based abundance estimate. Based on adipose fin clips and adjusting for unmarked hatchery fish using Kalama Falls Hatchery's mass mark rates, the proportion of hatchery-origin spawners for the South Fork Toutle fall Chinook subpopulation was 76.1%. Most adults were age-4. Subpopulation abundance, origin, sex, and age estimates are reported in Tables 49-51.

Table 43. Estimates of abundance, including sex- and origin-specific estimates, for the adult Toutle fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	949	50	854	947	1,053
Males	504	42	425	502	589
Females	445	40	369	444	528
HOS	693	47	604	692	790
NOS	256	32	197	255	322
Marked	683	46	595	682	778
Unmarked	266	32	208	265	332

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 44. Estimates of abundance by age and origin for the adult Toutle fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	276	29	222	275	336
HOS Age-4	290	33	230	289	361
HOS Age-5	125	20	89	124	167
HOS Age-6	2	3	0	0	10
NOS Age-3	61	15	35	59	93
NOS Age-4	125	21	87	124	171
NOS Age-5	68	14	43	67	99
NOS Age-6	2	3	0	0	10

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 45. Estimates of proportions of the adult Toutle fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.531	0.034	0.463	0.531	0.597
pFemale	0.469	0.034	0.403	0.469	0.537
pHOS	0.730	0.031	0.669	0.731	0.788
pNOS	0.270	0.031	0.212	0.269	0.331
pMark	0.719	0.030	0.659	0.720	0.776
pUnmark	0.281	0.030	0.224	0.280	0.342
p Age-3 HOS	0.399	0.034	0.334	0.399	0.468
p Age-4 HOS	0.420	0.036	0.350	0.420	0.490
p Age-5 HOS	0.181	0.027	0.132	0.180	0.236
p Age-6 HOS	0.002	0.004	0.000	0.001	0.015
p Age-3 NOS	0.239	0.049	0.150	0.236	0.341
p Age-4 NOS	0.493	0.056	0.385	0.493	0.602
p Age-5 NOS	0.269	0.047	0.183	0.266	0.366
p Age-6 NOS	0.006	0.011	0.000	0.001	0.039

Table 46. Estimates of abundance, including sex- and origin-specific estimates, for the adult Green fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	684	37	610	684	757
Males	362	34	298	361	429
Females	322	33	260	322	388
HOS	492	36	421	491	564
NOS	192	27	144	192	247
Marked	484	36	415	484	555
Unmarked	200	26	151	199	254

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 47. Estimates of abundance by age and origin for the adult Green fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	249	27	200	248	303
HOS Age-4	138	19	102	137	178
HOS Age-5	104	17	73	103	139
HOS Age-6	1	2	0	0	8
NOS Age-3	43	11	24	42	67
NOS Age-4	86	16	58	85	119
NOS Age-5	62	13	39	61	90
NOS Age-6	1	2	0	0	7

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 48. Estimates of proportions of the adult Green fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.529	0.040	0.451	0.529	0.606
pFemale	0.471	0.040	0.394	0.471	0.549
pHOS	0.719	0.036	0.647	0.719	0.786
pNOS	0.281	0.036	0.214	0.281	0.353
pMark	0.708	0.035	0.637	0.709	0.774
pUnmark	0.292	0.035	0.226	0.292	0.363
p Age-3 HOS	0.508	0.037	0.436	0.508	0.582
p Age-4 HOS	0.281	0.034	0.218	0.280	0.349
p Age-5 HOS	0.211	0.031	0.153	0.210	0.275
p Age-6 HOS	0.002	0.005	0.000	0.000	0.017
p Age-3 NOS	0.225	0.046	0.139	0.223	0.321
p Age-4 NOS	0.450	0.054	0.347	0.450	0.557
p Age-5 NOS	0.325	0.052	0.228	0.323	0.430
p Age-6 NOS	0.005	0.011	0.000	0.000	0.040

Table 49. Estimates of abundance, including sex- and origin-specific estimates, for the adult South Fork Toutle fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	265	30	215	262	333
Males	142	24	100	140	193
Females	123	23	84	121	171
HOS	202	28	153	199	262
NOS	63	17	34	62	101
Marked	199	27	151	197	258
Unmarked	66	17	37	65	104

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 50. Estimates of abundance by age and origin for the adult South Fork Toutle fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	27	12	9	25	53
HOS Age-4	153	25	108	151	207
HOS Age-5	22	10	6	20	46
HOS Age-6	1	2	0	0	5
NOS Age-3	18	10	4	16	41
NOS Age-4	39	14	16	38	71
NOS Age-5	6	6	0	4	22
NOS Age-6	1	2	0	0	6

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 51. Estimates of proportions of the adult South Fork Toutle fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.536	0.066	0.409	0.536	0.664
pFemale	0.464	0.066	0.336	0.464	0.591
pHOS	0.761	0.059	0.637	0.764	0.866
pNOS	0.239	0.059	0.134	0.236	0.363
pMark	0.749	0.058	0.628	0.752	0.853
pUnmark	0.251	0.058	0.147	0.248	0.372
p Age-3 HOS	0.133	0.054	0.046	0.127	0.255
p Age-4 HOS	0.758	0.068	0.613	0.762	0.878
p Age-5 HOS	0.107	0.049	0.031	0.100	0.221
p Age-6 HOS	0.003	0.008	0.000	0.000	0.025
p Age-3 NOS	0.278	0.134	0.064	0.263	0.568
p Age-4 NOS	0.617	0.146	0.318	0.624	0.875
p Age-5 NOS	0.097	0.088	0.000	0.073	0.324
p Age-6 NOS	0.009	0.028	0.000	0.000	0.088

Upper Cowlitz/Tilton Population

Fall Chinook salmon are captured at the Barrier Dam fish collection facility, trucked, and released into the Tilton, Upper Cowlitz, and Cispus rivers. Prior to being transported, Chinook salmon are classified as males, females, and jacks and their mark status are recorded. However, scales are not taken to determine ages. We subtracted the angler harvest from the number of salmon released and assumed no fall back or mortality due to transportation.

Abundance for the Upper Cowlitz fall Chinook population was estimated to be 5,564 adults (95% CI 5,424-5,699) and the proportion of hatchery-origin fish was 65%. Total abundance for the Tilton River fall Chinook subpopulation was estimated to be 2,374 adults (95% CI 2,258-2,489). Adjusting for unmarked hatchery-origin fish using Cowlitz Salmon Hatchery's mass mark rates, the proportion of hatchery-origin spawners in the Tilton subpopulation was 18%. Abundance for the Upper Cowlitz/Cispus fall Chinook salmon subpopulation was estimated to be 3,190 adults (95% CI 3,115-3,264). Adjusting for unmarked hatchery-origin fish using Cowlitz Salmon Hatchery's mass mark rates, the proportion of hatchery-origin spawners in the Tilton fall Chinook subpopulation was 100%. Upper Cowlitz/Tilton fall Chinook population abundance estimates and proportions by origin, sex, and age can be found in Tables 52-53. Tilton fall Chinook subpopulation abundance estimates and proportions by origin, sex, and age are reported in Tables 54-55. Upper Cowlitz/Cispus fall Chinook subpopulation abundance and proportions by origin, sex, and age estimates are reported in Tables 56-57.

Table 52. Estimates of abundance, including sex- and origin-specific estimates, for the adult Upper Cowlitz/Tilton fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	5,564	70	5,424	5,565	5,699
Males	2,583	35	2,514	2,584	2,651
Females	2,980	35	2,911	2,981	3,048
HOS	3,618	71	3,477	3,619	3,755
NOS	1,946	1	1,945	1,946	1,947
Marked	3,613	70	3,473	3,614	3,748
Unmarked	1,951	0	1,951	1,951	1,951

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 53. Estimates of proportions of the adult Upper Cowlitz/Tilton Chinook salmon population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.464	0.000	0.463	0.464	0.465
pFemale	0.536	0.000	0.535	0.536	0.537
pHOS	0.650	0.005	0.641	0.650	0.659
pNOS	0.350	0.005	0.341	0.350	0.359
pMark	0.649	0.004	0.640	0.649	0.658
pUnmark	0.351	0.004	0.342	0.351	0.360

Table 54. Estimates of abundance, including sex- and origin-specific estimates, for the adult Tilton fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	2,374	59	2,258	2,375	2,489
Males	1,199	29	1,141	1,199	1,256
Females	1,176	29	1,118	1,176	1,233
HOS	428	60	311	429	545
NOS	1,946	1	1,945	1,946	1,947
Marked	423	59	307	424	539
Unmarked	1,951	0	1,951	1,951	1,951

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 55. Estimates of proportions of the adult Tilton fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.505	0.000	0.505	0.505	0.505
pFemale	0.495	0.000	0.495	0.495	0.495
pHOS	0.180	0.021	0.138	0.181	0.219
pNOS	0.820	0.021	0.781	0.819	0.862
pMark	0.178	0.020	0.136	0.179	0.216
pUnmark	0.822	0.020	0.784	0.821	0.864

Table 56. Estimates of abundance, including sex- and origin-specific estimates, for the adult Upper Cowlitz/Cispus fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	3,190	38	3,115	3,190	3,264
Males	1,385	19	1,348	1,385	1,422
Females	1,805	19	1,768	1,805	1,842
HOS	3,190	38	3,115	3,190	3,264
NOS	0	0	0	0	0
Marked	3,190	38	3,115	3,190	3,264
Unmarked	0	0	0	0	0

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 57. Estimates of proportions of the adult Upper Cowlitz/Cispus fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.434	0.001	0.433	0.434	0.436
pFemale	0.566	0.001	0.564	0.566	0.567
pHOS	1.000	0.000	1.000	1.000	1.000
pNOS	0.000	0.000	0.000	0.000	0.000
pMark	1.000	0.000	1.000	1.000	1.000
pUnmark	0.000	0.000	0.000	0.000	0.000

Coweeman Population

Abundance estimates were based on a combination of two different methods. Above the weir site, we used Petersen mark-recapture based on live tagging at the weir in conjunction with spawning ground surveys above the weir and any carcasses recovered on the weir structure. Below the weir site, we used redd-based estimates from census counts of unique redds.

The weir on the Lower Coweeman River was operated over the entire spawning run and 176 adults were tagged and released above the weir. We used generalized linear models (GLM) assuming a binomial distribution and using a logit link function to estimate the probability of recovery for Floy tagged Chinook salmon during spawning ground surveys to determine whether a pooled Petersen abundance estimates was appropriate. Covariates included sex, origin, and categorical size (≥ 80 cm or < 80 cm), and all subsets of main effects models were compared and ranked using AICc (Burnham and Anderson 2002). The null model, indicating homogeneous recovery probabilities, was marginally supported ($\Delta AICc = 3.3$). The best Chinook salmon recovery probability model included a single main effect of categorical size, where recovery probability was significantly greater for large fish (27%) than for small fish (12%). We stratified to estimate abundance of large fish and small fish separately then combined those estimates for an overall estimate of adult Chinook salmon passing the weir site. This estimate was not significantly different from the pooled Petersen estimate, so we have chosen to report on the pooled Petersen estimate. To estimate the number of spawners upstream of the weir, we subtracted sport harvest (zero) then multiplied the run size estimate by the proportion of successful spawners, which resulted in an estimate of 310 adults (95% CI 234-409). The redd-based estimate of adult spawners below the weir was 153 (95% CI 82-243). Combining the estimate of spawners above and below the weirs yielded an abundance estimate of 463 adults (95% CI 357-593). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Kalama Falls Hatchery's mass mark rates, the proportion of hatchery-origin spawners for the Coweeman population was 11.0%. Most fish were age-4. Population abundance, origin, sex, and age estimates are reported in Tables 58-60.

Table 58. Estimates of abundance, including sex- and origin-specific estimates, for the adult Coweeman fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	463	60	357	459	593
Males	232	44	155	228	328
Females	231	37	165	229	311
HOS	51	17	24	49	91
NOS	412	54	315	408	529
Marked	51	17	24	49	90
Unmarked	412	54	316	409	530

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 59. Estimates of abundance by age and origin for the adult Coweeman fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	18	11	5	16	46
HOS Age-4	21	11	6	19	50
HOS Age-5	7	9	0	4	32
HOS Age-6	4	8	0	1	29
NOS Age-3	127	31	73	125	195
NOS Age-4	177	37	113	175	257
NOS Age-5	106	29	57	103	171
NOS Age-6	1	3	0	0	11

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 60. Estimates of proportions of the adult Coweeman fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.499	0.059	0.384	0.500	0.614
pFemale	0.501	0.059	0.386	0.501	0.616
pHOS	0.110	0.032	0.056	0.107	0.182
pNOS	0.890	0.032	0.818	0.893	0.944
pMark	0.109	0.032	0.056	0.106	0.181
pUnmark	0.891	0.032	0.819	0.894	0.944
p Age-3 HOS	0.361	0.164	0.110	0.335	0.726
p Age-4 HOS	0.416	0.166	0.143	0.397	0.774
p Age-5 HOS	0.139	0.142	0.004	0.086	0.528
p Age-6 HOS	0.084	0.135	0.000	0.012	0.478
p Age-3 NOS	0.308	0.062	0.193	0.306	0.438
p Age-4 NOS	0.431	0.069	0.298	0.430	0.569
p Age-5 NOS	0.258	0.063	0.147	0.254	0.389
p Age-6 NOS	0.003	0.008	0.000	0.000	0.026

Kalama Population

Abundance estimates were based on AUC methods using counts of live adult Chinook salmon classified as spawners. The abundance for the Kalama fall Chinook population was estimated to be 8,599 adults (95% CI 6,983-10,820). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Kalama Falls Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the Kalama fall Chinook population was 94.2% and greater than 69% of the marked adults were age-3. Kalama fall Chinook abundance estimates and proportions by origin, sex, and age are reported in Tables 61-63.

Table 61. Estimates of abundance, including sex- and origin-specific estimates, for the adult Kalama fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	8,599	982	6,983	8,490	10,820
Males	4,307	497	3,485	4,253	5,421
Females	4,293	497	3,468	4,238	5,430
HOS	8,102	926	6,570	8,001	10,200
NOS	497	69	379	491	654
Marked	8,035	918	6,517	7,935	10,110
Unmarked	564	76	436	557	735

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 62. Estimates of abundance by age and origin for the adult Kalama fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	1,817	301	1,307	1,793	2,481
HOS Age-4	5,621	687	4,478	5,556	7,165
HOS Age-5	661	162	391	645	1,023
HOS Age-6	3	11	0	0	32
NOS Age-3	202	78	70	194	372
NOS Age-4	122	72	4	114	283
NOS Age-5	169	73	52	161	331
NOS Age-6	4	13	0	0	41

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 63. Estimates of proportions of the adult Kalama fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.501	0.009	0.483	0.501	0.519
pFemale	0.499	0.009	0.481	0.499	0.517
pHOS	0.942	0.005	0.933	0.942	0.951
pNOS	0.058	0.005	0.049	0.058	0.067
pMark	0.934	0.005	0.925	0.935	0.943
pUnmark	0.066	0.005	0.057	0.066	0.075
p Age-3 HOS	0.224	0.027	0.174	0.224	0.278
p Age-4 HOS	0.694	0.030	0.634	0.695	0.750
p Age-5 HOS	0.082	0.018	0.051	0.080	0.119
p Age-6 HOS	0.000	0.001	0.000	0.000	0.004
p Age-3 NOS	0.406	0.146	0.147	0.398	0.707
p Age-4 NOS	0.246	0.138	0.009	0.235	0.542
p Age-5 NOS	0.340	0.137	0.107	0.329	0.634
p Age-6 NOS	0.008	0.026	0.000	0.000	0.083

Lewis Population

The Lewis fall Chinook population consists of the North Fork Lewis, East Fork Lewis, and Cedar subpopulations. Additionally, the Lewis fall Chinook salmon populations may be further divided into a Tule stock population, which has earlier spawn timing and a Bright stock population. Generally, most of the Bright stock population spawns in the North Fork Lewis River with minimal Bright stock spawning occurring in the East Fork Lewis River or Cedar Creek. Tule stock adults are present in all three of the subpopulations. We are only reporting estimates for the Tule stock populations in the East Fork Lewis River and Cedar Creek in this document.

Abundance estimates were based on AUC methods for East Fork Lewis fall Chinook subpopulation. Abundance estimates for the Cedar fall Chinook subpopulation were the sum of the Grist Mill ladder trap count, which is assumed to be a census count of adults above the site, and PCE for the area below the ladder. These two subpopulation estimates were summed to form a Lewis Tule stock population estimate, which excludes any North Fork Lewis Tule stock adults.

Our study was designed to estimate abundance below the Grist Mill ladder trap using carcass tagging applied to the JS model. However, due to low abundance and a lack of recaptures, the JS estimate was not a valid option. We used an alternative method of PCE using abundance estimates generated from 2010 and 2011 carcass-tagging studies divided by the peak count of adult carcasses within that reach in each respective year. We generated a mean of the 2010 and 2011 expansions, which was 3.63 (95% CI 2.84-5.08), and multiplied it by the 2012 peak count

of adult carcasses in that reach to estimate the 2012 adult abundance below the Grist Mill ladder trap.

The estimated abundance for the Lewis Tule stock population was 791 adults (95% CI 671-950). The proportion of hatchery-origin fish was 17.9% and the age structure was relatively balanced between age-3, age-4, and age-5 fish. The estimated abundance for the East Fork Lewis Tule stock subpopulation was 610 adults (95% CI 495-768). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Kalama Falls Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the East Fork Lewis Tule stock subpopulation was 5.2%. Age-4 fish comprised almost half of the spawning population. The estimated abundance for the Cedar Tule stock subpopulation was 181 adult s (95% CI 158-222). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Kalama Falls Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the Cedar Tule stock subpopulation was approximately 60% with equal numbers of age-3 and age-4 fish that comprised over 80% of adult spawning population. Lewis Tule stock abundance estimates and proportions by origin, sex, and age can be found in Tables 64-66. East Fork Lewis River Tule stock abundance estimates and proportions by origin, sex, and age can be found in Tables 67-69. Cedar Tule stock abundance and proportions by origin, sex, and age estimates can be found in Tables 70-72.

Table 64. Estimates of abundance, including sex- and origin-specific estimates, for the adult Lewis (excluding North Fork Lewis) Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	791	71	671	783	950
Males	375	42	302	372	466
Females	416	47	333	412	519
HOS	141	21	104	139	187
NOS	650	68	538	643	802
Marked	140	21	103	138	186
Unmarked	651	68	539	644	804

The sum of abundance by marked status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 65. Estimates of abundance by age and origin for the adult Lewis (excluding North Fork Lewis) Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	44	15	21	43	79
HOS Age-4	74	19	41	72	115
HOS Age-5	21	12	4	19	50
HOS Age-6	1	3	0	0	11
NOS Age-3	205	31	152	202	273
NOS Age-4	293	42	221	290	384
NOS Age-5	152	28	103	149	213
NOS Age-6	1	2	0	0	5

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 66. Estimates of proportions of the adult Lewis (excluding North Fork Lewis) Tule fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.474	0.034	0.408	0.474	0.542
pFemale	0.526	0.034	0.458	0.526	0.592
pHOS	0.179	0.026	0.131	0.177	0.234
pNOS	0.821	0.026	0.766	0.823	0.869
pMark	0.177	0.026	0.130	0.176	0.233
pUnmark	0.823	0.026	0.767	0.824	0.870
p Age-3 HOS	0.315	0.094	0.155	0.307	0.520
p Age-4 HOS	0.526	0.107	0.314	0.527	0.727
p Age-5 HOS	0.149	0.082	0.029	0.136	0.338
p Age-6 HOS	0.010	0.022	0.000	0.002	0.076
p Age-3 NOS	0.315	0.037	0.246	0.314	0.390
p Age-4 NOS	0.451	0.041	0.371	0.451	0.530
p Age-5 NOS	0.233	0.035	0.169	0.232	0.304
p Age-6 NOS	0.001	0.002	0.000	0.000	0.008

Table 67. Estimates of abundance, including sex- and origin-specific estimates, for the adult East Fork Lewis Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	610	70	495	602	768
Males	277	40	207	273	365
Females	333	45	256	329	433
HOS	32	12	13	31	58
NOS	578	67	467	571	729
Marked	32	12	13	30	58
Unmarked	578	67	468	571	729

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 68. Estimates of abundance by age and origin for the adult East Fork Lewis Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	16	8	4	14	36
HOS Age-4	15	8	3	14	36
HOS Age-5	0	2	0	0	5
HOS Age-6	0	2	0	0	5
NOS Age-3	161	30	109	158	227
NOS Age-4	279	42	207	276	369
NOS Age-5	137	27	91	135	197
NOS Age-6	0	1	0	0	4

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 69. Estimates of proportions of the adult East Fork Lewis Tule fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.454	0.040	0.375	0.453	0.533
pFemale	0.546	0.040	0.467	0.547	0.625
pHOS	0.052	0.018	0.023	0.050	0.093
pNOS	0.948	0.018	0.907	0.950	0.977
pMark	0.052	0.018	0.023	0.050	0.093
pUnmark	0.948	0.018	0.907	0.950	0.977
p Age-3 HOS	0.486	0.184	0.146	0.485	0.834
p Age-4 HOS	0.484	0.184	0.143	0.482	0.832
p Age-5 HOS	0.015	0.045	0.000	0.000	0.148
p Age-6 HOS	0.015	0.045	0.000	0.000	0.154
p Age-3 NOS	0.278	0.040	0.203	0.277	0.361
p Age-4 NOS	0.483	0.045	0.395	0.483	0.571
p Age-5 NOS	0.238	0.038	0.167	0.236	0.316
p Age-6 NOS	0.001	0.002	0.000	0.000	0.008

Table 70. Estimates of abundance, including sex- and origin-specific estimates, for the adult Cedar Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	181	17	158	178	222
Males	99	13	75	97	128
Females	83	14	58	82	115
HOS	109	18	79	107	149
NOS	73	11	56	71	99
Marked	108	18	78	107	148
Unmarked	73	11	56	72	99

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 71. Estimates of abundance by age and origin for the adult Cedar Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	29	12	11	27	58
HOS Age-4	59	17	30	57	95
HOS Age-5	20	12	4	18	49
HOS Age-6	1	3	0	0	9
NOS Age-3	44	6	34	44	56
NOS Age-4	14	4	8	14	22
NOS Age-5	14	7	5	13	32
NOS Age-6	0	1	0	0	2

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 72. Estimates of proportions of the adult Cedar Tule fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.544	0.061	0.425	0.544	0.664
pFemale	0.456	0.061	0.336	0.456	0.575
pHOS	0.598	0.062	0.461	0.605	0.705
pNOS	0.402	0.062	0.295	0.395	0.539
pMark	0.594	0.062	0.457	0.600	0.701
pUnmark	0.406	0.062	0.299	0.400	0.543
p Age-3 HOS	0.266	0.106	0.103	0.252	0.505
p Age-4 HOS	0.538	0.125	0.292	0.541	0.770
p Age-5 HOS	0.187	0.103	0.036	0.172	0.425
p Age-6 HOS	0.009	0.025	0.000	0.001	0.082
p Age-3 NOS	0.610	0.070	0.468	0.612	0.743
p Age-4 NOS	0.196	0.049	0.111	0.193	0.298
p Age-5 NOS	0.190	0.070	0.076	0.183	0.342
p Age-6 NOS	0.003	0.007	0.000	0.000	0.022

Washougal Population

The Washougal fall Chinook population primarily consists of Tule stock Chinook salmon but there is some evidence of a Bright stock population in the lower river. Currently, it is unknown whether the Bright stock population is genetically distinct from the Washougal fall Chinook population. Consequently, we treated all fall Chinook salmon in the basin as a single population for reporting purposes.

The study was designed to estimate abundance using a combination of two methods. Carcass tagging using a JS model for the area downstream of the Washougal Salmon Hatchery’s fixed panel weir and a census count of Chinook salmon passed upstream of fixed panel weir. However, due to a lack of recoveries we were forced to pool the first five periods in the JS model. We believe there were likely heterogeneous capture probabilities between these periods and, in this instance, pooling violates several assumptions of the model resulting in a biased abundance estimate. Therefore, we choose to instead use AUC methods to estimate abundance for the area downstream of the fixed panel weir. This yielded an adult Chinook salmon abundance estimate of 1,738 (95% CI 1,424-2,177). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Washougal Salmon Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the Washougal fall Chinook population was 72.3%. The majority of fish were age-3 and age-4. Population abundance, origin, sex, and age estimates are reported in Tables 73-75.

Table 73. Estimates of abundance, including sex- and origin-specific estimates, for the adult Washougal fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	1,738	192	1,424	1,718	2,177
Males	717	90	566	709	916
Females	1,022	121	822	1,008	1,294
HOS	1,256	144	1,020	1,242	1,582
NOS	482	67	369	476	630
Marked	1,238	142	1,005	1,223	1,558
Unmarked	501	68	385	494	652

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 74. Estimates of abundance by age and origin for the adult Washougal fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	391	58	291	386	517
HOS Age-4	730	93	574	722	939
HOS Age-5	135	30	84	132	201
HOS Age-6	1	2	0	0	5
NOS Age-3	299	47	218	295	402
NOS Age-4	97	25	55	95	153
NOS Age-5	85	22	48	83	135
NOS Age-6	0	2	0	0	5

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 75. Estimates of proportions of the adult Washougal fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.412	0.024	0.366	0.412	0.460
pFemale	0.588	0.024	0.540	0.588	0.634
pHOS	0.723	0.022	0.678	0.724	0.766
pNOS	0.277	0.022	0.234	0.277	0.323
pMark	0.712	0.022	0.668	0.713	0.754
pUnmark	0.288	0.022	0.246	0.287	0.333
p Age-3 HOS	0.311	0.030	0.255	0.311	0.371
p Age-4 HOS	0.581	0.032	0.519	0.581	0.643
p Age-5 HOS	0.107	0.020	0.070	0.106	0.150
p Age-6 HOS	0.000	0.001	0.000	0.000	0.004
p Age-3 NOS	0.620	0.050	0.520	0.621	0.717
p Age-4 NOS	0.202	0.042	0.124	0.200	0.291
p Age-5 NOS	0.177	0.039	0.107	0.175	0.260
p Age-6 NOS	0.001	0.003	0.000	0.000	0.010

Upper Gorge Population

The Upper Gorge fall Chinook population consists of the Wind and Little White Salmon subpopulations. Additionally, the Upper Gorge fall Chinook population may be divided into a native Tule stock population and a Bright stock population, which is thought to have descended from hatchery-origin strays from Upriver Bright programs. Abundance and biological information are reported for the Bright and Tule stock populations as well as reported separately and combined for the Wind and Little White Salmon subpopulations.

Abundance estimates were based on PCE methods for both subpopulations of the Upper Gorge fall Chinook population. The Wind subpopulation abundance was estimated using a PCE factor from a 1964 carcass tagging study based on the JS model. The expansion factor for this subpopulation, based on a combined peak count of live and dead Chinook salmon, was 1.19 (95% CI 1.13-1.28) (Rawding et al. 2014). For the Little White Salmon subpopulation, a PCE factor was developed based on a 1966 carcass tagging study based on the JS model. The 1966 expansion factor for this population, based only on carcasses only, is 3.79 (95% CI 2.92-5.18) (Rawding et al. 2019).

The abundance for the Upper Gorge Tule fall Chinook population was estimated to be 916 adults (95% CI 794-1,101). The proportion of hatchery-origin fish was 68.8% and age-3 hatchery-origin fish comprised over half of the adult Tule stock return for this population. The estimated abundance for the Wind Tule stock Chinook subpopulation was 407 adults (95% CI 383-436). Based on adipose fin clips and adjusting for unmarked hatchery-origin adults using Spring Creek National Fish Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the

Wind Tule stock Chinook subpopulation was 83.7% and greater than 80% of the marked adults were age-3. The estimated abundance for the Little White Salmon Tule stock Chinook subpopulation was 509 adults (95% CI 392-694). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Spring Creek National Fish Hatchery’s mass mark rates, the proportion of hatchery-origin spawners for the Little White Salmon Tule stock Chinook subpopulation was approximately 57%. Greater than 83% of the hatchery-origin adults were age-3 while natural-origin adults were predominately age-4 (75.7%). Upper Gorge Tule stock Chinook population abundance estimates and proportions by origin, sex, and age can be found in Tables 76-78. Wind Tule stock Chinook subpopulation abundance estimates and proportions by origin, sex, and age are found in Tables 79-81. Little White Salmon Tule stock Chinook subpopulation abundance and proportions by origin, sex, and age estimates are found in Tables 82-84.

The estimated abundance for the Upper Gorge Bright stock Chinook population (Wind and Little White Salmon Bright stock subpopulations combined) was 593 adults (95% CI 469-788). Adults from this population were equally comprised of age-3 and age-4. We estimated 54 adults (95% CI 51-58) in the Wind Bright stock subpopulation. Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Little White Salmon National Fish Hatchery’s mass mark rates, the proportion of hatchery-origin spawners was 40.8% and most adults were age-3 and age-4. For the Little White Salmon Bright stock Chinook subpopulation, we estimated 539 adults (95% CI 415-736). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Little White Salmon National Fish Hatchery’s mass mark rates, the proportion of hatchery-origin spawners was 69.1% and most adults were age-4. Upper Gorge Bright stock Chinook population abundance estimates and proportions by origin, sex, and age can be found in Tables 85-87. Wind Bright stock subpopulation abundance estimates and proportions by origin, sex, and age are found in Tables 88-90. Little White Salmon Bright stock subpopulation abundance and proportions by origin, sex, and age estimates are found in Tables 91-93.

Table 76. Estimates of abundance, including sex- and origin-specific estimates, for the adult Upper Gorge Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	916	79	794	904	1,101
Males	363	41	293	360	455
Females	552	56	461	546	681
HOS	629	53	542	623	750
NOS	286	43	214	282	384
Marked	605	51	522	600	722
Unmarked	310	44	237	305	410

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 77. Estimates of abundance by age and origin for the adult Upper Gorge Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	514	48	433	510	621
HOS Age-4	114	20	79	113	158
HOS Age-5	1	2	0	0	6
HOS Age-6	1	2	0	0	5
NOS Age-3	92	21	56	90	136
NOS Age-4	189	34	132	185	267
NOS Age-5	5	5	0	4	17
NOS Age-6	1	2	0	0	6

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 78. Estimates of proportions of the adult Upper Gorge Tule fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.397	0.030	0.340	0.396	0.457
pFemale	0.603	0.030	0.543	0.604	0.660
pHOS	0.688	0.031	0.626	0.689	0.747
pNOS	0.312	0.031	0.253	0.311	0.374
pMark	0.662	0.030	0.602	0.663	0.719
pUnmark	0.338	0.030	0.281	0.338	0.398
p Age-3 HOS	0.817	0.029	0.756	0.818	0.870
p Age-4 HOS	0.181	0.029	0.128	0.180	0.242
p Age-5 HOS	0.001	0.003	0.000	0.000	0.009
p Age-6 HOS	0.001	0.003	0.000	0.000	0.008
p Age-3 NOS	0.321	0.057	0.213	0.320	0.434
p Age-4 NOS	0.660	0.058	0.545	0.660	0.770
p Age-5 NOS	0.017	0.015	0.001	0.012	0.057
p Age-6 NOS	0.003	0.006	0.000	0.000	0.019

Table 79. Estimates of abundance, including sex- and origin-specific estimates, for the adult Wind Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	407	14	383	405	436
Males	168	18	134	167	204
Females	239	19	203	239	277
HOS	340	18	305	340	377
NOS	66	14	40	65	96
Marked	328	17	294	327	363
Unmarked	79	14	54	78	108

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 80. Estimates of abundance by age and origin for the adult Wind Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	273	20	235	273	313
HOS Age-4	66	13	42	66	95
HOS Age-5	0	1	0	0	3
HOS Age-6	0	1	0	0	3
NOS Age-3	43	12	22	42	69
NOS Age-4	23	9	9	22	42
NOS Age-5	0	1	0	0	3
NOS Age-6	0	1	0	0	3

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 81. Estimates of proportions of the 2012 adult Wind Tule fall Chinook subpopulation by sex and origin, and proportions of each origin by age. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.412	0.042	0.331	0.412	0.495
pFemale	0.588	0.042	0.505	0.588	0.669
pHOS	0.837	0.035	0.766	0.839	0.901
pNOS	0.163	0.035	0.099	0.161	0.234
pMark	0.806	0.033	0.737	0.807	0.866
pUnmark	0.194	0.033	0.134	0.193	0.263
p Age-3 HOS	0.803	0.038	0.722	0.805	0.873
p Age-4 HOS	0.195	0.038	0.126	0.194	0.275
p Age-5 HOS	0.001	0.003	0.000	0.000	0.009
p Age-6 HOS	0.001	0.003	0.000	0.000	0.009
p Age-3 NOS	0.648	0.110	0.419	0.653	0.848
p Age-4 NOS	0.343	0.109	0.146	0.337	0.571
p Age-5 NOS	0.005	0.015	0.000	0.000	0.046
p Age-6 NOS	0.005	0.015	0.000	0.000	0.047

Table 82. Estimates of abundance, including sex- and origin-specific estimates, for the adult Little White Salmon Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	509	77	392	497	694
Males	196	37	136	192	280
Females	313	53	231	306	437
HOS	289	50	210	282	406
NOS	220	41	154	215	314
Marked	278	48	202	272	391
Unmarked	231	42	164	226	327

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 83. Estimates of abundance by age and origin for the adult Little White Salmon Tule fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	240	43	171	235	342
HOS Age-4	48	15	23	46	83
HOS Age-5	0	1	0	0	4
HOS Age-6	0	1	0	0	4
NOS Age-3	49	17	22	47	86
NOS Age-4	166	33	113	162	242
NOS Age-5	4	4	0	3	16
NOS Age-6	0	1	0	0	4

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 84. Estimates of proportions of the adult Little White Salmon Tule fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.385	0.043	0.302	0.384	0.469
pFemale	0.615	0.043	0.531	0.616	0.698
pHOS	0.567	0.045	0.478	0.568	0.656
pNOS	0.433	0.045	0.344	0.432	0.522
pMark	0.546	0.043	0.460	0.546	0.631
pUnmark	0.454	0.043	0.369	0.454	0.540
p Age-3 HOS	0.832	0.045	0.736	0.836	0.912
p Age-4 HOS	0.165	0.045	0.086	0.161	0.260
p Age-5 HOS	0.002	0.005	0.000	0.000	0.015
p Age-6 HOS	0.001	0.004	0.000	0.000	0.013
p Age-3 NOS	0.221	0.060	0.112	0.218	0.346
p Age-4 NOS	0.757	0.062	0.630	0.759	0.870
p Age-5 NOS	0.020	0.019	0.001	0.015	0.071
p Age-6 NOS	0.002	0.006	0.000	0.000	0.018

Table 85. Estimates of abundance, including sex- and origin-specific estimates, for the adult Upper Gorge Bright fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	593	82	469	580	788
Males	258	51	174	253	375
Females	335	59	238	329	470
HOS	395	67	287	387	549
NOS	198	43	125	194	296
Marked	388	66	282	381	541
Unmarked	205	44	132	201	303

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 86. Estimates of abundance by age and origin for the adult Upper Gorge Bright fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	172	42	102	168	268
HOS Age-4	206	48	127	202	314
HOS Age-5	15	13	2	12	48
HOS Age-6	1	3	0	0	11
NOS Age-3	78	27	35	74	141
NOS Age-4	60	23	26	56	115
NOS Age-5	59	25	21	56	119
NOS Age-6	1	4	0	0	11

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 87. Estimates of proportions of the adult Upper Gorge Bright fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.436	0.061	0.318	0.435	0.558
pFemale	0.564	0.061	0.443	0.565	0.682
pHOS	0.665	0.059	0.544	0.667	0.774
pNOS	0.335	0.059	0.226	0.333	0.456
pMark	0.654	0.058	0.535	0.656	0.761
pUnmark	0.346	0.058	0.239	0.344	0.465
p Age-3 HOS	0.436	0.078	0.287	0.435	0.593
p Age-4 HOS	0.523	0.079	0.366	0.523	0.675
p Age-5 HOS	0.039	0.030	0.005	0.030	0.117
p Age-6 HOS	0.003	0.009	0.000	0.000	0.027
p Age-3 NOS	0.393	0.105	0.201	0.388	0.609
p Age-4 NOS	0.304	0.097	0.141	0.295	0.515
p Age-5 NOS	0.298	0.101	0.122	0.291	0.508
p Age-6 NOS	0.006	0.017	0.000	0.000	0.054

Table 88. Estimates of abundance, including sex- and origin-specific estimates, for the adult Wind Bright fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	54	2	51	54	58
Males	24	4	18	24	31
Females	30	4	23	30	37
HOS	22	4	15	22	29
NOS	32	4	25	32	39
Marked	22	3	15	21	28
Unmarked	32	4	25	32	39

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 89. Estimates of abundance by age and origin for the adult Wind Bright fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	11	3	6	10	17
HOS Age-4	9	3	4	9	15
HOS Age-5	2	2	0	2	6
HOS Age-6	0	0	0	0	1
NOS Age-3	9	3	5	9	15
NOS Age-4	19	3	12	19	26
NOS Age-5	4	2	1	3	8
NOS Age-6	0	0	0	0	1

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 90. Estimates of proportions of the adult Wind Bright fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.451	0.063	0.328	0.450	0.576
pFemale	0.549	0.063	0.424	0.550	0.672
pHOS	0.408	0.064	0.287	0.407	0.534
pNOS	0.592	0.064	0.466	0.594	0.713
pMark	0.400	0.062	0.281	0.399	0.523
pUnmark	0.600	0.062	0.477	0.601	0.719
p Age-3 HOS	0.487	0.103	0.287	0.487	0.688
p Age-4 HOS	0.407	0.101	0.219	0.405	0.614
p Age-5 HOS	0.102	0.065	0.014	0.088	0.262
p Age-6 HOS	0.005	0.014	0.000	0.000	0.044
p Age-3 NOS	0.298	0.077	0.158	0.295	0.459
p Age-4 NOS	0.585	0.084	0.418	0.586	0.744
p Age-5 NOS	0.114	0.055	0.028	0.106	0.242
p Age-6 NOS	0.003	0.009	0.000	0.000	0.029

Table 91. Estimates of abundance, including sex- and origin-specific estimates, for the adult Little White Salmon Bright fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	539	82	415	526	736
Males	234	51	150	229	351
Females	305	59	209	299	440
HOS	373	67	265	365	527
NOS	167	43	94	162	264
Marked	367	66	261	359	520
Unmarked	173	43	100	168	270

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 92. Estimates of abundance by age and origin for the adult Little White Salmon Bright fall Chinook subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	161	42	92	157	257
HOS Age-4	197	48	119	193	305
HOS Age-5	13	12	0	9	46
HOS Age-6	1	3	0	0	10
NOS Age-3	68	27	26	65	132
NOS Age-4	41	23	8	38	95
NOS Age-5	56	25	17	52	115
NOS Age-6	1	4	0	0	11

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 93. Estimates of proportions of the adult Little White Salmon Bright fall Chinook subpopulation by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.434	0.067	0.305	0.434	0.568
pFemale	0.566	0.067	0.432	0.566	0.695
pHOS	0.691	0.065	0.558	0.693	0.810
pNOS	0.309	0.065	0.190	0.307	0.442
pMark	0.680	0.064	0.549	0.682	0.797
pUnmark	0.320	0.064	0.203	0.318	0.451
p Age-3 HOS	0.433	0.083	0.276	0.432	0.599
p Age-4 HOS	0.530	0.084	0.363	0.530	0.690
p Age-5 HOS	0.035	0.032	0.001	0.025	0.118
p Age-6 HOS	0.003	0.009	0.000	0.000	0.028
p Age-3 NOS	0.412	0.126	0.185	0.407	0.669
p Age-4 NOS	0.247	0.114	0.057	0.235	0.499
p Age-5 NOS	0.335	0.121	0.125	0.328	0.585
p Age-6 NOS	0.006	0.021	0.000	0.000	0.064

White Salmon Population

The White Salmon fall Chinook population may be divided into a native Tule stock population and a Bright stock population that is thought to have descended from hatchery-origin strays from Upriver Bright stock programs. Abundance and biological information are reported separately for Bright and Tule stock populations. For AUC estimates, October 31 was used as the last date for Tule stock live counts. After October 31, we assumed all live counts were Bright stock. In general, the same date cutoff was used for carcasses. However, since carcasses can persist in the system for several weeks, surveyors made a call on whether the carcass was a Tule or Bright stock.

Abundance estimates were based on PCE methods. The White Salmon population was estimated using a PCE factor from a 1989 Bright stock carcass tagging study based on the JS model. The expansion factor generated from this study, based on a combined peak count of live and dead Chinook salmon, was 2.42 (95% CI 2.28-2.54) (Rawding et al. 2019). This expansion factor was used for both the Tule and Bright stock subpopulations in 2012.

The estimated abundance for the White Salmon Tule stock Chinook population was 553 adults (95% CI 511-597). Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Spring Creek National Fish Hatchery’s mass mark rates, the proportion of hatchery-origin spawners was low (6.5%) when compared to other LCR Tule stock populations. White Salmon Tule stock Chinook abundance estimates and proportions by origin, sex, and age can be found in Tables 94-96.

