

Lewis River Bull Trout (Salvelinus confluentus) Annual Operations Report



North Fork Lewis River – 2015

Merwin Yale Swift No. 1 Swift No. 2 FERC No. 935 FERC No. 2071 FERC No. 2111 FERC No. 2213

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1.0 INTRODUCTION

PacifiCorp and the Public Utility District No. 1 of Cowlitz County, Washington (Cowlitz PUD) (collectively the Utilities) are involved in various bull trout (*Salvelinus confluentus*) and salmonid monitoring programs on the North Fork Lewis River in southwest Washington. These monitoring programs and this report are designed to meet requirements pursuant to Article 402 in the Utilities' Federal Energy Regulatory Commission (FERC) operating licenses for the Merwin, Yale, Swift No. 1 and Swift No. 2 hydroelectric projects as well as requirements pursuant to sections 4.9, 9.6 and 14.2.6 of the Lewis River Settlement Agreement (SA). This Report and listed monitoring programs also serve to meet requirements contained in the 2006 Biological Opinion issued to PacifiCorp and Cowlitz PUD by the U.S. Fish and Wildlife Service (USFWS).

All activities are developed in consultation with the USFWS. This Report provides results from programs that are either ongoing or have been completed in 2015. For methods and general descriptions of all programs please refer to the Bull Trout Annual Operating Plan for the North Fork Lewis River 2015 that was submitted to the USFWS, members of the Lewis River Aquatic Coordination Committee (ACC) and the FERC within the ACC/TCC Annual Report in April 2015.

2.0 STUDY AREA

Bull trout monitoring activities are performed on the North Fork Lewis River and its tributaries upstream of Merwin Dam commencing at river mile (RM) 19.5 and ending at Lower Falls, a complete anadromous and resident fish barrier at RM 72.5. The North Fork Lewis River above Merwin Dam is influenced by three reservoirs created by the hydroelectric facilities; 4,000 acre Merwin Reservoir, 3,800 acre Yale Reservoir, and the largest and furthest upstream 4,600 acre Swift Reservoir. From Lower Falls downstream, the North Fork Lewis is free-flowing for approximately 12 miles until the river reaches the head of Swift Reservoir at RM 60. A map of the study area for all programs is shown in Figure 2.0-1.

Bull trout are found in all three reservoirs as well as the Swift No. 2 Power Canal, with the bulk of the population residing in Swift Reservoir. Only three known bull trout spawning streams are found in the study area; Rush and Pine Creeks, tributaries to the North Fork Lewis River upstream of Swift Reservoir, and Cougar Creek a tributary to Yale Reservoir. Recent genetic analysis performed in 2011 identified three distinct local populations residing within the basin; Rush, Pine, and Cougar Creek bull trout (Dehaan and Adams 2011).



Figure 2.0-1. Map of North Fork Lewis River study area.

3.0 METHODS AND RESULTS

During 2015 the Utilities participated in, funded, or initiated eight monitoring programs.

Bull Trout Programs completed in 2015:

- 1. Swift Reservoir adult migration, Survival (S), and Genetic Estimation of Breeder Population (Nb) estimates
- 2. Half-duplex Passive Integrated Transponder (PIT) tag antenna arrays in Cougar, Pine, P8 and Rush Creeks and the Muddy River
- 3. Yale tailrace collection and transport
- 4. Swift bypass reach collection and transport
- 5. Swift Power Canal collection and transport
- 6. Bull trout redd surveys of Cougar Creek
- 7. Bull trout redd surveys of Pine Creek and Pine Creek tributary P8
- 8. Bull trout Condition Factor (k) assessment

3.1 FERC PROJECT LICENSE ARTICLE 402(B) AND LEWIS RIVER SETTLEMENT AGREEMENT SECTION 9.6 – SWIFT RESERVOIR BULL TROUT POPULATION EVALUATION

3.1.1 ESTIMATE OF THE NUMBER OF STAGING BULL TROUT THAT MIGRATED UP THE NORTH FORK LEWIS RIVER FROM THE HEAD OF SWIFT RESERVOIR

EAGLE CLIFFS BULL TROUT COLLECTION (MARK):

Tangle net collection activities at the upper end of Swift Reservoir began May 13, 2015 and continued through July 8, 2015 (Appendix A). Eleven netting days were completed during the period. A total of 83 bull trout were captured in the Eagle Cliffs area of Swift Reservoir. Of these, 64 were tagged with two pink colored three inch Floy® T-bar anchor tags between the last two posterior dorsal fin-rays. Of the remaining 19 captures, six did not meet minimum fork length tagging requirements, and 13 were current year recaptures (Appendix A).

Of the 70 maiden bull trout captures in 2015, 22 had Floy® or PIT (Passive Integrated Transponder) tags from previous years bringing the total capture rate of previously handled fish to 31 percent (22 fish of a total of 70).

To catch Swift Reservoir staging bull trout, tangle nets are typically drifted along the stream bottom by means of a power boat or allowed to passively soak for up to ten minutes in slow-water areas of high bull trout concentration. Tangle nets consist of dyed green 6# monofilament, with depths of approximately 2 meters (m), varying lengths of 25 - 40 m, and varying mesh sizes of 2.5 - 7.5 centimeter (cm) stretch. 2015 was a unique year in terms of typical catch methods experienced historically. Due to drought conditions the North Fork Lewis River inflow and Swift Reservoir were extremely low, to the point that it excluded boat passage to typical capture areas from the middle of June until capture activities ceased in July. Tangle nets were still utilized but were no longer deployed and drifted from a boat, instead biologists in drysuits deployed tangle

nets in bull trout holding areas and either drifted the nets downstream or used them as seines to capture staging bull trout.

Keeping with previously established methods, all Floy® tagged bull trout captures received a second same colored tag on the opposite side of the fish. It is anticipated that double-tagging bull trout captures will refine tag-loss estimates and assumptions within the annual migration estimate. Tag retention was evaluated by snorkelers during the recapture surveys performed of the confluence areas of Muddy River and Rush and Pine Creeks. Surveyors paid careful attention to the number of pink tags observed in tagged bull trout in order to determine the proportion of bull trout missing a pink tag.

All <u>newly</u> captured bull trout received Floy® (if larger than 350mm) and half-duplex (HDX) PIT tags (if greater than 250mm dorsal sinus PIT tag location, if less than 250mm but greater than 120mm, these fish received a full-duplex (FDX) PIT tag).

The preferred tagging location for the 23mm HDX tag was the dorsal sinus. A small incision was made with a scalpel just anterior to the dorsal sinus and the tag was then gently pushed toward the caudal peduncle into the sinus (Tranquilli et. al 2003). If a bull trout was recaptured containing a Full Duplex (FDX) PIT tag, these fish were double-tagged with an HDX PIT tag as well. Research conducted by the United States Geological Survey (USGS) in 2007 identified that, when the copper coils of an FDX tag came within 1 centimeter (cm) of the copper coils within an HDX tag, the FDX tag interfered with the HDX tag signal and the HDX tag was not detected by the tag reader (Compton 2007). To alleviate the problem of tag interference between the two tag types in double-tagged bull trout, HDX tags were inserted in the dorsal sinus on the opposite side of the original FDX tagging location. Since 2010, this location has been incorporated with no known interference.

Along with tagging activities, all captured bull trout (minus same year recaptures) were measured to their caudal fork and, when feasible, weighed to the nearest gram. Recording bull trout weights is a data collection activity that was first implemented in 2008 and, along with fork lengths, will be used to assess the condition factor (K-factor) of bull trout residing in Swift Reservoir (Fulton 1902). When available, this biological information will be recorded with each fish captured and individual metrics will be compared with each recapture to evaluate trends in reservoir productivity and how this pertains to bull trout behavior. In order to not skew Kfactors, bull trout that had recently fed on large fish (evidenced by a caudal fin protruding from the jaw) were not weighed. All true maiden captures were also sampled for genetic material. Genetic analysis will be performed at a later date.

SNORKEL SURVEYS OF THE CONFLUENCE AREAS OF MUDDY RIVER, PINE, AND RUSH CREEKS WITH THE NORTH FORK LEWIS RIVER (RECAPTURE):

Snorkel surveys of the three confluence areas occurred weekly from August 27 to October 15 for a total of eight weeks. Due to poor snorkeling conditions (poor water clarity) the surveys were only completed for six of the eight weeks (Table 3.1-1).

Snorkel surveys of the Muddy, Pine, and Rush confluence areas began upstream of each confluence in the North Fork Lewis and continued downstream until bull trout were no longer

observed, usually a distance of approximately 100m. Given the short distance between the mouth of Pine Creek and the Muddy River, this area was also surveyed for bull trout during each confluence survey day (Figure 3.1-2).

Table 3.1-1. 2014 bull trout snorkel survey results for the Muddy River, F	Rush and Pine Creeks confluence areas
with the North Fork Lewis River (recapture).	