The estimated abundance for the White Salmon Bright stock Chinook population was 1,031 adults (95% CI 952-1,113). This is almost twice the Tule stock population estimate of 553 adults. Based on adipose fin clips and adjusting for unmarked hatchery-origin fish using Little White Salmon National Fish Hatchery's mass mark rates, the proportion of hatchery-origin spawners was 33.7% and most adults were age-4. White Salmon Bright stock Chinook population abundance estimates and proportions by origin, sex, and age can be found in Tables 97-99.

Table 94. Estimates of abundance, including sex- and origin-specific estimates, for the adult White Salmon Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	553	22	511	553	597
Males	125	21	87	124	169
Females	428	27	375	428	480
HOS	36	12	16	35	64
NOS	517	24	470	517	564
Marked	35	12	15	33	62
Unmarked	518	24	472	518	565

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 95. Estimates of abundance by age and origin for the adult White Salmon Tule fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	30	11	12	28	55
HOS Age-4	5	5	0	4	19
HOS Age-5	0	2	0	0	5
HOS Age-6	0	1	0	0	4
NOS Age-3	129	22	90	129	174
NOS Age-4	373	28	319	373	427
NOS Age-5	14	8	3	13	33
NOS Age-6	0	1	0	0	4

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 96. Estimates of proportions of the adult White Salmon Tule fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.226	0.037	0.159	0.225	0.304
pFemale	0.774	0.037	0.696	0.775	0.841
pHOS	0.065	0.022	0.029	0.063	0.115
pNOS	0.935	0.022	0.885	0.937	0.972
pMark	0.062	0.021	0.027	0.060	0.111
pUnmark	0.938	0.021	0.889	0.940	0.973
p Age-3 HOS	0.825	0.132	0.506	0.854	0.990
p Age-4 HOS	0.150	0.123	0.006	0.118	0.457
p Age-5 HOS	0.013	0.039	0.000	0.000	0.129
p Age-6 HOS	0.013	0.037	0.000	0.000	0.122
p Age-3 NOS	0.250	0.041	0.176	0.249	0.333
p Age-4 NOS	0.722	0.042	0.637	0.723	0.800
p Age-5 NOS	0.027	0.015	0.006	0.024	0.063
p Age-6 NOS	0.001	0.003	0.000	0.000	0.008

Table 97. Estimates of abundance, including sex- and origin-specific estimates, for the adult White Salmon Bright fall Chinook population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Abundance	1,031	40	952	1,030	1,113
Males	246	37	178	245	323
Females	785	47	693	785	878
HOS	347	43	267	346	436
NOS	684	49	589	684	781
Marked	334	42	257	334	421
Unmarked	696	48	604	696	792

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 98. Estimates of abundance by age and origin for the adult White Salmon Bright fall Chinook population, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
HOS Age-3	59	20	26	56	104
HOS Age-4	215	36	150	213	292
HOS Age-5	73	23	35	71	124
HOS Age-6	1	2	0	0	7
NOS Age-3	64	21	30	62	110
NOS Age-4	465	46	378	464	557
NOS Age-5	155	32	98	153	221
NOS Age-6	1	2	0	0	7

The sum of abundance by mark status, sex, and age may not equal the abundance estimate due to rounding errors.

Table 99. Estimates of proportions of the adult White Salmon Bright fall Chinook population by sex and origin, and proportions of each origin by age, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
pMale	0.239	0.035	0.174	0.238	0.310
pFemale	0.761	0.035	0.690	0.762	0.826
pHOS	0.337	0.040	0.261	0.336	0.417
pNOS	0.663	0.040	0.583	0.665	0.739
pMark	0.324	0.038	0.252	0.324	0.403
pUnmark	0.676	0.038	0.597	0.677	0.748
p Age-3 HOS	0.169	0.054	0.079	0.164	0.288
p Age-4 HOS	0.619	0.070	0.478	0.620	0.752
p Age-5 HOS	0.210	0.060	0.105	0.206	0.338
p Age-6 HOS	0.002	0.006	0.000	0.000	0.020
p Age-3 NOS	0.093	0.029	0.044	0.090	0.157
p Age-4 NOS	0.680	0.047	0.584	0.680	0.770
p Age-5 NOS	0.226	0.043	0.147	0.225	0.315
p Age-6 NOS	0.001	0.003	0.000	0.000	0.010

Population Summary

Individual population estimates were summed to provide a LCR ESU-scale estimate for Washington populations of Tule, North Fork Lewis Brights, Rogue River Brights, and Bonneville (BON) Pool Brights stocks. We estimated 22,963 adult Tule stock Chinook salmon in the WA LCR ESU (Table 100). The proportion of natural-origin Tule stock was estimated to be 32.5%, which yields an estimate of 7,362 hatchery-origin Tules. The estimate of North Fork

Lewis Brights stock was 8,143 (Shane Hawkins, personal communication, WDFW). The estimate for BON Pool Brights stock in the WA portion of the LCR ESU totaled 1,624, of which 45.7% were hatchery-origin (Table 101).

Table 100. Abundance and origin estimates of adult Tule stock Chinook salmon populations in the Washington portion of the LCR ESU, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
WA Adult Tules	22,963	1,006	20,991	NA	24,936
WA HOS Tules	15,502	939	13,661	NA	17,343
WA NOS Tules	7,362	139	7,090	NA	7,634
Marked WA Tules	15,371	931	13,546	NA	17,196
Unmarked WA Tules	7,495	142	7,216	NA	7,774
pHOS WA Tules	0.675	0.051	0.576	NA	0.774
pNOS WA Tules	0.325	0.015	0.295	NA	0.355
Prop Of Marked WA Tules	0.669	0.050	0.571	NA	0.768
Prop Of Unmarked WA Tules	0.331	0.016	0.300	NA	0.361

**includes Cowlitz and North Fork Lewis Tule estimate from Chris Gleizes and Shane Hawkins, personal communication, WDFW.*

Table 101. Abundance and origin estimates of adult Bright run Chinook salmon populations in the Washington portion of the LCR ESU, 2012. Hatchery- (HOS) and natural-origin (NOS) spawner abundance estimates account for tag loss and clipping rates at contributing hatcheries, whereas marked and unmarked estimates are based solely on the presence of adipose fin clips and CWTs.

Parameter	Mean	SD	2.50%	Median	97.50%
BON Pool Brights	1,624	91	1,445	NA	1,803
WA HOS BON Pool Brights	742	80	585	NA	898
WA NOS BON Pool Brights	882	66	754	NA	1,011
Marked WA BON Pool Brights	723	78	570	NA	875
Unmarked WA BON Brights	901	65	774	NA	1,028
pHOS WA BON Brights	0.457	0.055	0.348	NA	0.565
pNOS WA BON Brights	0.543	0.051	0.444	NA	0.643
Prop Of Marked WA BON Brights	0.445	0.054	0.339	NA	0.551
Prop Of Unmarked WA BON Brights	0.555	0.051	0.456	NA	0.654
Rogue River Brights in Grays/Elochoman	99	42	NA	NA	NA
Lewis/Cowlitz River Brights	8,849	NA	NA	NA	NA

The largest unmarked populations of Tule stock Chinook salmon were found in the upper Cowlitz (1,946) and Lewis (excluding North Fork Lewis) (650) while the smallest unmarked populations were found in the Mill (MAG) (24), Grays/Chinook (43), and Elochoman/Skamokawa (65) populations (Figure 3).

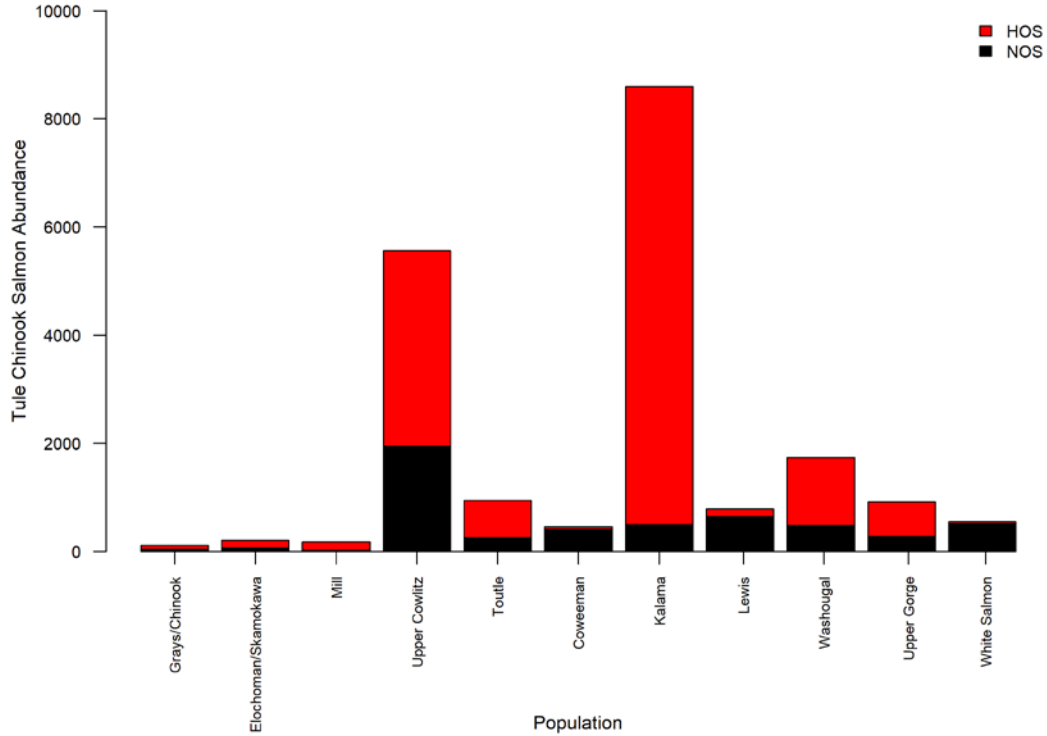


Figure 3. Tule Fall Chinook salmon Abundance by Origin and Population, 2012. The proportion of hatchery-origin spawners in Tule stock Chinook populations was lowest in the White Salmon (6.5%), Coweeman (11.0%), and Lewis (excluding North Fork Lewis) (17.9%) populations while the Kalama (94.2%) and Mill (MAG) (87.1%) populations had the greatest pHOS values (Figure 4).

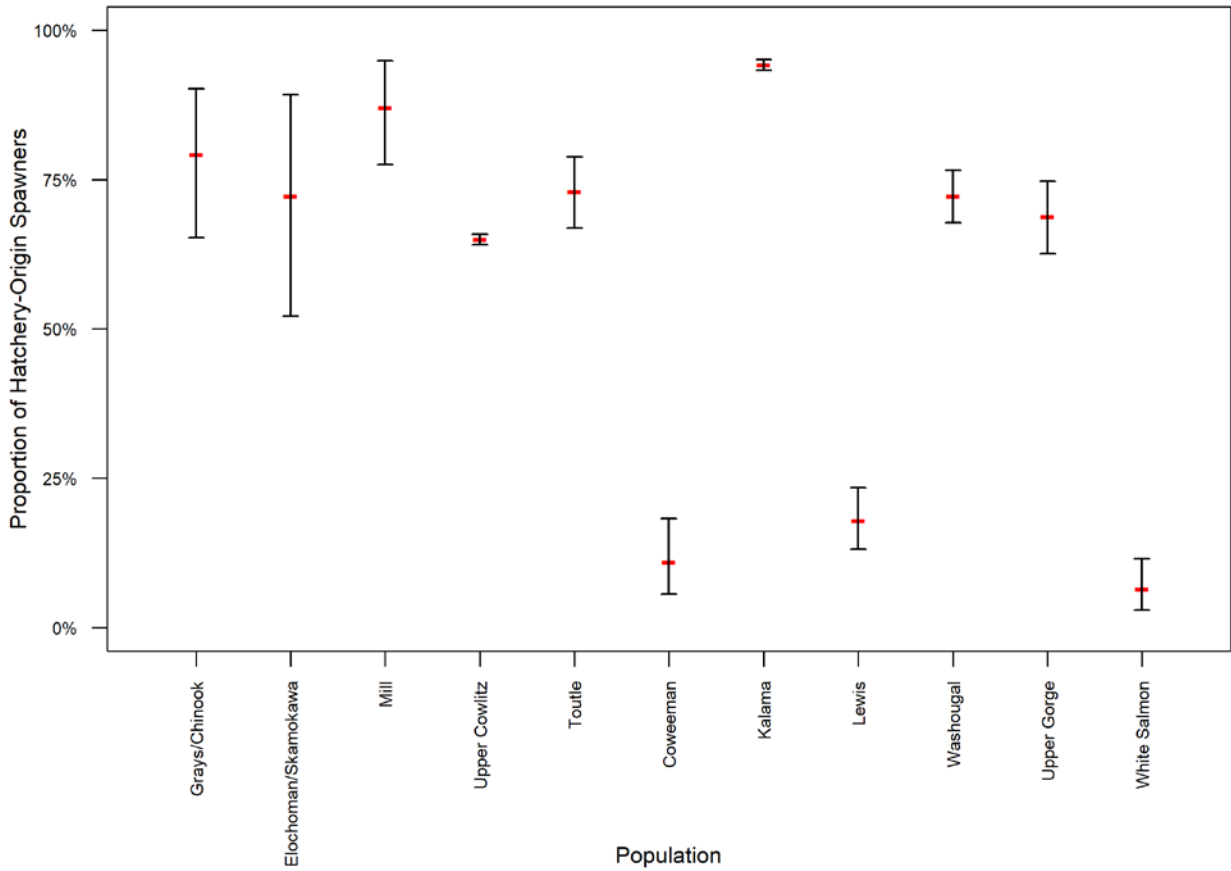


Figure 4. Proportion of Hatchery-Origin Spawners by Fall Chinook Salmon Population (Tule stock only), 2012.

Hatchery-origin Rogue River Brights are included in the Grays River pHOS calculation due to a lack of temporal separation between tule stocks and Rogue River Bright stocks.

Timing

The cumulative timing for Tule stock Chinook subpopulations are shown in Figure 5.

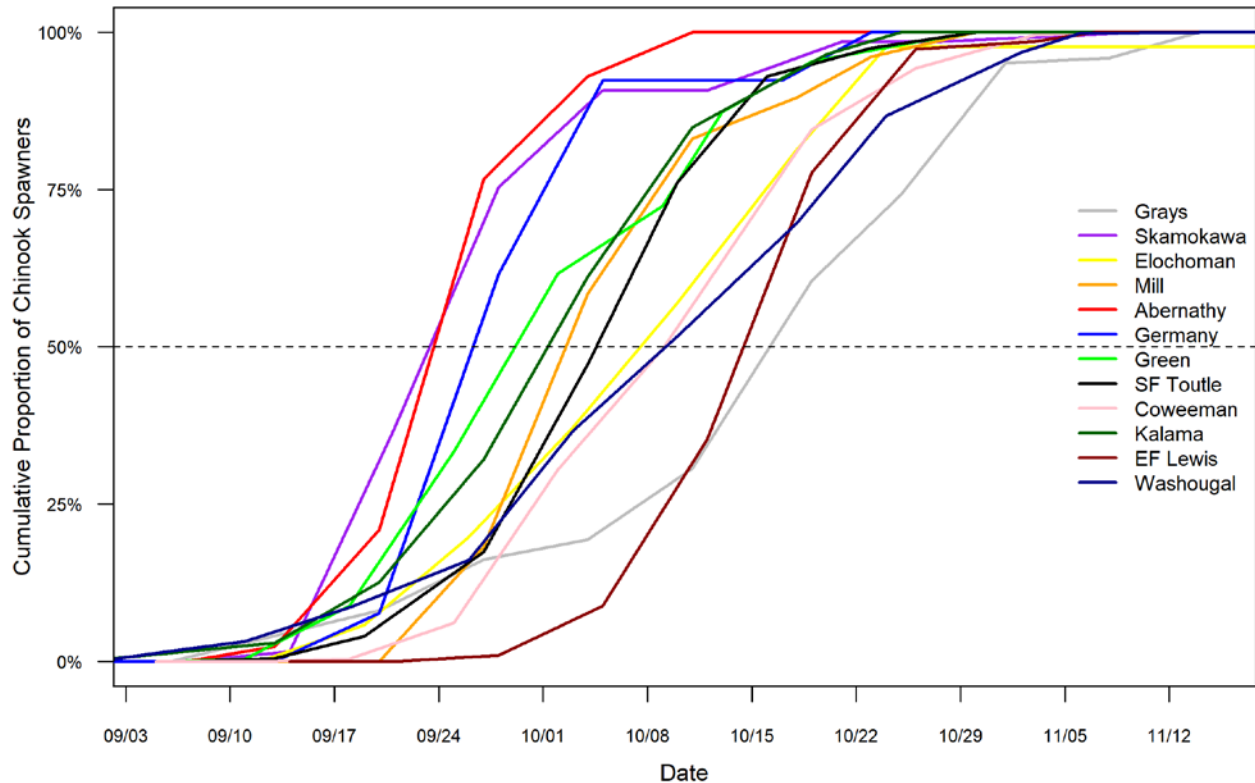


Figure 5. Tule stock fall Chinook salmon spawn timing for Washington populations within the Coast and Cascade strata based on period (weekly) counts of Chinook salmon classified as spawners, 2012.

CWT Program

The Chinook salmon CWT recoveries in the fall of 2012 were uploaded to the RMIS system during 2013-14. The uploaded data include: 1) freshwater sport fishery recoveries, 2) hatchery facility recoveries, 3) trap and weir recoveries, and 4) spawning ground recoveries.

There were no CWT recoveries made during stream surveys in the Elochoman, Mill, Abernathy, Germany, Coweeman, and Green fall Chinook subpopulations (Table 102). The lack of recoveries in these subpopulations was likely due to low overall Chinook salmon abundance in the Elochoman, Mill, Abernathy, and Germany subpopulations, a nearly fish-tight weir on the Lower Green River that removed most, if not all, of the hatchery-origin Chinook before they reached the spawning grounds, and the Coweeman population had low proportions of hatchery-origin fish present in the population. For CWT released from Washington hatcheries, most were recovered in the basin from which they were released. However, some hatchery programs had quite a few out-of-basin CWT recoveries (e.g. CWT released into the Kalama basin were recovered in four different subpopulations outside of the basin). CWTs released from the Little White Salmon Hatchery had the largest number of spawning ground survey recoveries with a total of 62 recovered. CWT fish released from Oregon hatcheries were generally recovered at a low rate in at fall Chinook management weirs and spawning ground surveys in Washington, with

the largest number of recoveries coming from the South Fork Klaskanine Hatchery. CWT data for fisheries and carcass recoveries are presented in annual reports for missing production groups (e.g. Harlan 2014).

Table 102. Unexpanded CWT recoveries by population and hatchery of origin for Chinook salmon, 2012. Gray boxes indicate the CWTs were recovered in the same basin as released. CWTs released from Spring Cr. Hatchery and recovered in the White Salmon were considered in-basin recoveries.

		Release Basin												Grand Total
Recovery Basin	Subpopulation	North Fork Klask H.	South Fork Klask H.	Big Cr H.	Cowlitz H.	N. Toutle H.	Kalama Falls/Fallert Cr. H.	North Fork Lewis Wild	Wash H.	Bonn H.	Little WS H.	Spring Cr H.	Out of ESU	
		Grays	0	2	0	0	0	0	0	0	0	0	0	0
	Skamokawa	1	0	0	0	0	0	0	0	0	0	0	0	1
	Elochoman	0	0	0	0	0	0	0	0	0	0	0	0	0
	Mill	0	0	0	0	0	0	0	0	0	0	0	0	0
	Abernathy	0	0	0	0	0	0	0	0	0	0	0	0	0
	Germany	0	0	0	0	0	0	0	0	0	0	0	0	0
	Lower Cowlitz	0	0	0	5	0	2	1	0	0	0	0	0	8
	Coweeman	0	0	0	0	0	0	0	0	0	0	0	0	0
	Green	0	0	0	0	0	0	0	0	0	0	0	0	0
	South Fork Toutle	0	0	0	0	0	1	0	0	0	0	0	0	1
	Kalama	0	0	0	0	0	34	0	0	0	0	0	0	34
	North Fork Lewis	0	0	1	0	1	5	60	1	0	0	0	0	68
	Cedar	0	0	0	0	0	0	0	0	0	0	0	0	0
	East Fork Lewis	0	0	0	0	0	1	0	0	0	0	0	0	1
	Washougal	0	0	0	0	0	0	0	3	0	1	0	0	4
	Wind	0	0	0	0	0	0	0	0	0	24	0	0	24
	Little White Salmon	0	0	0	0	0	0	0	0	1	37	1	1	40
	White Salmon	0	0	0	0	0	0	0	0	0	0	1	0	1
	TOTAL	1	2	1	5	1	43	61	4	1	62	2	1	184
	% Out of Basin	100%	100%	0%	0%	100%	21%	2%	25%	100%	40%	50%	100%	

Discussion

This is the third consecutive year we completed a comprehensive analysis of fall Chinook salmon returning to Washington's portion of the Lower Columbia River ESU. The programs study design prioritized the use of weir census and mark-recapture estimates when possible, followed by AUC and redd-based estimates, and PCE when other methods were not possible. We adopted a Bayesian approach, but with vague priors, which lets the results be driven by the data. We used a combination of frequentist and Bayesian hypothesis testing to identify mark-recapture models that met the required assumptions for unbiased estimates. We developed statistical methods to estimate the uncertainty in the abundance estimates and the proportions of natural- and hatchery-origin spawners by age.

Weir Estimates

Although the use of weirs in this study was primarily for broodstock collection and management purposes, such as limiting the number of hatchery fish on spawning grounds, in some cases the weirs were able to provide a census or very precise estimates of the Chinook salmon runs. When possible, we subtracted harvest and pre-spawn mortality estimates from the abundance estimate to provide an estimate of the number of adult Chinook salmon spawners. We did not have an estimate of the pre-spawn mortality or the number of transported fish that fell back and did not spawn in the Tilton and Upper Cowlitz/Cispus rivers. Therefore, in these cases, it is likely we overestimated the number of spawners.

We were not successful in operating weirs on the Washougal and Grays rivers to obtain abundance estimates of Chinook salmon. The run and spawn timing of the Chinook salmon population in the Washougal is later than many other LCR populations (Figure 5) and operating the weir later in the season makes it more susceptible to freshets and, thus, more challenging. On the Grays River, we were able to successfully operate the weir during the Tule stock return and spawning period. However, Rogue River Bright stock Chinook salmon from the Oregon's Selective Area Fisheries Enhancement (SAFE) program have a broader run timing and stray into the Grays basin. As is the case on the Washougal River, our ability to successfully operate a weir on the Grays River after mid-October is challenging. However, both of these weirs were successful at reducing the proportion of hatchery-origin spawners, which was their primary purpose.

Closed Population Estimates

We developed closed population estimates for adult Chinook salmon in the Green, Elochoman, and Coweeman rivers. Using the "pooled" Petersen model, the estimate for Chinook salmon passing the weir site was different from the actual weir counts at each of the three weirs. Since our estimates of abundance are adjusted by observed pre-spawning mortality rates, our reported abundance estimate is less than the pooled Petersen estimate and the weir count at the Elochoman and Green weirs. Assuming the pooled Petersen model estimate is correct, there were 134 adult Chinook salmon that passed the weir un-sampled, or arrived after the weir had been removed, on the Coweeman, 36 on the Green, and 57 on the Elochoman. Weir capture efficiencies estimates are reported in the appendix of this report.

Schwarz and Taylor (1998) indicate that the following assumptions must be met to provide a consistent estimate of abundance: 1) Tag Loss - there is no mark loss, 2) Handling Mortality - there are no marking effects, 3) Tag Reporting - all tagged and untagged fish are correctly identified and enumerated, 4) Closure - the population is closed, and 5) Equal Capture - all fish in the population have the same probability of being tagged; or all fish have the same probability of being captured in the second sample; or marked fish mix uniformly with unmarked fish.

We addressed tag loss by adding a permanent secondary mark, which was a shaped punch applied to the operculum that was rotated weekly. All Chinook salmon were handled carefully to minimize mortality, but even if it did occur it did not affect our results since the population was closed and the estimate of abundance was at the time of tagging. All surveyors were trained and carefully inspected all carcasses for tags, so we believe there was high probability that all tagged and untagged fish were correctly identified and enumerated. The weirs and stream surveys were operated/conducted over the entire migration and spawning period and carcass recoveries were spatially representative, so the closure assumptions was met. We conducted hypothesis testing for the equal capture assumption. The results from our GLM indicated that categorical size was a factor in the recovery probably of fish tagged at the weir and later recovered as carcasses on spawning ground surveys or on the weir structure. In all three cases, approximately 27% of the tagged large fish (≥ 80 cm) were recovered while 12-16% of the tagged small (< 80 cm) fish were recovered. The null model was equally supported in the Elochoman basin ($\Delta AICc = 0.7$) so we used that to generate our final estimate. For the Coweeman and Green population estimates, the null model was marginally supported ($\Delta AICc = 3.3$) and not supported ($\Delta AICc = 7.7$), respectively. In both of these cases, we stratified our dataset into small and large fish and retested the equal capture of assumption using GLM. By stratifying, the null model was supported for the small and large fish group for each basin. We generated estimates of small and large fish then combined two groups to generate a combined, or overall, adult estimate. The combined estimate was then compared to the estimate generated with the null model and in both instances they were not significant different from one another. Therefore, we choose to report the estimates generated with the null model. In these situations, there is a bias/precision tradeoff, and in these cases, it made sense to not stratify by large and small adults.

Open Population Estimates

Carcass tagging studies were executed in several basins (Grays, Skamokawa, Mill, Abernathy, Germany, and Washougal) in 2012 with the intent of using the JS model to estimate abundance. However, an insufficient number of marks and/or recaptures prevented us from using this method for any of the above basins. In mark-recapture experiments, five to ten marked animals should be recovered per release group in order to produce unbiased estimates (Schwarz and Taylor 1998). Additionally, Seber (1982) recommends more than nine recaptures per recovery period for unbiased estimates of open populations. The low abundance of returning Chinook salmon in these Lower Columbia River tributaries made achieving these benchmarks difficult. In the Grays and Washougal basins, removal of hatchery-origin fish at the weir sites further exacerbated this problem. When running the JS model, we were forced to pool multiple periods for each dataset to ensure at least one recapture per analysis period. While pooling allowed us to run the model, we believe there were likely heterogeneous capture probabilities between these periods and thus pooling in this instance would violate several assumptions of the model resulting in biased abundance estimates. All of the JS estimates generated for 2012 (not

reported) were substantially (35-62%) less than the redd-based or AUC estimates reported in this document.

PCE Estimates

WDFW has been using PCE factors for over 40 years because they are generally the most cost-effective method for estimating abundance. The PCE factors for the Wind, Little White Salmon, and White Salmon rivers were based on a single study for each subpopulation conducted 20 to 40 years ago. Except for some concerns regarding the GOF test in the JS abundance estimates from carcass tagging in the White Salmon population analysis, the PCE factors provide a statistical based population estimate. The following assumptions are used in the PCE method: 1) the peak day of abundance is known and the survey takes place on the peak, 2) if the entire spawning distribution is not surveyed, the proportion of fish used in the index or indices is similar to that of the years used to develop the PCE factor, 3) observer efficiency is similar in all years, and 4) the proportion of fish observed on the peak day is similar over all years. Since the expansion factors were generated at least 20 years ago, there are concerns about changes over time in proportions of spawners using the index reaches and proportion of carcasses and live fish present on the peak day due to changes in run timing. Additionally, these studies lack of replication to better estimate the variability in the PCE factors. Representative biological data and CWT recoveries often does not occur using the PCE method because it relies on a single, or a few surveys, near the peak. This is especially true when the population may be comprised of a mixture of different populations (i.e., hatchery & natural-origin) with different timing.

Redd and AUC Estimates

Concurrent observer efficiency and residence time studies are costly, so AUC abundance estimates often rely on observation efficiency and residence time from adjacent populations or from the same populations in other years. The use of these kinds of surrogate estimates in calculations of abundance should be carefully considered. Our intent was to generate concurrent census or mark-recapture estimates and periodic counts of spawners for several populations in 2012 to develop a year-specific ART for 2012. However, we believe our JS abundance estimates were biased due to sparse data, which resulted in pooling multiple periods in each of the datasets. We developed unbiased abundance estimates in the Elochoman, Coweeman, and Green basins using the closed population model, but we believe there may be a weir effect (migration delay) that is causing the ART to be biased low in these basins. As a result, applying ART from basins with weirs to basins without weirs may result in biased abundance estimates. Therefore, we chose to use the 2011 mean ART to develop 2012 AUC-based estimates. The 2011 ART value was based on concurrent mark-recapture estimates and periodic counts of adults classified as spawners in the Grays, Abernathy, Germany, and Washougal basins.

Since we had only one population in 2012 where we had concurrent mark-recapture estimates and a census count of unique redds (Coweeman), we used this dataset and seven previous redd and mark-recapture estimates on the Coweeman and East Fork Lewis fall Chinook populations to estimate a mean females per redd value for our 2012 redd-based estimates.

Recommendations

Over the last decade or so there has been a significant shift in the monitoring of fall Chinook salmon populations in the LCR to estimate VSP parameters (McElhany et al. 2000), and other important management indicators (Rawding and Rogers 2013). While great progress has been made in the LCR region, opportunities remain for improvement of estimates of fall Chinook salmon VSP and indicator parameters. Therefore, we recommend the following:

- 1.) Incorporating the results from the US Geological Surveys' radio tag study into future models to account for pre-spawn mortality and fall back in the Tilton and Upper Cowlitz/Cispus estimates.
- 2.) Change of weir locations (Washougal and Grays rivers) if possible to be more effective at trapping during fall freshets.
- 3.) As funding allows, transition away from PCE estimates on the Wind, Little White Salmon, and the Big White Salmon rivers and more representative sampling of carcasses for biological and CWT data.
- 4.) Continue to improve current modeling that estimates abundance and proportions by exploring covariates, hierarchical and space-state models.
- 5.) Expand the Chinook VSP monitoring program to ensure timing and georeferenced redd data are being collected for all subpopulations within the ESU.
- 6.) Redevelop the genetic baseline for the Lower Columbia River Tule stock Chinook salmon populations. The current baseline was developed shortly after the listing decision in the late 1990s. At that time, hatchery-origin fish could not be differentiated from natural-origin fish as mass marking had not begun. Additionally, egg takes were frequently transferred between LCR hatchery facilities. In general, the current genetic baseline shows a homogenized group across populations. It would be beneficial to redevelop with baseline with known natural-origin genetic collections across the different populations.

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**Lower Columbia River Fall Chinook Salmon Management Weirs –
2012 Summary and Evaluation**

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Introduction

Chinook salmon (*Oncorhynchus tshawytscha*) in the Lower Columbia River (LCR) Evolutionarily Significant Unit (ESU) were listed for protection under the Endangered Species Act (ESA) in 1999. In a recent five-year review, the National Oceanic and Atmospheric Administration (NOAA) Fisheries concluded that these fish should remain listed as threatened under the ESA (NOAA 2011). The LCR Chinook salmon ESU is composed of spring and fall populations split between the states of Washington and Oregon (Myers et al. 2006).

The Lower Columbia Fish Recovery Board's (LCFRB) Recovery Plan (2010) describes a recovery scenario for Lower Columbia River Chinook salmon. The plan identifies each population's role in recovery as a primary, contributing, or stabilizing population generally based on its baseline viability level and the desired recovery viability level. In 2007, the Hatchery Scientific Review Group's (HSRG) memo to the Columbia River Hatchery reform Steering Committee stated that one of the key factors limiting recovery of naturally spawning populations is interaction with hatchery-origin fish on the spawning grounds. The HSRG recommended management targets of less than 5% hatchery-origin spawners for primary populations and less than 10% hatchery-origin spawners for contributing populations without integrated hatchery programs. For populations with integrated hatchery programs, the goal is less than 30% hatchery-origin spawners for both primary and contributing populations (HSRG 2009).

In an effort to reduce the proportion of hatchery-origin spawners (pHOS) to meet HSRG standards and improve abundance estimates to meet NOAA's accuracy and precision guidelines, WDFW began installing and operating river-spanning weirs for the purposes of fall Chinook salmon management in LCR basins in 2008. This coincided with the phased implementation of LCR fall Chinook salmon mass marking (adipose clipping of all hatchery production) which began in 2005 and was fully realized in 2012 with all age-2-6 returns being marked. The Grays River Weir, installed in the fall of 2008, was the first LCR weir focused on fall Chinook salmon management. In the fall of 2009, the Elochoman River Weir was added, followed by the Green River Weir in the fall of 2010 and then the Coweeman and Washougal river weirs were added in the fall of the 2011.

This appendix reports on the weirs operated in the fall/winter of 2012 on the lower Grays, Elochoman, Green, Coweeman, and Washougal rivers. For all five weir locations, operations are primarily focused on fall Chinook salmon abundance monitoring, management, and broodstock collection (Green and Washougal river weirs only); however, information gathered from other returning salmonids (chum, coho, and steelhead) is also used to improve monitoring and management when possible.

At all five locations removal of known hatchery fish (identified by an adipose and/or left ventral (LV) fin clip) is utilized as a tool to promote recovery of wild stocks and meet management guidelines and objectives. The proportion of hatchery fish removed at each weir varies to meet management goals and objectives in the basin, and in some cases, is used to evaluate hatchery reform actions. WDFW annually conducts fall Chinook salmon spawning ground surveys on the Grays, Elochoman, Green, Coweeman, and Washougal rivers. Staff funded by these weir projects assist in these surveys to collect data necessary to estimate total abundance and proportions of hatchery- and natural-origin Chinook salmon, and evaluate weir effectiveness.

These projects have three objectives: 1) to complement existing adult salmonid monitoring efforts by developing accurate and precise estimates of total abundance, especially for fall Chinook salmon, 2) to promote recovery of fall Chinook salmon populations by meeting management guidelines/objectives for hatchery-origin Chinook salmon allowed to spawn naturally (pHOS), and 3) for collection of hatchery broodstock in the Green and Washougal rivers for WDFWs North Toutle and Washougal hatcheries, respectively.

Methods

Study area

The LCR Chinook salmon ESU extends from the mouth of the Columbia River up to, and including, the Big White Salmon River in Washington and Hood River in Oregon, and includes the Willamette River in Oregon up to Willamette Falls. Within this ESU, there are a total of 13 Washington populations, 8 Oregon populations, and 2 populations (Lower and Upper Gorge) that are split between the states. As of 2011, WDFW has installed temporary weirs in five of these populations in Washington for the purpose of fall Chinook salmon management: the Grays/Chinook population, the Elochoman/Skamokawa population, the Toutle Population (Green River), the Coweeman population, and the Washougal population (Figure 1). The Grays/Chinook population is comprised of two subpopulations: the Grays and Chinook, and is identified as a contributing population with pHOS target of less than 10%. Only one weir is operated within this population, located on the lower Grays River at rkm 16.50, and therefore only controlling pHOS within the Grays subpopulation. The Elochoman/Skamokawa population is also comprised of two subpopulations: the Elochoman and Skamokawa, and is identified as a primary population with a pHOS target of less than 5%. Only one weir is operated within this population, located on the lower Elochoman River at rkm 4.39, and is therefore only controlling pHOS within the Elochoman subpopulation. The Toutle population is made up of three subpopulations within the Toutle River basin: the Green River, SF Toutle River, and NF Toutle River. The Toutle population is classified as a primary population that includes an integrated hatchery program and therefore has a pHOS target of less than 30%. Only one weir is operated within this population, located on the lower Green River at rkm 0.64, and is therefore only controlling pHOS for the Green River subpopulation. The Coweeman population is made up of a single population and is classified as a primary population with a pHOS target of less than 5%. The weir is located on the lower Coweeman River at rkm 10.94. The Washougal population is made up of a single population and is classified as a primary population with a pHOS target of less than 5%. The weir is located on the lower Washougal River at rkm 19.15.

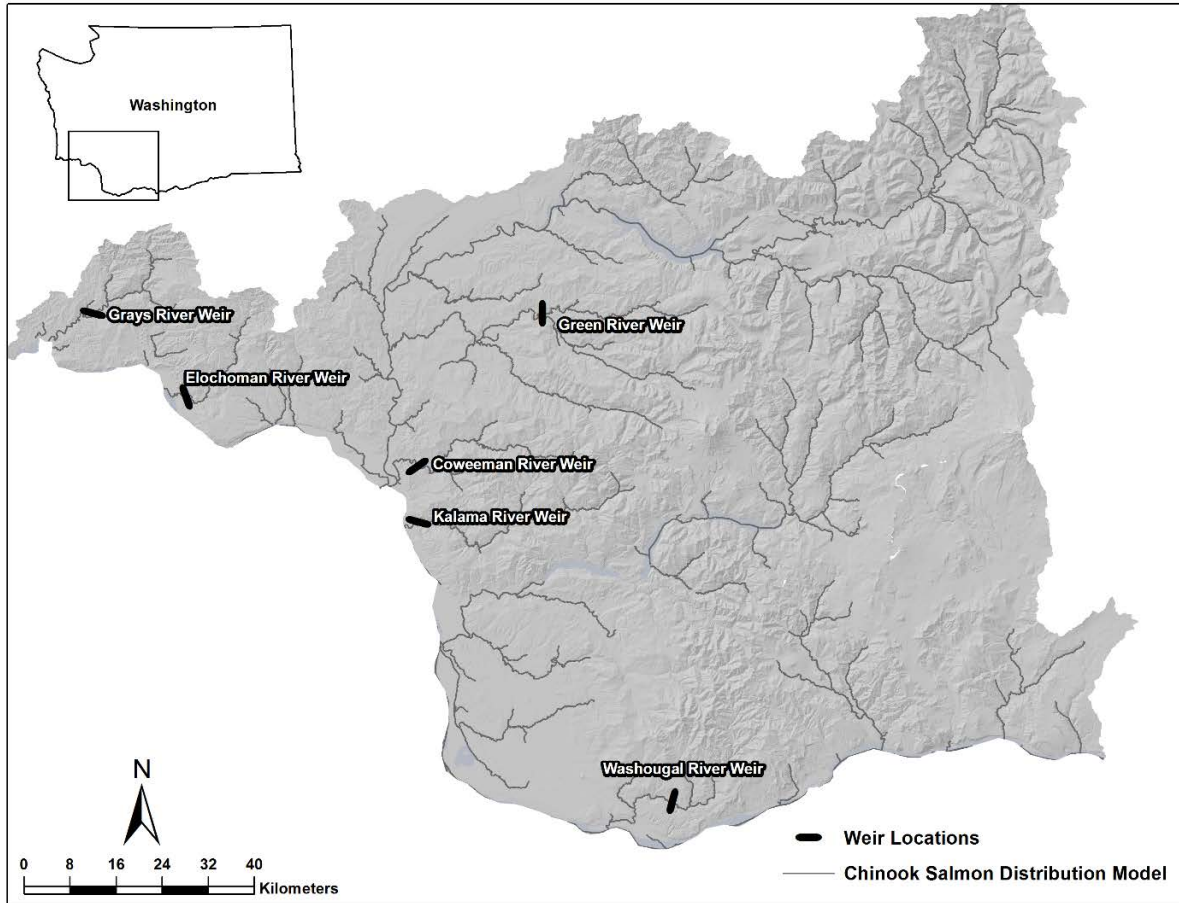


Figure 1. Location of weirs used for fall Chinook salmon management in the Lower Columbia River, 2012.

Fish Capture

Weir designs varied by location based on the available infrastructure and goals. In general, three weir designs were used: a fixed panel design, a resistance board design, and a hybrid fixed/resistance design. Fixed panel weirs have been used for decades in LCR tributaries to collect hatchery broodstock needs. Fixed panel weirs can be highly effective at low constant flows, especially when paired with in-stream infrastructure such as a concrete sill. This design was used in the Elochoman River with an existing concrete sill and trap box. A hybrid resistance board/fixed panel design utilizes fixed wooden panels on the perimeter and a floating resistance board section constructed primarily of PVC pipe in the center. This design was used in the Green River with an existing concrete sill and fish ladder that diverted fish into the North Toutle Hatchery adult holding pond. A resistance board design utilizes floating resistance board sections made of PVC pipe river-wide. It is typically anchored using duckbill anchors and cables (Figure 2). This design was used in the Grays, Coweeman, and Washougal rivers. All weirs had 3.8 cm spacing to limit any size bias.

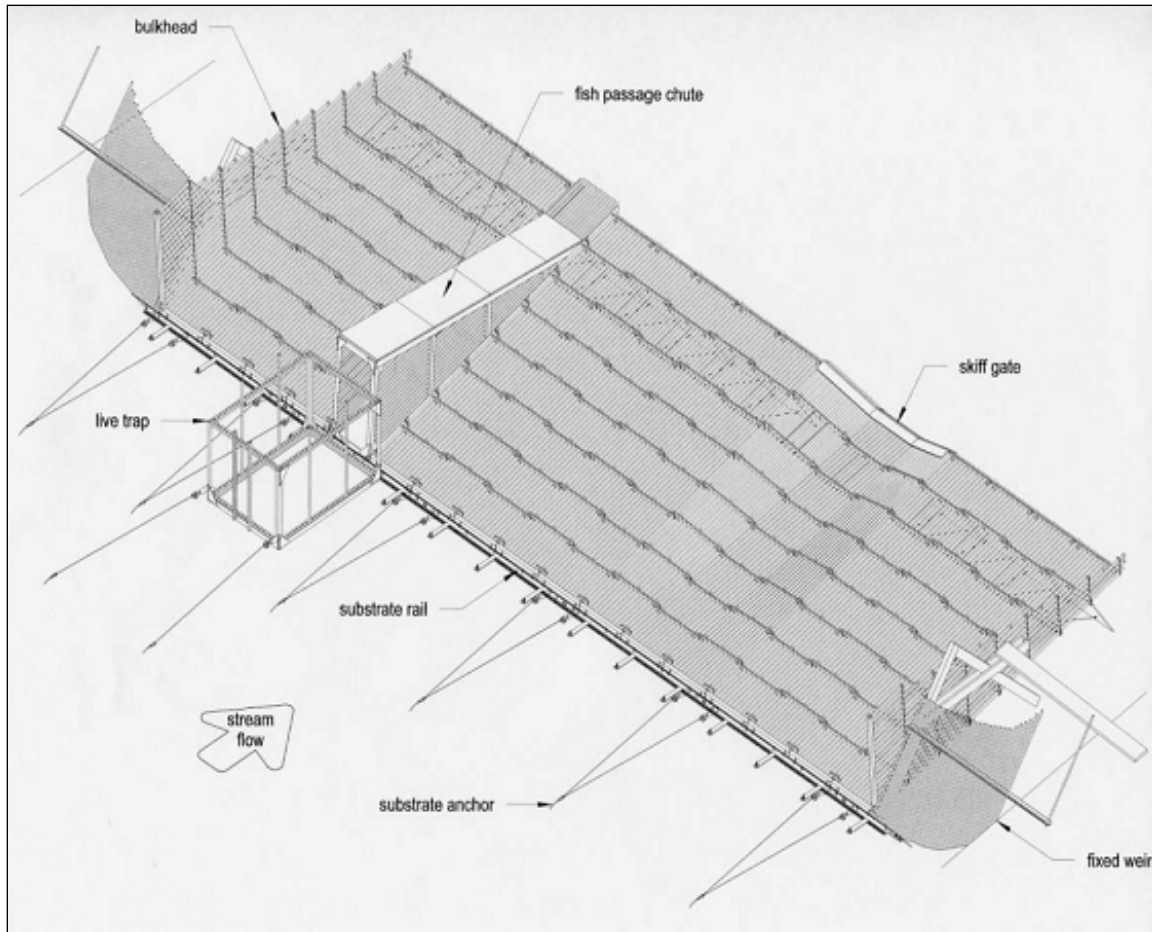


Figure 2. Schematic of a resistance board weir (Stewart 2003).

Weir Operation and Sampling Protocols

Weirs and traps were staffed continuously while installed and the trap box was checked daily (multiple times per day when necessary). Close attention was paid to the recruitment of fish into trap boxes and the accumulation of fish below the trap. When the abundance of salmonids exceeded the ability of staff to efficiently work through fish, modifications were made to trapping protocols to facilitate passage without handling. This was accomplished by opening the upstream gate on the trap box and allowing fish to pass through without handling or submerging a section of the resistance weir to allow fish passage.

Stream flow and weather forecasts were monitored closely to ensure the well-being of captured fish in the live box. The Washington Department of Ecology (WDOE) operates telemetry stream flow gauges that provide near real-time information on stream flows. Stream flow, weather forecast information, and ultimately direct observation, determined when flows began to limit accessibility to the trap box. When these conditions were encountered, the upstream door on the trap box would be opened to allow passage through the trap box. Tagging of fish captured at the weirs combined with stream surveys provided a means for estimating abundance and weir efficiency when fish were allowed through the trap unsampled and/or high flows compromised the ability to trap fish at the weir.

Adult fall Chinook salmon captured at each weir were sampled and tagged prior to release above the weir to evaluate weir efficiency and generate population estimates. Tagging was coordinated with spawning ground surveys to re-sight/recover these marks. Independent estimates of spawner abundance were made for fall Chinook salmon via mark/recapture, redd count expansion, and/or Area-Under-the Curve (AUC) methods for comparison to weir counts. All adult salmonids that were bio-sampled, except those able to be retained in sport fisheries upstream of weir sites, were anaesthetized with tricaine methanesulfonate (MS-222) prior to handle/tagging at the weir. All anaesthetized fish were allowed to fully recover before being released upstream of the weir. Table 1 outlines the planned disposition by species and origin at the Grays, Elochoman, Coweeman, Green, and Washougal weirs in 2012.

Table 1. Planned disposition of adult salmonids by species and origin for the Grays, Elochoman, Coweeman, Green, and Washougal river weirs, 2012.

Species	Origin	Grays	Elochoman	Coweeman	Green	Washougal
Fall Chinook	Unmarked	U	U	U	1 in 2 U	U
	Marked	R	R	R	1 in 3 U*	1 in 10 U*
Coho	Unmarked	U	U	U	U*	U
	Marked	U	R	R	R*	U
Chum	Unmarked	U	U	U	U	U
	Marked	U	U	U	U	U
Steelhead	Unmarked	U	U	U	U	U
	Marked	U	U	U	R	U

Unmarked fish are assumed to be of natural origin (NOR) and marked fish are assumed to be of hatchery origin (HOR)

U=Upstream, R=Removed

* denotes in excess of weekly broodstock needs

North Toutle (Green) has integrated fall Chinook and coho salmon programs – any unmarked Chinook and coho salmon not released upstream were taken for brood.

All LV-clipped fall Chinook salmon were removed at the weirs.

Data Analysis

Adult weir capture efficiency, pHOS without hatchery Chinook salmon removals at weirs, change in pHOS due to weir removals, and the proportion of Chinook salmon spawning occurring below the weir sites was estimated by adding additional equations, summary statistics, and parameters to the models already developed to estimate abundance for each subpopulation (Rawding et al. 2014). This analysis was conducted under a Bayesian framework utilized WinBUGS (Spiegelhalter et al. 1999) called from within R using the R2WinBUGS package (Sturtz et al. 2005). Table 2 and Table 3 outline the summary statistics, parameters, and equations used to calculate these metrics.

Table 2. Summary statistics used for weir reporting.

Statistic	Definition
N_{aw}	Adult Chinook salmon abundance above the weir site
N_{bw}	Adult Chinook salmon abundance below the weir site
W_{up}	Adult Chinook salmon passed upstream at weir
W_{hrem}	Adult Hatchery Chinook salmon removed at weir
W_{wrem}	Adult unmarked adult Chinook salmon taken for brood or trap mort
H_{swim}	Adult Chinook salmon swim-ins to hatchery facility above weir
pHOS	Proportion of marked spawners based on the presence of an adipose and/or ventral fin clip and/or coded wire tag (CWT)
HOS_{aw}	Hatchery-origin Chinook salmon spawners above weir

Table 3. Derived parameters for weir reporting.

Parameter	Definition/Equation
W_{eff}	Weir Capture Efficiency $((W_{up} + W_{hrem} + W_{wrem}) / (N_{aw} + W_{hrem} + W_{wrem} + H_{swim}))$
nwpHOS	Estimated pHOS without hatchery removals. $((pHOS_{aw} + W_{hrem}) / (N_{aw} + W_{hrem} + W_{wrem}))$
cpHOS	Estimated change in pHOS from removal of hatchery fish at the weir site. $nwpHOS - pHOS$
% spbw	Proportion of the spawning population that spawned downstream of the weir site. $N_{bw} / (N_{bw} + N_{aw})$

We provide estimates of age structure by mark type for Chinook salmon removed at each of the weirs based scale ageing.

Results and Discussion

The five weirs were installed prior to the start of fall Chinook salmon upstream migration with the intent of operating them through the migration period. A total of 64, 319, 244, 2,603, and 4,203 Chinook salmon were captured at the Grays, Elochoman, Coweeman, Green, and Washougal weirs, respectively. Table 4 lists the catch at each weir site by species, origin, and disposition. Weir totals represent total number of fish that were captured at each weir site. Total spawning escapement above each weir site may be more or less than weir totals depending on weir capture efficiency, sport harvest above weir sites, and pre-spawning mortality. Escapement reported in the main body of the report is less removal from fisheries and/or pre-spawning mortality.

Table 4. Weir capture totals by location, species, origin, and disposition, 2012.

		Number Trapped (Male/Female/Jack)					
Species	Mark	Grays	Elochoman	Coweeman	Green	Washougal	Disposition
Chinook	LV or ADLV	26 (11/10/5)	15 (6/5/4)	0	0		0 Removed
	LV or ADLV	2 (0/0/2)	0	0	0		0 Trap Mortality
	AD only	22 (8/9/5)	94 (42/49/3)	57 (36/21/0)	1026 (552/372/102)	1036 (332/263/441)	Removed
	AD only	0	0	0	449 (245/182/22)	70 (35/28/7)	Released upstream
	AD only	0	175 (93/78/4)	0	528 (229/296/3)	2800 (1370/1297/133)	Trucked/Held for Brood
	AD only	0	2 (0/1/1)	0	210 (114/80/16)	21 (1/6/14)	Trap Mortality
	None	12 (3/7/2)	31 (13/17/1)	186 (122/60/4)	212 (126/69/17)	269 (185/55/29)	Released upstream
	None	2 (0/2/0)	2 (0/2/0)	0	0		0 Released downstream
	None	0	0	0	160 (105/48/7)		0 Trucked/Held for Brood
None	0	0	1 (0/1/0)	18 (7/9/2)		2 (0/1/1) Trap Mortality	
Unknown	0	0	0	0		5 (0/1/4) Trap Mortality	
Coho	AD	105 (39/62/4)	0	0	0	25 (17/7/1)	Released upstream
	AD	0	6 (2/4/0)	1 (0/0/1)	952 (500/444/8)		0 Removed
	AD	0	0	0	713 (352/358/3)		0 Trucked/Held for Brood
	AD	0	0	0	323 (141/174/8)		0 Trap Mortality
	None	45 (29/15/1)	72 (33/39/0)	66 (41/23/2)	341 (220/117/4)		4 (4/0/0) Released upstream
	None	15*	0	0	144 (68/73/3)		0 Trucked/Held for Brood
	None	0	0	0	23 (14/9/0)		0 Trap Mortality
Chum	None	45 (29/16/0)	5 (2/3/0)	0	1 (0/1/0)		0 Released upstream
Steelhead	AD	3 (1/2/0)	25 (6/19/0)	4 (0/1/0)	0	17 (4/13/0)	Released upstream
	AD	0	0	0	38 (19/19/0)		0 Released downstream
	AD	1 (0/1/0)	0	0	275 (96/179/0)		0 Removed
	AD				2 (1/1/0)		1 (1/0/0) Trap Mortality
	None	1 (0/1/0)	0	6 (0/6/0)	8 (4/4/0)		13 (7/6/0) Released upstream
	None	0	0	0	0		0 Trap Mortality
Sockeye	None	2 (2/0/0)	0	0	0		0 Released upstream
	None	1 (1/0/0)	0	0	0		0 Released downstream

AD only = Fish with an adipose fin clip – indicates hatchery-origin

LV or ADLV = Fish with a left ventral or a left ventral and an adipose fin clip – indicates hatchery-origin Select Area Brights (SABs) from Oregon Select Area Fisheries Enhancement (SAFE) releases.

None = All fins intact – indicates natural-origin or a fish that was not mass marked

It should be noted that fish called jacks in the weir totals table (Table 4) are based fork length. In this analysis, only Chinook salmon with fork lengths ≥ 60 cm are considered adults. All abundance, pHOS, and weir efficiency estimates in this report are for adults only.

Grays River Weir

The Grays River Weir was initially established and operated in the fall of 2008 using Pacific Coast Salmon Restoration Fund (PCSRF) dollars; in 2009, funding to install and operate the weir shifted to Mitchell Act Monitoring Evaluation and Reform (MA MER) programs. The Grays River Weir is a resistance board design with 3.8 cm spacing between panel bars. In 2011, the Grays River weir was moved from its original location, just downstream of the Grays River Covered Bridge (rkm 17.22), to rkm 16.50 due to landowner constraints. The weir configuration has changed slightly each year to try and improve fish recruitment and to adapt to changing site conditions. For the fall 2012 season, the weir was weir installed at the same location fished in 2011 and was operational on August 4. The first and last Chinook salmon were captured on August 23 and October 23, 2012, respectively. The weir was submerged on two occasions due to high flow events. The first submersion began on October 15 and lasted until October 18. A

second high flow event caused the weir to submerge again on October 24 through October 25 when the weir was removed for the season. Figure 3 shows the 2012 Grays River Weir configuration.



Figure 3. Grays River Weir configuration, 2012.
Photo credit: Josh Laeder (WDFW).

A total of 64 Chinook salmon were trapped at the Grays River Weir in 2012. Over 78% of the Chinook salmon catch were marked (AD, LV or ADLV). Select Area Brights (SABs) comprised almost 44% of the total Chinook salmon catch. SABs are hatchery fall Chinook salmon that are released into Youngs Bay on the Oregon side of the Columbia River as part of the Select Area Fisheries Enhancement (SAFE) program. This is a non-local hatchery stock that originated from the Rogue River. Adult weir capture efficiency was estimated to be 29.0% (95% CI 19.6 – 42.7%) and removal of hatchery Chinook salmon at the weir site was estimated to have reduced pHOS by 3.4% (95% CI 1.4 – 6.6%). Approximately 36.1% of the Chinook salmon spawning in the basin occurred downstream of the weir site (Table 5). Age-3 fish dominated the age structure of fish removed at the weir (Table 6). We were unable to examine run timing by mark type past the weir site due to low weir capture efficiency.

Table 5. Adult weir capture efficiency, pHOS, and percent spawning below weir for the Grays River Chinook salmon subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Weff	29.0%	5.9%	19.6%	28.2%	42.7%
pHOS	79.2%	6.5%	65.3%	79.6%	90.2%
nwpHOS	82.6%	5.5%	70.7%	83.0%	92.0%
cpHOS	3.4%	1.3%	1.4%	3.2%	6.6%
% spbw	36.1%	0.0%	36.1%	36.1%	36.1%

Table 6. Age structure by mark type of Chinook salmon removed at the Grays River Weir based on scale ageing, 2012.

Age Read	AD-clipped		LV-or ADLV-clipped	
	Scale samples	Proportion	Scale samples	Proportion
Age-2	6	27.3%	9	36.0%
Age-3	11	50.0%	12	48.0%
Age-4	5	22.7%	4	16.0%
Age-5	0	0.0%	0	0.0%
n	22		25	

Note that not all Chinook salmon removed were sampled for scales.

Elochoman River Weir

The Elochoman River Weir was a full fixed panel weir design that is installed on a permanent concrete sill with adjoining live box (Figure 4). The site is located just above the Risk Road Bridge near the head of tide at rkm 4.39. For several decades, this site and configuration were used to collect broodstock for the WDFW Elochoman Salmon Hatchery fall Chinook salmon program. In 2009, after the closure of the Elochoman Hatchery and discontinuation of the Elochoman Hatchery fall Chinook salmon program in 2008, responsibility for the weir transferred to WDFW Region 5 Fish Management and MA MER funding was used to operate the weir. During this transition, weir panels were re-built with 3.8 cm spacing (instead of the previous 7.6 cm spacing) between panel bars. Weir installation began on August 17, 2012, and the weir was operational later that same day. The first and last Chinook salmon were captured on August 23 and October 22, 2012, respectively. The weir fished continuously until it was removed on October 26, 2012.



Figure 4. Elochoman River Weir configuration, 2012.

Photo credit: Claire Landry (WDFW).

A total of 319 Chinook salmon were trapped at the Elochoman River Weir in 2012. Adult weir capture efficiency was estimated to be 72.0% (95% CI 47.3 – 90.9%) and removal of hatchery Chinook salmon at the weir site was estimated to have reduced pHOS in the Elochoman River subpopulation by 11.1% (95% CI 0 – 29.9%). Approximately 37.2% (95% CI 14.9 – 69.2%) of the spawning occurred downstream of the weir site (Table 7). The age structure of adipose-clipped Chinook salmon was balanced with age-4 fish comprising over 44% of the adipose-clipped fish removed. LV-clipped Chinook salmon tended to be younger than adipose-clipped Chinook salmon removed at the weir (Table 8). The 50% passage date for unmarked Chinook salmon was almost two weeks later than adipose-clipped Chinook salmon (Figure 5).

Table 7. Adult weir capture efficiency, pHOS, and percent spawning below weir for the Elochoman River Chinook salmon subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Weff	72.0%	11.8%	47.3%	73.4%	90.9%
pHOS	59.3%	14.8%	30.4%	59.4%	87.2%
nwpHOS	70.4%	9.4%	50.5%	71.2%	86.9%
cpHOS	11.1%	10.6%	0.0%	11.6%	29.9%
% spbw	37.2%	14.0%	14.9%	35.6%	69.2%

Table 8. Age structure by mark type of Chinook salmon removed at the Elochoman River Weir based on scale readings, 2012.

Age Read	AD-clipped		LV-clipped	
	Scale samples	Proportion	Scale samples	Proportion
Age-2	1	2.6%	6	46.2%
Age-3	10	26.3%	4	30.8%
Age-4	17	44.7%	3	23.1%
Age-5	10	26.3%	0	0.0%
n	38		13	

Note that not all Chinook salmon removed were sampled for scales.

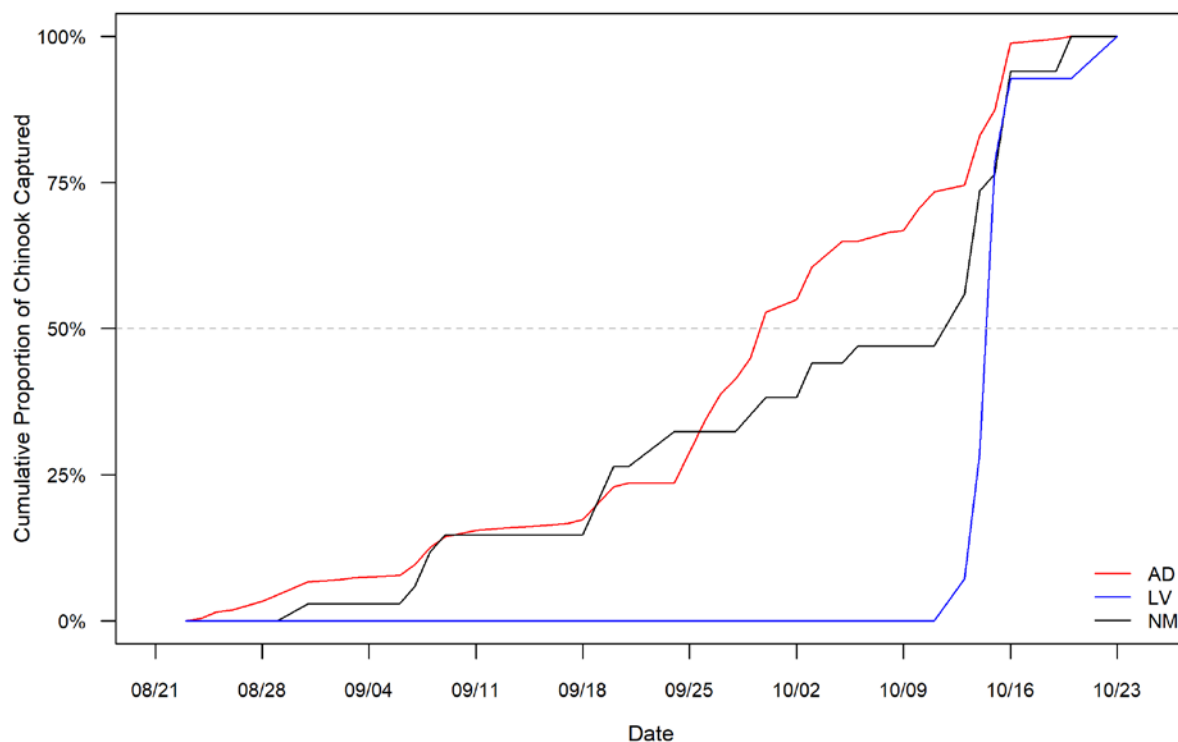


Figure 5. Chinook salmon run timing by mark type at Elochoman River Weir, 2012. AD = adipose fin clipped (indicates hatchery-origin), LV = left ventral fin clipped (indicates hatchery-origin SAB stock), NM = no mark or all fins intact (assumed to be natural-origin).

Coweeman River Weir

The Coweeman River Weir was first installed and operated in 2011. This weir utilizes a full resistance board design with 3.8 cm spacing between panel bars. The site is located at rkm 10.94 approximately 0.8 kilometers above the head of tide. The weir was installed and operational on August 28, 2012. The first and last Chinook salmon were captured on August 31 and October 19, 2012, respectively. The weir was fished nearly continuously while installed with a known outage on September 29 and partial outages on October 15 and 16. The weir was removed on October 25, 2012. Figure 6 shows the 2012 Coweeman River weir configuration.



Figure 6. Coweeman River Weir configuration, 2012.

Photo credit: Patrick Hulett (WDFW).

A total of 244 Chinook salmon were trapped at the Coweeman River Weir in 2012. Adult weir capture efficiency was estimated to be 62.4% (95% CI 49.3 – 74.2%) and removal of hatchery Chinook salmon at the weir site was estimated to have reduced pHOS by 10.0% (95% CI 7.8 – 12.7%). It was estimated that 32.9% (95% CI 20.1 – 46.0%) of the Chinook salmon spawning in the Coweeman River basin spawned below the weir site (Table 9). Age-3 and age-4 fish dominated the age structure of fish removed at the weir (Table 10). Run timing past the weir site was nearly the same between unmarked and marked Chinook salmon (Figure 7).

Table 9. Adult weir capture efficiency, pHOS, and percent spawning below weir for the Coweeman River Chinook salmon population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Weff	62.4%	6.4%	49.3%	62.7%	74.2%
pHOS	11.0%	3.2%	5.6%	10.7%	18.2%
nwpHOS	21.1%	3.0%	16.0%	20.8%	27.6%
cpHOS	10.0%	1.2%	7.8%	10.0%	12.7%
% spbw	32.9%	6.6%	20.1%	32.9%	46.0%

Table 10. Age structure by mark type of Chinook salmon removed at the Coweeman River Weir based on scale ageing, 2012.

Age Read	AD-clipped	
	Scale samples	Proportion
Age-2	1	1.8%
Age-3	23	41.8%
Age-4	29	52.7%
Age-5	2	3.6%
n	55	

Note that not all Chinook salmon removed were sampled for scales.

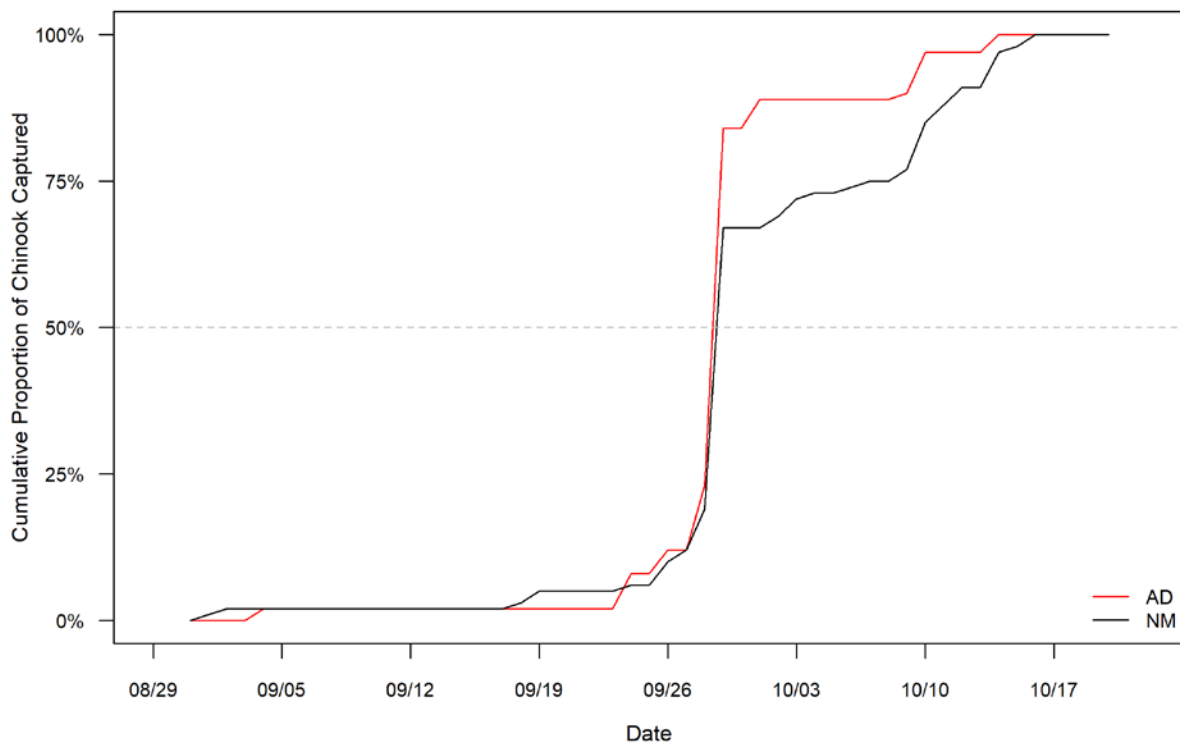


Figure 7. Chinook salmon run timing by mark type at Coweeman River Weir, 2012. AD = adipose fin clipped (indicates hatchery-origin), NM = no mark or all fins intact (assumed to be natural-origin).

Green River Weir

The Green River Weir was first installed and operated for fish management purposes in 2010. The weir has been used for many years prior to 2010, but was solely used to collect broodstock for the North Toutle Hatchery's Chinook and coho salmon programs. This weir utilizes a hybrid resistance board design with 3.8 cm spacing between panel bars. The site is located at rkm 0.64 adjacent to the North Toutle Hatchery. The weir was installed and operational on August 16, 2012. The first and last Chinook salmon were captured on August 27 and November 1, 2012, respectively. The weir removed on November 14, 2012. Figure 8 shows the 2012 Green River weir configuration.



Figure 8. Green River Weir configuration, 2012.
Photo credit: Amanda Danielson (WDFW).

A total of 2,603 Chinook salmon were trapped at the Green River Weir in 2012. Adult weir capture efficiency was estimated to be 94.8% (95% CI 92.7 – 96.6%) and removal of hatchery Chinook salmon at the weir site was estimated to have reduced pHOS at the Toutle River subpopulation level by 11.8% (95% CI 7.0 – 16.9%). Approximately 5.2% (95% CI 4.1 – 6.5%) of the Chinook salmon spawning in the Green River subpopulation occurred below the weir site (Table 11). The 50% passage date past the weir site for Chinook salmon was one week later for unmarked adults compared to marked adults (Figure 9). Age data from Chinook salmon removed at the weir was combined with Chinook salmon spawned at North Toutle Hatchery. Therefore, we cannot report on age structure of weir removals only in 2012.

Table 11. Adult weir capture efficiency, pHOS, and percent spawning below weir for the Green River Chinook salmon subpopulation, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Weff	94.8%	1.0%	92.7%	94.9%	96.6%
pHOS	71.9%	3.6%	64.7%	71.9%	78.6%
nwpHOS	83.6%	1.1%	81.5%	83.7%	85.6%
cpHOS	11.8%	2.5%	7.0%	11.7%	16.9%
% spbw	5.2%	0.6%	4.1%	5.1%	6.5%

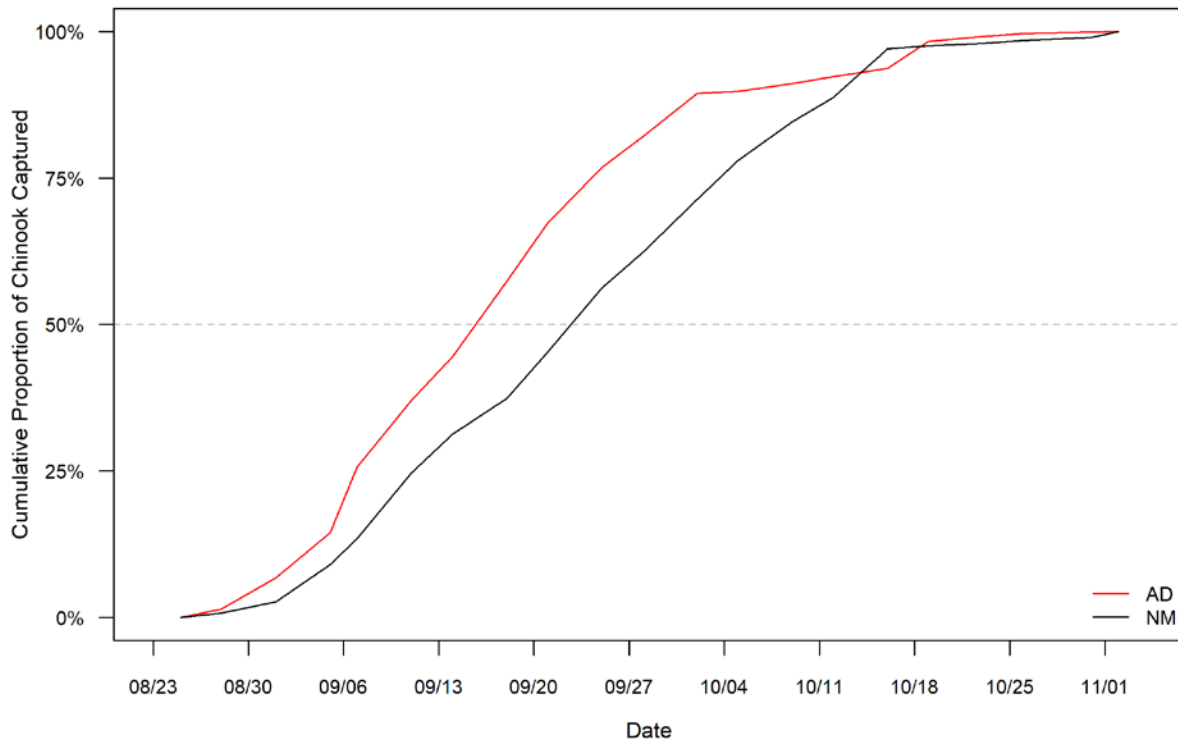


Figure 9. Chinook salmon run timing by mark type at Green River Weir, 2012.

AD = adipose fin clipped (indicates hatchery-origin), NM = no mark or all fins intact (assumed to be natural-origin).

Washougal River Weir

The Washougal River Weir was first installed and operated in 2011. This weir utilizes a resistance board hybrid design with 3.8 cm spacing between panel bars. The weir is located at rkm 19.15 and currently serves as both a broodstock collection point for the WDFW Washougal Salmon Hatchery fall Chinook salmon program as well as a monitoring and management platform. Weir installation began in mid-July and the weir was fully operational on September 4, 2012. The first and last Chinook salmon were captured on September 5 and October 22, 2012, respectively. Known weir outages occurred on October 15-17. October 22 was the last day the trap was fully operational due to high flows. The weir was removed as flows subsided. Figure 10 shows the 2012 Washougal River weir configuration.



Figure 10. Washougal River Weir configuration, 2012.
Photo credit: Jeremy Wilson (WDFW).

A total of 4,203 Chinook salmon were trapped at the Washougal River Weir in 2012. Adult weir capture efficiency was estimated to be 54.9% (95% CI 52.3 – 56.9%) and removal of hatchery Chinook salmon at the weir site was estimated to have reduced pHOS by 18.1% (95% CI 15.0 – 21.3%). This may be biased high as some of the fish removed at the weir would have recruited to Washougal Hatchery upstream but it is unclear what proportion would have done so. In 2012, it was estimated that 16.0% (95% CI 13.8 – 18.3%) of the Chinook salmon spawning in the Washougal population occurred below the weir site (Table 12). Age-2 fish dominated the age structure of Chinook salmon removed at the weir (Table 13). We were unable to examine run timing by mark type due to low weir capture efficiencies late in the season.

Table 12. Adult weir capture efficiency, pHOS, and percent spawning below weir for the Washougal River Chinook salmon population, 2012.

Parameter	Mean	SD	2.50%	Median	97.50%
Weff	54.9%	1.2%	52.3%	55.0%	56.9%
pHOS	72.3%	2.2%	67.8%	72.4%	76.6%
nwpHOS	90.4%	1.0%	88.2%	90.5%	92.3%
cpHOS	18.1%	1.6%	15.0%	18.1%	21.3%
% spbw	16.0%	1.1%	13.8%	16.1%	18.3%

Table 13. Age structure by mark type of Chinook salmon removed at the Washougal River Weir based on scale ageing, 2012.

Age Read	AD-clipped	
	Scale samples	Proportion
Age-2	42	42.0%
Age-3	32	32.0%
Age-4	22	22.0%
Age-5	4	4.0%
n	100	

Note that not all Chinook salmon removed were sampled for scales.

Coded-Wire-Tag Recoveries

All of the CWT recoveries at the Grays River Weir, and 75% of the CWT recoveries at the Elochoman River Weir, in 2012 were from Big Creek Hatchery (an Oregon Dept. of Fish and Wildlife facility) and SAFE program releases. Returns from the recently terminated Elochoman Hatchery fall Chinook salmon program made up the other 25% of the CWT recoveries at Elochoman River Weir. The only CWT recovery at the Coweeman Weir was from a Kalama River release. For the Green and Washougal river weirs, we were unable to parse out weir surplus vs. hatchery surplus CWT recoveries due to the way in which data were collected. Therefore, we report weir surplus and hatchery surplus CWT recoveries combined. These were almost entirely from in-basin hatchery programs (93% and 99% for the Green and Washougal weirs, respectively) (Table 14).

Table 14. Origin and recovery site of CWT recoveries from Chinook salmon removed at the Grays, Elochoman, Coweeman, Green, and Washougal weirs and surplus at the North Toutle and Washougal hatcheries, 2012.

		Recovery Location				
		Grays Weir	Elochoman Weir	Coweeman Weir	Green Weir	Washougal Weir
Release Basin	NF Klaskanine H.	1				
	SF Klaskanine H.	1	1		1	
	Big Creek H.	1	1			
	Deep River Net Pens		1			
	Elochoman H.		1			
	Fallert H.				1	
	N. Toutle H.				51	
	Kalama Falls H.			1	2	
	Washougal H.					134
	Cedar Cr. H. (Sandy R.)					1
	Total CWT Recoveries	3	4	1	55	135

Weir Effects

Displaced spawning due to the weir structure was a problem at most of the weir sites in 2012 due to low water. Prior to 2012, this had not been a widespread problem. We need to evaluate ways to improve fish recruitment into the trap boxes in the future or submerge the weir to allow a proportion of the fish to pass the weir site.

In 2011, we assessed the effects of handling on live fish by examining the number of pre-spawn mortalities in basins where we had “leaky” weirs but still had adequate sample sizes of tagged (handled) and untagged (not handled) Chinook salmon. We had planned to do the same analysis in 2012 but we were unable to due to small sample sizes.

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**Coho Salmon Escapement Estimates and Coded-Wire-Tag
Recoveries in Washington's Lower Columbia River Tributaries in
2012**

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August, 2019

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Abstract

The Lower Columbia River (LCR) coho salmon Evolutionary Significant Unit (ESU) is composed of 24 populations split between the states of Washington and Oregon. The Oregon Department of Fish and Wildlife (ODFW) began comprehensive monitoring of coho salmon populations in Oregon portion of this ESU in 2002. Minimum adult coho salmon estimates in Washington's portion of this ESU have been limited primarily to counts at hatchery facilities and a few fish ladder traps. This is the third year the Washington Department of Fish and Wildlife (WDFW) has implemented a program to estimate coho salmon spawner abundance, the proportion of hatchery origin spawners (pHOS), the proportion of spawning reaches occupied, spatial distribution, sex ratio including the proportion of jacks, and to recover Coded Wire Tags (CWT). We recovered nine CWT mostly in the Grays and Kalama basins. The adult coho salmon population monitoring program used trap and haul census counts, mark-recapture, smolt expansion, and redd-based methods to monitor adult coho salmon. We estimated a mean escapement of 34,174 (95% CI 24,720 – 51,680) adults and 7,656 jacks (95% CI 5,089 – 12,980) for the Washington portion of this ESU below Bonneville Dam excluding the Lower Cowlitz and mainstem Toutle/ lower North Fork Toutle (below the Sediment Retention Structure). Individual population estimates for spawners ranged from a high of 6,832 adults for the combined upper Cowlitz/Cispus population to a low of 313 adults for the Kalama population. As expected, populations with an operating coho salmon hatchery, including the Grays, Elochoman, Upper Cowlitz/Cispus, Tilton, and Kalama rivers, generally had higher proportions of hatchery spawners (mean = 19%, 25%, 75%, 78%, and 81%, respectively). The converse was true for populations without hatcheries, such as the Mill-Abernathy-Germany, Coweeman, South Fork Toutle, and EF Lewis populations, where we observed low percentages of marked adults (mean = 3%, 2%, 5%, 13%, and 8% respectively). The total mean estimate of unmarked coho salmon adults was 21,083 (95% CI 12,870 – 36,580). Estimates of precision for the aggregate estimate for all adults and unmarked adults as measured by the coefficient of variation (CV) were 21% and 30%, respectively. The precision of individual estimates of unmarked adults based on redd surveys was low, the most precise estimate occurring in the Green River with a CV of 48%. In two study streams, redd surveys were conducted in conjunction with mark-recapture to estimate the number of redds per female in order to expand redd counts throughout the ESU. The mean estimate of observed redds per female was 0.567 (95% CI 0.179 – 0.957), which indicates that we likely only observed about 57% of the redds assuming each female constructed one redd. This estimate was consistent with poor water clarity and periods of high discharge which limited observer efficiency and erased physical evidence of redds. Trap counts and mark-recapture estimates of coho salmon abundance were more precise than the redd-based estimates. To improve the precision of adult coho salmon redd-based estimates, we recommend obtaining more precise estimates of redds per female, increasing the number of reaches surveyed per population, and exploring possible density-based stratification of the Generalized Random Tessellation Stratified (GRTS) sampling design used to select redd survey reaches.

Introduction

Coho salmon (*Oncorhynchus kitsuch*) in the Lower Columbia River (LCR) Evolutionarily Significant Unit (ESU) were listed for protection under the Endangered Species Act (ESA) in 2005. In a recent five-year review, the National Oceanic and Atmospheric Administration (NOAA) Fisheries concluded that these fish should remain listed as threatened under the ESA (NOAA 2016). The LCR coho salmon ESU is composed of 24 populations split between the states of Washington and Oregon (Myers et al. 2006). The Oregon Department of Fish and Wildlife (ODFW) began comprehensive monitoring of LCR coho salmon populations in 2002 (Suring et al. 2006). However, estimates of adult coho salmon escapement in Washington's portion of the LCR were limited primarily to counts at hatchery facilities and a few fish ladder traps until this project was funded in 2010.

The coastwide Coded-Wire-Tag (CWT) program was developed in the 1970's to evaluate the contribution of different salmonid populations and hatchery programs to various fisheries and to estimate salmon fishery harvest rates, along with evaluation of hatchery rearing practices. The initial protocols for the CWT program included the insertion of a CWT into the snout of a juvenile hatchery salmon, which was accompanied by an adipose fin clip. A proportion of hatchery fish released from selected facilities had a CWT inserted. When salmon were recovered from fisheries and spawning areas, the snout of fish with missing adipose fins were taken to fisheries agency labs for decoding. Later the purpose of the CWT program was expanded to include forecasting run sizes to meet conservation and harvest objectives. For conservation purposes, the vast majority of coho salmon released from hatcheries are now adipose fin clipped (sometimes referred to as mass marked) and WDFW has implemented selective fisheries, which require the release of all adipose-intact (assumed to be natural origin) fish. CWTs are now detected electronically by scanning fish with handheld or stationary detectors, rather than using the adipose fin clip as an indicator of CWT presence. Upon implementation of mass marking, standard CWT protocols were modified to include inserting a CWT into a proportion of a hatchery release that was not adipose fin clipped—referred to as a Double Index Tag (DIT) group. The DIT groups were released from a few select hatcheries. These DIT groups are unmarked hatchery fish with a CWT that allow the evaluation of the harvest rates specific to selective fisheries and these DIT groups serve as surrogates for wild coho harvest rates for stocks subject to selective fisheries.

In 2010, the Washington Department of Fish and Wildlife (WDFW) initiated a program to sample LCR spawning grounds for coho salmon. This program had dual objectives: 1) to estimate Viable Salmonid Population (VSP) indicators (McElhany et al. 2000) and measure specific indicators to assess coho salmon viability (Rawding and Rodgers 2013) including coho salmon spawner abundance, the proportion of hatchery origin spawners, the proportion of spawning reaches occupied, spatial distribution, and sex ratio including the proportion of jacks; and 2) to recover CWT from spawning fish to provide complete accounting of CWT, so that harvest rates could accurately be determined. The first objective addressed a salmon recovery monitoring gap while the second objective addressed a gap identified from the CWT expert panel (Hankin et al. 2005). The framework of Rawding et al. (2014, 2015) was modified from 2010 and 2012 to summarize population monitoring of VSP indicators for LCR coho salmon returns and CWT recoveries in 2012, which are detailed in this report.