Date	Location	# marked	# Unmarked	Total	% of total with mark	Single tags observed	Tag loss % (survey day)
27-Aug	Pine, Rush, Muddy confluence areas	7	64	71	10%	1	14%
3-Sep	Pine, Rush, Muddy confluence areas	4	43	47	9%	0	0
9-Sep	Pine, Rush, Muddy confluence areas	3	56	59	5%	0	0
16-Sep	Pine, Rush, Muddy confluence areas	7	50	57	12%	0	0
24-Sep	Pine, Rush, Muddy, confluence areas	4	47	51	8%	0	0
1-Oct	Pine, Rush, Muddy, confluence areas	3	49	52	6%	0	0
8-Oct	Poor Visibility, no snorkel						
15-Oct	Poor Visibility, no snorkel						
TOTAL	Pine, Rush, Muddy confluence areas	28	309	337	8%		

During each snorkel survey all bull trout were enumerated (Tables 3.1-1). Care was taken to determine the presence of any pink Floy® tagged bull trout, and due to the current Floy® tag retention study, biologists also recorded any pink Floy® tag loss (i.e. a bull trout with only one pink tag as opposed to two). During the six confluence snorkel surveys, bull trout missing pink Floy® tags were rarely observed. Given individual tagged fish cannot be distinguished during each snorkel survey, cumulatively counting tag-loss during subsequent surveys would be erroneous. The only way to accurately express tag-loss without the chance of double-counting is to record the percentage of fish with only one tag for each survey (Table 3.1-1). Peak tag-loss (14 percent) was observed on August 27 when one bull trout was observed with only one pink Floy® tag.

The Swift Reservoir bull trout migration data was analyzed and a migration estimate obtained using program NOREMARK®. NOREMARK® computes an estimate of population size for a closed population with a known number of marked animals and one or more re-sighting events (White 1996). Program NOREMARK® utilizes four mark-resight estimators of population abundance; for all four estimators, the marked fish are assumed to have been drawn randomly from the population. That is, the marked fish are a representative sample of the population (White 1996).

For 2015, utilizing data collected during Muddy River, Rush, and Pine Creek confluence snorkels, the estimate of adult bull trout that migrated upstream from Eagle Cliffs is 697 (95% CL 509-1,006) (Table 3.1-2 and Figure 3.1-1).

A key assumption within the NOREMARK® mark/recapture estimate is that each tagged individual has an equal probability of being "recaptured" and counted during recapture activities (closed population). Being iteroparous, bull trout have the ability to migrate and spawn one year and not the next and as such, captured individuals tagged in the Eagle Cliffs area of the reservoir may not migrate upstream to the recapture survey areas after release.

Currently, the rate associated with tagged non-migrating bull trout in Swift Reservoir is unknown. It is assumed that the rate of non-migration fluctuates from one year to the next and is most likely closely related to size of fish and reservoir productivity. Thus, care should be taken during evaluation of this migration estimate, as this variable non-migration rate may positively bias migration abundance estimates. An un-validated ten percent in-season Floy® tag loss is assumed within the current estimate. At this time, an in-season mortality rate is unknown and therefore unaccounted for.



Figure 3.1-1. Estimates of bull trout that migrated from Swift Reservoir up the North Fork Lewis River for the years 1994 through 2015. (1994-2000 Peterson Estimator, 2001- 2014 Program NOREMARK[®], Smith 1996)

Year	Lower Bound (95% CL)	Upper Bound (95% CL)	Migration Estimate			
1994	85	118	101			
1995	193	326	246			
1996	173	782	325			
1997	235	361	287			
1998	345	571	437			
1999	181	365	248			
2000	242	352	288			
2001	439	689	542			
2002	701	1092	792			
2003	745	1140	911			
2004	1084	1556	1287			
2005	1042	1354	1181			
2006	865	1198	1011			
2007	436	596	505			
2008	298	507	380			
2009	367	554	445			
2010	430	690	536			
2011 (tribs.)	278	502	364			
2011 (confluences)	362	539	436			
2011 (tribs. and confl. combined)	354	493	414			
2012 (tribs.)	235	425	308			
2012 (confluences)	279	381	323			
2012 (tribs. and confl. combined)	277	364	316			
2013	377	564	455			
2014	198	274	230			
2015	509	1,006	697			

 Table 3.1-2. Tabular data of Swift Reservoir bull trout mark-recapture migration estimates for

 1994 - 2015. (1994-2000 Peterson Estimator, 2001-2014 Program NOREMARK[®], Smith 1996)



Figure 3.1-2. Snorkel sites (for recapture) associated with the Swift Reservoir bull trout migration estimate.

3.1.2 EVALUATION OF SWIFT AND YALE RESERVOIR BULL TROUT POPULATION THROUGH THE USE OF PIT TAG DETECTIONS AND PROGRAM MARK

"Program MARK is a computer program used to estimate survival based on the available history of detections for each individual tagged and re-sighted during capture and detection efforts" (White and Burnham 1999). All PIT tag and detection data was separated into two "capture periods" including:

- "Tagging periods" when fish were physically recovered (by a variety of methods) and (potentially) tagged, and
- "Antenna periods" when fish were detected at one of the stationary antenna, presumably on attempted spawning excursions.

The 2015 Swift and Yale reservoir PIT tag detection data was analyzed by statisticians from the consulting firm of Stillwater Sciences using the population structure software program MARK. In 2015, Program Mark generated probability estimates for a random fish making a spawning migration of 0.772 for Yale and 0.437 for Swift. MARK analysis of the probability that a fish will survive from one year to the next in Swift had a value of 0.841 and for Yale a value of 0.586.

Parameter Interpretation		Estimate	95% Interval				
	Yale Reservoir						
Model 4 $\phi_{2014t2014a} \times \phi_{2014a2015t}$	Survival from 2014 reservoir-sampling period to 2015 reservoir-sampling period	0.586	0.305-0.868				
Model 3 $\phi_{2014a2015t}$	Survival from 2014 antenna-detection period to 2015 reservoir-sampling period	0.794	0.560-0.996				
Model 3 $\phi_{2015t2015a}$	Survival from 2015 reservoir-sampling period to 2015 antenna-detection period	0.926	0.811-0.998				
Model 2 p_{2015a}	Probability of making a spawning excursion in 2015	0.772	0.564-0.993				
	Swift Reservoir	•					
Model 4 $\phi_{2014t2014a} \times \phi_{2014a2015t}$	Survival from 2014 reservoir-sampling period to 2015 reservoir-sampling period	0.841	0.696–0.986				
$\begin{array}{c} \text{Model 3} \\ \phi_{2014a2015t} \end{array}$	Survival from 2014 antenna-detection period to 2015 reservoir-sampling period	0.922	0.817-0.999				
$\begin{array}{c} \text{Model 3} \\ \phi_{2015t2015a} \end{array}$	Survival from 2015 reservoir-sampling period to 2015 antenna-detection period	0.891	0.754–0.997				
$ \begin{array}{c} \text{Model 2} \\ p_{2015a} \end{array} $	Probability of making a spawning excursion in 2015	0.437	0.341-0.539				

 Table 3.1.2-1.
 Summary table of survival (S) estimates and metrics for Yale and Swift reservoirs in 2015, analysis courtesy of Stillwater Sciences.

For more detailed Results, Analysis, Methods and Equations, please see the technical memorandum "Analysis of Bull Trout PIT tag and Detection Data" from Stillwater Sciences to Jeremiah Doyle located in Appendix A of this Report (Stillwater Sciences 2016).

3.1.3 EVALUATION OF THE SWIFT RESERVOIR BULL TROUT EFFECTIVE POPULATION (NE)

The Effective Population (N_e) size of bull trout within Swift Reservoir was evaluated in 2015 in order to fulfill bull trout objective number one within Objective 17 of the M&E Plan which states, "Provide an "unbiased" estimate of bull trout spawner abundance in Swift Reservoir".

Estimation of effective population size can provide information on the level of genetic variation within a population and how fast genetic variation may be lost through genetic drift (Luikart et al. 2010). The effective population size represents the size of an ideal population that would have the same rate of loss of genetic variation as the observed population (Wright 1931). Although general guidelines for minimum effective population sizes have been suggested (e.g., the 50/500 rule; Franklin 1980), evaluating temporal trends in estimates of N_e are often more useful than determining whether a population meets some minimum threshold number. For example, a population that shows a large decrease in N_e over the course of one or two generations could be experiencing a genetic bottleneck or decline in abundance. Alternatively, an increase in effective size following implementation of new management actions could be one indication that the population is responding positively (Pers. Comm. Pat DeHaan, USFWS).

To evaluate N_e , genetic tissue from juvenile bull trout from the same cohort (presumably age 0) was attained from utilized spawning tributaries (Rush, Pine, and Cougar Creeks, Figures 3.1.3-1 to 3.1.3-3). In order to get maximum genetic representation, fish captures were spatially balanced as much as practical along the length of usable habitat within each stream. Surveys were timed such to ensure capture of prior year's brood fish, with less than 70 mm fork length the cut-off used to determine age 0 bull trout (Fraley/Shepard 1989).

Areas within Rush Creek were sampled with a backpack electrofishing unit on July 7, July 17, and July 22 (Figure 3.1.3-1). In all, 53 juvenile bull trout were captured and sampled for genetic tissue. Of these 53 samples, 50 were less than 70 mm fork length and assumed to be of 2014 brood year origin and so were included within the N_e analysis. The length range of the bull trout used within the analysis was 31 mm – 60 mm, with an average fork length of 47 mm.



Figure 3.1.3-1. Electrofishing sites within Rush Creek during 2015 juvenile bull trout collection.