Methods

Study area

The LCR coho salmon ESU extends from the mouth of the Columbia River up to and including the Big White Salmon River in Washington and Hood River in Oregon, and includes the Willamette River to Willamette Falls, Oregon. Within this ESU, there are a total of fifteen Washington populations, seven Oregon populations, and two populations (Lower and Upper Gorge) that are split between the states (Figure 1). In this document we report on 13 populations in Washington. The upper Cowlitz and Cispus populations are combined into a single population because there is currently no way to determine spawning locations from the Cowlitz River trap and haul program for fish that are placed above Cowlitz Falls Dam. In 2012, Lower Cowlitz mainstem and tributaries, Toutle, and the Upper Gorge populations (including the Big White Salmon River) were not surveyed. It should be noted that coho salmon in the Lower Gorge population spawn in both states, but this report only contains information on the Washington proportion of the Lower Gorge population.

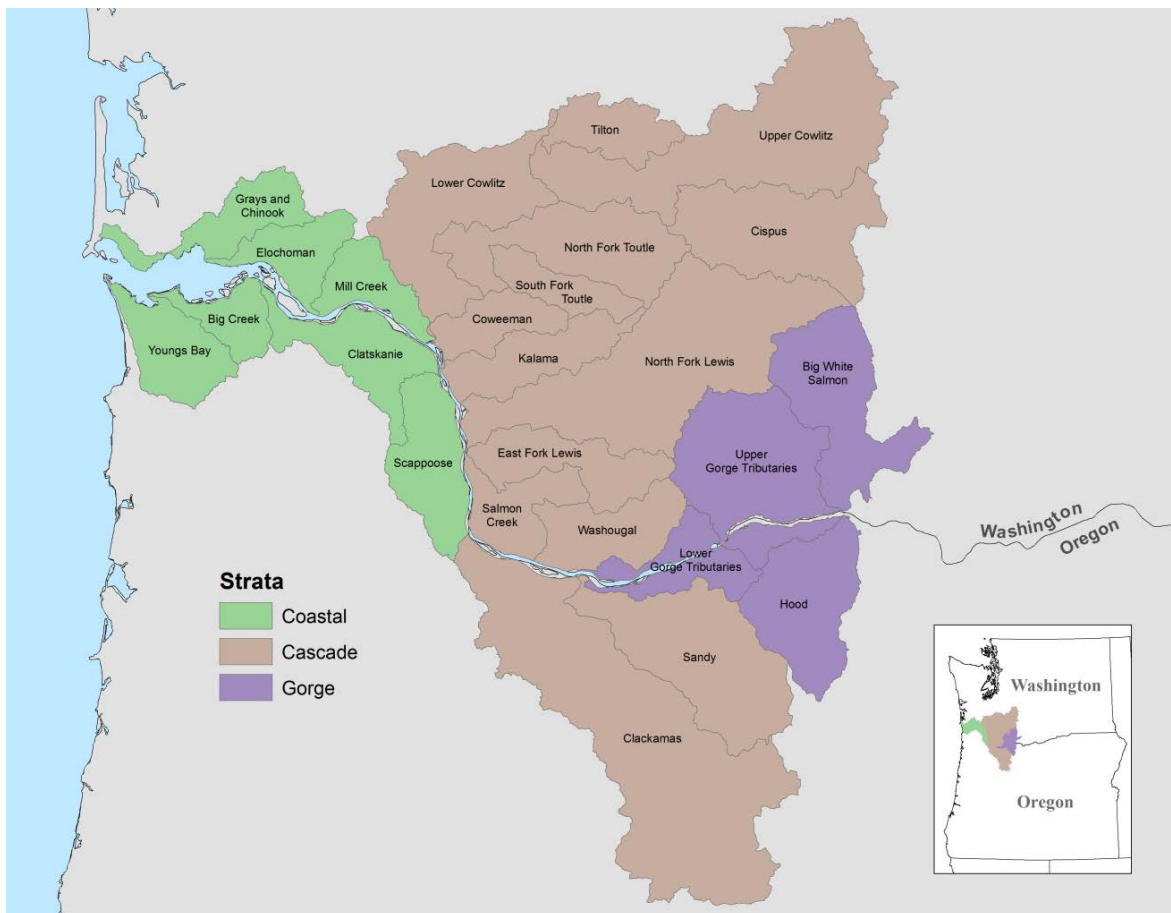


Figure 1. Lower Columbia River coho salmon populations and the regional groupings (i.e., strata) in which they occur within the LCR subunit recovery domain. The White Salmon population is considered part of the Upper Gorge Population.

Monitoring Design

We used dam counts and trapping, mark-recapture, and spawning ground surveys to estimate population parameters of LCR coho salmon (Figures 2 & 3). Field personnel were experienced and/or trained on adult salmon identification. Field data collection protocols varied but were based on the methods from the American Fisheries Society Salmonid Field Protocols Handbook (Johnson et al. 2007). Coho salmon redd, live fish, and carcass counts along with environmental and header information collected during coho salmon surveys were stored in the WDFW Spawning Ground Survey (SGS) database. Biological data collected on spawning ground surveys was stored in the WDFW Region 5 Age and Scales (A&S) database. Individual trap counts, tagging, and recovery data were stored in individual watershed databases or spreadsheets.

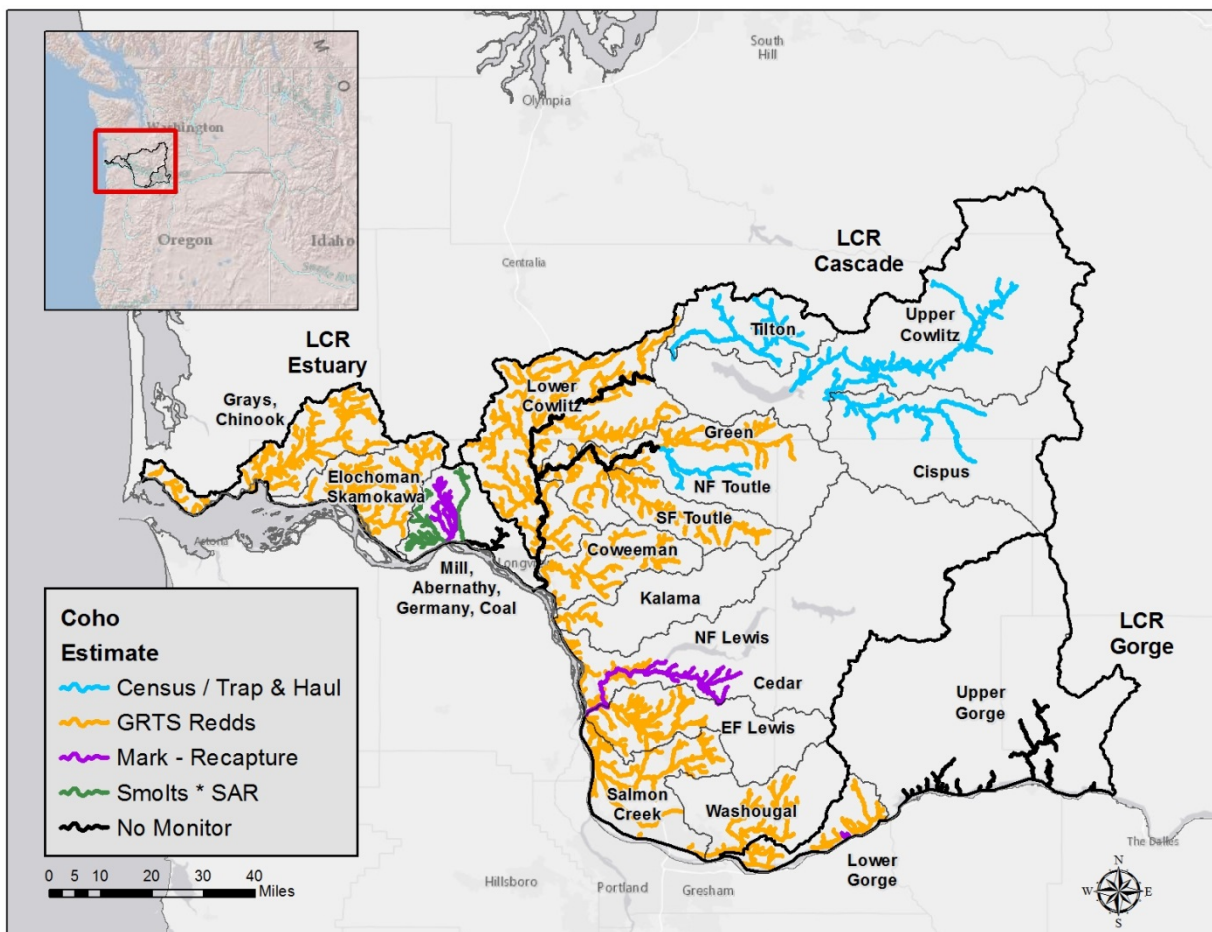


Figure 2. Watersheds containing the Washington populations of the Lower Columbia River coho salmon ESU and the methods WDFW used to estimate their abundance in 2012.

Trap & Haul

Dam counts were used at the Barrier dam on the Cowlitz River (RM 50), and the Toutle Fish Collection Facility (TFCF) on the NF Toutle River (RM 12). Depending on management objectives, coho salmon collected at these facilities were used for hatchery broodstock, surplused (donated to food banks, sold to the state fish buyer, or used for nutrient enhancement) or transported and released above the facility. We made the following key assumptions for the

trap and haul programs: 1) the count of all transported fish was without error, 2) all unmarked fish released survived to spawn, 3) transported fish spawned in the watershed where they were released (there was no fall back), 4) when fisheries in the Upper Cowlitz, Cispus, and Tilton rivers occurred only marked (adipose clipped fish) were harvested in accordance with regulations and there was no illegal harvest, 5) survival of all unmarked released fish was 100% (catch and release mortality was negligible), and 6) the WDFW methodology to expand catch record card (CRC) reported catch to total harvest and variance are correct.

Mark-Recapture

Petersen mark-recapture estimates for adult coho salmon were attempted in the Green River and Abernathy, Cedar, and Duncan creeks. However, high water undermined the weir at the Green River so escapement in this basin was determined using spawning ground surveys. Coho salmon were captured in adult traps located adjacent to the resistance board weir in Abernathy Creek at RM 0 (Kinsel et al. 2009), the fishway in Cedar Creek (RM 2), and Duncan Creek fishway (RM 0). Traps were installed prior to immigration of adult coho and fished through the end of migration in January or February. Recapture of fish occurred at upstream traps or during spawning ground surveys. The study design at all three locations was based on the Darroch estimator, which was developed for time stratified Petersen mark-recapture abundance estimates (Darroch 1961, Seber 1982). Schwarz and Taylor (1998) indicate that the following assumptions must be met to provide a consistent estimate of abundance: 1) there is no mark loss, 2) there are no marking effects, 3) all marked and unmarked fish are correctly identified and enumerated, 4) the population is closed, and 5) all fish in the population have the same probability of being tagged or all fish have the same probability of being captured in the second sample; or marked fish mix uniformly with unmarked fish.

The Jolly-Seber (JS) model estimates population abundance in mark-recapture studies where the population is open (Jolly 1965; Seber 1965) and has been widely used in estimating Pacific salmon spawning escapement from live fish (Schwarz et al. 1993; Jones and McPherson 1997; Rawding and Hillson 2003) but also using salmon carcasses (Parker 1968; Stauffer 1970; Sykes and Botsford 1986). The carcass tagging model has been used extensively in the Lower Columbia River to estimate Chinook salmon abundance (McIssac 1977; Rawding et al. 2006a). The JS model utilized carcass tagging for mark-recapture and was the method used for estimating escapement on the mainstem NF Lewis. Seber (1982) and Pollock et al. (1990) provide details of study design, assumptions, and analysis of mark-recapture experiments using the JS model. Five assumptions of the Jolly Seber model must be met in order to obtain unbiased population estimates from the model (Seber 1982) are: 1) equal catchability 2) equal survival between periods, 3) no handling mortality, 4) no tag loss, and 5) instantaneous sampling. For more details on the application of this approach to Lower Columbia River tributaries see Rawding et al. (2014).

Smolt Expansion

The number of coho salmon smolts emigrating from Mill, Abernathy, and Germany creeks are estimated annually based on a mark-recapture design (Kinsel et al. 2009). In addition, adult coho salmon returning to Abernathy Creek are estimated based on a mark-recapture study design. All three creeks enter the Columbia River within a few miles of each other. We assumed that the smolt to adult return (SAR) and stray rates were the same between the three sites, and were

therefore able to estimate the number of returning unmarked adults in Mill and Germany creeks by dividing their smolt estimates by the estimated Abernathy Creek SAR.

Spawning Ground Surveys

The monitoring design components for spawning ground surveys consist of basic elements (Stevens et al. 2007). These included: 1) the development of the sampling frame covering the entire spawning area, 2) a probabilistic sampling design to representatively survey the spawning area, 3) a temporal component to ensure the entire spawning period was sampled, and 4) a decision on the metric (e.g., live fish, carcass, or redd counts) used to estimate escapement, the observer efficiency, and the relationship between the metric and the escapement.

Spawning Distribution

The upper extent of the coho salmon spawning distribution was estimated based on the methods of Fransen et al. (2006). The upper extent of adult and juvenile coho salmon presence was estimated from focused and randomly selected surveys over two years. For sampled streams, fish presence protocols from the Washington Forest Practices Board (WFPB) for juveniles were followed. Following AFS electroshocking protocols (Temple et al. 2007), juveniles were continuously sampled moving in an upstream direction until fish were not observed for at least ¼ mile or a waterfall was encountered. This protocol was adapted for adult salmon except fish presence was based on visual sampling of live or dead adult coho salmon or their redds. The uppermost presence of fish was recorded using a global position satellite (GPS). This location was plotted on the WDFW Geographic Information Systems (GIS) stream and attribute layer. GIS attributes were recorded for the last reach where coho salmon were found, as well as the seven reaches downstream and eight reaches upstream of that point. Using logistic regression, a model was developed to predict the upper extent of coho distribution as a function of the GIS covariates including drainage area, mean annual flow, annual precipitation, confinement, elevation, and gradient. Akaike Information Criterion (AIC) was used to compare models and select the best model following Burnham and Anderson (2002). The coefficients for GIS covariates included in the best predictive model of upstream coho extent were drainage area, gradient, and elevation. The model was used to predict upstream extent throughout the ESU; the upstream extent was then further truncated by applying the WDFW fish passage barriers layer. The lower extent of coho salmon spawning was defined by the lowest location surveyed for steelhead or Chinook salmon redds in previous years; typically the downstream most extent of gravel in each watershed. More complete details of the upstream extent model development for Chinook salmon are provided in Rawding et al. (2010), which was adapted as described above for coho salmon. The spawning distribution drainage network as described above was the sampling frame used to develop the spatial sampling design for redd surveys.

GRTS Survey Sampling Design

A spatial sampling design was developed for 14 of the 17 coho salmon populations in Washington. The Upper Gorge population was excluded due to limited resources, the Mill-Abernathy-Germany (MAG), Upper Cowlitz/Cispus, and Tilton populations were excluded because we used alternate methods. For each population a Generalized Random Tessellation Stratified (GRTS) sampling design was used to establish a set of random, spatially balanced sample points for coho salmon surveys (Stevens 2002). Reach selection was based on the LCR GRTS web-based sampling tool developed by Oregon State University (OSU) through the

Pacific Northwest Aquatic Monitoring Partnership (PNAMP) with assistance from Don Stevens (OSU). Reaches, one mile in length, were established based on these points. In a few cases the reach length was less than one mile. This occurred when the GRTS point was located in a small tributary less than one mile in overall length, or there was an anadromous fish barrier falls less than a mile from the mouth. In the case of a tributary being less than 1 mile in length, the reach length was extended to the top fork of the 24k Washington Lakes and Rivers Information System (WLRS) stream layer regardless of sample frame.

A three-year rotating panel design was established for each coho salmon population (Firman and Jacobs 2004). In this design about 1/3 of the surveys for the 9-year period are repeated annually, 1/3 are repeated every third year, and new points are chosen each year for the remaining 1/3 of all surveys. For Oregon coastal coho salmon, the ODFW surveys 30 sites for each population, or enough sites to cover 30% of the coho spawning habitat for each coho salmon population (Lewis et al. 2009). The 30 sites or 30% of the habitat, whichever is lower, is expected to yield an average coefficient of variation (CV) near 15% (Jeff Rodger, ODFW, pers. comm.). However, due to limited resources, WDFW only sampled from 6 to 24 reaches per population (Appendix 1).

Weekly spawning ground surveys were scheduled for each reach from the start of spawning in mid-to late October until there was no observed spawning activity, which usually occurred in December or January depending on the population. However, due to high turbid flows and personnel challenges the designed temporal pattern did not always occur and some scheduled weekly surveys were missed.

Data Collection

Trap & Haul

Returning adult coho salmon from populations originating above dams in several Lower Columbia River watersheds were trapped and fish were hauled above those dams allowing for their enumeration and the collection of biological data. These watersheds included areas above the Sediment Retention Structure (SRS) on the North Fork Toutle River and the upper Cowlitz watershed above the Barrier Dam, including separate populations in the Tilton River and the Upper Cowlitz/Cispus Rivers. NF Toutle River coho salmon were trapped, anesthetized in CO₂, and sampled for biological data including length, sex, origin, and age. Adipose intact fish were transported and released in Alder and Bear Creeks, while hatchery fish, those with adipose fin clips, were recycled below the TFCF. Cowlitz River coho salmon captured at the Barrier Dam were anesthetized using electro-anesthesia and sampled for sex and origin. In addition, male coho salmon were classified as jacks or adults based on size. Adult salmon captured at the Barrier Dam were transported to their natal watersheds based upon differential marking they received as smolts when they were transported downstream of the Cowlitz dams; since smolts and parr caught at the Mayfield trap were tagged with CWT and not adipose fin clipped, these fish were released in the Tilton River which empties into Mayfield Lake, whereas unmarked adipose intact fish were transported to the Upper Cowlitz and Cispus Rivers where they presumably originated. In addition, adipose clipped hatchery coho salmon were released in the Tilton, Upper Cowlitz and Cispus rivers to provide recreational fishing opportunity and spawners to seed the available habitat. This action is needed because the current juvenile collection at the Cowlitz Falls dam is approximately 30%, too low to support self-sustaining runs (Serl and

Morrill 2009). Other adipose clipped coho salmon collected at the Barrier dam were used for broodstock, or surplused.

Mark-recapture

Fish in good condition were anesthetized, bio-sampled, double Floy (FD 68BC T-bar Anchor tags, Floy Tag & Mfg., Inc. Seattle, WA) tagged and released upstream in Duncan Creek at RM 0.8, Abernathy Creek at RM 0, and Cedar Creek at RM 2. Opercle punches were applied as a secondary mark allowing assessment of Floy tag (ft) loss and assignment of a recovered fish back to the weekly release group in Duncan and Abernathy creeks. In Cedar Creek, an opercle punch was not used, instead a third plastic tag was stapled to the inside of the opercle (op) to assess tag loss. Live recapture events occurred at the Abernathy Fish Technology Center (AFTC) located at RM 4, the Cedar Creek resistance board weir (RM 6). In addition to the recapture events described above, carcass recovery events occurred in Duncan and Abernathy creeks along with re-sight events of live tagged and untagged spawning fish during scheduled weekly spawning ground surveys. Recovery events were concurrent with spawning ground surveys in all creeks. Due to their small size, the sample frame for Duncan and Abernathy Creeks was the entire spawning distribution, which resulted in a redd census rather than a probabilistic sample (e.g., from a GRTS design).

On the North Fork Lewis River, carcasses were tagged to estimate abundance. During weekly spawning ground surveys, untagged carcasses were tagged on both opercles with uniquely numbered plastic tags (McIssac 1977). Tags were placed on the inside of the opercle to limit predation and potential bias in recovery rates due to observation of brightly colored tags. Tagged carcasses were then placed into moving water to facilitate mixing with untagged carcasses (Sykes and Botsford 1986). When tagged carcasses were recovered, surveyors recorded the tag numbers, the tags were removed and fish were marked by removing the tail (denoted as loss on capture in the Jolly-Seber model).

Spawning Ground Surveys.

Redd surveys followed the protocols of Gallagher et al. (2007). The start and end of each survey reach based on the GRTS design was geo-referenced and its coordinates were recorded on a Garmin Oregon 550 unit set in NAD 83. Surveyors typically located the upper most point in the reach and walked downstream to the coordinates at the end of the reach. Surveys were scheduled weekly and followed methods in Rawding et al. (2006a and 2006b). All identifiable redds were flagged and their location (latitudinal and longitudinal coordinates) was recorded. GPS units were allowed to acquire satellite locations until an accuracy of ± 100 feet or less was obtained, most often accuracies ranged from 5 to 50 feet. In subsequent surveys, previously flagged redds were inspected to determine if they should be classified as “still visible” or “not visible”. A redd was classified as “still visible” if it would have been observed and identified without the flagging present, and was recorded as “not visible” if it did not meet this criteria. These data were collected to allow us to estimate the time period redds were visible to surveyors.

In addition, all observed live adult and jack salmonids were recorded by species (Crawford et al. 2007a). Salmon were identified as either spawning or holding. A fish was identified as holding if it was observed in an area not considered spawning habitat, such as pools, in areas of large cobble and boulder riffles (Parken et al. 2003). Salmon were classified as spawners if they were

on redds or not classified as holders. Counts of live adult Chinook, coho, and chum salmon and steelhead were recorded separately for each survey reach. During these surveys, counts of tagged and untagged coho salmon occurred in the Abernathy, Cedar, and Duncan watersheds to provide one potential method to estimate abundance based on a mark-resight estimator (Jacobs et al. 2002).

All coho salmon carcasses that were not totally decomposed were sampled for external tags (Floy T-bar or opercle tags) and sampled for fork length, sex, adipose fin presence, spawn success (females only), DNA, and scales were collected for aging. Sex was determined based on morphometric differences between males and females and/or by cutting open the abdominal cavity to confirm sex and determine spawning success. The spawning success was approximated based on visual inspection, ranging from 100% to 0% success. A fish with 0% success was considered a pre-spawning mortality. Scale samples were collected by selecting scales from the preferred area as described in Crawford et al. (2007b). Preferred scales are samples in an area ~ 1-6 scale rows high, and ~15 scale rows wide, above the lateral line in a diagonal between the posterior insertion of the dorsal fin and anterior insertion of the anal fin. Scale samples were removed with forceps with special care to select scale samples that were of good quality (round shape, non-regenerated) and not adjacent to one another (to minimize the effects of regeneration) as described in a WDFW technical report (Cooper et al. 2011). Scales were placed on the gummed portion of WDFW scale cards with their exterior surfaces facing up. Scale cards were entered into the TWS database (Trap, Weir, Survey database).

All coho carcasses were sampled for CWT following standard protocols (NWMFT 2001). The surface of the CWT wand with radiating arrows was placed in contact with the snout and moved from the right to the left eye, and then up and over the snout area. For large fish, the wand was also inserted into the mouth with the radiating arrows rubbed against the roof of the mouth in vertical strokes. If a CWT is detected, the red LED will light up and a beep is emitted from the wand. When a CWT was detected, the snout was severed by cutting across the head straight down behind the eyes (Crawford et al. 2007b). The snout was placed in a plastic bag with a tag number linking the snout to biological data (length, sex, fin clips, spawning success for females, and scale sample number) recorded on the scale card, stream survey card, or other datasheet. Snouts were stored in a freezer and periodically delivered to the WDFW CWT lab in Olympia for processing.

Sample Processing

Scale Analysis

Scale preparation and analysis followed WDFW protocols (Cooper et al. 2011). Acetate impressions were made of the scale samples by a scale card press, where samples were covered with clear acetate (0.5mm thickness) and pressed under 1200-1300 PSI @ 100 degrees C for 30 seconds to 1 minute. Acetate impressions were then slightly cooled and removed from the scale card. Acetate impressions of scale samples were aged using a modified Gilbert/Rich ageing notation (Groot and Margolis 1991), where annuli are counted along with the scale edge to produce a total age in years. Annuli are defined as an area of narrowly spaced circuli that represent winter/early spring growth. Age was recorded as the total age in years followed by the year at outmigration. For example a typical coho salmon adult is age 3₂. This notation indicates a total age of 3 and the juvenile salmon left its natal freshwater habitat within its second year of

life. After being aged in Olympia by an aging specialist, scale samples were returned to Vancouver for entry into the Age & Scales database.

CWT Lab Analysis

The recovery of CWT tags at the WDFW lab follows the procedures outlined in the tag recovery chapter (Blankenship and Hiezer 1978) of the Pacific Coast Coded Wire Tag Manual and is briefly repeated here. Each snout is passed through a magnetic detector to determine tagged and untagged snouts. Untagged snouts are set aside and rechecked after magnetizing the tag. To ensure the tag is magnetized the length of the tag must pass through the horseshoe magnet in a plane parallel with a straight line collecting the poles. If the tag angle is off more than 40 degrees the tag may not be magnetized. Therefore, the head is passed through the magnet in three positions corresponding to the X, Y, and Z axes and then through the detector. Large heads are often dissected to maximize tag detections. Snouts with no tags detected are saved and an x-ray machine is periodically used to determine tag presence in these “no tagged” snouts. After determining a tag is present, the snout is dissected and the tag is located by process of elimination. After recovering the tag, the binary code is read using a microscope and recorded. CWT data is then entered into WDFW CWT access database, and provided to managers as needed and uploaded into the Regional Mark Information System (RMIS).

Data Analysis

Overview

Coho salmon abundance estimation was relatively straightforward for mark-recapture and trap and haul areas, but required combining multiple sources of information for GRTS survey areas (Figure 3). Briefly, a spawning habitat model developed for the ESU was parameterized with data from each GRTS survey sub-basin to predict the spawning habitat sampling frame. A subsample of reaches in this area was surveyed for redds, live fish, and carcasses, and the mean redd density was multiplied by the spawning habitat frame to estimate total redds for the GRTS sub-basin. Total redds were converted to total females by applying an ESU-wide estimate of redds per female based on the ratio of female abundance to census redd counts in mark-recapture basins. Female abundance was converted to adult abundance which could also be assigned marked and unmarked proportions based on hierarchically modeled sex ratios and marked to unmarked ratios from carcass recoveries in GRTS surveys. Jack abundance was estimated based on total male abundance from an ESU-wide estimate of the proportion of males that were jacks sampling at adult fishway traps.

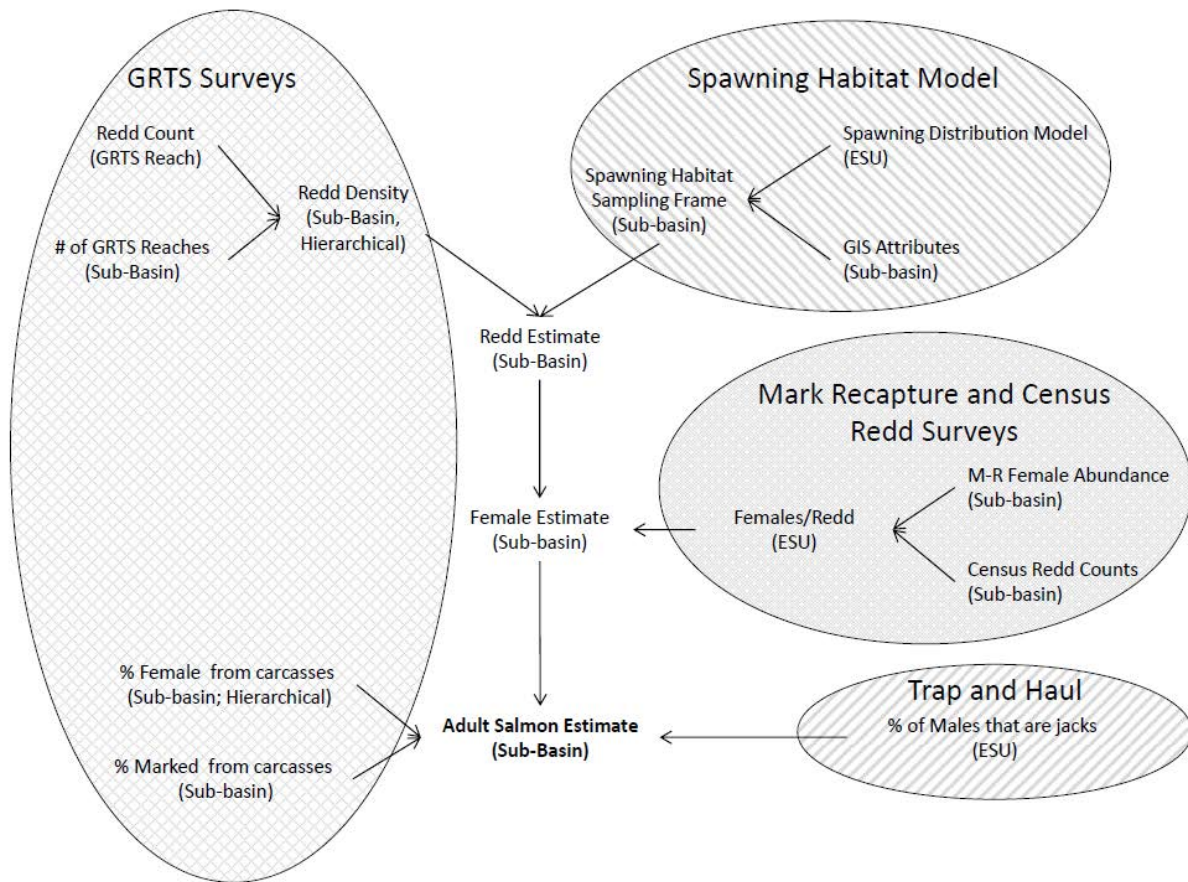


Figure 3. Overview of study design and data inputs used to generate coho salmon abundance estimates for GRTS survey sub-basins. Shaded circles show general information sources while wording describes specific parameters and arrows show how specific parameters were combined to generate estimates. Spatial scales are listed below parameters and hierarchically modeled parameters are noted.

Modeling Approach

Data analysis was conducted using a Bayesian framework. Bayes rule states the posterior distribution, $p(\theta|y)$, is the product of the prior distribution, $p(\theta)$, and the probability of the data given the model or likelihood, $p(y|\theta)$, which is expressed by

$$p(\theta | y) = \frac{p(\theta)p(y|\theta)}{p(y)} \quad (1)$$

Where y are the data, θ are the parameters, and $p(y) = \sum_{\theta} p(\theta)p(y|\theta)$ for all discrete values or $p(y) = \int p(\theta)p(y|\theta)d\theta$ for continuous data (Gelman et al. 2004). The formula of the posterior distribution may be complex and difficult to directly calculate. Samples from the posterior distribution can often be obtained using Markov chain Monte Carlo (MCMC) simulations (Gilks et al. 1995). WinBUGS is a software package that implements MCMC simulations using a Metropolis within Gibbs sampling algorithm (Spiegelhalter et al. 2003) and has been used to estimate abundance and densities in fish and wildlife studies (Rivot and Prevost 2002, Wyatt

2000, Link and Barker 2010). All of the modeling results described in this paper have undergone tests to assess chain convergence and the uncertainty in the parameter estimates due to Markov Chain variability (Plummer et al. 2005, Su et al. 2001). We used multiple chains starting at divergent initial values and monitored the chains until they reached equilibrium, which was assessed visually and using the Brooks-Gelman-Rubin statistic (Lunn et al. 2013). Values less than 1.1 are considered to have converged (Gelman et al. 2004). After discarding the burn-in, iterations before convergence, we monitored the Monte Carlo standard error (MCSE) until it was less than 5% of the standard deviation to obtain accurate parameter estimates (Lunn et al. 2013). We also monitored the estimate of effective parameters; Rafferty and Lewis (1992) suggested that if the effective parameters equaled 4,000 then the estimate of the 2.5% and 97.5% quantiles are within ± 0.01 with a 95% probability. It is therefore assumed that our reported estimates are accurate and represent the underlying stationary distributions of the estimate's parameters.

The mode, median, and mean are commonly reported measures of central tendency for posterior distributions, which are reported in the form of point estimates. The mode is the most frequent value in the dataset. The middle value of the data is the median and the mean is the sum of the numbers in the dataset divided by the numbers in the dataset. For symmetric distributions these measures of central tendency are the same. However, for asymmetric distributions it is not always clear on which measure of central tendency to report. The median is often used because it is intermediate to the mode, which can be a poor choice when it is distant to the middle of the distribution and the mean, which can give substantial weight to extreme values (Carlin and Louis 2009). Many of our estimates include the combination of two distributions (e.g. the number of fish by age which include the multinomial distribution for age and various distributions for abundance). Because these two distributions are often asymmetrical for fish monitoring data when we sum the medians of abundance by age they may not equal the median abundance estimate. Therefore, to limit confusion we have decided that the reported estimate will be the mean, which has a property that the individual estimates sum to the total estimate. The summary table will also include the median and the standard deviation based on the posterior distribution. We reported the equal-tailed or symmetric 95% credible intervals which exclude 2.5% from each tail of the posterior distribution rather than the highest probability interval, which is the shortest 95% interval of the posterior mass and is sometimes preferred (Lee 2004).

We specified vague priors for parameters. First, because this was the first study to estimate coho salmon in the Washington's portion of LCR, there was little prior information. Second, vague priors are developed not to influence the posterior distribution and therefore "let the data speak for themselves". We chose Beta and Dirichlet priors parameterized with $\alpha = \beta = 1, 0.5, \text{ or } 0.01$ for binomial or multinomial distributions, which are referred to as the Bayes-LaPlace, Jefferys', and Haldane, respectively. We used the Jefferys' prior in the model and tested sensitivity using the other priors. For abundance estimates in mark-recapture, we chose a Uniform prior, so that the minimum and maximum bounds did not truncate the posterior distribution. When hierarchical modeling binomial proportions, we chose the logit-normal model with mean having a vague Normal (0,100) and a Uniform (0,100) for the standard deviation (Gelman 2006). We also considered a Gamma (0.001, 0.001) constrained to less than 100 for each of the alpha and beta hyper-priors in the hierarchical models to test the sensitivity of the logit-normal priors.

In some cases we used hierarchical models (e.g., Gelman et al. 2004). For example, we believe that the sex ratio of adult coho salmon in each LCR population should be near 50% females (Sandercock 1991, Dittman et al. 1998), but may vary slightly between populations, and may be subject to measurement error due to small carcass sample sizes. In this case, hierarchical models should adequately describe the percentage of females in each spawning population while allowing the hierarchical posterior distribution of sex ratio estimates to reduce the influence of small sample sizes in contributing to measurement error. Following this same logic, hierarchical models were used to estimate the percentage of jacks within the male population from trap data and to estimate watershed redd density based on the negative binomial distribution, which is appropriate for over-dispersed count data. The hierarchical redd density model was also necessary for some populations because the small number of reaches surveyed resulted in challenges obtaining stable numerical redd density estimates unless the method of moments was used to estimate parameters for the negative binomial distribution.

A key assumption in hierarchical models is that of exchangeability (Kery and Schaub 2012). In our sex ratio model, this means that all the individual population sex ratios are assumed to come from a common distribution of sex ratios for all LCR coho salmon populations, and their ordering does not affect the results. An important characteristic of hierarchical models is that the individual estimates borrow strength from the group estimate. This results in shrinkage of the individual estimates toward the population mean (Gelman et al. 2004). The amount of shrinkage depends on the variance between the populations and their sample sizes. We chose the hierarchical approach as a compromise between treating each population's sex ratio independently and pooling all data to estimate a single sex ratio. An advantage of this approach is less over-fitting of the data than would occur in generating independent estimates for each population, while still accounting for individual variability to influence estimates for a particular population (Kery and Schaub 2012).

Goodness of Fit (GOF) Tests

The purpose of GOF tests are to identify potential inadequacies in the fit of the model to the observed data. One Bayesian approach used for GOF testing is posterior predictive checking, which is a comparison of the posterior predictive distribution of replicated data from the model with the data analyzed by the model (Gelman et al. 2004). In other words, the predictive data ($y.rep_i$) is the expected observation after replicating the study, having observed the data (y_i) and assuming the model is true. When using MCMC simulations, a measure of discrepancy (D) is computed for the actual and replicated datasets for each iteration. An assessment of the posterior distributions of $D(y^{rep}, \theta)$ and $D(y, \theta|y)$ provides individual and overall GOF measures. The posterior or Bayesian p -value = $\Pr(D(y^{rep}, \theta) > D(y, \theta|y))$. The interpretation of the Bayesian p -value is the proportion of the times the discrepancy measure of the replicated data is more extreme than the observed data. If there is a good fit of the model to the data, we would expect the observed data to be similar to the replicated data, resulting in a Bayesian p -value of 0.50 while values near 0 or 1 indicate that the model does not fit the data.

There are many possible types of discrepancy measures including the Freeman-Tukey, standardized Pearson residual, chi-square, and deviance statistics (Brooks et al. 2000, Lunn et al. 2012). Residuals measure the difference between observed and fitted data. The standardized Pearson residual is one measure of this difference and is expressed by

$$r_i(\theta) = \frac{y_i - E(y_i | \theta)}{\sqrt{\text{Var}(y_i | \theta)}} \quad (2)$$

where r_i is an individual residual, y_i is an individual data point, and $E(y_i|\theta)$ is the fitted value of for y_i based on the function to determine the parameters θ . We used standardized Pearson residuals to assess GOF in hierarchical binomial models following Kery (2010). To assess the GOF for redd densities and to test GOF for the recapture portion of the JS model, we used the Freeman-Tukey statistic (Brooks et al. 2000). Our binned redd count data consisted of many zero counts and this test statistic does not require the pooling of bins with small or zero values. The Freeman-Tukey statistic is expressed as

$$d_i(\theta) = \sqrt{y_i} - \sqrt{E(y_i | \theta)} \quad (3)$$

where d_i is an individual discrepancy, y_i is an individual data point, and $E(y_i|\theta)$ is the fitted value of y_i based on the function to determine the parameter θ . When estimating independent values, such as the proportion of hatchery fish in a single population, Bayesian p -values are typically near 0.5. Therefore, we conducted GOF tests for hierarchical estimates and not independent estimates. Although Bayesian p -values are commonly used for model checking, there have been criticisms of this approach. First, it uses the data twice to build and check the model, which may not be as robust as other methods for testing model adequacy (Carlin and Louis 2009, Kery 2010). Second, it is unclear what cut off values to use for the interval (5% to 95%) to indicate lack of model fit. Third, the posterior distribution is influenced by the prior distribution, thus a Bayesian p -value is influenced by the prior distribution (Brooks et al. 2000). These concerns have been addressed, but are beyond the scope of this paper (Gelman et al. 2004, Carlin and Louis 2009, and Brooks et al. 2000). Due to these concerns, we used posterior predictive model checking as a qualitative measure of model adequacy, if a Bayesian p -value indicated the model did not fit the data, we considered this to indicate significant lack of model fit (Link and Barker 2010).

In some cases we tested the probability that one estimate was greater than another. These tests included determining if female density was greater than the density needed to seed habitat and greater than NOAA proposed occupancy rates (Crawford and Rumsey 2010). In these cases we monitored the difference between these two variables and assigned a value of 1 when the first estimate was higher than the second for each iteration. The proportion of times the first estimate was higher than the second estimate was the sum of the “1s” divided by the total iterations. We refer to this probability as a p -value, which is different than the Bayesian p -value described above.

Modeling Approach

In our coho salmon study, data were sparse and thus formal model selection techniques were unlikely to be very informative. Therefore, model development relied more on our knowledge of LCR coho salmon biology and population dynamics than formal model selection (Mäntyniemi and Romakkaniemi 2002). The exception to this was the use of Deviance Information Criteria (DIC) developed by Spiegelhalter et al. (2002) for formal model selection between the Negative

Binomial and Poisson distribution for the redd counts, and model selection for the Jolly-Seber model using carcass tagging to estimate population abundance on the mainstem NF Lewis.

Due to computational challenges it is difficult to estimate Bayes Factors when using MCMC approaches (Ntzoufras et al. 2009, Lunn et al. 2012) and this occurred in mark-recapture model selection. As a practical solution we limited the number of JS models to four (Table 1), and used DIC for model selection:

$$DIC = Dev(\theta_m) + pv \quad (4)$$

where $D(\theta_m)$ is the posterior mean deviance for the model and $pv = Var(D(\theta|Y))/2$ and is a measure of the number of effective terms in the model. We choose pv over the more commonly used pD for an estimate of effective parameters, because pv performs well when there is weak prior information and is invariant to parameterization (Gelman et al. 2004). DIC is a Bayesian analog of Akaike Information Criteria (AIC) but is based on MCMC outputs. Similar to the model support scale developed by Burnham and Anderson (2002), Spiegelhalter et al. (2002) suggested that models ΔDIC of less than 2 have considerable support, models with ΔDIC having 3-7 have less support, and models with $\Delta DIC > 10$ have negligible support.

Table 1. Model notation used for JS carcass tagging (from Lebreton et al. 1992). Models names indicate whether capture, survival, or entrance probabilities were allowed to vary over time (“t”) or were held constant (“s” = same).

Model	Probability of capture (p)	Probability of survival (ϕ)	Probability of entry (b^*)
t t t	varies over periods	varies over periods	varies over periods
s t t	equal over periods	varies over periods	varies over periods
t s t	varies over periods	equal over periods	varies over periods
s s t	equal over periods	equal over periods	varies over periods

Trap & Haul Escapement Estimates

The coho salmon abundance estimate for unmarked adults was simply the number of unmarked coho salmon trapped, hauled, and released into the upper NF Toutle, Tilton, and Upper Cowlitz/Cispus rivers. There were no marked adults released into the upper NF Toutle River. In the Tilton and Upper Cowlitz/Cispus rivers a recreational fishery occurred for marked coho salmon. All anglers retaining a marked coho salmon are required to record the fish on a CRC. At the end of the season, CRCs are returned to WDFW. However, successful anglers are more likely to return CRCs than unsuccessful anglers (Bob Leland, WDFW, pers. comm.). To account for this bias, WDFW contacts a random sample of anglers not returning their CRC by mail and they are reminded to turn in their CRC. Phone calls are then made to a random set of anglers receiving the reminder that still did not return their CRC in order to obtain their harvest information (Eric Kraig, WDFW pers. comm.). For each month the mean catch and variance are estimated (Kraig 2014). To obtain the total marked catch, the means and variances are summed. Therefore, we estimate the marked catch of adults and jacks by

$$Ad_Catch_j \sim Normal(a\mu_j, asd_j) \quad (5)$$

$$J_Catch_j \sim Normal(j\mu_j, jsd_j) \quad (6)$$

where Ad_Catch and J_Catch is the estimated catch assuming a normal distribution, $a\mu$ and $j\mu$ are the means for the adult and jack marked catch, asd and jsd are the standard deviation for the adult and jack marked catch, and j is an index for the Tilton and Upper Cowlitz/Cispus populations. The escapement of marked adults and jacks is the number trapped and hauled minus the catch

$$ATHm_j = AHm_j - Ad_Catch_j \quad (7)$$

$$JTHm_j = JHm_j - J_Catch_j \quad (8)$$

where $ATHm$ and $JTHm$ is the estimated adult and jack escapement and AHm and JHm are the number of transported adults and jacks, respectively.

Mark-Recapture Adult Escapement Estimates

Adult salmon escapement estimates were made using Peterson mark-recapture methods in Duncan, Abernathy, and Cedar creeks. The tagging event occurred near the mouth and the recovery events consisted of recoveries of live fish at adult traps upstream of the tagging site in Abernathy and Cedar creeks, and carcass recoveries in all three creeks during spawning ground surveys. Due to the sparseness of data and the results from 2010 (Rawding et al. 2014) we used the pooled Petersen estimator to estimate abundance by

$$rb_h \sim Binomial(q_h, tb_h) \quad (9)$$

$$cb_h \sim Binomial(q_h, Nb_h) \quad (10)$$

where tb , rb , and cb are the number of tagged, recaptured or re-sighted fish, and fish captured or observed in the second sample, respectively. The recapture efficiency and the population estimate are denoted by q and Nb and estimated by:

$$q_h \sim Beta(a, b) \quad (11)$$

$$Nb_h \sim Uniform(\min, \max). \quad (12)$$

This was assessed in 2010 with double tagging experiments and marking experiments. Since the mark was permanent and the low tag loss was observed in our 2010 study (Rawding et al. 2014), we did not assess tag loss in 2012.

We parameterized the Schwarz et al. (1993) “super population” JS model into a Bayesian framework. Rather than using individual capture histories we used summary statistics to increase the computational speed (Table 2). It is important to note that in the more popular Schwarz and Arnason (1996) model the super population and other fundamental parameters are based on births while in the Schwarz et al. (1993) model the super population is the total of gross births or salmon escapement (Table 3). This model allows salmon escapements to be hierarchically modeled (Rivot and Prevost 2002) and probability of entry to be modeled based on various distributions (Hilborn et al. 1999). Derived parameter estimates in Table 4 are based on Schwarz et al. (1993) and Manske and Schwarz (2000). We included the later author’s derived estimates for cases when the mark-recapture study ends early, as they proposed a method to

estimate escapement based on the residence time estimated from the mark-recapture data and AUC method, which is a plot of the population size at each sampling period. The JS likelihood is the product of three likelihoods: 1) the probability of first capture based on a super population (N) that enter the population (b^*_i) following a multinomial distribution, 2) the probability of release on capture (v_i) from a binomial distribution using total fish sampled (n_i) and number of n_i that are released (R_i), and 3) the probability of recapture which is the product of two binomial distributions to estimate the probability of capture (p_i) and survival (ϕ_i) (Burnham 1991) (Table 5).

Table 2. Summary statistics used in the Jolly-Seber model.

Statistic	Definition/Equation
m_i	Number of fish captured at sample time i that were previously marked.
u_i	Number of fish captured at sample time i that were unmarked.
n_i	Number of fish captured at sample time i . $n_i = m_i + u_i$.
l_i	Number of fish lost on capture at time i .
R_i	Number of fish that were released after the i th sample. R_i need not equal n_i if there were losses on capture or injections of new fish at sample time i .
r_i	Number of R_i fish released at sample time i that were recaptured at one or more future sample times.
z_i	Number of fish captured before time i , not captured at time i , and captured after time i .
T_i	Number of fish captured at before time i and captured at or after time i . $T_i = m_i + z_i$.

Table 3. Fundamental parameters for the Jolly-Seber model under the salmon escapement super population model (Schwarz et al. 1993).

Parameter	Definition/Equation
s, tm	Number of sample times and length of interval between samples
p_i	Probability of capture at sample time i , $i = 1, \dots, s$.
ϕ_i	Probability of a fish surviving and remaining in the population between sample time i and sample time $i + 1$, given it was alive and in the population at sample time i , $i = 1, \dots, s-1$.
b^*_i	Probability that a fish enters the population between sample times i and $i + 1$, $i = 0, \dots, s-1$ under the constrain that $\sum b^*_i = 1$. These are referred to as entry probabilities.
v_i	Probability that a fish captured at time i will be released, $i = 1, \dots, s-1$.
N	Total number of fish that enter the system before the last sample time or the escapement. This is referred to as the super population.

Table 4. Derived parameters for the Jolly-Seber model under the salmon escapement super population model (Schwarz et al. 1993) and the stream residence time model (Manske and Schwarz 2000).

Parameter	Definition/Equation
λ_i	Probability that a fish is seen again after sample time i , $i = 1, \dots, s$. $\lambda_i = \varphi_i p_{i+1} + \varphi_i (1 - p_{i+1}) \lambda_{i+1}$, $i = 1, \dots, s-1$; $\lambda_s = 0$.
τ_i	Conditional probability that a fish is seen at sample time i given that it was seen at or after sample time i , $i = 1, \dots, s$. $\tau_i = p_i / (p_i + (1 - p_{i+1}) \lambda_i)$.
ψ_i	Probability that a fish enters the population between sample time $i-1$ and i and survives to the next sampling occasion. $\psi_i = b^*_i$, $\psi_{i+1} = \psi_i (1 - p_i) \varphi_i + b^*_i (\varphi_i - 1) / \log(\varphi_i)$
B_i	Number of fish that enter after sample time i and survive to sample time $i+1$, $i = 0, \dots, s-1$. These are referred to as net births. $B_0 = B^*_0$, $B_i = B^*_i (\varphi_i - 1) / \log(\varphi_i)$.
B^*_i	Number of fish that enter between sampling occasion $i-1$ and i , $i = 0, \dots, s-1$. These are referred to as gross births. $B^*_i = N (b^*_i)$
N_i	Population size at time i , $i = 1, \dots, s$. $N_1 = B_0$, $N_{i+1} = (N_i - n_i + R_i) \varphi_i + B_i$
N^-_i	Number of fish alive immediately before sample time i , $i = 1, \dots, s$. $N^-_1 = B_0$; $N^-_{i+1} = N^+_i \varphi_i + B_i$
N^+_i	Number of fish alive immediately after sampling time i , $i = 1, \dots, s$. $N^+_i = (N_i - n_i + R_i)$. N^+_i may differ from N_i if there were losses on capture or injections of new fish.
RT	Average residence time; for $i = 1, \dots, s-1$. $RT = 0.5 \sum t m_i N^+_i (\varphi_i + 1) + 0.5 t m_s N^+_s + 0.5 t m_0 B_0 + \sum B_i t m_i (\varphi_i / \varphi_{i-1} - 1 / \log(\varphi_i))$
AUC	Aggregate residence time over all spawner. This is referred to as the total fish days or Area-Under-the-Curve. $AUC = 0.5 t m_0 N^-_1 + \sum 0.5 t m_i (N^+_i + N^-_i) + 0.5 t m_s N^+_s$.
ESC	Escapement. $ESC = AUC / RT$. This is slightly greater than N , which is also a measure of escapement due to accounting for fish before and after sampling.

Table 5. The likelihoods for the Schwarz et al. (1993) model

Description	Likelihood
Pr(first capture part a)	$u_i \sim \text{Binomial}(\sum \psi_i p_i, N)$, $i = 0, \dots, s-1$. $u_i = \sum u_i$
Pr(first capture part b)	$u_i \sim \text{Multinomial}(\psi_i p_i / \sum \psi_i p_i, u_i)$, $i = 0, \dots, s-1$.
Pr(release on capture)	$R_i \sim \text{Binomial}(v_i, n_i)$, $i = 1, \dots, s-1$.
Pr(recapture part a)	$m_i \sim \text{Binomial}(\tau_i, T_i)$, $i = 2, \dots, s-1$.
Pr(recapture part b)	$r_i \sim \text{Binomial}(\lambda_i, R_i)$, $i = 1, \dots, s-1$.

Expanded Smolts Abundance Estimates

Weekly redd surveys were not conducted over the entire spawning area in Mill and Germany creeks so adult abundance in these watersheds was estimated by applying the smolt-to-adult return rate (SAR) from neighboring Abernathy Creek to smolt estimates from these basins. Smolt estimates following standard protocols are available for Mill, Germany, and Abernathy Creeks (Mara Zimmerman, WDFW, unpublished data), and a mark-recapture estimate is available for adults in Abernathy Creek. The Abernathy Creek SAR was estimated for Abernathy Creek by

$$Ab_SAR = AMRum_2 / Ab_smolts \quad (13)$$

where Ab_SAR is the Abernathy Creek smolt to adult return rate, Ab_smolts is the estimated smolt outmigration in 2009, and $AMRum_2$ is the mark-recapture estimate of adult abundance for unmarked fish. The unmarked adult abundance for Mill and Germany creeks is estimated by

$$ASum_f = smolts_f / Ab_SAR \quad (14)$$

where $ASum$ is the unmarked adult abundance estimate using the smolt expansion method and $smolts$ is the estimated smolt abundance from Mill and Germany creeks in 2009 based on a stratified estimator (Volkhardt et al. 2007).

Redd based Abundance Estimates

To estimate the adult coho salmon spawning escapement, the following estimates are required: 1) the number of redds per female, 2) the proportion of adult spawners that are females, and 3) the total number of redds in the population. In Duncan and Abernathy creeks we estimated the total abundance based on a mark-recapture study above trapping sites located at the mouth of these creeks (equations 9, 10, 11 and 12). Morphometric characteristics of live fish and carcass recoveries were used to estimate the proportion of females and the number of female spawners by

$$FMR_h \sim Binomial(pFMR_h, AMR_h) \quad (15)$$

$$NbF_h = pFMR_h * Nb_h \quad (16)$$

$$pMC_k \sim Beta(a, b) \quad (17)$$

where FMR and AMR are the number of unique females and adults sampled in the mark-recapture study, respectively, while $pFMR$ is the proportion of female adults in the mark-recapture study and NbF is the estimated number of female spawners in the population. The redd counts and female spawners from Duncan and Abernathy creeks were summed and the redds per female was estimated using the Binomial distribution with a Beta distribution for the proportion of females by

$$MRF = \sum_{h=1}^2 NbF_h \quad (18)$$

$$DA_redds \sim Bin(RpF, MRF) \quad (19)$$

$$RpF \sim Beta(a, b) \quad (20)$$

where MRF is the sum of the mark-recapture estimate of females in Duncan and Abernathy creeks, DA_redds is the sum of the Duncan and Abernathy creek redd counts, and RpF is the estimated number of redds per female.

For each one mile redd survey reach, the sum of the new redds counted was the redd density for that reach. To estimate the redd density for the sampled reaches, parametric statistics were not considered due to concerns about the lack of fit using standard sampling theory (Courbois et al. 2008). The starting point for analysis of count data is often the Poisson distribution. However, in the Poisson distribution the mean is equal to the variance, which is often an unrealistic

assumption for count data. The negative binomial distribution is a more flexible distribution for the analysis of count data and allows for over dispersion in count data (Link and Barker 2010). The Poisson distribution is a special case of the negative binomial distribution as the over dispersion parameter approaches ∞ the Poisson distribution is recovered (Hilborn and Mangel 1997). Redd counts were modeled using a hierarchical negative binomial distribution, with an adjustment to accommodate WinBUGS parameterization by

$$y_{ik} \sim \text{NegativeBinomial}(p_k, r_k) \quad (21)$$

$$\mu_k = r_k * (1 - p_k / p_k) \quad (22)$$

where y is the number of redds in reach i for population k , with hyperparameters p and r . Both hyperparameters were assigned vague hyperpriors including

$$\text{logit}(p_k) \sim \text{Normal}(p_mu, p_sd) \quad (23)$$

$$r_k \sim \text{Gamma}(a_1, a_2) \quad (24)$$

$$p_mu \sim \text{Normal}(0,100) \quad (25)$$

$$p_sd \sim \text{Uniform}(0,100) \quad (26)$$

where the a , b , p_mu , and p_sd are the hyperpriors.

The redd density for each population is estimated by

$$\lambda_k \sim \text{NegativeBinomial}(p_k, r_k) \quad (27)$$

where λ is the redd density. Ntzoufras (2009) noted that the dispersion index is equal to $\text{Var}(Y)/E(Y)$. This is estimated by

$$DI_k = 1 / p_k \quad (28)$$

where DI is the dispersion index and p is the hyperparameter of the negative binomial distribution. Since by definition the variance equals the mean for the Poisson distribution, a dispersion index greater than one indicates support for the Negative Binomial over the Poisson distribution for each population, which was assessed with a Bayesian GOF test. The female and adult redd density, and the proportion of females are estimated by

$$FD_k = \lambda_k / RpF \quad (29)$$

$$AD_k = FD_k / pF_k \quad (30)$$

$$FC_k \sim \text{Binomial}(pF_k, AC_k) \quad (31)$$

where FD is the female density, AD is the adult density, pF is the proportion of females, FC is the number of female carcasses, and AC is the number of adult carcasses. We estimate p -values to estimate the probability that our observed female redd densities for each population was

greater than the mode of the female density required to seed freshwater habitat from Bradford et al. (2000). The proportion of females was hierarchically modeled by

$$\text{logit}(pF_k) \sim \text{Normal}(pF_mu, pF_sd) \quad (32)$$

$$pF_mu \sim \text{Normal}(0,100) \quad (33)$$

$$pF_sd \sim \text{Uniform}(0,100) \quad (34)$$

where pF_mu and pF_sd are the hyperpriors.

The total escapement based on redd surveys was estimated by

$$AT_k = \left(y_k + yc_k + \sum_{i=1}^{\text{mis_miles}} \lambda_k \right) / RpF \quad (35)$$

where y is the observed number of redds in GRTS reaches, yc is the number of redds in non GRTS reaches (typically index Chinook or chum salmon reaches), λ is the redd density, and mis_miles is the number of unsurveyed miles in the GRTS sampling frame from which to expand redd counts in GRTS reaches.

Estimates of Hatchery and Wild Adults

We used the carcasses collected during the stream surveys to estimate the proportion of marked and unmarked adults by

$$MC_k \sim \text{Binomial}(pMC_k, SC_k) \quad (36)$$

$$pUMC_k = 1 - pMC_k \quad (37)$$

$$pMC_k \sim \text{Beta}(a, b) \quad (38)$$

where MC_k is the number of marked adult carcasses sampled, SC_k is the number of sampled adult carcasses, pMC_k is the proportion of marked adults based on the carcasses sampled, and $pUMC_k$ is the proportion of unmarked adults. The estimated number of marked and unmarked adult coho salmon based on the stream surveys was estimated by

$$ARm_k = pMC_k * AT_k \quad (39)$$

$$ARum_k = pUMC_k * AT_k \quad (40)$$

where ARm_k is the estimate of marked adults and $ARum_k$ is the estimate of unmarked adult coho salmon. The same equations (36-38) were used to estimate the proportion of marked and unmarked adults in the mark-recapture studies except the subscript used was h instead of k to denote the difference between the mark-recapture and redd based proportions. Equations 36 to 38 were used to estimate the marked and unmarked adult abundance in the mark-recapture estimates.

Combining Data Sources to Generate Population Estimates

Finally, the adult marked and unmarked abundance estimates from redd, mark-recapture, and trap and haul methods were summed as needed to estimate population abundance. These population abundances were summed to estimate the total adult coho salmon abundance below Bonneville Dam except for areas not sampled including the mainstem of the Toutle, lower NF Toutle, and Cowlitz rivers.

Estimating the Proportion of Males that are Jacks

Due to differential capture probabilities between jack and adult coho salmon carcasses during spawning ground surveys, we applied an aggregate estimate of the proportion of males that were jacks obtained from weirs and trap & haul operations to areas where redd counts were used. We used a hierarchical model to estimate the proportion of male coho salmon that were jacks based on trap data at Cedar Creek, Cowlitz Barrier Dam, and TFCF, and we used the subscript g to denote these four groups. The proportion of jacks was estimated by

$$TJ_g \sim \text{Binomial}(pJ_g, TM_g) \quad (41)$$

$$\text{logit}(pF_g) \sim \text{Normal}(pJ_mu, pJ_sd) \quad (42)$$

$$pJ_mu \sim \text{Normal}(0,100) \quad (43)$$

$$pJ_sd \sim \text{Uniform}(0,100) \quad (44)$$

where TJ_g is the count of jacks at a trap, TM_g is the number of trapped males, pJ_g is the proportion of jacks. We used the same hierarchical equations and priors based on the logit-normal distribution as in equations 32-34 provided in 42-44. The jack abundance for each population was estimated by

$$Jtot_k = AT_k * (1 - pF_k) * \text{mean}(\text{hier_}pJ) \quad (45)$$

where $Jtot_k$ is the estimate of jacks within the population where AT_k is the adult abundance from the redd or mark-recapture estimate, pF_k is the proportion of females, and $\text{mean}(\text{hier_}pJ)$ is the mean of the hierarchical estimate of the proportion of males that are jacks. .

Estimating the Proportion of One-Mile Reaches Occupied by Coho Salmon Spawners

The spawning reach occupancy rate of coho salmon was based on the redd surveys and estimated by

$$Oc_k \sim \text{Bin}(pOc_k, m_k) \quad (46)$$

where OC_k is the number of reaches in which at least one redd was observed, m_k is the number of reaches, and pOC_k is the percent of reaches occupied. In addition, we estimated the probability that 80% of the reaches in a population were occupied by recording the number of iterations the occupancy rate exceeded 80% by

$$p80Oc_k = pOc_k - 0.80 \quad (47)$$

where $p80OC_k$ is the probability that 80% of the surveyed reaches were occupied.

Results

Model convergence and diagnostics

We ran two chains with a thinning rate of 10 using the Gibbs sampler in WinBUGS. After discarding the 5,000 burn-in iterations, a total of 20,000 iterations for the posterior distribution of each parameter were saved. Visual inspection of the history plots suggested the chains mixed and converged. The BGR diagnostic test for convergence yielded values of less than 1.09 for each parameter, which is less than the recommended value of 1.1. While it is impossible to conclusively demonstrate a simulation has converged, the above diagnostic tests did not detect that the simulations did not converge. The MCSE was 1% of the standard deviation of the parameter estimates, which suggests our posterior distributions were accurate. In addition, the estimates effective number of parameters ranged from 1,200 to 20,000 for all monitored parameters but for the adult abundance parameters the minimum was 3,500 suggesting sufficient iteration for accurate estimates of 95% CI. It should be noted that some numbers presented in this report may not sum due to rounding.

We tested the sensitivity of our analysis based on the various priors. We used three vague priors for the beta distribution ($\alpha = \beta = 0.5, 1, \text{ and } 0.01$), which correspond to Jeffreys, LaPlace-Bayes, and Haldane priors. We used vague hyper-priors for the binomial and negative binomial hierarchical models based on the gamma distribution (0.001, 0.001) and normal distribution (0, 0.001) for the mean and a uniform distribution (0, 100) for the standard deviation for logit-normal model. Our results were not sensitive to the priors or hyperpriors except when we had few recoveries in some weeks during the NF Lewis River JS population estimate. In addition, for hierarchical models the logit-normal provided slightly better mixing than the Gamma distribution. Our population abundance estimates were similar for all priors and the results reported here are based on Jeffreys prior for the beta distribution, the logit-normal priors for the hierarchical binomial and negative binomial models mentioned above.

Trap and Haul Abundance Estimates

A total of 84 unmarked adult and 12 jack coho salmon were collected and released above the TFCF on the NF Toutle River (Table 6). These numbers are the total escapement above the TFCF. A total of 6,505 and 1,583 marked adult and jack coho salmon, respectively, were collected at Barrier Dam on the Cowlitz River and released into the Tilton River. Subtracting the fishery impacts for mass marked coho salmon left a mean Tilton River escapement of 5,193 and 1,465 marked adults and jacks, respectively. In addition, 1,442 unmarked adults and 142 unmarked jacks were released in the Tilton River and were not available for harvest, so were assumed to have spawned. For the Cowlitz/Cispus population a total of 5,334 and 2,917 marked adults and jacks, respectively, were captured at Barrier Dam and released above Cowlitz Falls Dam (CFD). Subtracting the expanded CRC catch of marked coho salmon leaves a mean escapement of 5,143 and 2,895 marked adults and jacks, respectively. Since we assumed no fishery impacts for unmarked fish, the Upper Cowlitz/Cispus escapements were the same as the release totals of 1,689 and 70 unmarked adults and jacks, respectively.

The proportion of male coho salmon that were classified as jacks was relatively consistent at three of four locations and ranged from 15.5% at the Cowlitz Barrier Dam to 43.4% on Abernathy Creek (Table 7). The Bayesian p -values ranged from 0.50 to 0.54 for these three populations based on an analysis of Pearson's residuals, which do not indicate any problems with

the GOF test for these data using the hierarchical model. The mean proportion of males that were jacks based on the hierarchical model for the trap data was 26.8%.

Table 6. Trap and haul counts at North Toutle Fish Collection Facility (TFCF), Cowlitz Barrier Dam counts transported to the Tilton and Upper Cowlitz/Cispus rivers, estimate of recreational harvest of marked fish, and marked and unmarked escapement in 2012.

Parameter	mean	sd	2.50%	50%	97.50%
Toutle FCF Unmarked Adult Release	84	---	---	---	---
Toutle FCF Unmarked Jack Release	12	---	---	---	---
Upper Cowlitz Unmarked Adult Release	1,689	---	---	---	---
Upper Cowlitz Unmarked Jack Release	70	---	---	---	---
Tilton Unmarked Adult Release	1,444	---	---	---	---
Tilton Unmarked Jack Release	142	---	---	---	---
Upper Cowlitz Marked Adult Release	5,334	---	---	---	---
Upper Cowlitz Marked Jack Release	2,917	---	---	---	---
Tilton Marked Adult Release	6,505	---	---	---	---
Tilton FCF Marked Jack Release	1,583	---	---	---	---
Upper Cowlitz Marked Adult Catch	191	39	115	191	266
Upper Cowlitz Marked Jack Catch	22	13	0	22	47
Tilton Marked Adult Catch	1,312	126	1,065	1,311	1,560
Tilton Marked Jack Catch	118	30	59	118	178
Tilton Marked Adult Escapement	5,193	126	4,945	5,194	5,440
Tilton Marked Jack Escapement	1,465	30	1,406	1,465	1,524
Upper Cowlitz Marked Adult Escapement	5,143	39	5,068	5,143	5,219
Upper Cowlitz Marked Jack Escapement	2,895	13	2,870	2,895	2,920

Table 7. Estimates of the proportion on male coho salmon that are jacks from trap data at the North Toutle Fish Collection Facility (TFCF), Cowlitz at Barrier dam, Abernathy trap, and Cedar trap in 2012.

Subpopulation	mean	sd	2.50%	50%	97.50%
Proportion of jacks (Toutle FCF)	15.5%	3.9%	8.6%	15.2%	23.7%
Proportion of jacks (Cowlitz-Barrier Dam)	43.4%	0.4%	42.5%	43.4%	44.2%
Proportion of jacks (Abernathy)	20.4%	3.7%	13.5%	20.2%	28.1%
Proportion of jacks (Cedar)	24.9%	2.3%	20.6%	24.9%	29.5%
Mean proportion of jacks	26.8%	13.8%	5.4%	24.9%	64.4%

Adult Mark-Recapture Results

For the JS model used to estimate carcass abundance on the NF Lewis river, DIC favored the tst model. The Δ DIC was 10.13 compared to the next best model, which was the stt model.

Bayesian p -values indicated that all models adequately fit the data so the tst model was therefore chosen. Abundance estimates were relatively similar across all models, thus not very sensitive to model choice, but the abundance estimates were higher using the Jeffreys prior for ϕ

and ρ compared to the uniform prior. The estimated escapement was 471 adult coho salmon with approximately 85% unmarked fish (401) (Table 8). Period abundance was low at the start of the study, peaked in the middle and declined toward the end.

Table 8. The estimated total, marked and unmarked escapement in the NF Lewis River in 2012 and the estimated escapement by period (Bstar).

Parameter	mean	sd	2.50%	50%	97.50%	CV
Escapement	471	86	334	460	669	18%
Unmarked Escapement	401	75	283	392	572	19%
Marked Escapement	70	19	40	67	114	27%
Bstar[1]	83	29	39	79	152	35%
Bstar[2]	65	41	7	58	163	63%
Bstar[3]	110	46	39	103	217	42%
Bstar[4]	107	45	29	102	207	42%
Bstar[5]	41	31	2	35	116	76%
Bstar[6]	45	30	3	40	118	67%
Bstar[7]	14	13	0	10	46	93%
Bstar[8]	7	8	0	5	28	106%

For other mark-recapture populations, the tagged adult recovery efficiency based on live fish ranged from 8% to 25%. The adult abundance estimates ranged from a low of 61 in Duncan Creek to 2,031 in Cedar Creek. The proportion of unmarked adults was high in both Abernathy Creek (99%) and Cedar Creek (86%). The estimates of marked and unmarked adult abundance with 95% CI for these creeks are found in Table 9. The number of female spawners in Duncan and Abernathy creeks was 17 and 118, respectively. The proportion of females was similar at both locations (Table 9). The estimate of redds per female for our study was 0.567 (95% CI 0.271 - 0.957). This estimate (0.567) equates to a detection efficiency (number of redds observed out of those actually constructed) of 57% if we assume one redd per female coho salmon.

Table 9. Results for mark-recapture populations in 2012 including estimates of mark-recapture tag recovery efficiency; total, unmarked, and marked adult escapement; proportions of marked, unmarked spawners, and female escapement; proportion of females; and redds per female.

Parameter	mean	sd	2.50%	50%	97.50%
Mark Recovery Efficiency					
Abernathy Creek	8.2%	2.1%	4.5%	8.1%	12.8%
Cedar Creek	25.7%	4.2%	18.1%	25.5%	34.5%
Duncan Creek	21.3%	7.7%	10.1%	19.9%	40.0%
Adult Escapement					
Abernathy Cr. (Total)	260	96	131	243	496
Abernathy Cr.(Unmarked)	252	94	126	235	481
Abernathy Cr. (Marked)	8	12	0	4	42
Cedar Cr. (Total)	2,032	355	1,461	1,991	2,839
Cedar Cr. (Unmarked)	1,739	305	1,246	1,705	2,430
Cedar Cr. (Marked)	293	60	196	286	430
Duncan Cr. (Total)	61	20	26	60	97
Proportion of Marked and Unmarked Adults					
Abernathy Cr.(Marked)	1.5%	4.2%	3.9%	1.3%	0.2%
Abernathy Cr. (Unmarked)	98.5%	1.0%	96.1%	98.7%	99.8%
Cedar Cr. (Unmarked)	85.6%	1.6%	82.4%	85.6%	88.5%
Cedar Cr. (Marked)	14.4%	2.9%	17.6%	14.4%	11.5%
Female Escapement, Proportions, and Redds per Female					
Duncan Cr. Female Escapement	17	9	4	15	38
Abernathy Cr. Female Escapement	118	45	59	110	227
Proportion of Females (Duncan)	27.4%	10.7%	9.3%	26.5%	50.6%
Proportion of Females (Abernathy)	45.4%	3.9%	37.9%	45.3%	53.2%
Redds per Female (Duncan & Abernathy)	0.567	0.179	0.271	0.545	0.957

SAR Expansion Adult Estimates

The 2011 coho salmon smolt emigration estimates ranged from 6,744 in Germany Creek to 14,298 in Mill Creek (Table 10). The 2011 smolt to adult return (SAR) in Abernathy Creek was 1.8% (95% CI 0.7% - 3.5%). Coho salmon escapement based on smolt abundance and Abernathy Cr. SAR in Mill and Germany creeks was 210 and 124 adults, respectively (Table 10). Unmarked and marked adult abundance in these basins based on the proportion of marked adults in Abernathy Cr. is also provided in Table 10.

Table 10. Estimates of 2011 smolt abundance and Smolt to Adult Return rate (SAR), and 2012 total, unmarked, and marked coho spawner abundance based on SAR expansions for Germany and Mill creeks.

Parameter	mean	sd	2.50%	50%	97.50%
2011 Smolt Abundance Estimate					
Abernathy Cr.	14,298	1,270	11,809	14,298	16,787
Germany Cr.	6,744	809	5,158	6,744	8,330
Mill Cr.	11,425	765	9,926	11,425	12,924
2011 Smolt to Adult Return					
Abernathy Cr.	1.78%	0.68%	0.86%	1.65%	3.47%
2012 Adult Escapement Estimates based on SAR Expansions					
Germany Cr. (Total)	124	50	57	114	246
Germany Cr. (Unmarked)	120	49	55	111	240
Germany Cr. (Marked)	4	6	0	2	20
Mill Cr. (Total)	210	81	101	194	411
Mill Cr. (Unmarked)	203	79	97	188	398
Mill Creek (Marked)	7	10	0	3	34

Redd Based Estimates

A total of 186 reaches across 13 populations were surveyed as part of the GRTS design (Appendix 1). The number of sites ranged from 6 to 24 per population and averaged 14 (Appendix 1). The mean dispersion index for the redd data ranged from 4.3 to 21.5 and the lower 95% CI exceeded 2.2, which all exceeded the expected dispersion index of 1 from the Poisson distribution (Table 11). The NB GOF test indicated the probability that the replicated dispersion index based on the Negative Binomial model was more extreme than the dispersion index, and based on the observed data, ranged from 0.05 to 0.95. The P GOF test indicated the probability that the replicated dispersion index based on the Poisson model was more extreme than the dispersion index, and based on the observed data, was between 0.00 and 0.13. This provides strong evidence that the data are over dispersed and are consistent with the Negative Binomial model, but not consistent with the Poisson model.

Table 11. The estimated dispersion index for the negative binomial distribution from GRTS surveys in 2012. The last two columns are a Bayesian p -values for GOF tests to measure the probability that the dispersion index is less than 1 (NB GOF), which would favor the Poisson distribution, or if the probability that the dispersion index is 1 which would favor the Poisson model (P GOF).

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	NB GOF	P GOF
Grays/Chinook	5.12	2.94	2.26	4.35	12.37	0.29	0.00
Elochoman/Skamakowa	4.26	1.76	2.18	3.85	8.69	0.67	0.00
Coweeman	18.58	7.48	9.21	17.04	37.48	0.59	0.00
NF Toutle	13.26	8.86	5.30	11.06	34.20	0.05	0.00
Green	6.12	2.13	3.21	5.71	11.36	0.89	0.00
SF Toutle	17.87	8.89	8.11	15.75	40.27	0.52	0.00
Kalama	5.78	3.39	2.35	4.91	14.28	0.61	0.00
NF Lewis	7.27	6.62	2.41	5.81	20.41	0.20	0.00
Cedar	5.28	2.02	2.68	4.88	10.35	0.92	0.01
EF Lewis	21.54	11.26	9.72	18.85	49.34	0.44	0.00
Salmon	7.44	4.58	3.01	6.32	18.25	0.21	0.00
Washougal	6.32	3.25	2.71	5.53	14.32	0.91	0.13
Lower Gorge	8.44	5.08	3.30	7.17	20.84	0.49	0.00

The hierarchical modeled redd densities followed a highly skewed (right-tailed) distribution, resulting in a mean being greater than the median. The observed mean redd density ranged from 1.3 to 11.1 (Table 12). The Bayesian p -values for the hierarchical Negative Binomial model for count data ranged from 0.08 to 0.88, indicating no significant lack of fit for the GOF test based on Freeman-Tukey test statistics. The Bayesian p -values from the Poisson model were not consistent with the data and 7 of 13 p -values were less than or equal to 0.02.

Table 12. Observed coho salmon redds per mile based on the negative binomial distribution from GRTS surveys in 2012. The last two columns are a Bayesian p -values for a GOF test to measure if the data are consistent with the Negative Binomial and Poisson models.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	NB GOF	P GOF
Grays/Chinook	1.25	2.81	0	0	9	0.30	0.01
Elochoman/Skamakowa	1.64	2.79	0	1	9	0.59	0.27
Coweeman	11.07	15.13	0	6	54	0.35	0.00
NF Toutle	4.36	9.64	0	1	27	0.35	0.00
Green	3.45	4.95	0	2	17	0.61	0.00
SF Toutle	8.63	13.58	0	4	45	0.09	0.00
Kalama	2.17	4.05	0	1	13	0.61	0.20
NF Lewis	2.35	5.18	0	1	15	0.44	0.08
Cedar	2.71	4.11	0	1	14	0.88	0.28
EF Lewis	10.19	16.40	0	4	56	0.08	0.00
Salmon	3.08	5.54	0	1	18	0.81	0.23
Washougal	3.08	5.01	0	1	17	0.19	0.02
Lower Gorge	3.95	6.70	0	2	22	0.60	0.06

Based on the mark-recapture estimates and redd census, we expanded the redd counts by 0.567 observed redds per female (Table 9) to convert the estimated redds to females (Table 13). The mean females per mile estimates ranged from 2.5 to 21.9. Based on a meta-analysis, Bradford et al. (2000) found the mode of female coho salmon per mile needed to seed freshwater habitat was 15 females. The probability that our population estimates exceeded 15 females per miles ranged from 0.03 to 0.41.

Table 13. The estimated number of coho salmon females/mile based on GRTS surveys in 2012. The p-value is the probability the observed female density is greater than the mode of the full habitat seeding density based on Bradford et al. 2000.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	p-value
Grays/Chinook	2.45	5.98	0.00	0.00	17.66	0.03
Elochoman/Skamakowa	3.24	6.17	0.00	1.16	19.56	0.04
Coweeman	21.85	33.43	0.00	10.55	109.40	0.41
NF Toutle	8.51	18.70	0.00	2.17	55.67	0.17
Green	6.83	10.64	0.00	3.12	35.78	0.13
SF Toutle	17.03	29.34	0.00	6.77	93.39	0.32
Kalama	4.24	8.49	0.00	1.44	26.06	0.07
NF Lewis	4.59	10.60	0.00	1.11	30.48	0.08
Cedar	5.32	8.73	0.00	2.30	28.41	0.09
EF Lewis	20.03	34.46	0.00	7.93	112.50	0.36
Salmon	6.04	11.71	0.00	2.05	36.00	0.11
Washougal	6.06	10.70	0.00	2.36	34.27	0.11
Lower Gorges	7.79	14.31	0.00	2.93	45.29	0.15

Using the hierarchical model we estimated the mean proportion of females among all adult coho salmon was 43.6% based on carcass recoveries. Population-specific estimates ranged from 41.5% to 44.5% and the 95% credible intervals overlapped with 50%, which is expected since the sex ratio should be near 1:1 (Table 14). The Elochoman population had the most extreme GOF test value of 0.95. However, this is due to the small number of female carcasses observed. The GOF test based on Bayesian *p*-values ranged from 0.24 to 0.95 for the 13 populations, which indicates no concern with model fit.

Table 14. Estimates of the proportion of adult females in the 2012 populations based on carcass recoveries during redd surveys. The last column is a Bayesian p -value for a GOF test.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	GOF
Grays/Chinook	41.5%	6.5%	26.2%	42.2%	52.5%	0.24
Elochoman/Skamakowa	43.4%	6.1%	30.9%	43.4%	56.0%	0.95
Coweeman	43.9%	5.3%	33.7%	43.8%	54.9%	0.78
NF Toutle	44.4%	6.3%	32.9%	44.0%	58.6%	0.65
Green	43.8%	5.8%	32.2%	43.7%	56.0%	0.86
SF Toutle	43.4%	5.4%	32.4%	43.4%	54.1%	0.81
Kalama	44.3%	5.7%	33.4%	44.0%	56.9%	0.75
NF Lewis	42.4%	5.9%	29.5%	42.7%	53.1%	0.63
Cedar	44.5%	5.6%	34.1%	44.2%	56.9%	0.67
EF Lewis	42.9%	5.0%	32.5%	43.0%	52.6%	0.70
Salmon	43.5%	6.1%	30.9%	43.5%	56.0%	0.93
Washougal	43.9%	5.7%	32.5%	43.8%	56.2%	0.84
Lower Gorge	44.3%	5.7%	33.5%	44.0%	57.0%	0.71
Mean Females	43.6%	6.7%	30.0%	43.6%	57.9%	

The female density estimates were expanded by the population-specific estimates of the proportion of females to estimate the adult densities (Table 15). The mean adults per mile ranged from a high of 50.5 in the Coweeman River basin to a low of 6.2 in the Green River basin. A total of 10 out of 13 population estimates had mean adult densities greater than 10 per mile.

Table 15. Expanded coho salmon adults per mile based on GRTS surveys in 2012.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	6.12	15.39	0.00	0.00	44.33
Elochoman/Skamakowa	7.64	14.74	0.00	2.61	46.78
Coweeman	50.56	78.48	0.00	24.33	258.00
NF Toutle	19.52	43.25	0.00	4.89	127.40
Green	15.88	25.19	0.00	7.25	82.79
SF Toutle	39.97	70.04	0.00	15.66	221.60
Kalama	9.76	19.81	0.00	3.24	59.50
NF Lewis	11.09	25.76	0.00	2.58	74.40
Cedar	12.16	20.20	0.00	5.21	65.57
EF Lewis	47.40	82.23	0.00	18.44	269.41
Salmon	14.23	28.38	0.00	4.73	86.32
Washougal	14.03	25.25	0.00	5.48	81.15
Lower Gorge	17.80	33.08	0.00	6.62	103.70

The adult densities were then expanded by the proportion of the sample frame surveyed to estimate the adult abundance (Table 16). Adult coho salmon abundance estimates followed variably skewed right-tailed distributions; the mean adult coho salmon abundance estimated

from redd surveys ranged from a low of 313 for the Kalama population to a high of 3,997 adults for the EF Lewis population.

Table 16. The estimated adult coho salmon escapement based on redd surveys in 2012.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	980	606	317	829	2,505
Elochoman/Skamakowa	674	358	250	591	1,579
Coweeman	3,097	1,481	1,274	2,770	6,810
NF Toutle	972	628	307	811	2,584
Green	781	352	337	705	1,677
SF Toutle	2,409	1,326	875	2,099	5,731
Kalama	313	207	91	262	851
NF Lewis	498	469	101	380	1,597
Cedar	435	196	186	393	921
EF Lewis	3,997	2,193	1,429	3,480	9,616
Salmon	2,468	1,744	677	2,033	6,736
Washougal	610	372	197	517	1,536
Lower Gorge	610	399	192	509	1,613

Based on carcass surveys we estimated the percentage of marked (clipped adipose fin or CWT) and unmarked adult coho salmon. Populations with hatcheries such as the Grays, Elochoman, Toutle, and Kalama Rivers had mean estimates of 19%, 25%, 21%, and 80% marked carcasses, respectively (Table 17). Except for the Toutle tribs (25%), the remaining populations had mark rates less than 20%. Thus, the mean percentage of unmarked fish exceeded 80% in these basins with the Coweeman, EF Lewis, NF Lewis, and Cedar having mean estimates of over 90% marked fish (Table 18).