Areas within Pine Creek and tributary P8 were sampled for juvenile bull trout with a backpack electrofisher on June 12, June 25, and July 9 (Figure 3.1.3-2). In all, 63 juvenile bull trout were captured from within P8 with 57 of these fish meeting the fork length criteria of less than 70 mm. 34 juvenile bull trout were captured from within areas of Pine Creek, with 33 captures meeting the fork length criteria used for the N_e analysis. The lengths of the 90 assumed 2014 brood year bull trout captured in the Pine system ranged from 45 mm – 70 mm with an average fork length of 61 mm.



Figure 3.1.3-2. Electrofishing sites within the Pine Creek system during 2015 juvenile bull trout collection.



Figure 3.1.3-3. Electrofishing sites within the Cougar Creek system during 2015 juvenile bull trout collection.

Areas within Cougar Creek were sampled with a backpack electrofishing unit on July 3 and July 15 (Figure 3.1.3-3). In all, 77 juvenile bull trout were captured and sampled for genetic tissue. Of these, 73 were less than 70 mm fork length and assumed to be of 2014 brood year origin and so were included within the N_e analysis. The length range of the bull trout used within the analysis was 47 mm – 70 mm, with an average fork length of 65 mm.

Based off of the sample of individual juveniles provided in 2015, the Genetic Estimation of Spawner Abundance in Pine Creek for brood year 2014 was assessed to be 19.5; (95% C.I.=15.2-25.1), Rush Creek had an estimate of 23.0; (95% C.I.=18.0-29.8), while Cougar Creek had an estimate of 18.7; (95% C.I.=15.2-23.2) (Table 3.1.3-1).

Methods, Materials, and Results for all genetic activities performed within the Lewis River in 2015 can be found in the Report titled "Rapid Response Genetic Analysis and Genetic Estimation of Spawner Abundance of Bull Trout Collected in the Lewis River, WA" (Adams/Doyle, 2016) located in Appendix B of this Report.

Table 3.1.3-1. Estimates of effective number of breeders (95% CI) in three Lewis River tributaries for multiple N_b estimators in 2015 (minimum allele frequencies of 0.02).

Tributary	N _b Estimator All Individuals	N _b Estimator Reduced Families	Colony
Cougar Creek	18.6 (15.5-22.3)	18.7 (15.2-23.2)	26.5 (16.0-45.5)
Pine Creek	16.5 (13.1-20.8)	19.5 (15.2-25.1)	31.5 (20.0-52.5)
Rush Creek	23.0 (18.0-29.8)	23.0 (18.0-29.8)	28.5 (17.0-49.0)

Juvenile bull trout/coho interactions

Numerous young of the year (YOY) coho were also found to be occupying the same habitat as YOY bull trout in the Rush and Pine Creek systems above Swift Reservoir and as such were inadvertently captured during electrofishing surveys. These coho were quantified and measured to their caudal fork as part of activities pursuant to Objective 18 within the M&E Plan, evaluation of resident/anadromous fish interactions. No coho were observed or captured during electrofishing surveys of Cougar Creek in 2015.

Coho YOY dominated the catch in both Pine and Rush Creeks, totaling 124 and 128 captured respectively. This corresponds to a YOY bull trout catch of 33 and 50, a difference in overall collected of 73 percent more YOY coho captures in Pine Creek and 61 percent more in Rush Creek. A marked contrast was observed in P8 Creek, with only three coho YOY captures compared to 57 bull trout, or a difference of 95 percent more bull trout than coho YOY (Figure 3.1.3-4).



Figure 3.1.3-4

Size of coho YOY in terms of average fork length was also assessed and compared to that of YOY bull trout occupying the same habitat within the Pine and Rush creek systems. Across the board coho YOY were marginally larger than bull trout YOY, with the biggest discrepancy occurring within Rush Creek were coho YOY were 16 percent larger and had an average fork length of 56mm compared to that of bull trout YOY at 47mm. The size difference in Pine and P8 Creeks was similar, with coho YOY fork lengths eight and ten percent larger than that of observed bull trout YOY fork lengths. Average observed coho YOY fork lengths in Pine Creek was 66mm as compared to 61mm of bull trout, and 68mm as compared to 61 mm average fork lengths in P8 Creek (Figure 3.1.3-5).



Figure 3.1.3-5

3.2 LEWIS RIVER PASSIVE INTEGRATED TRANSPONDER TAG ANTENNA ARRAYS

3.2.1 EVALUATION OF SWIFT AND YALE RESERVOIR BULL TROUT THROUGH THE USE OF STREAM-WIDTH HALF-DUPLEX PASSIVE INTEGRATED TRANSPONDER ANTENNAS IN RUSH, P8, PINE AND COUGAR CREEKS

Stream-width half-duplex PIT tag antennas were placed in Pine, and P8 Creeks and the Muddy River near their confluence's with the North Fork Lewis River in the late summer through fall time period. A dual reading full and half-duplex PIT tag antenna was also temporarily placed near the mouth of Rush Creek and was operated through the spawning migration period by Washington Department of Fish and Wildlife personnel (Figure 3.2.1-1). The remote PIT antenna array in Pine Creek was stream-spanning and located in a shallow riffle approximately 300 m upstream from the confluence with the North Fork Lewis River. The Rush Creek antenna array was located in a narrow shoot approximately 50 m upstream from the confluence with the North Fork Lewis River. The Rush Creek antenna utilized a weir to direct fish movement past the antenna. The array in P8 was stream-spanning and located approximately 150 m upstream from the confluence with Pine Creek. The array on the Muddy River was also stream-spanning and was located approximately 30 m upstream from the confluence with Pine Creek. The array on the Muddy River was also stream-spanning and was located approximately 30 m upstream from the confluence with Pine Creek. The array on the Muddy River was also stream-spanning and was located approximately 30 m upstream from the confluence of the North Fork Lewis River.

Each half-duplex antenna site consisted of two antennas (for directionality) that were multiplexed (synchronized) and spaced approximately two meters apart. Half-duplex antennas consisted of 10-gauge copper wire looped along the stream bottom starting from one stream bank, spanning the entire wetted-width of the stream along the stream bottom to the opposite bank, and then along the stream surface back to the original starting point creating a large swim thru rectangle shape. Each antenna wire or cable was connected to an Oregon RFID RI-Acc-008B antenna tuner unit. Copper twinax was then run from each tuner unit to an Oregon RFID RI-RFM-008 reader board and data logger. The antenna reader board and data logger were located in secure Joboxes near the stream bank and were powered by two large 12 volt deepcycle marine batteries run in parallel. Batteries at the Pine and Muddy site were charged via 120w solar panels hooked to a charge controller, while batteries at the P8 site were exchanged with fully-charged replacements every two to three weeks as necessary. The dual reading half and full-duplex tag antenna near the mouth of Rush Creek consisted of one swim thru loop antenna (no directionality) connected to a weir that forced fish to swim thru the antenna loop. The antenna was connected to a Biomark IS1001 Data Logger Board and powered by 12 volt deep-cycle batteries.



Figure 3.2.1-1. Half-duplex stream-width PIT tag antenna locations in the Upper Lewis River Basin – 2015.

Development of length prediction equations for use with PIT antenna detections

Analysis of size distribution of bull trout migrating up spawning/foraging tributaries may help to better understand the dynamics of the Lewis River bull trout populations. Unique identification of each PIT tag allows for an individual fish and its corresponding historical length data to be assigned to the particular stream in which it was detected. However, a problem occurs when fish tagged in prior season field efforts are detected in the current year assessment, that being there is no current length data for that fish. To address this problem, all available recapture data was analyzed and equations developed to estimate unknown fish lengths.

Individual equations were developed to predict fish lengths on a years-since-last-capture basis. That is, a unique length-prediction equation exists for fish measured one year, two years, and three years since the latest PIT tag detection. To develop these equations, all available recapture data was analyzed (dating back to 1998) and individual length-growth rates were recorded. For example, if a fish was tagged in 2008 and recaptured in 2009, 2010, and 2011 then length-growth data is available for a one year interval (2008-2009 length change) a two-year interval (2008-2010 length change) and a three-year interval (2008-2011 length change). Individual length-growth rates were then compiled into their corresponding time interval data set, and data sets were then analyzed using linear regression to determine a best-fit relationship. The 2013 regressed length-prediction equations are shown in figures 3.2.1-2, 3.2.1-3, & 3.2.1-4 for one, two, and three years since last capture, respectively. Production of the length-prediction equations involved using all of the recapture data available (dating back to 1998). The use of this data-set was incorporated to provide a large enough sample to produce reliable estimates.

Length-prediction equations will be recomputed annually when additional recapture data becomes available, resulting in length-prediction equations that more accurately represent the year's population size distribution.



Figure 3.2.1-2. The length-prediction equation for fish tagged one year prior to the latest PIT antenna detection is shown. This equation yields the largest r-squared value out of the length-predicting equations due to the most data and the finest time interval (i.e. since fish length varies over time, the smaller the time interval the less variation observed). Each blue dot represents a recaptured individual bull trout.



Figure 3.2.1-3. The length-prediction equation for fish tagged two years prior to the latest recapture event is shown. Each blue dot represents a recaptured individual bull trout.



Figure 3.2.1-

4. The length-

prediction equation for fish tagged three years prior to the latest recapture event is shown. As expected, this three-year since last capture equation yields the smallest r-squared value out of the length-prediction equations due to the least data available and taking place over the largest time interval. Each blue dot represents a recaptured individual bull trout.

The Bull Trout size distributions are not continuous data sets, instead length data are assigned within discrete intervals of: <300, 300-399, 400-539, 540-599, 600-699, >700 (mm). For these reasons the length-prediction equations were compressed into a single comprehensive table, shown in Table 3.2.1-1.

 Table 3.2.1-1
 Table of the compressed length-prediction equations is shown. FL means fork length in mm.

 None means that the current FL does not exist to a prior year's corresponding size interval. For example, there are no fish lengths from three years ago that are currently 300-399 mm; all are currently greater than 399 mm. Unknown means the regressed equation becomes false at that particular size interval.

Years Since Capture 1998-2012 Model					
One Year	Two Years	Three Years			
Prior FL (mm)	Prior FL (mm)	Prior FL (mm)	Current FL (mm)		
0-184	none	none	<300		
185-309	0-160	none	300-399		
310-484	161-390	0-144	400-539		
485-559	391-489	145-404	540-599		
560-683	489-653	unknown	600-699		
>683	>653	unknown	>700		

In 2015 there were 139 unique PIT tag detections at stationary antennae in tributaries to Yale and Swift Reservoirs. The breakdown of detections by stream, as well as timing, spawning frequency and size of bull trout migrant is as follows:

Cougar Creek

The PIT antenna at the mouth of Cougar Creek was in operation from August 5 – October 30, continuous operation was experienced during this sampling timeframe except for one loss of power event from October 8 – October 10. During the migration period 398 detections occurred at the antenna resulting in 26 unique bull trout. All of the 398 upstream and downstream movement events occurred during the crepuscular period. Peak migration was observed on September 25 with a total of 12 individual bull trout moving past the antenna site (Figure 3.2.1-5).



Figure 3.2.1-5

The number of unique bull trout detections in 2015 mark the most observed at this site since activities began in 2010 (Figure 3.2.1-6). Of the 26 bull trout that migrated upstream, nine (35 percent) were consecutive spawners with one fish being detected for the last four consecutive years. Sixteen bull trout migrants (60 percent) were maiden detections in 2015 and one bull trout exhibited behavior of biennial spawning (detected in 2013 and again in 2015 with no 2014 detection).



Figure 3.2.1-6

Based off of known in-season 2015 captures and use of the length predicting equation referenced earlier, the size breakdown of Cougar Creek migrating bull trout is expressed in Figure 3.2.1-7.



Figure 3.2.1-7

Pine Creek

The PIT antenna at the mouth of Pine Creek was in operation from July 28 to October 27, no power loss was experienced during the survey period. 266 detections were experienced during the period of operation resulting in 61 discrete bull trout tags. 80 percent of detections at this site occurred during the crepuscular period, while 20 percent of detections were recorded during diurnal hours. Peak migration past this antenna was observed on September 23 when seven bull trout volitionally swam past (Figure 3.2.1-8).



Figure 3.2.1-8

The number of discrete detects at this site represent the most since PIT antenna operations started in 2011 (Figure 3.2.1-9). Of the 61 bull trout that migrated upstream past this antenna, 55 percent showed evidence of consecutive year migrations (2, 3, or 4 year consecutive), 30 percent

were maiden detections, 10 percent showed evidence of biennial migrations, and 5 percent were transported from out of basin during 2015 (two bull trout from the Swift Bypass Reach and one from the Swift Power Canal). 5 of the 61 (8 percent) bull trout interrogated at this site in 2015 were transferred at some point from the Swift Bypass Reach in Yale Reservoir and released into Swift Reservoir.



Figure 3.2.1-9

Based off of known in-season 2015 captures and use of the length predicting equation referenced earlier, the size breakdown of Pine Creek migrating bull trout is expressed in Figure 3.2.1-10.



Figure 3.2.1-10

Pine Creek Tributary P8

The PIT antenna at the mouth of Pine Creek tributary P8 was in operation from August 6 to October 19. Power loss was experienced for six days, from August 15 - 21 due to a faulty battery. 1,170 detections were recorded during the period of operation resulting in 30 discrete bull trout tags. 49 percent of detections at this site occurred during the crepuscular period, while 51 percent of detections were recorded during diurnal hours. Peak migration was observed on September 20 when eight bull trout volitionally swam past this antenna (Figure 3.2.1-11).



Figure 3.2.1-11

Discrete detections at this site dropped marginally from the previous two years (Figure 3.2.1-12). Of the 30 bull trout detected at this antenna in 2015, 57 percent showed evidence of consecutive year migrations, 27 percent were maiden detections, and 16 percent showed behavior of biennial migratory patterns.



As all bull trout detected at this site were also detected either migrating upstream or downstream past the PIT antenna at the mouth of Pine Creek, the migrant size breakdown at this site also reflects that of Figure 3.2.1-10.

Rush Creek

The PIT antenna near the mouth of Rush Creek was operated by staff from the Washington Department of Fish and Wildlife and was in operation from August 19 to October 6, no power loss was experienced during this sampling period. 113 total detections were recorded during this time frame resulting in fourteen discrete bull trout tags. 78 percent of detections were recorded during crepuscular hours, with the other 22 percent coming during the diurnal period. Peak migration past this antenna was observed on September 27 when six bull trout were interrogated (Figure 3.2.1-13).



Figure 3.2.1-13

Discrete detections at this antenna have been on a downward trend since operations began in 2006 (Figure 3.2.1-14). Of the fourteen bull trout interrogated at the Rush Creek antenna in 2015, 50 percent were maiden detections, 36 percent show evidence of consecutive year migrations, and fourteen percent exhibited behavior of biennial migratory patterns.



Figure 3.2.1-14 Courtesy of WDFW.

Based off of known in-season 2015 captures and use of the length predicting equation referenced earlier, the size breakdown of Rush Creek migrating bull trout is expressed in Figure 3.2.1-15.



Figure 3.2.1-15

Muddy River

The PIT antenna at the mouth of the Muddy River was in operation from August 20 to October 18. No power loss was experienced during the sampling period. 96 detections were recorded during the period of operation resulting in 7 discrete bull trout tags. All detections at this site occurred during the crepuscular period. Peak migration at this antenna site was observed on October 8 when three bull trout volitionally swam past (Figure 3.2.1-16).



Figure 3.2.1-16

Discrete detections at this antenna have been on a downward trend since operations began in 2013 (Figure 3.2.1-17). All of the seven bull trout interrogated at the Muddy River antenna in 2015 were maiden detections.



Figure 3.2.1-17

Based off of known in-season 2015 captures and use of the length predicting equation referenced earlier, the size breakdown of Muddy River migrating bull trout is expressed in Figure 3.2.1-18.



3.3 Lewis River Bull Trout Capture and Transport Activities

3.3.1 FERC PROJECT LICENSE ARTICLE 402(A) AND LEWIS RIVER SETTLEMENT AGREEMENT SECTIONS 4.9.1 & 4.9.2 - YALE TAILRACE CAPTURE AND TRANSPORT ACTIVITIES

Per Article 402(a) in the FERC licenses and the Lewis River SA section 4.9.1, PacifiCorp annually captures and transports bull trout from the Yale powerhouse tailrace (upper Merwin Reservoir) to the mouth of Cougar Creek, a Yale Reservoir tributary. A total of 151 bull trout have been captured from the Yale tailrace since the program began in 1995.

To capture bull trout from the Yale tailwaters, monofilament mesh tangle nets are used (typically 40 m long, 2 m deep, and consisting of 6.5 cm stretch mesh). Depending on catch rates, netting occurs for the most part on a weekly basis beginning in June and ending mid-August. Netting usually occurs between the hours of 0900 and 1200. During this time, the powerhouse generators are taken off-line to facilitate deployment and handling of the nets. Nets are tied to the powerhouse wall and then stretched across the tailrace area using a powerboat. The nets are then allowed to sink to the bottom. Depending on conditions or capture rate, the nets are either held by hand on one end or allowed to fish unattended. The maximum time nets are allowed to fish is 10 minutes.

Upon capture of a bull trout, it is immediately freed of the net (usually by cutting the net material) and placed in a live well. Captured fish are measured to their caudal fork, weighed with a hand-held scale to the nearest gram, and inserted with a uniquely coded HDX or FDX PIT tag (size dependent). All fish are scanned with a hand-held PIT tag detector to check for previous tags prior to inserting a PIT tag. Along with fork length information, the weights of

captured bull trout will be used to assess the condition factor (K-factor) of fish residing in Lake Merwin.

Use of Alternative Capture Methods

PacifiCorp continues to consider more effective and less intrusive methods to collect bull trout from the Yale tailrace. Past alternative methods investigated include; beach seines, purse seines, drifting tangle nets when the powerhouse is online, and angling.

In 2015, tangle nets and angling were the only methods used. To date, tangle nets remain the most effective. PacifiCorp continues research on possible alternative methods of effective capture and transport. However, upon investigation of each concept or pilot test conducted at other Northwestern dams, PacifiCorp has not been successful in finding a better alternative than the current method.

Yale Netting Results

At the Yale powerhouse tailrace, five capture attempts were completed from May 19 through July 21, 2015 yielding one bull trout. Unfortunately, the one individual captured expired during the capture and handling process. All procedures concerning Reporting a bull trout mortality and Handling of the bull trout carcass per the USFWS Biological Opinion for the Lewis River were followed and adhered to.