Table 17. The estimated percentage of adult coho salmon that are marked (adipose fin clipped or CWT) based on carcass recoveries during GRTS surveys in 2012.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	18.8%	13.1%	1.6%	16.0%	50.9%
Elochoman/Skamakowa	25.2%	16.4%	2.4%	22.3%	63.4%
Coweeman	2.4%	3.3%	0.0%	1.1%	11.8%
NFToutle	24.9%	16.4%	2.2%	22.0%	63.1%
Green	20.7%	11.2%	3.8%	19.1%	46.3%
SF Toutle	12.5%	7.2%	2.2%	11.2%	29.7%
Kalama	80.6%	10.5%	56.1%	82.2%	96.4%
NF Lewis	3.9%	5.1%	0.0%	1.9%	18.4%
Cedar	2.6%	3.6%	0.0%	1.3%	13.0%
EF Lewis	8.1%	4.8%	1.5%	7.2%	19.5%
Salmon	18.9%	13.1%	1.6%	16.1%	50.6%
Washougal	10.7%	8.0%	0.9%	8.8%	30.6%
Lower Gorge	19.2%	10.5%	3.7%	17.6%	43.6%

Table 18. The estimated percentage of adult coho salmon that are not marked (no adipose fin clip or CWT) based on carcass recoveries during GRTS surveys in 2012.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	81.2%	13.1%	49.1%	84.0%	98.4%
Elochoman/Skamakowa	74.8%	16.4%	36.6%	77.7%	97.6%
Coweeman	97.6%	3.3%	88.2%	98.9%	100.0%
NF Toutle	75.1%	16.4%	36.9%	78.0%	97.8%
Green	79.3%	11.2%	53.7%	80.9%	96.2%
SF Toutle	87.5%	7.2%	70.3%	88.8%	97.8%
Kalama	19.4%	10.5%	3.6%	17.8%	43.9%
NF Lewis	96.1%	5.1%	81.6%	98.1%	100.0%
Cedar	97.4%	3.6%	87.0%	98.8%	100.0%
EF Lewis	91.9%	4.8%	80.5%	92.8%	98.5%
Salmon	81.1%	13.1%	49.4%	83.9%	98.4%
Washougal	89.3%	8.0%	69.4%	91.2%	99.1%
Lower Gorge	80.8%	10.5%	56.4%	82.4%	96.3%

There was a low percentage of marked fish in the NF Lewis and Cedar Creek, however these basins are heavily supplemented with hatchery fry releases originating from remote site incubators (RSI) within the basin (Table 19). Returning adults from these hatchery-origin releases are not externally marked. Therefore, our estimates of unmarked fish are a combination of unmarked hatchery-origin and natural-origin fish in these basins.

In addition, it should be noted that we reported on marked fish, which include hatchery fish that are adipose fin-clipped or CWT only, such as the NF Lewis River hatchery double index group. There are also a small percentage of hatchery fish that are unintentionally released unmarked due to machine or human error during marking. Therefore, estimates of the true proportion of hatchery fish would increase slightly if adjusted for the percentage of unmarked hatchery fish.

Table 19. Off station hatchery releases (primarily from remote site incubators) of coho salmon expected to return in 2012.

Brood Yr	Month	Basin	Stage	UnMark	MassMark	Totals
2009	Mar	Salmon Cr.	Fry	377,870	0	377,870
2009	Apr	Salmon Cr.	Fry	17,500	0	17,500
2009	Jan-Feb	Lewis	Fry	769,600	0	769,600
2009	Jan-Mar	Cowlitz	Fry	276,700	0	276,700
2009	Jun	Cowlitz	Fingerling	0	1,000	1,000
						1,442,670

Estimates of marked and unmarked adult coho abundance for GRTS areas followed variably-skewed distributions and were generally right-tailed. The mean estimate of marked adult abundance ranged from 12 in Cedar Creek to 464 in the Salmon Creek (Table 20). Mean estimates of unmarked adult abundance ranged from a low of 61 for the Kalama population to a

high of 3,675 for the EF Lewis population (Table 21). In the Cowlitz, Lewis, and Salmon Creek populations a total of 1,442,670 fry were released primarily from RSIs (Table 19). Since these hatchery fish are not externally marked, they are likely included in some of the unmarked samples in these populations and possibly other populations. At this time there is no straightforward method to determine the percentage of unmarked RSI releases in these populations.

Table 20. Estimated adult marked coho salmon abundance from 2012 GRTS surveys.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	184	185	11	130	680
Elochoman/Skamakowa	170	155	12	129	574
Coweeman	74	118	0	30	396
NF Toutle	242	252	15	172	880
Green	162	119	24	132	470
SF Toutle	301	255	38	232	961
Kalama	252	171	69	209	695
NF Lewis	19	39	0	7	112
Cedar	12	18	0	5	61
EF Lewis	322	280	42	246	1,047
Salmon	464	507	26	319	1,738
Washougal	65	70	4	44	248
Lower Gorge	117	109	15	87	391

Note the sum of abundance by marked status may not equal the abundance estimate due to rounding.

Table 21. Estimated adult unmarked coho salmon abundance from 2012 GRTS surveys.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%
Grays/Chinook	796	520	232	668	2,088
Elochoman/Skamakowa	504	295	151	436	1,254
Coweeman	3,023	1,451	1,239	2,710	6,650
NF Toutle	730	503	188	603	2,028
Green	620	297	246	554	1,385
SF Toutle	2,108	1,179	747	1,829	5,049
Kalama	61	58	7	45	206
NF Lewis	479	451	97	365	1,525
Cedar	423	192	180	383	898
EF Lewis	3,675	2,029	1,301	3,202	8,878
Salmon	2,004	1,482	505	1,625	5,682
Washougal	545	337	172	460	1,394
Lower Gorge	493	331	147	408	1,342

Note the sum of abundance by marked status may not equal the abundance estimate due to rounding.

The percentage of GRTS reaches having at least one redd ranged from 30% in the Grays to 80% for the Coweeman population (Table 22). Some populations with high occupancy rates included the Elochoman, Green, Kalama, and Washougal which also have intensive hatchery programs; however, some populations with low hatchery influence, as measured by the percentage of marked fish, also had high occupancy rates including the SF Toutle, Coweeman, Cedar, and EF Lewis. We calculated the probability that 80% of the reaches were occupied based on observed redd counts, which is the NOAA occupancy rate standard (Table 22). The Coweeman was the only populations for which there was a greater than 50% probability that 80% of reaches were occupied (Table 22). For most populations the probability that the occupancy rate was greater than 80% was less than 20%, indicating that most populations were below the NOAA guideline. It should be noted that we are reporting on the observed occupancy rate based on redds. This is less than the true occupancy rate because our redd detection rate was about 57%, assuming 1 redd per female, and males and jacks were not included in the occupancy rate.

Table 22. Occupancy rate or the percentage of GRTS reaches in 2012 that were occupied (had at least one redd) and the probability that the occupancy rate was above 80% (last column).

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	<i>p-value</i>
Grays/Chinook	30.0%	8.9%	14.1%	29.5%	49.0%	0.00
Elochoman/Skamakowa	54.4%	10.2%	34.5%	54.6%	73.8%	0.00
Coweeman	80.6%	9.1%	60.0%	81.9%	94.8%	0.58
NF Toutle	46.0%	13.8%	20.2%	45.8%	72.9%	0.00
Green	78.1%	8.1%	60.3%	78.9%	91.7%	0.44
SF Toutle	65.4%	12.7%	38.9%	66.3%	87.6%	0.13
Kalama	50.0%	14.5%	22.2%	50.1%	77.8%	0.02
NF Lewis	35.8%	16.9%	7.6%	34.4%	71.3%	0.01
Cedar	70.5%	9.5%	50.4%	71.0%	87.2%	0.16
EF Lewis	65.2%	12.7%	38.8%	66.0%	87.4%	0.12
Salmon	65.0%	14.3%	34.8%	66.0%	89.3%	0.16
Washougal	68.3%	13.4%	39.7%	69.4%	90.7%	0.20
Lower Gorge	68.8%	15.4%	35.4%	70.5%	93.5%	0.26

We also estimated the density of unmarked females (Table 23). The mean density ranged from a low of 0.82 to a high of 21.3 females/mile in the Kalama and Coweeman basins, respectively. Using a significance level of 0.05, there is a low probability that the Grays, Elochoman, and Kalama basins have unmarked female seeding levels that exceed the mode from Bradford's analysis. As discussed earlier, the mean unmarked females densities in the NF Lewis, Cedar, and Lower Cowlitz basins are influenced by an unknown number of unmarked hatchery fish.

Table 23. The estimated number of unmarked coho salmon females/mile based on GRTS surveys in 2012. The *p*-value is the probability the observed wild female density is greater than the mode of the full habitat seeding density based on Bradford et al. 2000.

GRTS Survey Basin	mean	sd	2.50%	50%	97.50%	<i>p</i>-value
Grays/Chinook	1.99	4.89	0.00	0.00	14.16	0.02
Elochoman/Skamakowa	2.42	4.67	0.00	0.73	15.03	0.03
Coweeman	21.34	32.67	0.00	10.28	107.40	0.41
NF Toutle	6.42	14.72	0.00	1.58	43.49	0.12
Green	5.42	8.58	0.00	2.43	28.29	0.09
SF Toutle	14.91	25.89	0.00	5.91	81.72	0.29
Kalama	0.82	1.89	0.00	0.17	5.54	0.00
NF Lewis	4.40	10.16	0.00	1.06	29.11	0.08
Cedar	5.18	8.51	0.00	2.25	27.73	0.09
EF Lewis	18.40	31.76	0.00	7.25	103.81	0.34
Salmon	4.91	9.54	0.00	1.64	29.84	0.09
Washougal	5.41	9.61	0.00	2.11	30.57	0.09
Lower Gorge	6.30	11.64	0.00	2.33	37.08	0.11

Coho Salmon Escapement Estimates

Estimates for populations as designated by the NOAA Technical Recovery Team (TRT) were calculated by summing redd-based, mark-recapture, and trap and haul based estimates as appropriate. The mean estimates ranged from 313 to 6,832, Kalama and Upper Cispus/Cowlitz populations, respectively (Table 24). For the Upper Cispus/Cowlitz, and Tilton populations the CVs were less than the NOAA guideline of 15% (Crawford and Rumsey 2011). Precise estimates were obtained for these populations because of the trap and haul program. In contrast, the CV for all redd based estimates did not meet the standard and had CVs ranging from 48% to 71%, Coweeman and Salmon populations, respectively. The NF Lewis and MAG estimates were primarily mark-recapture estimates and their CVs were 38% and 29%, respectively.

Table 24. Adult coho salmon population estimates by TRT Recovery population. The Upper Gorge populations were not monitored in 2012 and there were no GRTS surveys for the mainstem Toutle/mainstem NF Toutle or mainstem Lower Cowlitz populations.

Population	mean	sd	2.50%	50%	97.50%	CV
Grays/Chinook	980	606	317	829	2,505	62%
Elochoman/Skamakowa	674	358	250	591	1,579	53%
Mill/Abernathy/Germany	593	222	295	552	1,139	38%
Coweeman	3097	1,481	1,274	2,770	6,810	48%
Green	1,891	850	870	1,696	4,060	45%
SF Toutle	2,409	1,326	875	2,099	5,731	55%
Upper Cowlitz/Cispus	6,832	39	6,757	6,832	6,908	1%
Tilton	6,637	126	6,389	6,638	6,884	2%
Kalama	313	207	91	262	851	66%
NF Lewis	3,001	594	2197	2916	4,297	20%
EF Lewis	3,997	2,193	1,429	3,480	9,616	55%
Salmon	2,468	1,744	677	2,033	6,736	71%
Washougal	610	372	197	517	1,536	61%
Lower Gorge	671	400	245	571	1,678	60%

Note the sum of abundance by marked status may not equal the abundance estimate due to rounding.

As expected, the marked population estimates were highest in basins with hatcheries (Table 20; Appendix 2). The population with the greatest number of marked fish was in the Upper Cispus/Cowlitz and Tilton populations where hatchery fish are released as part of a program to re-establish natural production above the Barrier dam. These population estimate of 5,143 and 5,193 adults accounted for slightly less than 79% of the total marked population (Table 25). The largest producers of unmarked adults include the EF Lewis (3,675), and Coweeman (3,023) populations (Table 26).

Table 25. Marked adult coho salmon population estimates by TRT Recovery population. Note: the Upper Gorge population was not surveyed in 2012 and there were no surveys for the mainstem NF Lewis, mainstem Toutle/mainstem NF Toutle, or mainstem Lower Cowlitz populations.

Population	mean	sd	2.50%	50%	97.50%	CV
Grays/Chinook	184	185	11	130	680	101%
Elochoman/Skamakowa	170	155	12	129	574	91%
Mill/Abernathy/Germany	18	27	0	8	95	148%
Coweeman	74	118	0	30	396	160%
Green	404	295	84	331	1,144	73%
SF Toutle	301	255	38	232	961	85%
U Cowlitz/Cispus	5,143	39	5,068	5,143	5,219	1%
Tilton	5,193	126	4,945	5,194	5,440	2%
Kalama	252	171	69	209	695	68%
NF Lewis	382	74	268	373	548	19%
EF Lewis	322	280	42	246	1,047	87%
Salmon	464	507	26	319	1,738	109%
Washougal	65	70	4	44	248	107%
Lower Gorge	119	109	16	89	393	92%

Note the sum of abundance by marked status may not equal the abundance estimate due to rounding.

Table 26. Unmarked adult coho salmon population estimates by TRT Recovery population. Note the Upper Gorge populations were not surveyed in 2012 and there were no surveys for the mainstem Toutle/mainstem NF Toutle and mainstem Lower Cowlitz populations. An unknown number of NF Lewis and L. Cowlitz unmarked adults originated from hatchery-origin RSI releases.

Population	mean	sd	2.50%	50%	97.50%	CV
Grays/Chinook	796	520	232	668	2,088	65%
Elochoman/Skamakowa	504	295	151	436	1,254	59%
Mill/Abernathy/Germany	575	217	283	535	1,105	38%
Coweeman	3,023	1,451	1,239	2,710	6,650	48%
Green	1,488	682	667	1,331	3,244	46%
SF Toutle	2,108	1,179	747	1,829	5,049	56%
U Cowlitz/Cispus	1,689	---	---	---	---	0%
Tilton	1,444	---	---	---	---	0%
Kalama	61	58	7	45	206	95%
NF Lewis	2,619	549	1,893	2,536	3,826	21%
EF Lewis	3,675	2,029	1,301	3,202	8,878	55%
Salmon	2,004	1,482	505	1,625	5,682	74%
Washougal	545	337	172	460	1,394	62%
Lower Gorge	552	333	197	468	1,397	60%

Note the sum of abundance by marked status may not equal the abundance estimate due to rounding.

Applying the estimate of the percentage of males that were jacks from Table 7 leads to an estimate of jacks by population (Table 27). Jack estimates ranged from 47 to 2,965, Kalama and Upper Cispus/Cowlitz populations, respectively. Jack data used to estimate jack proportions and calculate jack abundance elsewhere, were from trap and haul programs only, since sampling of jacks is likely biased and incomplete due to their small size elsewhere.

Table 27. Jack coho salmon population estimates by TRT Recovery population. Note the Upper Gorge population was not surveyed in 2012 and there were no surveys for the mainstem Toutle/mainstem NF Toutle, or mainstem Lower Cowlitz populations.

Population	mean	sd	2.50%	50%	97.50%	CV
Grays/Chinook	156	142	20	118	514	91%
Elochoman/Skamakowa	104	85	14	82	322	83%
Mill/Abernathy/Germany	87	58	14	73	236	66%
Coweeman	471	365	69	384	1,402	78%
Green	277	203	51	227	803	73%
SF Toutle	369	306	52	291	1,133	83%
U Cowlitz/Cispus	2,965	13	2,940	2,965	2,990	0%
Tilton	1,607	30	1,548	1,607	1,666	2%
Kalama	47	45	6	35	161	95%
NF Lewis	392	233	73	348	991	59%
EF Lewis	617	515	85	485	1,916	83%
Salmon	379	377	45	280	1,313	100%
Washougal	93	83	12	71	306	89%
Lower Gorge	92	86	11	69	305	93%

The combined LCR ESU estimates for WA populations are found in Table 28. We estimated a mean total of 34,174 adults: 7,656 jacks, 13,091 marked adults, and 21,083 unmarked adults. The CV for marked adults met the NOAA standard and the CV for the total adults was 21% compared to the 15% NOAA standard. The CV for unmarked adults was 30%, which is double the NOAA standard. It should be noted that no adult population estimates were made for the mainstem Toutle/mainstem NF Toutle below the SRS, mainstem and tributaries of the Lower Cowlitz, or Upper Gorge population. Without these, the total ESU population estimate should be considered a minimum. We believe these missed areas do not represent substantial production due to the observed level of coho salmon spawning during Chinook spawning ground surveys there.

The proportions of unmarked and marked adult coho salmon by population are found in Table 29. As described above, basins with hatcheries tended to have higher proportions of marked fish while basins without hatcheries tend to have higher proportions of unmarked fish. The precision estimates generally exceeded the 95% CI half width of 5% guideline except for populations with traps (Rawding and Rodgers 2013).

Table 28. Washington’s LCR ESU coho salmon population estimates for 2012. Note the Lower Cowlitz and the Upper Gorge populations were not surveyed in 2012 and there were no surveys for the mainstem Toutle/mainstem NF Toutle, or mainstem Lower Cowlitz populations.

Population	mean	sd	2.50%	50%	97.50%	CV
Marked Adults	13,091	1,147	11,620	12,840	15,950	9%
Unmarked Adults	21,083	6,299	12,870	19,800	36,580	30%
Total Adults	34,174	7,212	24,720	32,700	51,680	21%
Total Jacks	7,656	2,041	5,089	7,209	12,980	27%

Note the sum of abundance by marked status may not equal the total abundance estimate due to rounding.

Table 29. Estimates of the proportions of unmarked and marked adult coho salmon by TRT Recovery population in 2012. An unknown number of NF Lewis and Cowlitz unmarked fish included in the proportions are from hatchery-origin RSI releases.

Proportion Unmarked				Proportion Marked			
Population	mean	sd	95%CI-1/2w	Population	mean	sd	95%CI-1/2w
Grays/Chinook	81.2%	13.1%	24.6%	Grays/Chinook	18.8%	13.1%	24.6%
Elochoman/Skamakowa	74.8%	16.4%	30.5%	Elochoman/Skamakowa	25.2%	16.4%	30.5%
Mill/Abernathy/Germany	96.9%	4.2%	7.5%	Mill/Abernathy/Germany	3.1%	4.2%	7.5%
Coweeman	97.6%	3.3%	5.9%	Coweeman	2.4%	3.3%	5.9%
Green	79.0%	9.6%	18.4%	Green	21.0%	9.6%	18.4%
SF Toutle	87.5%	7.2%	13.7%	SF Toutle	12.5%	7.2%	13.7%
U Cowlitz/Cispus	24.7%	0.1%	0.3%	U Cowlitz/Cispus	75.3%	0.1%	0.3%
Tilton	21.8%	0.4%	0.8%	Tilton	78.2%	0.4%	0.8%
Kalama	19.4%	10.5%	20.1%	Kalama	80.6%	10.5%	20.1%
NF Lewis	87.1%	1.8%	3.6%	NF Lewis	12.9%	1.8%	3.6%
EF Lewis	91.9%	4.8%	9.0%	EF Lewis	8.1%	4.8%	9.0%
Salmon	81.1%	13.1%	24.5%	Salmon	18.9%	13.1%	24.5%
Washougal	89.3%	8.0%	14.8%	Washougal	10.7%	8.0%	14.8%
Lower Gorge	82.6%	9.4%	17.9%	Lower Gorge	17.4%	9.4%	17.9%

CWT Program

The CWT recoveries of coho salmon in the fall of 2012 were uploaded to the RMIS system during 2012-14. The uploaded data include: 1) freshwater sport fishery recoveries and hatchery facility coho recoveries uploaded in December 2012, and coho spawning ground recoveries uploaded in April 2015. RMIS is a coastwide database that stores CWT tag and release data along with recovery and sampling data.

CWT recoveries from carcass recoveries found during stream surveys are presented in Table 30. These do not include hatchery recoveries, thus the recoveries and percent of out of basin recoveries only apply to coho salmon that spawned in streams. There were no recoveries in the

MAG, Elochoman, Coweeman, Green, SF Toutle, EF Lewis, Salmon, and Washougal populations. These recoveries are consistent with the low proportion of marked fish sampled in these populations (Table 15). High numbers of CWT fish were recovered in the Grays and Kalama basin. CWT data for fisheries and carcass recoveries are presented in annual reports for missing production groups (e.g. Harlan 2013).

Table 30. Unexpanded CWT recoveries by TRT Recovery population and hatchery for adult coho salmon in 2012. Gray boxes indicate CWT was recovered in the same basin as released.

		Release Basin								
Recovery Basin	Population	Grays H	Deep River Net pens	Toutle H.	Kalama H	Lewis H	Cascade H. Beaver Cr. Pond	Cascade H. Icicle Cr.	S. Fork Klaskanine Pond	Total
	Grays	1	1						1	3
	S. Fork Toutle			1						1
	Kalama				1		1	1		3
	NF Lewis					1				1
	Lower Gorge						1			1
	Total	1	1	1	1	1	2	1		9
	% Out of Basin	0%	100%	0%	0%	0%	NA	NA	NA	

Discussion

One of the most controversial aspects of the Bayesian approach is the specification of priors. We used vague priors because this was only the third year of study on LCR coho and because it was unclear if other coho salmon information was applicable to the LCR (see below) given differences in climate, habitat, and experience of surveyors in conducting coho salmon surveys. In such a case, vague priors allow the posterior distribution to be dominated by the observed data, yielding Bayesian parameter estimates similar to those obtained by maximum likelihood methods (Kery 2010). The Bayesian framework provides an approach to account for this type of information in future years.

We used census counts and mark-recapture estimates to estimate coho salmon population abundance where feasible. These methods are preferred because all the data needed to make an abundance estimate are collected annually. However, this left a large area for which alternate methods, such as Area-Under-the-Curve (AUC) and redd surveys, had to be used to estimate abundance. Unfortunately, AUC and redd surveys require assumptions about observer efficiency, survey life, and redd identification that may or may not be applicable to data collected from other basins or from other years (Irvine et al. 1992). We considered the use of AUC estimates, but survey life (e.g., the duration of time that live coho remained in the survey area) and observer efficiency (of live adults) for LCR coho salmon are unknown. Suring et al. (2006) assumed the estimates for the Oregon coast are applicable for the Lower Columbia River. However, Jacobs et al. (2002) noted that for some years the mark-recapture estimates for the Smith River, an Oregon coastal stream, were higher than the AUC estimates for the same area. If the Smith River mark-recapture estimates are correct, one possible explanation for this discrepancy is that the standard Oregon coastal estimates of survey life and/or observer efficiency are biased high for those years

on the Smith River. Therefore, application of the standard Oregon coastal observer efficiency and survey life estimates may lead to underestimates of Washington LCR coho salmon abundance.

In addition, a review of the literature by Perrin and Irvine (1990) demonstrated high variability in survey life for coho salmon. Gallagher et al. (2010) estimates of survey life for coho were approximately two times or greater than those used by ODFW. However, Gallagher et al. 2010 estimates include residence time from entry, while ODFW estimates (~11 days) focus more on residence time in spawning tributaries (Willis 1954). Lestelle and Weller (2002) used an average residence time of 15 days. Estimates of observer efficiency for coho salmon averaged 75.5% for Oregon coastal streams (Solazzi 1984), 22% (range 20-24%) for a Northern California stream (Szerlong and Rundio 2007), 65% (range 22-100%) for an Alaskan stream (Hetrick and Nemeth 2003), and 86.5% for a coho stream on Vancouver Island (Holt 2002). Gallagher et al. (2010) indicated that AUC estimates were very sensitive to survey life and observer efficiency estimates; consequently, concluding they were less reliable than redd counts. Lestelle and Weller (2002) believed that AUC estimates under estimated escapement at low density because it is difficult to observe fish when their abundance is low. However, at higher escapement they believed redd counts are likely to underestimate abundance due to superimposition and difficulty in identifying individual redds.

After our AUC method review, we were uncomfortable in applying this method without LCR-specific observer efficiency and apparent residence time estimates over varying spawning escapements, so we opted to use redd-based estimates because we could obtain a specific annual LCR estimate of redds per female. While redd surveys are widely used (WDFW 2011) and can provide unbiased estimates, they have their own set of challenges (Muhlfeld et al. 2003, Dunham et al. 2001). The key assumptions for redd surveys are: 1) the spatial spawning distribution is known and either sampled completely or expanded for in an unbiased manner as part of the sampling design, 2) surveys cover the entire temporal spawning period, 3) all redds are consistently identified with the same protocols, and 4) the variability in redds per adult or female is measured annually for that population or if derived from other population or years is similar to the population where redd surveys are conducted.

The first two assumptions indicate that redd surveys must be spatially or temporally complete otherwise redd abundance will be under estimated. We believe that we had a good spatial survey design based on using GRTS. However, our temporal coverage was more problematic and there were missed scheduled surveys, particularly due to high and turbid water conditions. Training was provided to all staff to help with consistent redd identification (Crisp and Carling 1989) and to differentiate coho, chum, and Chinook salmon and steelhead redds, which were all potentially visible during the coho salmon spawning time. We used physical differences in substrate size and location within the basin to help classify redds from different species (e.g., Gallagher and Gallagher 2005). In addition, we used two locations to estimate redds per female and these locations were geographically distant from each other, had different habitat, and survey conditions. A key assumption was that the number of redds constructed by females in these basins and the observer efficiency in identifying these redds together were representative of redds per female in all other redd survey reaches in the ESU. Provided this assumption was met, our design did address the key assumptions needed for an unbiased redd survey.

Curbois et al. (2008) noted that the 95% CI based on normally distributed data and large sample theory was not adequate to estimate redd abundance. This resulted from the clumpiness of the redd data and many reach counts of zero, particularly when population sizes were low. To address this problem, we used the Negative Binomial distribution, which is commonly used for over dispersed count data (Hilborn and Mangel 1997). Based on Bayesian p -values, the negative binomial distribution adequately fit the data. However, the precision of our estimates was worse than we anticipated. This occurred because the data were over dispersed resulting in large variances, which were consistent with our observations. Another factor that affected precision was the reach sample sizes, which were fewer than expected due to limited resources. Finally, our escapement estimates include most sources of uncertainty. Our redd based estimates included spatial uncertainty as with the Oregon coast surveys, but also include uncertainty in redds per female, adult sex ratio, and jack to adult male ratio. The trap and haul estimates included uncertainty associated with harvest of marked fish.

We explored a number of approaches to see if our estimates of adult coho abundance seemed reasonable. One approach we used was to compare our estimate of redds per female with other studies. For example, Gallagher et al. (2010) found that adult coho salmon redd-based abundance estimates were positively correlated with, and similar to, mark-recapture estimates in northern California streams. However, they noted that the coho salmon spawner to redd ratio varied annually and with the exception of 2006 the average adults per redd was 2.2; assuming a 1:1 sex ratio this would equate to 1.16 females per redd, which equates to an average of 0.86 redds per female. However, their annual point estimates for redds per female ranged from 0.55 to 1.67. In 2006, Gallagher et al. (2010) observed ~0.20 redds per female for each of three surveyed populations because of challenging observation conditions, which likely decreased redd detectability and life. Lestelle and Weller (2002) estimated coho salmon escapement in two Washington coastal streams between 1996 and 2000. They judged four mark-recapture experiments to be successful and in these years the redd based estimates were positively biased by ~15% in three of the four years. In one year the redd based estimate was negatively biased by ~7% compared to the mark-recapture estimate. Assuming equal sex ratio the redds per female from Lestelle and Weller (2002) was approximately 0.87, which is similar to the average estimate from Gallagher et al. (2010).

Our estimate was 0.57 redds per female (95% CI 0.18 to 0.96), which was within the range from the California and Washington studies. However, if our estimate of redds per females is biased low and the true estimate is closer to 0.87 redds per female from the other Washington study (Lestelle and Weller 2002) or 1.0 as found for Chinook salmon (Murdoch et al. 2009), the true population estimates would be less than those reported here.

Chinook salmon carcass recoveries may be biased by sex, age, and origin (Zhou 2000, Parken et al. 2003, and Murdoch et al. 2010). To minimize possible size bias in carcass recoveries for coho salmon, we estimated adult and jack abundance separately and used only trap data to estimate the proportion of males that were jacks. For coho salmon, carcass recoveries may be biased because females tend to guard the nest after spawning (Sandercock 1991). If we assume the sex ratio for coho salmon should be approximately 50% females (Dittman et al. 1998), our hierarchical sex ratio estimate for adults from carcasses surveys (44% females) may indicate a bias that males are recovered at a higher rate. If this is the case, our redd-based population

estimates may be slightly biased high; however, some populations of coho salmon are known to maintain female-biased sex ratios (Holtby and Healey 1990), in which case our estimates may remain unbiased. Most coho spawning carcass recoveries occurred in small streams and were based on weekly surveys using a spatially balanced design, so both the size of streams and the representative sampling design should minimize carcass recovery bias by origin.

We provided direct estimates of marked and unmarked coho salmon adults as surrogates for hatchery- and natural-origin adults. If all hatchery-origin juveniles were adipose fin clipped and/or CWT, then we could make the assumption that marked fish were hatchery-origin fish and all unmarked fish were natural-origin fish. However, when examining the actual hatchery marking QA/QC data, ~ 99.8% of the hatchery fish were mass marked and/or CWT. Therefore, our estimates of unmarked and marked fish as surrogates for hatchery- and natural-origin spawners are slightly biased. In addition, we found no reliable method for correction for the unmarked hatchery-origin RSI and unfed fry releases, which may decrease the number of natural-origin spawners reported in the NF Lewis and Lower Cowlitz populations.

We used two metrics to compare LCR coho salmon populations to other populations, including occupancy rate and the seeding level based on females spawners (Crawford and Rumsey 2011 and Bradford et al. 2000). The 80% occupancy guideline was based on coho salmon observations in small Oregon coastal streams. Since our sample frame included large rivers, an area less preferred by coho salmon for spawning (Sandercock 1991), the comparison is not equitable; we would expect lower occupancy rates when sampling over all possible spawning distribution as compared to a subset of preferred spawning sites, which is what we observed. The populations analyzed by Bradford et al. (2000) consisted of many low gradient productive habitats for coho salmon; thus, it is expected that the seeding level (female spawners per mile) would be higher in these areas than in less productive habitat such as the higher gradient habitat in most LCR populations. Both of these metrics should be further reviewed as they are currently applied to the LCR. For example, given sufficient monitoring sites, we could use the methods of Bradford et al. (2000) to develop LCR specific estimates of seeding.

The last NOAA status review suggested that all coho salmon populations in Washington's portion of the Lower Columbia ESU were at high risk for extinction because limited surveys suggested that the ESU was comprised of greater than 90% hatchery-origin spawners. However, there was great uncertainty in the NOAA status due to the lack of comprehensive coho salmon surveys (NMFS 2011). In this report we estimate that ~21,000 unmarked adult coho salmon spawned in the WA portion of the LCR ESU in 2011. The actual estimate is likely higher since we did not include the mainstem Cowlitz, mainstem Toutle/lower NF Toutle rivers, and the Upper Gorge populations in our estimates. It is likely a small percentage of the unmarked population is comprised of unmarked hatchery-origin fish as a result of human or machine error during mass marking and CWT application, and resulting from returns of unmarked Remote Site Incubator plants of hatchery origin coho. The total proportion of hatchery origin spawners (pHOS) estimate, not corrected for missing mass marks, was 38%. If we subtract the hatchery adults released to spawn in the upper Cowlitz and Tilton to maintain that population until better juvenile passage exists, the total pHOS estimate decreases to 13% for the remainder of the Washington portion of the ESU. In contrast to the status review, we found no population had greater than 90% hatchery-origin spawners. Excluding the NF Lewis and Salmon populations,

due to the release of unmarked hatchery-origin fish, a total of eight WA populations had proportions of natural origin spawners (pNOS) greater than 75%, with the Coweeman and Mill populations having pNOS greater than or equal to 95%.

Recommendations

This was the third year WDFW conducted coho salmon spawning ground surveys. This was an enormous undertaking and it was met with considerable success; however, many improvements can be made to reduce possible bias, improve precision, and improve repeatability of our study and results. Our recommendations for improvement include:

- 1) Develop a standardized manual of protocols for conducting coho salmon spawning ground surveys. This should at a minimum cover species and redd identification, a detailed description of the methods used to conduct surveys and how to record information, methods for data storage and frequency of downloading information, and the methods used to establish and modify survey reaches based on GRTS points.
- 2) One key assumption is that the redd identification methods in Duncan and Abernathy creeks are the same as those used in all other basins. While difficult to test, supervisors and crew leaders should schedule periodic surveys following surveyors to ensure standard techniques described in the manual are being implemented during surveys. Standardized methods and proper training can minimize differences between surveyors (Willis 1964).
- 3) It is likely that early-timed hatchery-origin coho salmon that spawned in the Kalama and possibly the NF Lewis River are under-represented by redd counts since these fish may be spawning in the same areas and at the same times as Chinook salmon. The coho sampling design should be refined to address this issue.
- 4) Redd locations are recorded electronically. However, the remainder of the data is transcribed on field datasheets then entered into electronic databases after the surveys are completed. WDFW should pursue the use of technology to electronically record data in the field to save time and reduce error generation during data entry. However, data storage devices must be rugged and waterproof to minimize loss of data in these difficult survey conditions.
- 5) Currently data for this analysis is obtained from different ARC-GIS databases, trapping spreadsheets, the WDFW corporate spawning ground survey database, and a regional age and scales database. We have consolidated databases and are moving toward unified corporate databases which improved the analysis but there is still room for improved database management (WDFW 2011b).
- 6) The current coho survey design used GRTS location draws developed for other purposes. One result is that there were a limited number of data points available to develop the coho salmon spawning ground survey design. A denser GRTS draw for the LCR area would eliminate this problem and should be pursued.
- 7) We recommend that the Upper Gorge populations be monitored for redds, and other methods be explored to develop estimates for the mainstem Lower Cowlitz River.

- 8) The precision of the redd-based estimates is low due to sampling a low fraction of the spawning area, over dispersed data, and the sampling design. To address these concerns, we recommend increasing the number of samples per population and consider stratification of sampling effort corresponding to higher and lower density coho spawning areas. Stratification may lead to more precise estimates if a denser GRTS draw is available and homogeneous strata can be developed (Liermann et al. 2015).
- 9) Since the precision for the mark-recapture estimates was low, the resulting redds per female estimate had low precision. Besides the clumpiness in our redd densities, theredds per female estimate is the largest source of error in our abundance estimates. We recommend efforts to improve trap operations at these sites to mark more fish to improve estimates or consider alternate approaches for estimating escapement such as those detailed in Labelle et al. (1994) or a modification of Korman et al. (2002, 2007).
- 10) Over 0.76 million unmarked fry releases occurred in the NF Lewis population and over 0.27 million unmarked fry releases occurred in the Lower Cowlitz. Since these groups are too small to be mass marked, we cannot use the mass mark to identify hatchery-origin fish. Analysis should be undertaken to determine the extent to which these plants are contributing to adult returns and whether the receiving waters they are planted in are being fully seeded by natural spawning. If these programs are to be continued, we recommend funding of otolith marking and recovery to identify hatchery-origin fish. Rawding and Groesbeck (2006) used this method in Cedar Creek to estimate the proportion of hatchery- and natural-origin fish in the coho smolt outmigration. These methods could be extended to adults. Alternatively, parental based tagging using genetic markers could be used (Anderson and Garza 2006).
- 11) Rawding and Rodgers (2013) suggested that efficiencies may be obtained by WDFW and ODFW working together on salmon and steelhead escapement estimates in the LCR ESU. Since both agencies are estimating coho salmon abundance, we suggest annual workshops/coordination meetings to review and learn about different study designs, protocols, database management, and statistical analysis to explore these efficiencies would be beneficial.
- 12) The original coho sampling frame for redd surveys was developed based on a few years of adult and juvenile survey data. There are now three additional years of adult and juvenile data available since the frame was developed. The sample frame should be updated based on these additional data.
- 13) When GRTS draws lead to reaches near hatcheries redd densities may be extreme in these reaches. This was not observed in 2012, but was observed in 2011. Additional consideration should be given to outlier detection, reaches next to hatcheries, and reaches downstream from weirs should be more carefully evaluated (Liermann et al. 2015).