Other species captured besides bull trout included kokanee (*Oncorhynchus nerka*), largescale suckers (*Catostomus macrocheilus*), northern pikeminnow (*Ptychocheilus oregonensis*), mountain whitefish (*Prosopium williamsonii*), coho salmon (*O. kisutch*), coastal cutthroat trout (*O. clarkii*), and rainbow trout (*O. mykiss*) all of which were returned to the tailrace.

YEAR	No. captured at the Yale tailrace	No. transferred to mouth of Cougar Creek	No. transferred to Swift Reservoir	No. released back into Merwin Reservoir	MORTALITIES
1995	15	9	0	6	0
1996	15	13	0	2	0
1997	10	10	0	0	0
1998	6	6	0	0	0
1999	6	0	0	6	0
2000	7	7	0	0	0
2001	0	0	0	0	0
2002	6	5	0	1	0
2003	19	8	0	1	10^
2004	8	3	0	5	0
2005	5	5	0	0	0
2006	5	5	0	0	0
2007	13	13	0	0	0
2008	15	15	0	0	0
2009	5	5	0	0	0
2010	1	0	0	0	1
2011	6	5	0	0	1
2012	3	3	0	0	0

Table 3.3.1-2. Number of bull trout collected from Yale tailrace (Merwin Reservoir) and transferred to the mouth of Cougar Creek (Yale tributary) or Swift Reservoir: 1995 – 2015.

2013	6	4	2	0	0
2014	0	0	0	0	0
2015	1	0	0	0	1
TOTAL	151	112	2	21	13

^Please refer to the 2003 PacifiCorp Threatened and Endangered Species Monitoring Report for a description of mortalities

3.3.2 FERC PROJECT LICENSE ARTICLE 402(A) AND LEWIS RIVER SETTLEMENT AGREEMENT SECTIONS 4.9.1 & 4.9.2 - SWIFT BYPASS REACH CAPTURE AND TRANSPORT ACTIVITIES

The Swift Bypass Reach is the former Lewis River channel between the Swift No. 1 and Swift No. 2 hydroelectric projects. Since 2010, a minimum flow of 65 cubic feet per second (cfs) has flowed in the Bypass Reach through what the SA termed the "Upper Release Point" and the "Canal Drain". The Upper Release Point flows from the Swift No. 2 Power Canal directly upstream from the Swift No. 1 spill plunge pool and provides 51 – 76 cfs of water depending on the time of year. The Canal Drain flows from the Swift No. 2 Power Canal into an approximately 350 m long reach (termed the Constructed Channel) that is relatively unaffected by Swift No. 1 spill events and provides a continual 14 cfs of water flow. This Constructed Channel then joins the main channel Bypass Reach. Along with Ole Creek, these two water release points provide most of the flow into the Bypass Reach.

In 1999, The Utilities began netting the Swift No. 2 powerhouse tailrace as part of requirements contained in amendments to Article 51 of the former Merwin license. The tailrace was not netted from 2001 to 2005 because of the Swift No. 2 canal failure in 2001 and subsequent reconstruction. Capture efforts were then restarted in 2006 pursuant to sections 4.9.1 and 4.9.2 of the Lewis River Settlement Agreement and in 2008 pursuant to Article 402(a) of the new FERC licenses for Swift No. 1 and No. 2.

At the 2007 annual bull trout coordination meeting (attended by USFWS, WDFW, and PacifiCorp), the Utilities proposed to discontinue netting the Swift No. 2 tailrace (since only two fish had been captured since 1999) and move the collection site to an area near the International Paper (IP) Bridge within the Swift Bypass Reach (Figure 3.3.2-1). As noticed in past Swift Bypass Reach snorkel surveys, this area was found to contain adult bull trout between the months of June thru October. The USFWS and those in attendance at the 2007 coordination meeting approved this recommendation (see Utilities 2007 Annual Bull Trout Monitoring Plan for meeting notes

http://www.pacificorp.com/content/dam/pacificorp/doc/Energy_Sources/Hydro/Hydro_Licensin g/Lewis River/Annual Bull Trout Monitoring Plan 2007.pdf).



Figure 3.3.2-1. Map showing bull trout sampling areas between Swift No.1 and Swift No. 2 powerhouse's.

2015 collection activities typically focused on capturing bull trout from the agreed-upon sampling area of the bypass reach below the International Paper Bridge and from the confluence of the bypass reach with Yale Reservoir (Figure 3.3.2-1). Angling was the primary method of capture in this area early in the season (when bull trout are aggressive and still actively feeding) due to its effectiveness and low rate of incidental catch of other species present in the survey area.

As the season progressed and bull trout became increasingly indifferent to fishing lures, the method of capture switched to utilizing passively set tangle nets. Nets similar in length, depth and mesh size to those used at Eagle Cliffs and the Yale powerhouse tailrace were used for the Swift Bypass efforts. Unlike other collection areas within the Lewis River basin where nets are allowed to passively "soak" unattended, bull trout captured in the bypass reach are corralled by biologists in snorkel gear into set nets and as such, are constantly checked. When a bull trout became entangled, the net was immediately pulled in and the bull trout freed and placed in a holding container (aerated cooler or live box in the stream).

The Swift Bypass Reach was sampled seven times from May 27 to July 27, 2014. During this sampling time-frame, 24 bull trout were captured. Of these, 21 were maiden captures, two were past year recaptures, and one was a same year recapture (Appendix B). Maiden captures were tagged with a uniquely coded HDX PIT tag, sampled for genetic tissue, weighed, and measured to their caudal fork. Recaptured bull trout from this area were simply interrogated for their PIT code, measured and weighed.

In past collection activities, Swift Bypass Reach captured bull trout, after tagging and biologically sampling, were simply released back to the point of capture. With the completion of the Lewis River bull trout genetic baseline in 2011, all new bypass reach bull trout captures have been transported to Speelyai or Merwin Hatchery and held while rapid response genetic analysis of each individual fish is performed at the Abernathy Lab. The intent of the rapid response genetic analysis is to identify any Swift origin bull trout residing in Yale Reservoir that are prevented from returning to their natal stream to spawn, and to transport them back upstream into

Swift Reservoir. It is commonly accepted that bull trout are highly migratory and, over time, a portion of the Swift bull trout population has migrated downstream of Swift No. 1 dam either by passing through spill gates during spill events or passing through the turbine units in the powerhouse.

The 21 maiden bull trout captures in 2015 were transported to Merwin Hatchery and held in one of three circular tanks while awaiting results from the genetics lab. Circular tanks were approximately 2.5 meters in diameter and 2 meters in height, water was filled to within half a meter of the top of each tank. Circular tanks were fed with constantly moving water; and water temperature never exceeded 12° Celsius for the duration of the collection period. Only like-sized bull trout were held in the same tank. ³/₄ inch plywood was placed over the top of each circular tank to prevent bull trout from jumping out of the tank. The longest a bull trout was held while awaiting genetic analysis during 2015 activities was approximately 48 hours.

It was decided during 2015 planning meetings to continue to err on the side of caution when deciding which captured bull trout would be transported upstream for release into Swift Reservoir after Rapid Response genetic analysis. Therefore, only bull trout found to be genetically endemic to Rush Creek, Pine Creek, or a combination thereof at a Greatest Likelihood of Origin score of \geq .99 were transported upstream to Swift Reservoir in 2015. In contrast, bull trout with a likelihood score of less than 0.99 to Rush Creek, Pine Creek, a combination of the two, or with a Greatest Likelihood of Origin score greater than 0.02 to Cougar Creek were released back into Yale Reservoir. A sheet detailing genetic analysis of all previously captured bull trout that were simply sampled and released during prior years was onsite so as to determine real-time origin of any recaptured fish. If origin of recaptured fish was known, that fish was not held at a hatchery, but instead taken to one of the release points described above as determined by its greatest likelihood of origin score. For a description of Materials and Methods used by the lab for Rapid Response genetic analysis of Bull Trout Collected in the Lewis River, WA 2011 Annual Report" (DeHaan and Adams 2011).

Of the 24 bull trout captured in the Swift Bypass Reach in 2015, five were found to be of Pine or Rush Creek origin. The remaining nineteen captures either did not score high enough to be assigned to Rush or Pine, or scored a high likelihood to the Cougar Creek population and as such were returned to Yale Reservoir.

Figure 3.3.2-2 illustrates the size distribution of 2015 Swift Bypass Reach captures by area of final disposition.



Figure 3.3.2-2. Size distribution of transported bull trout from the Swift Bypass Reach in 2015.

YEAR	No. captured at the Swift Bypass Reach	No. transferred to Swift Reservoir	No. released back into Yale Reservoir	MORTALITIES
2007	15	0	15	0
2008	6	0	6	0
2009	25	0	25	0
2010	27	0	27	0
2011	32	15	17	0
2012	29	8	20	1
2013	24	8	16	0
2014	30	5	25	0
2015	21	5	15	1
TOTAL	209	41	166	2

Table 3.3.2-1. Number of bull trout collected from the Swift Bypass Reach (Yale Reservoir) and transferred to Swift Reservoir: 2007 – 2015.

Of particular note during 2015 Bypass reach collection efforts was the recapture in the bypass reach of a bull trout previously captured in 2010. This individual bull trout was first captured in the Swift Bypass Reach during 2010 activities at a fork length of 467 mm and a weight of 1140 grams. During this initial capture event it was simply PIT tagged, sampled for genetic material and released back to the point of capture. The genetic sample was then analyzed in early 2011 and analysis found this individual to be endemic to Pine Creek at a Greatest Likelihood Score of 100 percent. This bull trout was not handled again until this year, when it was recaptured in the Swift Bypass Reach on June 1, 2015, at a fork length of 755 mm and weight of 5340 grams. At this time this fish was transported and released to Swift Reservoir per its established genetic assignment. Though this fish was undoubtedly of spawning size and maturity, it had never been interrogated at the PIT antenna site in Cougar Creek.

3.3.3 SWIFT POWER CANAL BULL TROUT CAPTURE AND TRANSPORT ACTIVITIES

For the first time since 2012 the Swift Power Canal (Figure 3.3.2-1) was tangle-netted as part of bull trout capture and transport activities. Though the canal provides ample forage and thermal refugia for bull trout, it was deemed necessary to periodically collect and transport bull trout from the power canal based on the lack of any suitable bull trout spawning habitat (canal average depth of 10m) and because the only means of volitional migration is through the Swift No. 2 turbines.

The power canal was surveyed three times, May 14, June 17, and July 9, using methods similar to Yale Tailrace Capture and Transport activities (Section 3.3.1). Like Yale Tailrace collection activities the powerhouse generators were taken offline and netting usually consisted of a three hour block of time. Nets were typically deployed near the Swift No. 1 powerhouse. One bull trout measuring 537 mm was captured during the June 17 survey date. This fish was placed in a fish tank and transported for release into Swift Reservoir. No rapid response genetic analysis was performed or necessary given the only entry into the Swift Power Canal is via turbine passage at Swift No. 1 from Swift Reservoir. This captured bull trout was subsequently interrogated moving upstream past the Pine Creek PIT antenna on July 29 and then interrogated at the same antenna site moving back downstream on September 29, a total of two months within the Pine Creek system. Figure 3.3.3-1 illustrates historical capture numbers within the Swift Power Canal.



Figure 3.3.3-1. Historical bull trout captures from within the Swift Power Canal. Zero bull trout were captured in 2012 and no netting activities occurred during 2013 or 2014.

3.4 LEWIS RIVER BULL TROUT SPAWNING SURVEYS

3.4.1 FERC PROJECT LICENSE ARTICLE 402(B) AND LEWIS RIVER SETTLEMENT AGREEMENT SECTION 9.6 - COUGAR CREEK SPAWNING ESTIMATE

Since 1979, PacifiCorp biologists, along with various state and federal agencies, have conducted annual surveys to estimate spawning escapement of kokanee in Cougar Creek. Along with the kokanee, surveyors also count the number of bull trout and bull trout redds observed within the creek. In 2015, the Utilities conducted six Cougar Creek bull trout redd surveys from September 10 to October 29.

Surveys begin at the mouth of the creek and end at the creek's spring source, a distance of approximately 2100 m. Though redd count methodology has effectively replaced live peak counts as the metric used to estimate spawner abundance, peak counts are still performed during redd surveys in order to continue this established trend for comparison and calibration of the redd count expansion method.



Figure 3.4.1-1. GPS locations of bull trout redds in Cougar Creek in 2015. Each red dot represents an individual bull trout redd (n=19).

Due to the wide range use of redd counts to quantify bull trout spawner abundance, multiple research studies have been performed in an effort to gauge the precision of this methodology and also to question the efficacy of redd counts as a population estimator (Dunham et al. 2001,

Muhlfeld et al. 2006). Most often, redd surveys are conducted in large river systems with multiple different observers. The large systems necessitate the need for index areas mainly due to time and logistical constraints. The use of indices has been questioned based on their reliance of fish coming back to the same area at the same time every year to spawn. In addition, the use of multiple observer teams and a variety of observers on the same project, is considered to cause inaccuracies based on the variability between observers' experience with identifying redds.

The redd count methodology employed within Cougar Creek differs from most large-scale redd surveys in that the stream is small enough to feasibly cover the entire length during each survey, and currently is the only known bull trout spawning stream in Yale Reservoir. Cougar Creek also lends itself nicely to these types of surveys in that the water is extremely clear and has stable flow for most of the survey period. Also, redd life, the amount of time a redd remains visible, has an exceptionally long duration. Most, if not all, observed redds remain visible during the entire time-frame of the surveys.

In 2015, biologists walked the entire 2100 m of Cougar Creek during each redd survey. Surveys were completed over an extended period of time to address potential error associated with spawn-timing. To alleviate inter-observer variability, surveys were performed by the same experienced biologists every week. Dunham et al. (2001) specified that a sampling effort should not rely on indices and should use the same surveyors as effective ways of improving the reliability of bull trout redd counts.

The real challenge of using bull trout redds to quantify the bull trout spawning population size lies in determining the relationship between redd counts and actual numbers of fish (Budy et al. 2003). Much past and present research has been conducted that attempts to correlate the number of spawning adult bull trout per redd. These numbers range widely by basin (1.2 to 4.3 fish per redd) and it seems the number of bull trout per redd is most likely basin or watershed specific.

At this time, given that the exact number of bull trout that ascended Cougar Creek in 2015 to spawn is unknown, there is no reliable way to get an approximate number of fish per redd. Therefore, until we are able to find a method to obtain true numbers of adult bull trout spawners that enter Cougar Creek, PacifiCorp has elected to use two fish per redd as the interim index ratio.

During each 2015 redd survey, new redds were flagged and identified by Global Positioning Satellite (GPS) coordinates. The date, location of redd in relation to the flag, and GPS coordinates were all written on the flagging (Figure 3.4.1-1). Subsequent surveys inspected each redd to see if they were still visible. If a redd was still visible, that information was written on the flagging with the date, until the redd was no longer visible, at which time this was noted on the flagging. Biologists also counted any bull trout observed within the vicinity of each redd. Throughout the spawning season, new redds were flagged and identified as described above until bull trout adults and new redds were no longer observed in Cougar Creek.

19 individual bull trout redds were observed in Cougar Creek in 2015. Using the two fish per redd expansion, 38 spawning bull trout were estimated to have ascended Cougar Creek in 2015 (Figure 3.4.1-2). The first recorded redd was observed on September 22, and the last new redd was observed on October 29. Peak redd construction occurred during the week of October 12
when eight new bull trout redds were observed, this peak coincides with historical peak redd count data.

As in past years, the bulk of bull trout redds were observed in the upper half of the creek upstream of a log jam that in most years is impassable to kokanee (Figure 3.4.1-1).

A recent concern in Cougar Creek, first observed in 2008, are bull trout redds found to be superimposed over one another. During redd counts in 2015, no bull trout redds was observed superimposed over a previously excavated bull trout redd.

Flagging from redd surveys performed in 2014 were left in place over the course of the year and along with GPS coordinates, care was taken to document redd habitat areas used consecutively from the previous year. It was observed in 2015 that 10 of the 19 redds (52 percent) were constructed very near and often in nearly the exact spots as the previous year(s).

Along with redd counts, a peak visual count of bull trout was also performed in the same manner that began in 1979 (Figure 3.4.1-3). This count is not considered a spawning population estimate as it relies on a peak count of bull trout observed on a single sampling event. Rather, the annual peak counts are used to monitor Cougar Creek bull trout relative abundance trends from year to year. In 2015 the peak visual count was 5 adult bull trout.



Figure 3.4.1-2. Annual Cougar Creek bull trout spawning escapement based on redd surveys, 2007-2015.



Figure 3.4.1-3. Cougar Creek peak count based on foot and snorkel surveys, 1979-2015.

3.4.2 BULL TROUT REDD SURVEYS OF PINE CREEK AND PINE CREEK TRIBUTARY P8

Tributaries to Pine Creek are counted from the mouth of Pine Creek upstream. P8 (Figure 3.4.2-1) is the eighth and largest of the tributaries. Based on surveys performed in 1999 and 2000 to document the extent of available anadromous fish habitat within the North Fork Lewis River basin, P8 contains approximately 6400 m of accessible anadromous fish habitat and has relatively low gradient for the first 1600 m. P8 is a relatively small stream, with an average wetted width of 3.5 m, but it contains abundant annual flow and cold water (PacifiCorp and Cowlitz PUD 2004).

Redd surveys (consistent with methodology used for Cougar Creek) were performed on Pine Creek tributary P8 five times (September 14 – October 27) during the 2015 bull trout spawning season. The first recorded redd was observed on September 14 and the last observed redd was recorded on October 27. A peak count of 16 new redds was recorded during the survey on October 6, this is typical of historical peaks observed in years past. In all, GPS coordinates were collected from 42 bull trout redds which were observed and counted from the mouth of P8 to 2100 m upstream (Figure 3.4.2-1). Based on expansion factors of two adult bull trout per redd, 96 bull trout were estimated to have spawned within P8 (Figure 3.4.2-2).

For the past two seasons spawning coho have been observed within P8 during bull trout spawning surveys. No coho or coho redds were observed within P8 in 2015. This likely was a function of an extremely low coho return to the Lower Lewis River in 2015 which in turn lead to few coho being transported and released into Swift Reservoir.