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Appendices

Appendix 1

Appendix 1 a. GRTS reaches surveyed for Grays River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BLA	Grays/Chinook	Blaney Creek	1.00	0.00	1.00
CAB	Grays/Chinook	Cabin Creek	1.00	0.00	1.00
CRJ	Grays/Chinook	Crazy Johnson Creek	1.00	0.50	1.50
EGA	Grays/Chinook	East Fork Grays River	1.00	0.07	1.07
EGR	Grays/Chinook	East Fork Grays LB Trib 1	1.00	0.00	1.00
EGT	Grays/Chinook	East Fork Grays LB Trib 1	1.00	1.00	2.00
FOD	Grays/Chinook	Fossil Creek	1.00	0.00	1.00
GRH	Grays/Chinook	Grays River	1.00	17.47	18.47
GRN	Grays/Chinook	Grays River	1.00	24.07	25.07
GRO	Grays/Chinook	Grays River	1.00	25.07	26.07
GUR	Grays/Chinook	Grays Upper LB Trib	1.00	0.66	1.66
GUT	Grays/Chinook	Grays Upper LB Trib	1.00	1.66	2.66
HOA	Grays/Chinook	Honey Creek	1.00	0.00	1.00
HUE	Grays/Chinook	Hull Creek	1.00	1.81	2.81
HUF	Grays/Chinook	Hull Creek	1.00	2.81	3.81
HUI	Grays/Chinook	Hull Creek	1.00	3.78	4.78
MAE	Grays/Chinook	Malone Creek	1.00	1.92	2.92
MTB	Grays/Chinook	Mitchell Creek	1.00	0.13	1.13
NIA	Grays/Chinook	Nikka Creek	1.00	0.00	1.00
SGF	Grays/Chinook	South Fork Grays River	1.00	3.89	4.89
SGI	Grays/Chinook	South Fork Grays River	1.00	4.89	5.89
SGJ	Grays/Chinook	South Fork Grays River	1.00	6.61	7.61
WGB	Grays/Chinook	West Fork Grays River	1.00	2.99	3.99
WGC	Grays/Chinook	West Fork Grays River	1.00	3.99	4.99

Appendix 1 b. GRTS reaches surveyed for Elochoman River coho salmon in 2012

Section	Population	Stream Name	Miles	RM Start	RM Stop
BVA	Elochoman/Skamakowa	Beaver Creek	1	1.63	2.63
BVD	Elochoman/Skamakowa	Beaver Creek	1	0.63	1.63
BNA	Elochoman/Skamakowa	Birnie Creek	1	0.35	1.35
CLA	Elochoman/Skamakowa	Clear Creek	1	0	1
ELW	Elochoman/Skamakowa	Elochoman River	1	17.45	18.45
ELG	Elochoman/Skamakowa	Elochoman River	1	16.45	17.45
ELS	Elochoman/Skamakowa	Elochoman River	1	14.35	15.35
ELK	Elochoman/Skamakowa	Elochoman River	1	8.37	9.37
EFC	Elochoman/Skamakowa	Elochoman River - East Fork	1	0.7	1.7
WFC	Elochoman/Skamakowa	Elochoman River - West Fork	1	2.8	3.8
FAC	Elochoman/Skamakowa	FALK Creek 25.0222	1	4.08	5.08
FAI	Elochoman/Skamakowa	FALK Creek 25.0222	1	0.88	1.88
NLC	Elochoman/Skamakowa	Nelson Creek	1	2.03	3.03
NTA	Elochoman/Skamakowa	Nelson Creek Trib	0.8	0	0.8
NNA	Elochoman/Skamakowa	NF of NF ELOCHOMAN 25.0265	1	0	1
LSE	Elochoman/Skamakowa	Skamokawa Creek - Left Fork	1	1.13	2.13
LSB	Elochoman/Skamakowa	Skamokawa Creek - Left Fork	1	0.13	1.13
SKT	Elochoman/Skamakowa	Skamokawa Trib	0.47	0	0.47
SDE	Elochoman/Skamakowa	Standard Creek	1	1.4	2.4
WIL	Elochoman/Skamakowa	Wilson Creek	1	7	8
WIK	Elochoman/Skamakowa	Wilson Creek	1	6	7
WIH	Elochoman/Skamakowa	Wilson Creek	1	3.07	4.07

Appendix 1 c. GRTS reaches surveyed for Green River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
CAC	Green	Cascade Creek	1	1	2
CAA	Green	Cascade Creek	1	0	1
DVC	Green	Devils Creek	1	2.3	3.3
DVB	Green	Devils Creek	1	1.3	2.3
DVA	Green	Devils Creek	1	0.31	1.31
DTA	Green	Devils Creek West Fork	1	0	1
DT1	Green	Devils Trib 1	1	0	1
ELC	Green	Elk Creek	1	3.3	4.3
ELA	Green	Elk Creek	1	0	1
GNR	Green	Green River	1	21.66	22.66
GNQ	Green	Green River	1	20.66	21.66
GNP	Green	Green River	1	19.66	20.66
GNM	Green	Green River	1	18.66	19.66
GNK	Green	Green River	1	13.34	14.34
GNJ	Green	Green River	1	12.34	13.34
GNI	Green	Green River	1	11.34	12.34
GNH	Green	Green River	1	10.34	11.34
GNG	Green	Green River	1	7.33	8.33
GNE	Green	Green River	1	6.33	7.33
GNC	Green	Green River	1	5.33	6.33
GNB	Green	Green River	1	4.33	5.33
G1A	Green	Green Trib 1	1	0	1
G2A	Green	No Name Cr (LB trib below 2500 br)	1	0	1
SHA	Green	Shultz Creek	0.52	0	0.52

Appendix 1 d. GRTS reaches surveyed for mainstem and NF Toutle River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM	
				Start	RM Stop
HEC	NF Toutle	Hemlock Creek	1	4.11	5.11
OUA	NF Toutle	OUTLET Creek	1	0.45	1.45
OTA	NF Toutle	Outlet Trib	1	0	1
S2A	NF Toutle	Silver Trib 2	1	0.66	1.66
KYB	NF Toutle	Stankey Creek	1	0	1
T2B	NF Toutle	Toutle Trib 2	1	0	1
N2A	NF Toutle	UNNAMED Cr to TOUTLE	1	0	1
WYG	NF Toutle	WYANT Creek	1	4.64	5.64
WYD	NF Toutle	WYANT Creek	1	2.64	3.64
WYA	NF Toutle	WYANT Creek	1	0.29	1.29
WTB	NF Toutle	Wyant Trib 1	1	0.78	1.78

Appendix 1 e. GRTS reaches surveyed for SF Toutle River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM	
				Start	RM Stop
HAQ	SF Toutle	Herrington Creek	1	0	1
JOH	SF Toutle	Johnson Creek	1	0.75	1.75
LOC	SF Toutle	Loch Creek	0.85	0	0.85
STP	SF Toutle	Studebaker Creek	1	1	2
STL	SF Toutle	Studebaker Creek	1	0	1
SLA	SF Toutle	Studebaker Creek LB Trib 1	1	0	1
SFJ	SF Toutle	SF Toutle River	1	21.41	22.41
SFF	SF Toutle	SF Toutle River	1	14.99	15.99
TSC	SF Toutle	SF Toutle River	1	9.58	10.58
SFY	SF Toutle	SF Toutle River	1	7.25	8.25
SFB	SF Toutle	SF Toutle River	1	0.49	1.49
TRE	SF Toutle	Trouble Creek	1	1.47	2.47

Appendix 1 f. GRTS reaches surveyed for Coweeman River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BDA	Coweeman	Baird Creek	1	0	1
CAM	Coweeman	Coweeman River	1	29.6	30.6
CAL	Coweeman	Coweeman River	1	28.6	29.6
CAK	Coweeman	Coweeman River	1	27.6	28.6
CAH	Coweeman	Coweeman River	1	26.6	27.6
CAC	Coweeman	Coweeman River	1	24.6	25.6
CWY	Coweeman	Coweeman River	1	22.46	23.46
CWS	Coweeman	Coweeman River	1	19.59	20.59
CWJ	Coweeman	Coweeman River	1	12.12	13.12
CWC	Coweeman	Coweeman River	1	7.54	8.54
CWA	Coweeman	Coweeman River	1	6.54	7.54
C3A	Coweeman	Coweeman Trib 3	1	0	1
GBF	Coweeman	Goble Creek	1	2.41	3.41
GBC	Coweeman	Goble Creek	1	0.79	1.79
NGB	Coweeman	NF Goble Creek	1	0	1
MUH	Coweeman	Mulholland Creek	1	3.04	4.04
MUD	Coweeman	Mulholland Creek	1	0	1

Appendix 1 g. GRTS reaches surveyed for Kalama River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BRK	Kalama	Burke Creek	0.21	0.4	0.61
FSB	Kalama	Fish Pond Creek	1	0.59	1.59
INB	Kalama	Indian Creek	1	0	1
KAJ	Kalama	Kalama River	1	7.69	8.69
KAK	Kalama	Kalama River	1	6.63	7.63
KAB	Kalama	Kalama River	1	3.64	4.64
CAA	Kalama	Kalama River	1	1.67	2.67
SCA	Kalama	Schoolhouse Creek	1	0	1
SPB	Kalama	Spencer Creek	1	1	2
SPA	Kalama	Spencer Creek	1	0	1

Appendix 1 h. GRTS reaches surveyed for Cedar Creek coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BEB	Cedar	BEAVER Creek	1	1	2
BEA	Cedar	BEAVER Creek	1	0	1
BIB	Cedar	BITTER Creek	1	1	2
BIA	Cedar	BITTER Creek	1	0	1
CER	Cedar	CEDAR Creek	0.83	17.96	18.79
CEO	Cedar	CEDAR Creek	1	14.1	15.1
CEN	Cedar	CEDAR Creek	1	13.1	14.1
CEM	Cedar	CEDAR Creek	1	12.1	13.1
CEL	Cedar	CEDAR Creek	1	11.1	12.1
CEK	Cedar	CEDAR Creek	1	10.1	11.1
CEJ	Cedar	CEDAR Creek	1	9.1	10.1
CEI	Cedar	CEDAR Creek	1	8.1	9.1
CEH	Cedar	CEDAR Creek	1	7.02	8.02
CEF	Cedar	CEDAR Creek	1	6.02	7.02
NCB	Cedar	CHELATCHIE-NF Creek	1	0.47	1.47
CHF	Cedar	CHELATCHIE-SF Creek	1	5	6
CHE	Cedar	CHELATCHIE-SF Creek	1	4	5
CHA	Cedar	CHELATCHIE-SF Creek	1	0	1
JOA	Cedar	JOHN Creek 27.0335	0.85	0	0.85
PUA	Cedar	PUP Creek 27.0345	1	0.48	1.48
PTR	Cedar	Pup Creek Trib	1	0	1

Appendix 1 i. GRTS reaches surveyed for NF Lewis River coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BRA	Lower Lewis	Bratton Creek	1	0	1
GEE	Lower Lewis	Gee Creek	1	4.9	5.9
HYD	Lower Lewis	Hayes Creek	1	0.68	1.68
HOC	Lower Lewis	HOUGHTON Creek	1	1.26	2.26
JOA	Lower Lewis	JOHNSON Creek	1	0	1
RSC	Lower Lewis	ROSS Creek	1	0.38	1.38

Appendix 1 j. GRTS reaches surveyed for EF Lewis coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
DEA	EF Lewis	Dean Creek	1	0.15	1.15
JEN	EF Lewis	Jenny Creek	0.23	0	0.23
EFB	EF Lewis	Lewis River - East Fork	1	13.92	14.92
LWD	EF Lewis	LOCKWOOD Creek	1	1.22	2.22
LWA	EF Lewis	LOCKWOOD Creek	1	0	1
MNE	EF Lewis	MASON Creek 27.0200	1	2.68	3.68
MNC	EF Lewis	MASON Creek 27.0200	1	1.68	2.68
MNA	EF Lewis	MASON Creek 27.0200	1	0.23	1.23
MIC	EF Lewis	MILL Creek 27.0218	1	1.2	2.2
RCC	EF Lewis	ROCK Creek 27.0222	1	0	1
SLD	EF Lewis	Stoughton Creek	1	1.19	2.19

Appendix 1 k. GRTS reaches surveyed for Washougal coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
BOA	Washougal	Boulder Creek	1	0	1
LWC	Washougal	Little Washougal River	1	2.09	3.09
ELC	Washougal	EF Little Washougal River	1	0.81	1.81
WAX	Washougal	Washougal River	1	20.7	21.7
WAT	Washougal	Washougal River	1	19.7	20.7
WAQ	Washougal	Washougal River	1	17.51	18.51
WAF	Washougal	Washougal River	1	9.43	10.43
WAA	Washougal	Washougal River	1	7.11	8.11
WLB	Washougal	Wildboy Creek	1	0	1
WLE	Washougal	WINKLER Creek	1	0	1

Appendix 1 l. GRTS reaches surveyed for Lower Gorge coho salmon in 2012.

Section	Population	Stream Name	Miles	RM Start	RM Stop
CMP	Lower Gorge	CAMPEN Creek	1	0.35	1.35
CRP	Lower Gorge	Carpenter Creek	1	0	1
GFB	Lower Gorge	Greenleaf Creek	1	0.12	1.12
HMC	Lower Gorge	Hamilton Creek	1	1.72	2.72
LNC	Lower Gorge	LAWTON Creek	1	1	2
LNA	Lower Gorge	LAWTON Creek	1	0	1
WWD	Lower Gorge	Woodward Creek	1	2.43	3.43

Appendix 2

Appendix 2. Hatchery coho salmon smolt releases that occurred in 2011 from BY 2009. The two large releases of unmarked CWT fish (CWT-NoClip) from the Lewis River Hatchery are double index tag (DIT) group releases of early and late stock coho salmon to evaluate selective fisheries.

Release Site	Population	CWT-AdClip	CWT-NoClip	AdClip	NoClip	Total
Deep R Net Pens	Grays	26,500	0	664,169	1,331	692,000
Grays River Hatchery	Grays	25,000	0	129,740	260	155,000
Cowlitz Salmon Hatch	Cowlitz	823,180	251,270	1,994,836	7,109	3,069,286
North Toutle Hatchry	Green	28,429	250	134,037	2,269	164,985
Fallert Cr Hatchery	Kalama	52,724	0	52,715	0	105,439
Kalama Falls Hatchry	Kalama	30,240	0	618,652	0	648,892
Lewis River Hatchery	NF Lewis	75,411	75,411	676,585	1,288	828,695
Lewis River Hatchery	NF Lewis	76,178	76,178	647,830	1,689	801,875
Washougal Hatchery	Washougal	89,154	613	2,539,865	22,918	2,652,550
TOTAL		1,226,816	403,722	7,458,429	29,755	9,118,722

Detection Probabilities for Passive Integrated Transponder (PIT) Tags in Adult Salmon and Steelhead with Hand Held Scanners, 2012

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Executive Summary

Passive Integrated Transponder (PIT) tags are used throughout the Columbia River basin to measure survival, migration patterns, predation rates, and other life history and demographic attributes of salmon and steelhead populations. The use of PIT tags for estimating salmon and steelhead harvest rates in fisheries is a potential new application for PIT tags. However, the efficiency with which these tags may be detected in landed catch must be known for these estimates to be unbiased. We implemented a study to evaluate PIT detection rates for tagged adult salmonids using a variety of tag scanner types under conditions similar to those expected in sampling of fisheries catch. Fall Chinook salmon, coho salmon, and summer steelhead hatchery adults were tagged with 12.5 mm full-duplex PIT tags and released into hatchery raceways in the fall of 2012. A total of 300 tagged individual salmon and steelhead were sampled with four PIT tag reader types, including the Destron Fearing FS2001F-ISO with racquet antenna (DF), Biomark 601-3 (AF), Agrident AWR 100 Stick Reader (SR), and Biomark HPR plus (HPR). The probability of detection was estimated using series of general linear mixed models (GLMM) including combinations fish characteristics as well as reader type and sampling protocol characteristics.

The best model based on Deviance Information Criterion (DIC) included a random effect for fish, accommodating the repeated measures design, nested fish-level fixed effects for species and girth, and non-nested fixed effects of reader type, sampling method, use of a spacer to simulate scanning a fish without maintaining physical contact, and an interaction between sampling method and reader type. Since individual fish covariates are not measured for all fish during fishery sampling and sampling protocols help ensure protocol deviations are held to a minimum, a reduced model was fit to estimate detection efficiencies for each reader type under fishery sampling conditions for each species, with resulting detection probabilities of > 99.50% for Chinook salmon, coho salmon, and summer steelhead using DF, AF, and SR reader types. However, AF and SR readers were sensitive to simulated protocol violations, suggesting the DF reader may be most appropriate for applications when large numbers of fish are present (e.g., commercial fishery sampling) and protocol violations are more likely. Conversely, the cheaper AF readers may be a viable alternative for sport fishery sampling applications where fish volumes are lower and sampling protocol violations are less likely. Application of our detection rates to adult PIT tag fishery sampling programs allows for a bias correction due to PIT tags that are not detected, although this bias is negligible.

Introduction

Passive Integrated Transponder (PIT) tags are the primary means of estimating many demographic parameters for Columbia River Basin salmon and steelhead populations, including juvenile and adult survival, and mechanisms affecting survival (Connor et al. 1998, Zabel and Accord 2004, Buchanan et al. 2006) such as predation by bird and northern pikeminnow (Collis et al. 2001, Petersen and Barfoot 2003), and habitat characteristics (Paulsen and Fisher 2005). Despite the central role of PIT tags in monitoring Columbia River fish populations, estimates of fishery harvest removals remain one of the largest sources of lifetime mortality that is not currently estimated specifically for PIT tagged fish and could provide valuable information to researchers, managers, and policy makers. However, before PIT tags recovered from harvested fish may be used to estimate harvest rates, their detection probability in landed catch using handheld readers must be estimated. Without expansion, harvest estimates derived from sampling catch for PIT tags will underestimate the true harvest rate. The purpose of this study was to develop PIT tag sampling protocols for adult salmon and steelhead landed in fisheries and to estimate detection rates of PIT tags that may be applied to expand the raw number of PIT tags recovered in order to estimate harvest rates.

The number of juvenile and adult salmon and steelhead tagged for various research and monitoring purposes throughout the Columbia Basin has increased from less than 20,000 in 1988 to over 2,000,000 in 2009. Almost \$4,000,000 annually is dedicated to the purchase of PIT tags, and millions more are spent capturing and tagging fish, recovering tags, and storing data in the PIT Tag Information System (PTAGIS), a regionwide PIT tag database. Detection systems have advanced from hand held devices (Buzby and Deegan 1999) to juvenile bypass systems and adult traps and ladders (Harmon 2003) to instream arrays capable of detecting adult and juvenile passage (Connolly et al. 2008). As a result more than 30,000 PIT tagged adults have now been detected migrating past Bonneville Dam in some years, suggesting sample sizes may now be sufficient for use in estimating harvest rates in fisheries.

Columbia River fisheries operate on a mixture of dozens of distinct populations, yet fishery harvest is primarily monitored and managed for a small number of harvest reporting groups using coded-wire tags (CWT), body size, and migration timing, which are insufficient to estimate fishery mortality for specific populations. Thus, use of PIT tag recoveries from harvested fish may allow managers to better estimate fishery impacts to shape fisheries to reduce impacts on ESA-listed and other at-risk populations based on their spatial and temporal occurrence in fisheries. The current fishery sampling program operated by the Washington Department of Fish and Wildlife (WDFW), the Oregon Department of Fish and Wildlife (ODFW), and the Pacific States Marine Fisheries Commission (PSMFC), in collaboration with the Columbia River treaty tribes, provides a platform for sampling catch, and has recently been expanded to include sampling for the presence of PIT tags.

While it may be convenient to assume that all PIT tagged fish sampled will be detected, violation of this assumption would result in systematic underestimates of harvest rates on PIT tagged fish. PIT tag readers are designed to detect tags within a specific distance of

the reader, however readers may fail to detect tags if fish are scanned in a way that the reader does not pass close enough to the location where the tag is located either because of the size and girth of the fish, or because of variability in the technique used to scan the fish. Therefore, in 2010 and 2011 the Washington Department of Fish and Wildlife (WDFW) initiated a study to estimate the probability of detecting PIT tags in adult salmon and steelhead using standardized methods and a variety of commonly used portable PIT tag detectors and antennae. However, the study design precluded effectively estimating how fish characteristics and sampling methods affect detection rates. Herein, we report the results of the continuation of this detection study in 2012. Our objectives in 2012 were to measure the effects of PIT tag reader type, as well as fish characteristics and sampling methods on detection rates. Fish characteristics tested included length, girth, sex, and species. Sampling techniques tested included scanning fish with readers held at various distances from the fish, as well as a variety of scanning techniques.

Methods

Tagging

Adult salmon and steelhead that had returned to WDFW hatcheries were PIT tagged one week prior to culling and simulated fishery sampling occurred in order to evaluate detection rates. Adult Chinook salmon were tagged on October 2nd, 2012, at Skamania Hatchery; adult coho salmon were tagged on November 8th, 2012, at Fallert Creek Hatchery, and adult steelhead were tagged on January 24th, 2013, at Merwin Hatchery.

Standard Columbia Basin PIT tagging procedures from the Columbia Basin Fish and Wildlife Authority (CBFWA, 1999) developed for juveniles were adapted for adults. Briefly, fish were crowded in the hatchery raceway with seines or screens, netted, and released into a holding tank. The tank was filled with water and had a concentration of ~ 40mg of MS-222 per liter. After fish had become docile, they were tagged with a Destron Fearing TX1411SST full-duplex PIT tag (12.5mm 134.2 kHz) in the peritoneal cavity, and scanned with a Destron Fearing FS2001F-ISO Reader Base Unit with a racket antenna (DF) to record the tag number, and then released back into the raceway.

At the time of tagging we recorded species and sex, which was identified using morphological characteristics (Groot and Margolis 1991). A measuring board was used to measure fork length and a plastic tape measure was used to measure girth by measuring body circumference anterior to the dorsal fin (Table 1).

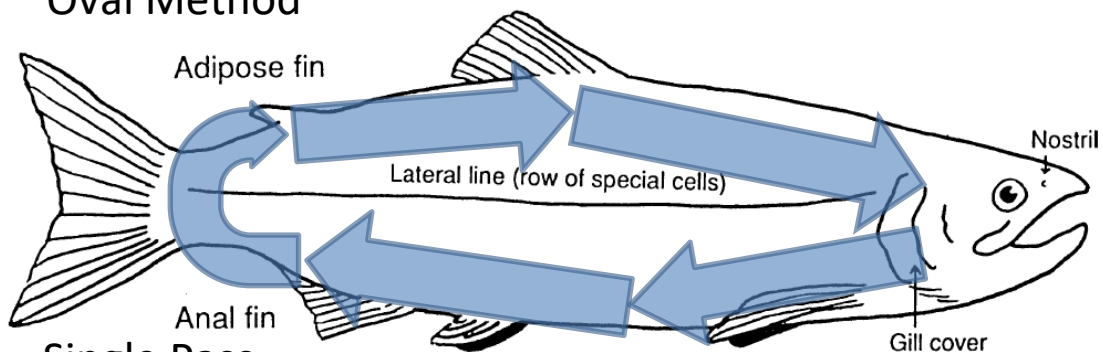
Detection Trials

Adult salmon and steelhead were euthanized on the respective day that the detection study was conducted for each species. Trials conducted on sacrificed Chinook (CK) and coho (Co) salmon and steelhead (Sth) took place on October 5th and November 16th, 2012, and on January 28th, 2013, respectively. These dates were chosen to ensure that fish were sacrificed prior to full maturation of the gonads because high rates of tag loss may occur immediately prior to spawning (Prentice et al. 1994). Locations for each field detection test matched the locations that initial tagging was conducted: adult Chinook salmon at Skamania Hatchery, adult coho salmon at Fallert Creek Hatchery and adult steelhead at Merwin Hatchery.

Carcasses were then scanned with a Destron Fearing FS2001F-ISO Reader Base Unit with a racket antenna (DF) to determine tag presence and only carcasses found to have tags were retained for the detection study (n = 100 per species). The carcasses were placed head to tail in the same orientation on tables with 0.75 meters distance between the noses of adjacent fish to avoid potential interference from PIT tags in adjacent carcasses.

Field protocols were developed to maximize PIT tag reader efficiency under realistic fishery sampling conditions. The PIT tag reader was placed in direct contact with a fish and moved in an oval-shaped pass from the ventral opercle area, across the ventral/lateral surface, crossing the caudal peduncle, and back to the anterior of the fish across the dorsal/lateral surface, the “Oval Method” (OM) (Figure 1.a.). However, under real fishery sampling conditions, high volumes of fish requiring rapid sampling may increase the tendency for samplers to violate this protocol, either conducting a “Single Pass” (SP), in which a the reader is moved in a single continuous pass down the lateral line of a fish (Figure 1.b.). In addition, samplers may not maintain continuous physical contact between the PIT tag reader and the fish.

a) Oval Method



b) Single Pass

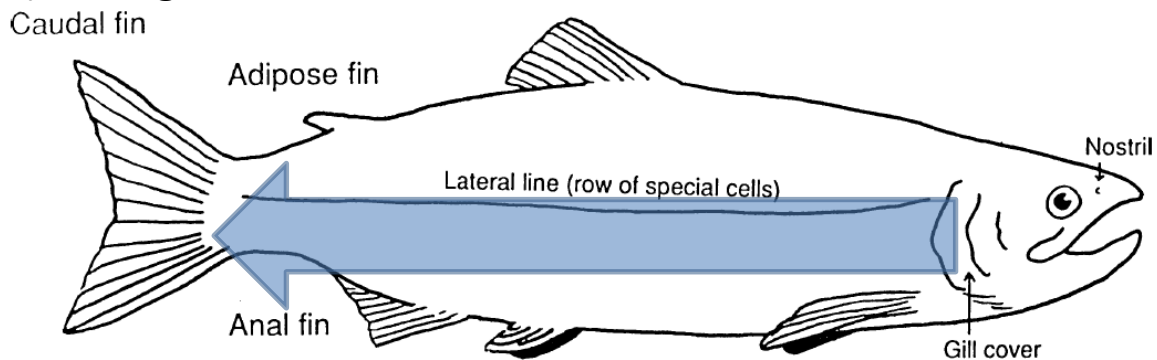


Figure 1. Pass over detection methods for scanning adult salmon for PIT Tags (Kaessey, 2017).

In order to determine the sensitivity detection efficiency estimates to these sampling protocol violations, trials were conducted using both the SP and OM sampling techniques, both with and without the use of 5 cm thick foam spacers taped to the readers to simulate the effect of holding the reader 5cm away from fish during sampling. Spacers were used to ensure consistent distance between the RFID readers and fish (Figure 2). The effect of foam spacers on read-range of the readers was tested and was found not to affect read range, although tests of read range suggested most readers had lower read ranges than reported by manufacturers (Appendix 1).

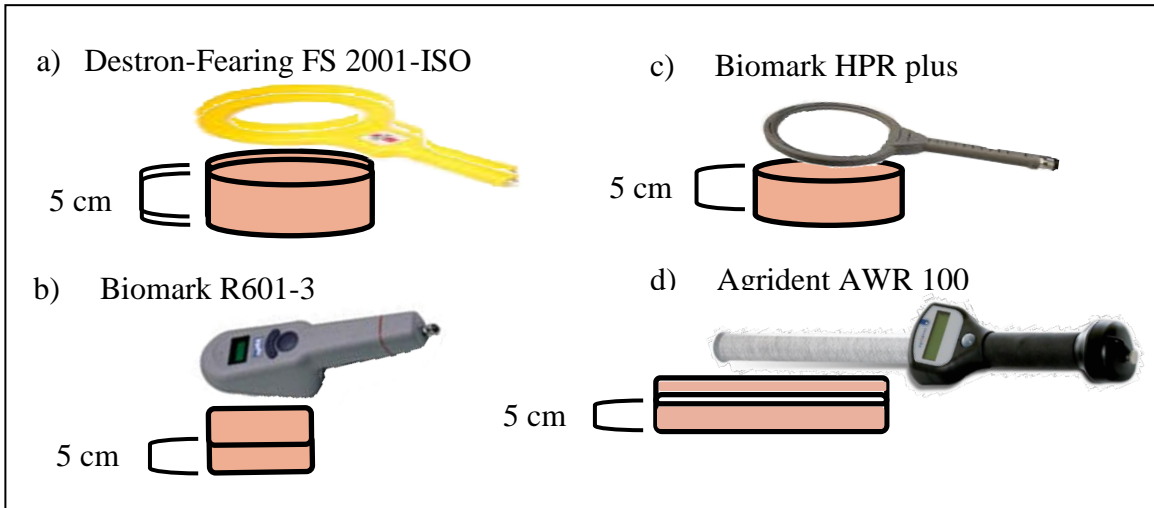


Figure 2. PIT tag detection antennae used in this study with schematic showing foam spacers. Reader types include: a) Destron Fearing FS2001F-ISO Reader Base Unit with racquet antenna (DF), b) Biomark R601-3 Reader (AF), c) Biomark HPR plus (HPR), and d) the Agrident AWR 100 Stick Reader (SR). Reader antennae are shown with schematics of 5 cm foam spacers used to simulate sampling protocol deviations in one set of trials (see methods).

Table 1. Fixed effects evaluated in statistical models for their influence on detection efficiency. Factor levels are reported for categorical variables and medians and ranges are reported for continuous variables. Individual fish characteristics were nested within a random effect (individual fish) to accommodate a repeated measures design which involved scanning individual fish multiple times.

Variable	Abbreviation	Factor Levels or Median (Range)
<i>Fish-Level (Nested) Fixed Effects</i>		
Species	Sp	Steelhead, Coho, Chinook
Girth	G	37 (22-52) cm
Sex	Sx	Male, Female (male only for CK)
Fork Length	FL	70 (40-89) cm
<i>Observation-Level (Non-Nested) Fixed Effects</i>		
Reader Type	RT	DF, SR, AF
Sample Method	SM	Single Pass, Oval Method
Spacer	Sr	Spacer, No Spacer

A single detection trial consisted of a sampler scanning every individual fish of a particular species with a unit of a particular reader type. Reader types included: Destron Fearing FS2001F-ISO Reader Base Unit with racquet antenna (DF), Biomark R601-3 Reader (AF), Agrident AWR 100 Stick Reader (SR), and Biomark HPR plus (HPR). To evaluate the variability in detection efficiency of each reader type, we used multiple handheld units for each of the four reader types: four DF reader units, four AF reader units, two SR reader units, and two HPR reader units (steelhead trials only). To evaluate (or control) the effect of sampler on detection efficiency, we employed a fully crossed study design. Here four different samplers exchanged reader units of a particular type so that each sampler (n = 4 samplers) used two of the four DF and AF units. For SR and HPR readers, since there were only two units, two samplers conducted trials with these units, and exchanged them so that each sampler used each unit. Trials were conducted with both OM and SP sampling methods as well as with and without foam spacers. Additionally HPR readers were tested in two modes with “Auto-tuning” (a manufacturer setting thought to affect detection probability) set to both on and off. Efforts were made to cross the various factors of the study design (Table 2).

Table 2. Detection trial sample sizes for each species ($n = 100$) by RFID reader type. HPR readers were only used in steelhead trials. The study design was crossed so total sample sizes may be obtained by multiplying down each column.

Detection Trial Factor	Reader Type			
Reader Type	AF	DF	SR	HPR
Number of reader units used by each sampler	2	2	2	2
Number of Samplers	4	4	2	2
Sampling Method (OM or SP)	2	2	2	2
Spacer (used or not used)	2	2	2	2
Auto-tune function (On or Off)	—	—	—	2
Number of Fish (per species)	100	100	100	100
Total Fish Scanned	3,200	3,200	1,600	3,200

Statistical Analysis

Our experimental design involved multiple individuals repeatedly scanning 100 salmon and steelhead of each species with various PIT tag units of each reader type and various sampling methods with and without spacers. This design necessitated the use of a repeated measures analytical framework with individual fish treated as a random effect. We used a generalized linear mixed modeling approach in which related the Bernoulli response (detected/not detected) to covariates on the logit scale.

Covariates included both fish-level and observation-level fixed effects. Fish-level fixed effects (species, sex, girth, length) were those that were nested within individual fish, which was a random effect, and were evaluated solely as main effects (Table 1). Lengths and girths were centered prior to completing the analysis. Observation-level fixed effects were non-nested fix effects that were evaluated as main effects and in combination as two way interactions. These included PIT tag reader type (DF, AF, SR), sampling method (Oval and Single Pass), presence/absence of a spacer, and two-way interactions between reader type and sampling method as well as reader type and spacer presence (Table 1). The two-way interaction between spacer presence and sampling method (e.g., that the effect of distance on detection efficiency would depend on sampling method in a non-additive manner) did not make logical sense, therefore this interaction as well as the three-way interaction between reader type, spacer presence, and sampling method, was not evaluated.

We analyzed detection efficiencies of the HPR readers separately since this reader type was only tested on steelhead and was tested with an additional fixed effect (use or non-use of “auto-tune” function).

The full model was specified by:

$$y_{f,i} \sim \text{Bernoulli}(p_{f,i}) \quad (1)$$

where y are individual scans of a fish (detected/not detected) with a probability of detection p , and the subscript f represents the individual fish, which were treated as a

random effect, and the subscript i represents an individual scan of an individual fish. The logit-transformed probability of detection was modeled as a linear function with a global intercept μ , and random adjustment to the global intercept α_f for each fish (Eq. 2) and series of indicator and continuous fixed effects, each with their own adjustment to the slope, β , some of which were nested within individual fish:

$$\text{logit}(p_{f,i}) = \mu + \alpha_f + \beta_1 Sp_f + \beta_2 Sx_f + \beta_3 FL_f + \beta_4 G_f + \beta_5 RT + \beta_6 SM + \beta_7 Sr + \beta_8 RTSM + \beta_9 RTSr \quad (2)$$

The random adjustment to the global intercept for each fish was normally distributed with a mean of zero and a common standard deviation:

$$\alpha_f \sim iid N(0, \sigma^2) \quad (3)$$

This model was then reparametrized to facilitate Markov chain Monte Carlo (MCMC) convergence using the package ‘glmmBUGS’ (Brown and Zhou 2010). Vague priors, $U(-10, 10)$, were defined for the intercept and fixed effects on the logit scale in order to confine the MCMC sampling to real parameter space on the normal scale (0-1) while ensuring the priors would have minimal influence on the posterior distribution relative to the likelihood and data.

The model was fitted using WinBUGS (Spiegelhalter 2003) via the ‘R2WinBUGS’ package (within the R statistical computing environment (R Development Core Team 2010)). For each model, three MCMC simulations were given a 1,000 iteration ‘burn-in’. Samples were ‘thinned’ to every 10th iteration, and a total of 9,000 samples per chain were obtained.

Model Selection

Our candidate model set included fish-level fixed effects which were nested within a random effect (fish), as well as observation-level fixed effects. We followed the mixed effects model selection procedures outlined in Bolker et al. (2009) and Brown and Zhou (2010). We began by constructing a full model with all fish- and observation-level fixed effects and performed model selection on random effects while holding the fixed effects constant, followed by performing model selection on fixed effects using the random effects selected in the previous phase of model selection Bolker et al. (2009). Model selection of fixed effects was accomplished in stages following the recommendations of Brown and Zhou (2010), first by identifying the best model of observation-level fixed effects while including all fish-level fixed effects. Once the best model of observation-level fixed effects was determined, these effects were included while allowing fish level effects to vary in order to select the best model of fish-level fixed effects. Evaluating random effects was accomplished using Deviance Information Criterion (DIC; Spiegelhalter 2002), where the model with the lowest DIC was considered the best model, and models within 2 units of this model were considered similarly plausible and preferable due to parsimony, if including fewer parameters. We used DIC for fixed effects model selection as well, but also computed 95% credible intervals for coefficients

of covariates, only including the fish-level variables that had 95% credible intervals which did not overlap zero.

Random effects not incorporated in statistical models and data censoring

Detection rates in our study were potentially influenced by the specific reader unit used among all readers of particular type as well as the particular person sampling fish among all samplers. We were interested in the average detection efficiency of particular reader types, and of the average individual sampler rather than among-unit variability in readers of a particular type or among-sampler variability. Therefore reader number and sampler number were not included as a fixed effect in models. Additionally, the crossed experimental design, which required samplers to rotate among reader units of particular type, and to scan all fish using both oval pass and single pass methods with and without spacers, ensured that any among-unit or among sampler variability would not be confounded with study variables of interest. Thus, it was unnecessary to include these variables as random effects in statistical models.

Nonetheless, we summarized detection data by unit for each PIT tag reader type to ensure that a defective unit of a particular type did not influence overall study results. We used contingency tables and χ^2 tests to test for significant among-unit variation within each reader type in order to censor data from reader units which were malfunctioning.

Detection data by individual sampler did not require similar screening and censoring since the samplers used for this study were a subset of the samplers who sample fish for WDFW in the field and we wanted results to encompass among-sampler variability. Although attempts were made to use the same individuals for this study on all days, some individuals were not available on all days. Therefore among-sampler variability may be somewhat confounded with species-specific detection efficiencies since trials for each species were conducted on different days.

Results

MCMC diagnostics suggested that models converged to the posterior distribution of the parameters. Gelman–Rubin convergence diagnostics for all parameters were good ($\hat{R} = \pm 0.0005$). Visual inspection of chains showed good mixing and an absence of initialization effects.

Overall detection rates by reader type

Detection rates were similar among all units of each type and were not significantly different from each other (DF: $\chi^2 = 2.4574$, $df = 3$, $p\text{-value} = 0.48$, AF: $\chi^2 = 6.9045$, $df = 3$, $p\text{-value} = 0.075$, SR: $\chi^2 = 1.8253$, $df = 1$, $p\text{-value} = 0.1767$) except for HPR units (HPR: $\chi^2 = 118.7122$, $df = 1$, $p\text{-value} < 2.2e-16$), for which unit 1 had a significantly lower mean detection efficiency than unit 2 (Table 3). For AF units, coho salmon sampling was excluded from tests since the data logger on unit 1 malfunctioned during coho trials.

Table 3. Detection data and rates by unit number for each reader type pooled across all species and trials. AF data are shown with and without coho trials since the data logger for unit one malfunctioned during this trial. HPR readers were only used during steelhead trials.

Reader Type	Unit #	Missed	Detected	% Detected
DF	1	2	2398	99.92%
DF	2	2	2398	99.92%
DF	3	2	2398	99.92%
DF	4	5	2395	99.79%
AF (not used for coho)	1	28	1572	98.25%
AF	2	26	2274	98.87%
AF	3	15	2385	99.38%
AF	4	26	2374	98.92%
AF (no coho trials)	1	28	1572	98.25%
AF (no coho trials)	2	18	1482	98.80%
AF (no coho trials)	3	12	1588	99.25%
AF (no coho trials)	4	24	1576	98.50%
SR	1	317	2083	86.79%
SR	2	285	2115	88.13%
HPR (sth only)	1	156	1444	90.25%
HPR (sth only)	2	16	1584	99.00%

Effects of fish characteristics, reader types, and protocol adherence on detection ratesThe best model of observation-level covariates (Model 1) included RT, SM, Sr, and an interaction between RT and SM ($\Delta\text{DIC} = 2.47$ for next best model) and all covariates had coefficients with credible intervals which did not overlap zero (Table 4). Model selection for fish-level covariates then proceeded including these observation-level covariates. Although model selection criteria for fish-level covariates weakly favored Model A over Models B and C ($\Delta\text{DIC} = 1.41$ and 1.85 , respectively), Model C was similarly plausible and contained fewer parameters, and was consequently selected as the best model (Table 5).

Table 4. Model selection criteria used to compare models of detection efficiency to identify the best set of observation-level fixed effects, using the full model of fish-level fixed effects.

Model	Fish-level Fixed Effects	Observation-level Fixed Effects	DIC	ΔDIC
1	Sp + G + Sx + FL	RT + SM + Sr + RT : SM	4118.64	0.00
2	Sp + G + Sx + FL	RT + SM + Sr + RT : SM + RT : Sr	4121.11	2.47
3	Sp + G + Sx + FL	RT + SM + Sr	4138.67	20.03
4	Sp + G + Sx + FL	RT + SM + Sr + RT : Sr	4141.10	22.46

Table 5. Model selection criteria used to compare models of detection efficiency to identify the best set of fish-level fixed effects, using the best model (model 1) of observation-level fixed effects.

Model	Fish-level Fixed Effects	Observation-level Fixed Effects	DIC	Δ DIC
A	Sp + G + Sx + FL	RT + SM + Sr + RT : SM	4118.64	0.00
B	Sp + G + Sx	RT + SM + Sr + RT : SM	4120.05	1.41
C	Sp + G	RT + SM + Sr + RT : SM	4120.49	1.85
D	G + Sx	RT + SM + Sr + RT : SM	4127.30	8.36
E	G	RT + SM + Sr + RT : SM	4129.36	10.39
F	Sp + Sx	RT + SM + Sr + RT : SM	4142.73	23.14
G	Sp	RT + SM + Sr + RT : SM	4145.99	27.35
H	Sx	RT + SM + Sr + RT : SM	4150.67	31.96

The best overall model of detection efficiency (Model C) included several fish- and observation-level fixed effects (Tables 5-6). Detection efficiency differed among species (CK > Sth > Co) and was negatively correlated with girth. Detection efficiency also differed among reader types (DF > AF > SR), sampling methods (OM > SP), and spacer presence (absent > present), and there was a significant interaction between reader type and spacer presence in which detection efficiency declined more for SR readers than for DF and AF readers, for which the effect of spacers did not differ (Table 6).

Table 6. Parameter values on the logit scale for fixed effects that were part of Model C, which was selected as the best overall model of detection efficiency.

Parameter	L 95 % CI	Median	U 95 % CI
<i>Fish-level Fixed Effects</i>			
Sp (Coho)	-0.85	-0.54	-0.24
Sp (Steelhead)	-0.87	-0.53	-0.20
G	-0.12	-0.10	-0.07
RT (DF)	1.71	2.32	3.05
RT (SR)	-2.74	-2.48	-2.23
SM (Oval Method)	1.43	2.01	2.64
Sr	-2.03	-1.82	-1.62
RT (DF) x SM (Oval Method)	-1.37	0.61	4.04
RT (SR) x SM (Oval Method)	-1.99	-1.34	-0.75

Detection rates by species and reader type for use in fisheries sampling

Although the best model identified differences in detection among PIT tag reader types, these differences were small in magnitude. In addition, the proportion of tags detected was close to 100% for all reader types (DF, AF, SR) that were tested on all species (CK, CO, Sth), and no reader type missed more than two tags out of 800 trials per species (400 for SR) when the OM sampling method was used without spacers (Tables 7-10), simulating complete sampling protocol adherence (Appendices 1 and 2). The DF reader was robust to simulated sampling protocol violations, detecting more than 99.5% of tags regardless of SM and spacer presence. In contrast, AF and SR readers were more

sensitive to protocol violations; under the worst case scenario (single pass sampling method with spacer) AF readers detected 94.38% – 98.00% of tags and SR readers detected 67.25% – 91.00% of tags, depending on the species (Tables 7-9). Owing to the large extent of among-unit variability in HPR readers and the limited number of units tested (n = 2), we chose not to report HPR modeling results or detection probabilities.

Table 7. Raw fall Chinook salmon (males only) detection data and proportions of tags detected by reader type and sample method using the oval method and single pass scanning techniques. Trials with no simulated protocol violations are bold face.

Reader Type	Sample Method	Spacer	Tags Detected	Trials	Proportion Detected
AF	Oval Method	N	799	800	99.88%
AF	Oval Method	Y	798	800	99.75%
AF	Single Pass	N	798	800	99.75%
AF	Single Pass	Y	755	800	94.38%
DF	Oval Method	N	800	800	100.00%
DF	Oval Method	Y	800	800	100.00%
DF	Single Pass	N	799	800	99.88%
DF	Single Pass	Y	798	800	99.75%
SR	Oval Method	N	394	400	98.50%
SR	Oval Method	Y	320	400	80.00%
SR	Single Pass	N	354	400	88.50%
SR	Single Pass	Y	364	400	91.00%

Table 8. Raw coho salmon detection data and proportions of tags detected by reader type and sample method using the oval method and single pass scanning techniques. AF total trials are reduced by one quarter owing to a defective unit during this trial. Trials with no simulated protocol violations are bold face.

Reader Type	Sample Method	Spacer	Tags Detected	Trials	Proportion Detected
AF	Oval Method	N	600	600	100.00%
AF	Oval Method	Y	599	600	99.83%
AF	Single Pass	N	600	600	100.00%
AF	Single Pass	Y	588	600	98.00%
DF	Oval Method	N	799	800	99.88%
DF	Oval Method	Y	800	800	100.00%
DF	Single Pass	N	800	800	100.00%
DF	Single Pass	Y	796	800	99.50%
SR	Oval Method	N	400	400	100.00%
SR	Oval Method	Y	308	400	77.00%
SR	Single Pass	N	345	400	86.25%
SR	Single Pass	Y	301	400	75.25%

Table 9. Raw steelhead detection data and proportions of tags detected by reader type and sample method using the oval method and single pass scanning techniques. AF total trials are reduced for spacer present trials as these trials inadvertently did not occur. Trials with no simulated protocol violations are bold face.