A one-time peak bull trout redd count was attempted of Pine Creek mainstem on September 28 and 29. On September 28 Pine Creek was broken up into manageable walking reaches with one

surveyor walking and recording bull trout redds from the mouth of Pine Creek to the mouth of P3 Creek, where six bull trout redds were marked by GPS; and another surveyor walking and recording bull trout redds from the mouth of P3 Creek to the mouth of P8 Creek, where 30 bull trout redds were marked by GPS. On September 29 the same two surveyors walked upstream within Pine Creek from the mouth of P8 Creek for approximately one mile, 34 bull trout redds were observed within this reach and marked by GPS (Figure 3.4.2-3).

Later attempts to complete the survey to the extent of anadromous fish habitat within Pine Creek were unsuccessful. In all, 70 bull trout redds were observed and marked by GPS. Of these 70 redds 20, or 29 percent, were observed to have bull trout actively constructing or guarding the redd. 32 bull trout were counted on the 20 redds that contained lives, corresponding to an observed fish per redd ratio of 1.6.



Figure 3.4.2-1. GPS locations of bull trout redds in Pine and P8 creeks in 2015. Each red dot represents an individual bull trout redd (n=112).



Figure 3.4.2-2. Pine Creek tributary P8 bull trout spawning population estimate based on redd expansion estimate of two fish per redd (2008 and 2009 data courtesy of WDFW).

3.5 BULL TROUT CONDITION FACTOR (K)

Since 2008, most captured bull trout encountered in the Lewis River basin were weighed to the nearest gram (Map 2.0-1). The goal of gathering this additional biological information is to quantify the condition factor of bull trout in Merwin, Yale, and Swift Reservoirs. This standardized information can then be utilized to compare the condition of reservoir bull trout populations from year to year. K-factor data may also offer insights into reservoir productivity and its potential influence on bull trout spawning migration frequency.

Condition factor is a simple weight-length relation that is generally thought to be one of several indices of healthy fish (Nielson and Johnson 1983). Fulton (1902) established the weight-length relation equation that was used to estimate K-factors in this study.

The Fulton-type equation used is as follows;

 $K = (W/L^3) X$

Where;

K = metric condition factor
W = weight in grams
L = length in millimeters
X = Arbitrary scaling constant (for our purposes 10⁵ was used)

A hand-held scale was used to weigh fish during Lewis River basin netting activities. To weigh bull trout, a landing net or water-filled bucket was attached to the hand-held scale, the scale was allowed to tare to zero, a bull trout was placed in the landing net or water-filled bucket, and the weight was recorded to the nearest gram. The entire time bull trout were out of water if weighed with a landing net was normally under 10 seconds. When feasible, bull trout were weighed on land. While in a boat, calm coves were sought out but a measure of inaccuracy was unavoidable due to the pitch and roll of the boat in response to wave action. Biologists felt this inaccuracy was acceptable if it alleviated any added undue stress to the captured bull trout due to overhandling or length of holding time.

A total of 86 bull trout were weighed from the Swift Power Canal, Yale and Swift Reservoirs in 2015. Of those fish, 64 were from Swift Reservoir, 21 from Yale Reservoir, and one from the Swift Power Canal (not all captured bull trout were weighed in 2015 due to the occasional lack of available equipment).

For salmonids, K factor values usually fall between 0.8 and 2.0 (Nielson and Johnson 1983). A K-factor scale was used to filter the data and to help analyze the values for comparison. The scale is based on direct visual observations of all weighed bull trout within the North Fork Lewis River basin to date, and may adaptively change in the future with the input of additional data. The scale used is as follows:

- less than 0.99 = Poor
- 1.00 1.19 = Fair
- 1.20 1.39 = Healthy
- greater than 1.40 = Exceptional

Figure 3.5-1 represents the percent distribution of weighed bull trout occurrences in the above mentioned K-factor scale. Bars in the graph are divided to represent bull trout from each sampling area. Figure 3.5-2 represents condition factors and their correlation to the corresponding fork length for all measured fish (n=86). The regression line indicates a slight statistical correlation existed in 2015 between fish length and condition factor; though not on the magnitude that was expected or observed in prior years, the larger size-class bull trout exhibited a slightly higher condition factor than the smaller size-class fish (Figure 3.5-2). A data set was unavailable from Merwin due to the lack of bull trout captures during 2015 activities.

Median condition factor values were 1.17 for fish sampled in Yale Reservoir, and 1.13 for fish sampled in Swift Reservoir. The median condition factor for all bull trout combined in 2015 was 1.15. When comparing numeric fish condition factors, care needs to be taken to only compare fish of like fork lengths (Anderson and Gutreuter 1983). Figure 3.5-3 compares bull trout lengths to weights recorded and the corresponding curve established by this relationship.

To quantify variation within the 2015 condition factor data-set, the coefficient of variation (%CV) was computed and represented in percent format. Coefficient of variation is the standard deviation of a sample divided by the arithmetic mean; this number is then multiplied by 100 to convert to percent CV. The coefficient of variation from the entire bull trout condition factor sample in 2015 was thirteen percent. Figures 3.5-4 and 3.5-5 are historical comparisons of collected Condition Factor data grouped by reservoir.



Figure 3.5-1. Percent distribution of all weighed bull trout in 2015 over established Lewis River condition factor scale.



Figure 3.5-2. Individual bull trout condition factors in relation to corresponding fork lengths for entire sample from all sample areas combined in 2015.



Figure 3.5-3. Bull trout length to weight relation curve observed in 2015. Each dot represents an individual fish (n=86).



Figure 3.5-4. Historical median K-factors observed from bull trout within Swift Reservoir.



Figure 3.5-5. Historical median K-factors observed from bull trout within Yale Reservoir.

4.0 **DISCUSSION**

As directed in Article 402 of the Federal Energy Regulatory Commission issued operating licenses for Merwin, Yale, Swift No.1, and Swift No.2 hydroelectric projects (issued June 26, 2008) and pursuant to Section 9.6 and 4.9 of the Lewis River Settlement Agreement, the Utilities are to monitor bull trout populations in Swift Reservoir and Yale Reservoir annually as well as annually capture and transport bull trout from the Yale powerhouse and Swift No.2 tailrace areas. The Utilities collected the data contained in this report to accomplish these mandated monitoring objectives.

The estimated number of bull trout that staged in the Eagle Cliffs area at the head of Swift Reservoir in the spring/summer and then migrated upstream the North Fork Lewis River in the summer/fall increased dramatically over the previous year in 2015. This number is likely grossly over-estimated and given the breadth within the 95 percent confidence intervals (almost +/-300 of 697), caution should be taken when evaluating. The uncertainty surrounding the migration estimate in 2015 stems from the lack of marked individuals observed during re-sight surveys. Though 64 bull trout were marked with double pink Floy® tags at Eagle Cliffs in the early summer, it seems very few of these fish actually left the marking area and ventured upstream in the late summer/early fall as evidenced by the high mark to no-mark ratio observed during snorkeling surveys (average of 1 mark to 12 no marks, or eight percent of total observed sample marked). High observer error during snorkeling surveys was no longer considered an issue after review of 2015 PIT antenna detections revealed that only 19 percent (12 of 64) of bull trout Floy® tagged during 2015 activities actually migrated past an antenna located at either Pine, P8, Muddy, or Rush during the sampling period (August – October).

At this time the specific reason for lack of 2015 Floy® marked bull trout to the re-sight area or spawning tributary's is unknown. Figure 4.1 below may lend insight to a possible explanation for non-migration of some tagged fish in 2015. Of the 64 bull trout Floy® tagged in 2015, only 51 percent (33) were greater than 500mm fork length. 88 bull trout were detected and recorded

moving upstream or downstream past a PIT antenna above Swift Reservoir in 2015, of these 88 fish none measured less than 500mm in fork length. It appears our minimum tag size of 360mm may be too small, especially if the expectation is one that the tagged fish will be migrating upstream to a spawning or tag re-sight area. Given all of the tag information from PIT antenna detections to date, the majority of migrating bull trout are 500mm or greater in fork length.

Though the above explanation may speak to the non-migration of tagged smaller-sized bull trout in 2015, it does not explain the disposition of the 21 tagged bull trout greater than 500mm fork length that never were observed migrating upstream or detected at a spawning tributary. At this time it is unknown what environmental or physical factor prohibited these individuals from completing a spawning tributary migration in 2015.



Figure 4-1

Genetic estimation of the Effective Number of Breeders (Nb) was again calculated for Pine and Rush creeks in 2015, and for the first time within Cougar Creek. Based on analysis of the sample of age 0 juvenile bull trout collected in the early summer from Pine, Rush, and Cougar creeks, Nb for Rush Creek was 23, Pine Creek was 19.5 and Cougar Creek 18.7. Nb increased in Rush Creek from 2014 (18) and decreased in Pine Creek from 2014 (21). Changes in both were slight and speak to some stability within the establishing trend line. Of particular interest when evaluating Nb for the 2014 brood year, specifically within Pine and Rush, is the decline in numbers in Pine Creek compared to Rush Creek. This is especially interesting when compared to known bull trout use as well as available habitat within each respective stream. If PIT antenna detections at the mouth of each stream are used as an indicator of overall bull trout spawning habitat usage, then the fact that Rush Creek had a higher Nb estimate than Pine while experiencing 84% less use in terms of migrating bull trout (10 bull trout detected in Rush compared to 60 detections in Pine in 2014), is somewhat concerning when evaluating bull trout abundance within Pine. Nb will continue to be analyzed in future years in hopes of further assessing the Effective Population (Ne) of these local bull trout populations. Methods, Materials, and Results for all genetic activities performed within the Lewis River in 2015 can be found in the Report titled "Rapid Response Genetic Analysis and Genetic Estimation of Spawner

Abundance of Bull Trout Collected in the Lewis River, WA" (Adams/Doyle, 2016) located in Appendix B of this Report.