Reader Type	Sample Method	Spacer	Tags Detected	Trials	Proportion Detected
AF	Oval Method	N	798	800	99.75%
AF	Oval Method	Y	744	750	99.20%
AF	Single Pass	N	794	800	99.25%
AF	Single Pass	Y	732	750	97.60%
DF	Oval Method	N	800	800	100.00%
DF	Oval Method	Y	800	800	100.00%
DF	Single Pass	N	800	800	100.00%
DF	Single Pass	Y	797	800	99.63%
SR	Oval Method	N	400	400	100.00%
SR	Oval Method	Y	351	400	87.75%
SR	Single Pass	N	392	400	98.00%
SR	Single Pass	Y	269	400	67.25%

Table 10. Model-fitted detection probabilities by species and reader type for the subset of trials using the OM method with no spacer. These detection probabilities are representative of fishery sampling detection rates when protocols are followed.

Species	Reader Type	Mean	sd	L 95%CI	Median	U 95%CI
Ck	AF	99.92%	0.07%	99.74%	99.93%	99.99%
Co	AF	99.99%	0.02%	99.93%	99.99%	100.00%
Sth	AF	99.98%	0.03%	99.90%	99.99%	100.00%
Ck	DF	99.97%	0.05%	99.82%	99.98%	100.00%
Co	DF	99.99%	0.01%	99.96%	100.00%	100.00%
Sth	DF	99.99%	0.02%	99.94%	100.00%	100.00%
Ck	SR	99.56%	0.38%	98.56%	99.67%	99.96%
Co	SR	99.92%	0.10%	99.65%	99.95%	100.00%
Sth	SR	99.88%	0.14%	99.49%	99.93%	100.00%

Discussion

Our results suggested that individual PIT tag detection rates with the three models of hand-held PIT tag detectors (DF, AF, SR) were greater than 99% when sampling protocols were followed. These results are consistent with a previous study on Pacific Halibut (*Hippoglossus stenolepis*) that used the same type of PIT tag with AF and DF readers Hauser (2003). The halibut study examined PIT tag detection rates in Pacific Halibut that were PIT tagged in the cheek and found each PIT tag reader had detection rates greater than 96% and no significant difference between readers ($P > 0.05$) in 19 trials. Although tag location in that study was different from ours (cheek for halibut versus peritoneal cavity for salmon), both yielded similar results.

Our results support that PIT tag detection rates in commercial and recreational fisheries can be high if well-designed protocols are developed and implemented. Since our detection rate approached 100%, the assumption that fishery sampling activities had perfect detection efficiency for salmon and steelhead would lead to only a slight negative bias in sampled PIT tags. The significant effect of girth and species on detection probabilities suggests that our results may be less applicable to fisheries sampling efforts encountering fish outside the range of girths tested in this study (e.g., very large chinook), or species with different body morphology, which may necessitate a different sampling method.

Reduced detection probabilities resulting from the simulated protocol deviations underscores the need for proper training of staff and quality assurance/quality control (QA/QC) programs. Current scanning protocols used by WDFW (Figure 1) call for the use of the OM sampling method while maintaining complete contact between the reader and the fish. Our results suggest that the DF reader maintains near-perfect detection efficiency in the presence of minor deviations from this protocol. While the AF reader maintains high but declining efficiency and the SR reader has markedly reduced performance in the presence of minor deviations from protocol. We therefore recommend the use of the DF reader in commercial fishery sampling applications where minor protocol violations are more likely to occur due to the high volume of fish sampled. In contrast, the AF reader may be a suitable and more cost effective alternative for sport fishery sampling where samplers only encounter small numbers of fish at a time, allowing better assurance that protocols are followed.

Although we tested the OM and SP sampling methods with all reader types in this study, many users of hoop-shaped PIT tag readers, including the DF, and HPR, use the “pass-through” method, where fish are passed through the open racquet-type antenna (C. Cochran, WDFW pers. comm.). It is likely that the pass through method has similar to or higher detection rates than those documented in our study. We implemented the OM sampling method because we wanted a consistent detection method in order to compare among reader types, and because we wanted our results to be applicable to real catch sampling, which sometimes does not allow for pass through detection. For example, large Chinook salmon cannot fit through the opening in the racquet-type antenna, eliminating the possibility of consistent use of the pass through method for all adult salmon with the DF. In addition, the pass through method cannot be implemented for the smaller hand

held detectors like the AF. We chose the OM method because this method can be consistently implemented under all hand held adult fishery sampling situations. WDFW adult PIT tag sampling protocols for commercial and sport fisheries are listed in Appendix 2 and 3, respectively.

Study Limitations

One of the major limitations in this study was our use of fish PIT tagged as adults rather than as juveniles, which is when the majority are tagged in the Columbia River basin. However, seeding PIT tags to estimate efficiency is an accepted practice for hand held detectors (Hauser 2003) and for flat plate detectors (Evans et al. 2012). We chose seeding (implanting previously untagged adults) as a practical solution to ensure sufficient sample sizes. A key assumption in seeding tags is that the tag location and orientation in newly tagged adults is similar to returning adults or that if tag placement and orientation are different, these factors do not affect detection rates.

Conclusions and Recommendations

This analysis indicates that handheld PIT tag readers are able to detect PIT tags with near-perfect efficiency in a realistic fishery sampling environment. The study also revealed that reader type, sampling method, and fish characteristics affect detection rates. Therefore, we recommend use of the OM method for sampling adult salmon and steelhead, which if protocols are followed results in near-perfect detection efficiencies for all reader types. In cases where sampling protocol violations are likely, or particularly large fish are present, use of the DF reader should help ensure near perfect detection efficiencies under conditions where detection rates of other reader types may decrease meaningfully.

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Appendix 1. Manufacturer reported* and measured read ranges for four hand held PIT tag readers.

Reader Type	Abbreviation	Manufacturer Read Range (cm)	Measured Read Range (cm)
Destron-Fearing FS2001-ISO	CB	28-39	16.168
Biomark R601-3 Reader	AF	16.5-20	13.259
Biomark HPR plus ISO Reader	HPR	23-32	12.8115
Agrident AWR 100 Stick Reader	SR	<32	6.235

**Biomark provides the following description of manufacturer reported read ranges: “Read range is affected by tag orientation and environmental noise. When a range is present the smaller number represents approximate read distance when tag is parallel to the antenna face (worst orientation) while larger number represents approximate read distance when tag is perpendicular to the antenna face (best orientation). Environmental noise can be caused by: power lines, dirty AC power, over head lights, pumps, etc.”*

Appendix 2: Procedures/Protocol for PIT sampling in the Columbia River Commercial/Treaty Fisheries, Version 6.0

Procedures/Protocol for PIT sampling in the Columbia River Commercial/Treaty Fisheries

It is essential to follow the protocols and procedures below. Failure to follow these will lead to undetected PIT tagged fish, which will provide biased estimates of harvest and stock composition. Therefore, all staff will follow these procedures and protocols daily.

PIT tag units will be assigned to crews and available for crew leaders to take on the table in the PIT /CWT/DNA sampler area (or in the cubical of crew leaders). The unit will be ready to sample with and fully charged.

On occasions where units are not specifically assigned to crew leaders due to time constraints or lack of sufficient PIT readers, the PIT tag coordinator will notify crew leaders and assign PIT readers for the entire week.

It will be the crew leaders' responsibility to insure that the unit they have been assigned is downloaded and charged after each sampling day unless otherwise notified.

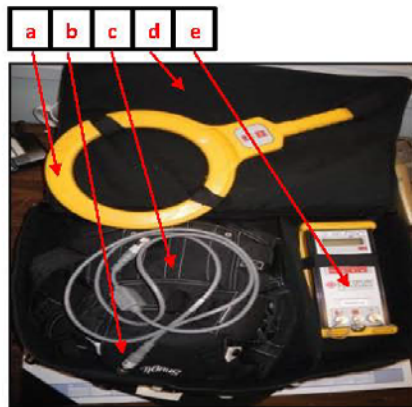
Commercial sampling using the Destron Fearing FS2001 (Cheese Block)

I – Parts of the FS2001 (Cheese Block) PIT tag reader

The primary PIT tag sampling unit that crews will use for the detection of PIT tagged fish is the Destron Fearing FS2001, "lovingly" known as the Cheese Block.

As seen in figure 1 below, a complete kit for Commercial PIT sampling will include:

- a) Antenna Racket
- b) Cable
- c) Snuggly*
- d) Bag (which should have a dummy tag and protocol in the front pocket)
- e) Cheese Block





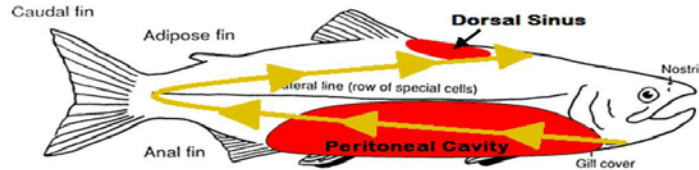
In order to connect the antenna racket to the Cheese Block in the correct configuration, the end with the ferrite choke box (circled) goes to the transceiver (Cheese Block).

Please be careful when attaching and detaching these cables. The best method is to gently wiggle the cable as you screw the connectors on and off. Please be sure that the cables are tightly secured, and when not in use, all caps are screwed on tightly.

II – Using the FS2001 (Cheese Block) PIT tag reader correctly while sampling

1. Select the PIT detector unit number into the header comments of each sampling form – This number is found on the front and base of the Cheese Block units – use the dropdown menu to select the correct unit type and number combination.
2. **Scan the test tag at the beginning and end of each session!!!** (Each Cheese Block bag has a test tag kept in front zipper pocket) *A session* changes when you start a new day or switch sampling locations (i.e. a new byer on the same day). It is very important to scan the test tag at the beginning and end of the sampling session, because it shows that the PIT tag unit is working both before and after sampling, and the times that it was tested. **It is mandatory to scan the test tag at the beginning and end of the sampling session.**
3. The preferred location for PIT tagging is the peritoneal cavity; gutted salmon **should not** be PIT tag scanned because it is unknown if PIT tag loss has occurred. It is very important that gutted fish be sampled on a separate, CWT-Only sample form.
4. **The Cheese Block is not waterproof!!!** Unfortunately, the Cheese Block units are not waterproof, and are not very water resistant. To combat this equipment shortfall, please try to keep the Cheese Block unit in hand and away from water. If it is raining (or may rain), please wrap both ends of the antenna cable in a plastic SNID bag, and use the zip ties located in the Cheese Block front zipper pocket to make the connections as water-tight as possible.

5. **The Cheese Block is not rugged!!!** Unfortunately, the Cheese Block units are not completely rugged. To combat this equipment shortfall, please try to keep the Cheese Block unit in hand and avoid placing the unit in any position where it may fall onto a hard surface. **Be AWARE of your surroundings.**
6. We will be using the **oval method** for scanning salmonids as illustrated below. The Cheese block is set to require the racquet antenna "scan" button to be pressed and held to scan for a PIT tag. Hold the button for 5 seconds, and *touching* the antenna parallel to the fish's lateral line, pass the antenna in an oval pattern over the fish as illustrated. Speed can affect the detection rate, so try to scan at a consistent medium speed, taking the full 5 seconds to complete the oval.



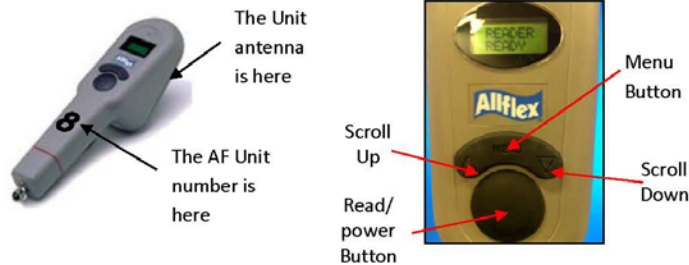
7. **Look at the Cheese Block screen!!!** There are many sources of noise while PIT tag sampling in a commercial or treaty fishery setting. The only way to insure that all PIT tags are accounted for is to look at the Cheese Block screen **for every fish scanned, every time.**

II – Using the R601-3 (All Flex) PIT tag reader correctly while sampling

Along with an assigned Cheese Block, each crew leader should have their sport-assigned R601-3 PIT tag reader, known as an All Flex. It is each crew leader's responsibility to make sure they have their All Flex as a backup in case of damage or malfunction to the Cheese Block during sampling.


Due to the hectic nature of Commercial and Tribal fishery sampling, it is even more important to follow strict adherence to protocol if samplers need to resort to using the All Flex unit for primary PIT tag scanning.

As covered above (Section II, 6) the **oval swipe method** will be used for scanning salmonids. The All Flex units are set to scan for 5 seconds. **You must** utilize the entire 5 seconds to scan the fish, and **you must** have the All Flex antenna physically pressing on the lateral side of the fish being scanned.



3

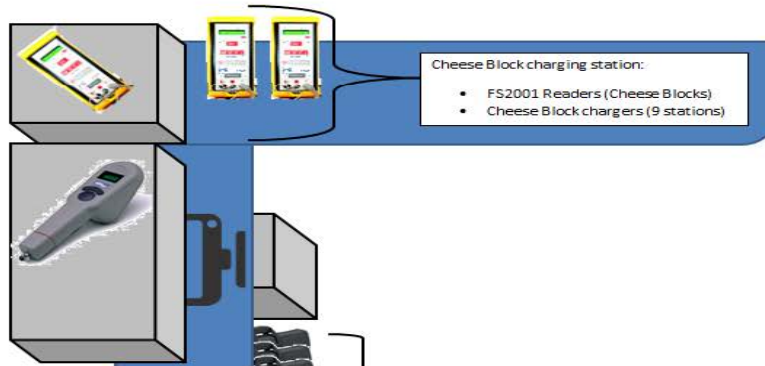
III - PIT tag recovery in a Commercial/Treaty fishery

1. During sampling, PIT tagged fish are treated the same as CWT positive fish. In most cases, they will be set aside to work up for bio data later – or given to the samplers working the board. *Make sure* that you keep track of fish that have PIT tags to maintain accurate data.
2. To use the Psion PDA to populate the PIT Tag # field:
 - a. Insure that the program AirWedge2 has been activated (you only need to check this at the beginning of the sampling period – not every time you scan a PIT tag)
 - b. Insure that the PIT Tag # field is selected
 - c. Press the  button on the PDA to begin scanning for the PIT tag
 - d. When the PIT Tag has been successfully interrogated, the PIT Tag # field will populate with a 14 digit decimal number.



IV – Downloading the PIT tag reader

1. At the end of each sampling session, it is expected that crew leaders will **download** their Cheese Block units, and **plug the Cheese Block into a charger**. The Cheese Block charging area is in back right corner of the CWT PIT tag office area, as shown below.

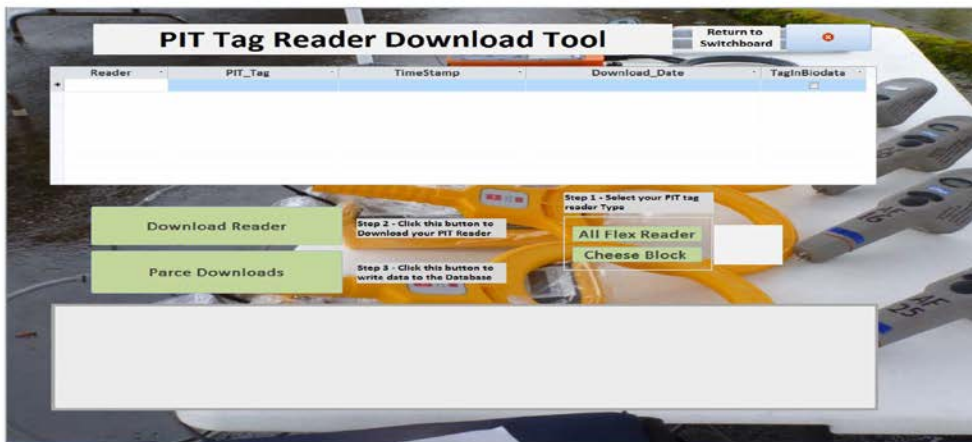


4.

- The Commercial and Sport Database now has a “PIT Tag Tools” section on the application switchboard.
- After you have returned from a commercial or treaty sample, select “Download Tool” from the menu.



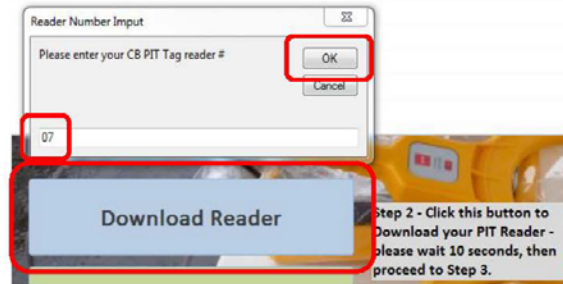
- The PIT Tag Reader Download Tool form will launch. Insure that your Cheese Block unit is connected to the computer by the grey screw-cable located on the desk by the download computer, and is **powered on**:



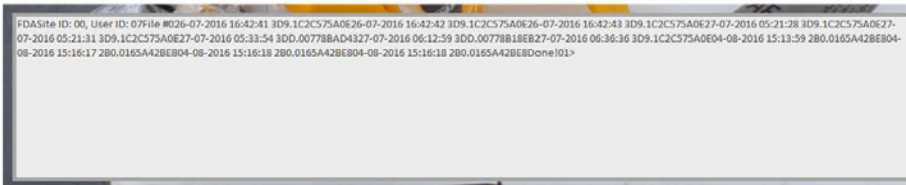
5. Select "Cheese Block" in the reader type selection box:



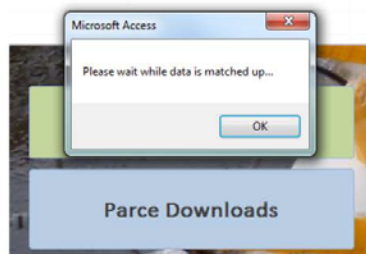
6. Next, select "Download Reader" from the operation buttons on the left of the tool. A dialogue box will appear and ask for your CB PIT Tag Reader #. This is the number printed on your Cheese Block. Enter that number and press "OK".



7. If the correct steps were followed, you will see a large string of text start to scroll out on the data window at the bottom of the tool, as shown below. Please allow at least 10 seconds to let the reader fully download its data to the database.




8. After you have waited at least 10 seconds, press the "Parse Download" button on the tool. This will allow the data that was downloaded from your Cheese Block to be written to the database. This process can take some time (up to one minute) depending on the amount of data stored on your Cheese Block. Select "OK" when the dialog box appears.



- Once the “parse downloads” action is finished, if you have any recovered PIT tags, those tags will appear in the Tag recovery window at the top of the tool:

Reader	PIT_Tag	TimeStamp	Download_Date
CB07	3D9.1C2DE425EF	06/17/2016, 11:37:51	6/17/2016 3:41:47 PM
CB07	3D9.1C2DE9CE8F	06/17/2016, 12:24:18	6/17/2016 3:41:47 PM
CB07	384.3B23B09EF2	06/22/2016, 10:50:07	6/23/2016 3:08:42 PM
CB07	3D9.1C2DE567E8	06/22/2016, 14:25:43	6/23/2016 3:08:42 PM
CB07	3DD.00778BAD43	07/27/2016, 05:33:54	7/27/2016 7:28:49 AM
CB07	3DD.00778818EB	07/27/2016, 06:12:59	7/27/2016 7:28:49 AM

- You can now exit out of the tool by using the red  button at the top right corner of the screen.

V – Other PIT tag functions

- Aside from the PIT Tag download Tool, there are two additional tools that are now available to samplers.

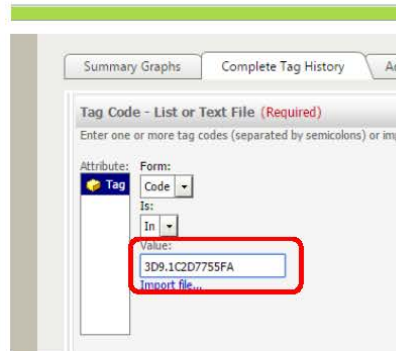
a. The Single Tag History Web Tool

- This tool allows the user to input any one PIT tag number to show the tag history of that PIT tag.

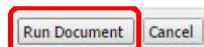
- When you select the “Single Tag History Web Tool” button, a web browser will open up to the PTAGIS Complete Tag History Tool.



- Simply input the full PIT tag number that you want information about into the “Value” input box, as shown:



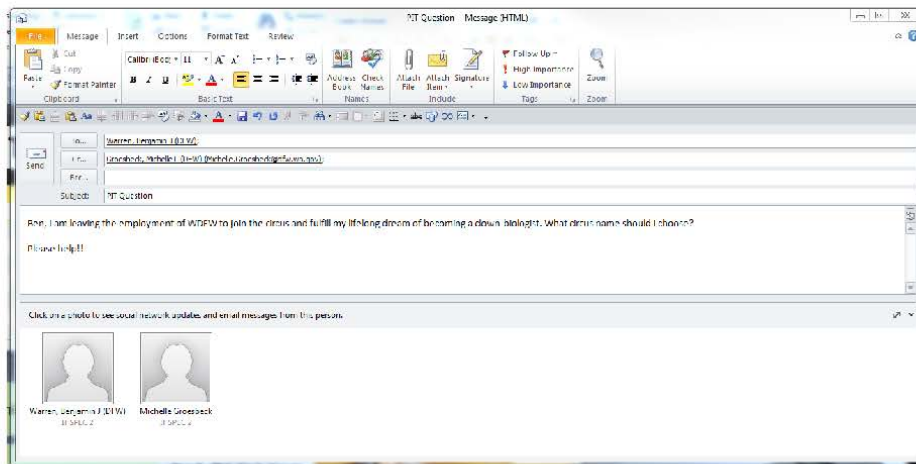
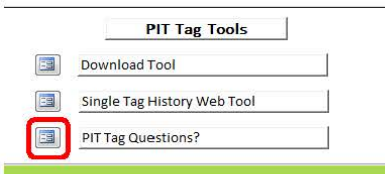
- Once you have put in a PIT tag number, click “Run Document” at the bottom of the page.



- The resulting document will contain the complete tag history of the PIT tag – including tagging, recapture, and dam passage information when available.

b. PIT Tag Questions Tool

- If you have any PIT tag questions and the PIT tag data coordinator or a crew leader is not available to answer them, you can now select the “PIT Tag Questions?” button to launch a new email addressed to Ben Warren:



(Note* – Please only occasionally email me about joining the circus...this is serious business, after all : P)

VI – Cleaning and returning the PIT tag reader

When a sampling session has been completed for the day, and *the test tag has been scanned to end the session* it is expected that samplers will clean the Cheese Block unit as best as they are able. Please follow these simple instructions to avoid damaging the Cheese Block while cleaning and returning the unit.

1. Turn off the PIT Tag reader
2. Detach each component
3. Cap each post on the cheese block before cleaning with water
4. Tightly cover the antenna racquet post with a hand before washing with water – do not let any water near the post.
5. Wash each component with light water - *please do not spray forcefully.*
6. Use the scrubbing wipes included in the Cheese Block bag to remove any fish blood/scales etc. still attached to the equipment.
7. Leave the Cheese Block bag partially open on one side for the trip back to the office to allow for air to circulate and dry the equipment.
8. **After downloading your Cheese Block**, please be sure to leave the Cheese Block bag and equipment on the sampling table in the CWT/PIT tag sampling area to dry, and **please make sure to plug in your Cheese Block at the end of each sampling day.** *Failure to charge your cheese block will result in not enough units to sample all fisheries throughout the week.*

Appendix 3: Procedures/Protocol for PIT sampling in the Columbia River Sport Fisheries, Version 4.0

Procedures/Protocol for PIT sampling in the Columbia River Sport Fishery

It is essential to follow the protocols and procedures below. Failure to follow these will lead to undetected PIT tagged fish, which will provide biased estimates of harvest and stock composition. Therefore, all staff will follow these procedures and protocols daily.

PIT tag units will be assigned to individual samplers at the beginning of their sampling season.

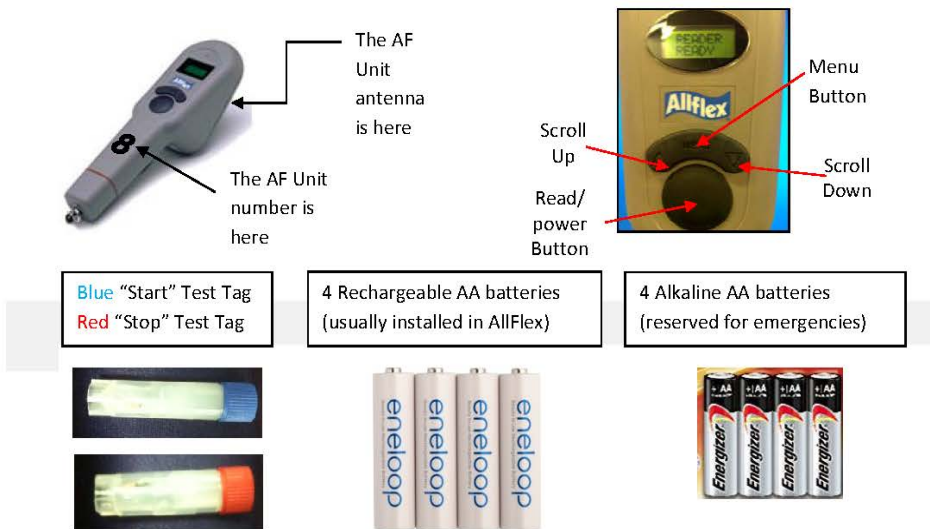
On occasions where units are not specifically assigned to samplers due to time constraints or last minute need, the PIT tag coordinator should be notified that a unit will be in use; crew leaders should insure that this occurs. It will be the sampler's responsibility to insure that the unit they have been assigned is operable and ready to sample with each sampling day, and to notify the PIT tag coordinator or their supervisor if any problems arise.

I – Parts of the R501-3 (AllFlex) PIT tag reader

The primary PIT tag sampling unit that will be used for the detection of PIT tagged fish in Sports fisheries is the Biomark R501-3 reader, "lovingly" known as the AllFlex.

As seen in Figure 1 below, a complete kit for Sport PIT tag sampling will include:

Figure 1: Biomark R501-3: the "AllFlex" RFID PIT Tag Reader



II – Using the R601-3 (AllFlex) PIT tag reader correctly while sampling

1. Select the PIT detector unit number into the header comments of each sampling form – This number is found on the front handle of the AllFlex units – use the dropdown menu to select the correct unit type and number combination.
2. Scan the **Blue** test tag at the beginning of each session!!! Each sampler will be given a blue “start” test tag.
3. Scan the **Red** test tag at the end of each session!!! Each sampler will be given a red “stop” test tag.

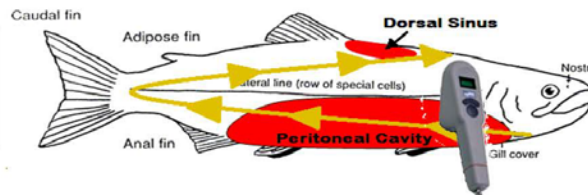
*2 Test tags are required for sport sampling because of hardware restrictions of the All-Flex units.

A *session* changes when you start a new sampling day or sampling type (i.e. – moving from a CREEL survey to a stream survey on the same day). It is very important to scan the blue test tag at the beginning of the session, and the red test tag at the end of the sampling session, because it shows that the PIT tag unit is working both before and after sampling, and the times that it was tested. **It is mandatory to scan the start test tag at the beginning of the sampling session, and the stop test tag at the end of the sampling session.**



4. The preferred location for PIT tagging is the peritoneal cavity; gutted salmon **should not** be PIT tag scanned because it is unknown if PIT tag-loss has occurred. It is very important that gutted fish be sampled on a separate, CWT-Only sample form.
5. **The AllFlex is not waterproof!!!** Unfortunately, the AllFlex units are not waterproof – only water resistant. To combat this equipment shortfall, please do not submerge the AllFlex units. If it is raining extremely hard, samplers should wrap the AllFlex unit in a SNID plastic bag to protect the unit.
6. **The AllFlex is not indestructible!!!** Unfortunately, the AllFlex units are not extremely rugged. To combat this equipment shortfall, please try to keep the AllFlex unit in hand or in your vest, and avoid placing the unit in any position where it may fall onto a hard surface / get crushed / get damaged. **Be AWARE of your surroundings.**
7. We use the **Pass-Over method** for scanning salmonids, as illustrated below. The AllFlex is set to turn on after pressing and holding the middle read button for one second. When the AllFlex unit is powered on, *touch* the unit antenna perpendicular to the fish’s lateral line. Press the center button once, and the unit will begin to scan for a PIT tag, and pass the antenna in an oval pattern over the fish as illustrated. Speed can affect the detection rate, so try to scan at a consistent medium speed, taking the full 5 seconds to complete the oval.

Figure 2: Correct application of the Pass-Over Method using the AllFlex unit.




8. **Look at the AllFlex screen!!!** There are many sources of distraction while sampling during peak times in a sport fishery. The only way to insure that all PIT tags are accounted for is to look at the AllFlex screen **for every fish scanned, every time.**

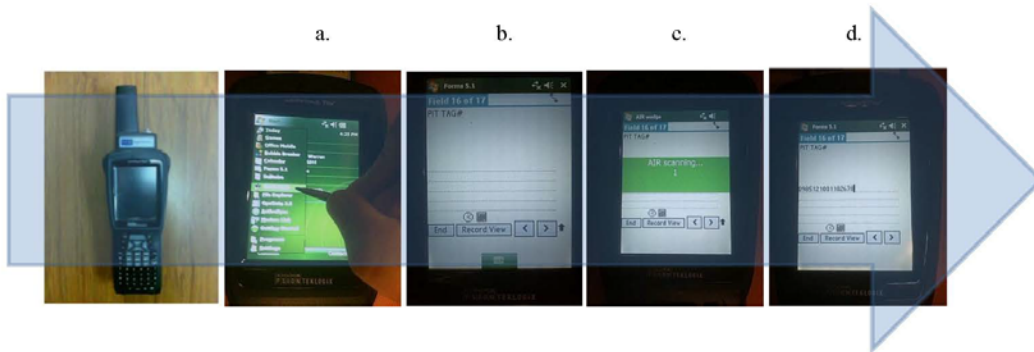
Figure 3: AllFlex display messages



2

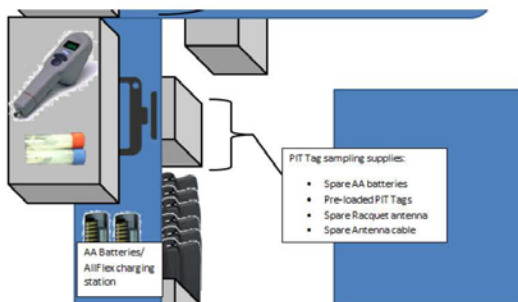
III - PIT tag recovery in a Sport fishery

1. During sampling, PIT tagged fish will be recorded in the Psion PDA's. To use the Psion PDA's to populate the PIT Tag # field:
 - a. Insure that the program AirWedge2 has been activated (you only need to check this at the beginning of the sampling period – not every time you scan a PIT tag)
 - b. Insure that the PIT Tag # field is selected
 - c. Press the  button on the PDA to begin scanning for the PIT tag
 - d. When the PIT Tag has been successfully interrogated, the PIT Tag # field will populate with a 14 digit decimal number.



IV – Downloading the PIT tag reader

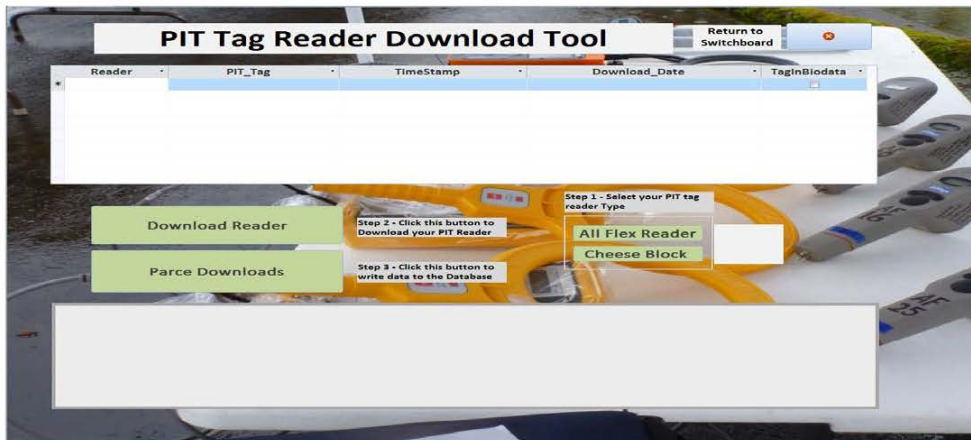
1. At the end of each sampling week, it is expected that samplers will **download** their AllFlex units, and **swap out the batteries** with fresh ones. Batteries will be available in the center drawer in the CWT PIT tag download area.



- The Commercial and Sport Database now has a “PIT Tag Tools” section on the application switchboard.
- At the end of your sampling week, select “Download Tool” from the menu.



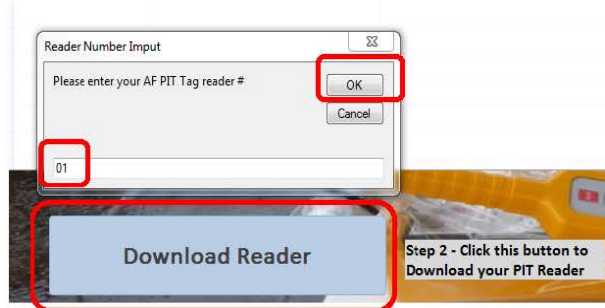
- The PIT Tag Reader Download Tool form will launch. Insure that your All-Flex unit is connected to the computer by the end-cap cable located on the desk by the download computer, and powered on:



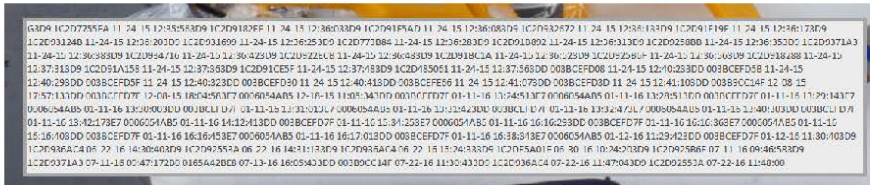
- Select “All Flex Reader” in the reader type selection box:



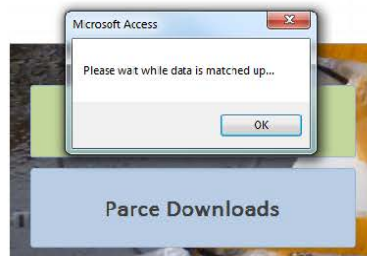
- Next, select “Download Reader” from the operation buttons on the left of the tool. A dialogue box will appear and ask for your AF PIT Tag Reader #. This is the number printed on your All Flex. Enter that number and press “OK”.



- If the correct steps were followed, you will see a large string of text start to scroll out on the data window at the bottom of the tool, as shown below. Please allow at least 10 seconds to let the reader fully download its data to the database.




- After you have waited at least 10 seconds, press the “Parse Download” button on the tool. This will allow the data that was downloaded from your All Flex to be written to the database. This process can take some time (up to one minute) depending on the amount of data stored on your All Flex. Select “OK” when the dialog box appears.



- Once the “parse downloads” action is finished, if you have any recovered PIT tags, those tags will appear in the Tag recovery window at the top of the tool:

Reader	PIT_Tag	TimeStamp	Download_Date
AF01	3D9.1C2D7755FA	11/24/2015, 12:35:56	7/27/2016 5:21:29 PM
AF01	3D9.1C2D9182FE	11/24/2015, 12:36:03	7/27/2016 5:21:29 PM
AF01	3D9.1C2D91F5AD	11/24/2015, 12:36:08	7/27/2016 5:21:29 PM
AF01	3D9.1C2D932672	11/24/2015, 12:36:13	7/27/2016 5:21:29 PM
AF01	3D9.1C2D91F19F	11/24/2015, 12:36:17	7/27/2016 5:21:29 PM
AF01	3D9.1C2D93124B	11/24/2015, 12:36:20	7/27/2016 5:21:29 PM
AF01	3D9.1C2D931699	11/24/2015, 12:36:25	7/27/2016 5:21:29 PM
AF01	3D9.1C2D773884	11/24/2015, 12:36:28	7/27/2016 5:21:29 PM

10. You can now exit out of the tool by using the red  button at the top right corner of the screen.

V – Other PIT tag functions

1. Aside from the PIT Tag download Tool, there are two additional tools that are now available to samplers.

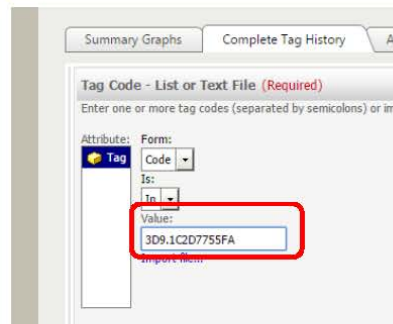
a. The Single Tag History Web Tool

1. This tool allows the user to input any one PIT tag number to show the tag history of that PIT tag.

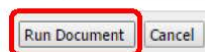
2. When you select the “Single Tag History Web Tool” button, a web browser will open up to the PTAGIS Complete Tag History Tool.



3. Simply input the full PIT tag number that you want information about into the “Value” input box, as shown:



4. Once you have put in a PIT tag number, click “Run Document” at the bottom of the page.



- The resulting document will contain the complete tag history of the PIT tag – including tagging, recapture, and dam passage information when available.

Complete Tag History Form (ID: 0377-4553)

Tag Info | Site Info | Canal Info | Distribution Info

Mark and Release Information

Species/Release type	Mark Site	Release Site	Release River: Kilometer
Mtl. Spring Chinook	GA31	GA31 - Rapid River Hatchery	522.533-146.037-965
Coordinator	Section Message	Tag File	
CO - Jerry McGinnis	TRAP PERIOD 2014 STR2	15838018-401	
Mark Date	Release Date	Conditional Comments (Flags)	Log (mm)
5/13/2014	03/17/2014	Adjuster File Clip	
Capture Method	Text Comments		
Exp. Net			

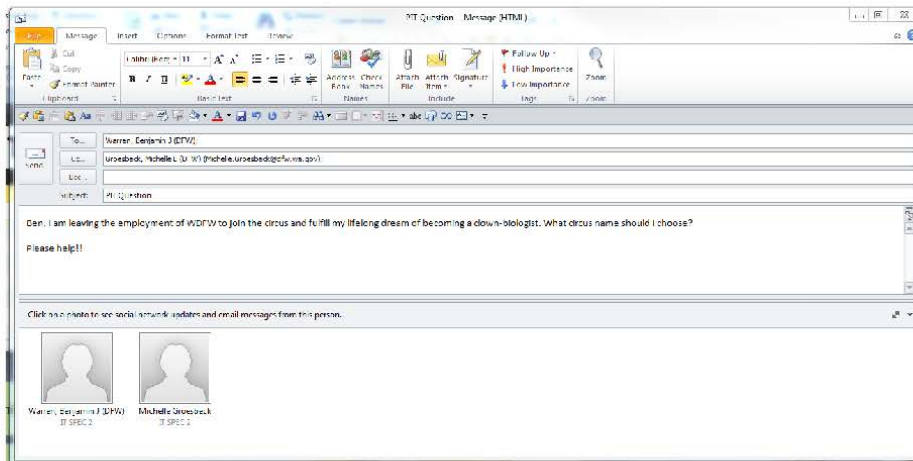
Recapture, Observation, and Mortality Information

History Summary | Observation Detail | Recap/Mortality Detail

Date	Event Type	Site Code	Site Name	Event Site Type	Catch Size (PWS)
04/16/2014	Obs	030	David Evans Hatchery Pond	Mark and Release Pond	650-533-146-307-506
05/16/2014	Obs	040	Michael P. Urebeck	Stream - River - Runoff	470
05/06/2014	Obs	001	Keenwell - NED's Leach	Stream - River - Runoff	734

b. PIT Tag Questions Tool

- If you have any PIT tag questions and the PIT tag data coordinator or a crew leader is not available to answer them, you can now select the “PIT Tag Questions?” button to launch a new email addressed to Ben Warren:



(Note* – Please only occasionally email me about joining the circus...this is serious business, after all : P)

VI – Cleaning and returning the PIT tag reader

When a sampling session has been completed for the day, and *the red test tags have been scanned to end the session*, it is expected that samplers will clean the AllFlex unit as best as they are able.

- Do not spray the AllFlex unit directly with strong jets of water
- Clean with a wet cloth – or cleaning wipes are available in the PIT/CWT samplers area

Each sampler will need to return the AllFlex unit that they have been assigned at the end of each season so it can be checked for operability, cleared and tuned. AllFlex units will be returned to each individual sampler at the beginning of each season for use.



This program receives Federal financial assistance from the U.S. Fish and Wildlife Service Title VI of the Civil Rights Act of 1964, Section 504 of the Rehabilitation Act of 1973, Title II of the Americans with Disabilities Act of 1990, the Age Discrimination Act of 1975, and Title IX of the Education Amendments of 1972. The U.S. Department of the Interior and its bureaus prohibit discrimination on the bases of race, color, national origin, age, disability and sex (in educational programs). If you believe that you have been discriminated against in any program, activity or facility, please contact the WDFW ADA Program Manager at P.O. Box 43139, Olympia, Washington 98504, or write to

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Chief, Public Civil Rights Division
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Washington D.C. 20240