PIT antenna detection data in 2015 was analyzed for bull trout Survival (S), migration timing, stream utilization and size at migration. Based on in-stream PIT tag interrogations at passive antennas in Pine and Rush Creeks, Pine Creek is increasingly becoming more utilized in terms of a greater proportion of the population making assumed spawning migrations. Though the sample size of available tags for recovery has increased every year since 2011, interrogations at the Rush Creek antenna have remained relatively the same and low with only 10-21 individual fish detected from one year to the next during this time-period (2011-2015, courtesy WDFW). Many of the fish interrogated at Rush Creek are also prior year migrants, lending additional credence to the apparent lack of new recruitment to this stream. Compare this to activity within Pine Creek, where bull trout usage has increased every year since operation of passive PIT antennas began in 2011. Seventeen individuals were detected in Pine Creek in 2011, 21 in 2012, fifty in 2013, sixty in 2014, and 62 in 2015. A more detailed analysis of PIT antenna detections as they correlate to an estimate of Survival (S) from one year to the next, as well as the probability that an individual fish will make a spawning excursion can be found in the Memo "Analysis of Bull Trout PIT Tag Detection Data" (Stillwater Sciences, 2016) located in Appendix A of this Report.

Bull trout captures in the Yale powerhouse tailrace remained low in 2015 (1) and similar to 2014 (0). Capture methods (tangle nets) were similar to past collection years as was total effort (five netting days). New methodologies to capture these fish continue to be investigated, though at this time tangle nets remain the most effective and efficient. With the construction in late 2009 of the Yale Entrainment Reduction Net, and the Yale Spillway Entrainment Reduction Net in 2013, pursuant to section 4.9.3 of the Lewis River Settlement Agreement, capture numbers of bull trout in the Yale powerhouse tailrace are anticipated to continue this current downward trend.

Collection and tagging methods within the Swift Bypass Reach continued relatively unchanged in 2015. Unless of known genetic origin from a previous capture, all captured Swift Bypass Reach bull trout in 2015 were held in circular tanks at Merwin Hatchery while rapid response genetic analysis was performed. Bull trout that scored high enough in a Likelihood of Origin Analysis (greater than 99 percent) to a Swift Reservoir population (or combination thereof) were transported upstream and released into Swift, while bull trout that did not meet the scoring criteria were released back into Yale Reservoir. Capture numbers in 2015 (23) were consistent with what has been encountered in recent years. Catch was slightly lower than expected but this may have been a function to the truncated survey period (May 27-July 27). Surveys were called off two weeks earlier than normal due to low water conditions in the survey area and higher than normal water temperatures not conducive to fish transport. Five of the 23 Swift Bypass Reach bull trout captures, after analysis, were found to be endemic to a Swift Reservoir local population (Rush or Pine) and were transported and released into Swift Reservoir. The remaining eighteen captures were either endemic to the Cougar Creek local population, or did not score high enough in the Likelihood of Origin analysis to Rush or Pine Creek and were released back to Yale Reservoir.

Bull trout redd count methodology continued in Cougar Creek to quantify the bull trout spawning population residing in Yale Reservoir. Though bull trout redds observed in the creek in 2015 (19) were only slightly less to what was observed in 2014 (22), they mark the second

year in a row of declining numbers. Multiple redd surveys encountered bull trout physically on redds and at times in the process of excavating. Information concerning a bull trout-per-redd expansion factor is still needed. 2015 bull trout redd counts in Pine Creek tributary P8 were second only to what was observed in 2014 which is highest on record (42 in 2015 compared to 49 in 2014). Similar to Cougar Creek surveys, bull trout in P8 were routinely observed physically paired up on and actively constructing redds. A high-flow event occurred in the basin on October 31, 2015 which may have scoured some existing redds. A portion of P8 was left dessicated as the stream jumped its banks and cut a new channel. It remains to be seen just how many bull trout redds were affected by this event, but it may prove to be difficult to find and collect 2015 brood year fry during Genetic Estimation of Breeder Population activities in the early summer of 2016.

Weights of most handled bull trout were again collected in 2015. Individual weights were then compared to corresponding fork lengths and fish condition factors were assigned. Due to the low catch numbers encountered this spring and summer during Eagle Cliffs netting, the number of weights recorded in Swift Reservoir in 2015 (64) remained low and comparable to 2014 (67). The number of weights recorded in Yale Reservoir in 2015 (22) dipped slightly to numbers recorded in 2014 (29). When the calculated condition factors of like-sized individuals were compared, the year 2015 showed a slight increase in overall bull trout condition factor in Yale, while Swift remained unchanged. Median values observed in Swift Reservoir in 2015 (1.13) remained exactly to what was observed in 2014 (1.13); while Yale, for the second year in a row, showed an increase in 2015 (1.17) to what was observed in 2014 (1.15). No bull trout were handled from Merwin Reservoir during 2015 activities. It is anticipated that condition factor information may offer insight into reservoir productivity as it relates to bull trout, and the overall health of individual bull trout. This information can then be related to how fish condition may affect bull trout behavior especially in terms of reproduction and year-to-year spawning behavior.

5.0 ACKNOWLEDGEMENTS

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6.0 LITERATURE CITED

- Adams, B., J. Doyle. 2016. Rapid Response Genetic Analysis and Genetic Estimation of Spawner Abundance of Bull Trout Collected in the Lewis River, WA. United States Fish and Wildlife Service Abernathy Fish Technology Center. Longview, WA.
- Akaike, H. 1974. "A new look at the statistical model identification". *IEEE Transactions on Automatic Control* 19 (6): 716–723.
- Anderson, R. and S.J. Gutreuter. 1983. Length, weight, and associated structural indices *In* L.A. Nielsen and D.L. Johnson, eds. Fisheries Techniques. American Fisheries Society. Bethesda, Maryland.
- Budy, P., R. Al-Chokhachy, and G.P. Thiede. 2003. Bull trout population assessment and lifehistory characteristics in association with habitat quality and land use in the Walla Walla River Basin: a template for recovery planning. 2002 Annual Progress Report to US Fish and Wildlife Service, Vancouver, Washington.
- Compton, R.I. 2007. Detection of half and full duplex PIT tags by half duplex PIT tag antennas and portable full duplex PIT tag readers. United States Geological Service, Wyoming Cooperative Fish and Wildlife research Unit.
- DeHaan. P., B. Adams. 2011. Analysis of Genetic Variation and Assessment of Population Assignment Methods for Lewis River Bull Trout. United States Fish and Wildlife Service Abernathy Fish Technology Center. Longview, WA.
- Dunham, J., B. Rieman, and K. Davis. 2001. Sources and magnitude of sampling error in redd counts for bull trout *Salvelinus confluentus*. North American Journal of Fisheries Management 21: 343-352.
- Fraley, J. J., and B. B. Shepard. 1989. Life history, ecology and population status of migratory bull trout (*Salvelinus confluentus*) in the Flathead Lake and River system, Montana. Northwest Science 63(4):133-143.
- Fulton, T.W. 1902. The rate of growth of fishes. 20th Annual Report of the Fishery Board of Scotland 1902 (3):326-446.
- Muhlfeld. C.C., M. Taper, D. Staples, and B. Shepard. 2006. Observer Error Structure in Bull Trout Redd Counts in Montana Streams: Implications for Inference on True Redd Numbers. Transactions of the American Fisheries Society 135:643-654.
- Nielson, L.A., and D.L. Johnson. 1983. Fisheries Techniques. American Fisheries Society.
- Stillwater Sciences. 2016. Technical Memorandum "Analysis of Bull Trout PIT tag and Detection Data" from Stillwater Sciences to Jeremiah Doyle.

- Tranquilli, J.V., M.G. Wade, C.K. Helms. 2003. Minimizing risks and mitigation of impacts to bull trout *Salvelinus confluentus* from construction of temperature control facilities at Cougar Reservoir, Oregon. Oregon Department of Fish and Wildlife. Salem, OR.
- White, G.C. 1996. NOREMARK: Population estimation from mark-resighting surveys. Wildlife Society Bulletin. 24: 50-52.
- White, G. C., and K. P. Burnham. 1999. Program MARK: survival estimation from populations of marked animals. Bird Study 46:120-139.

APPENDIX A

2015 Lewis River Bull Trout Survival Estimate

TECHNICAL MEMORANDUM

February 17, 2016
Jeremiah Doyle, PacifiCorp
Stillwater Sciences
Analysis of bull trout PIT tag and detection data

1 Introduction

From 2008 through 2014, bull trout (*Salvelinus confluentus*) were tagged with Passive Integrated Transponder (PIT) tags in Yale and Swift reservoirs, and in tributaries to Swift Reservoir including Pine, P8, Muddy, and Rush creeks. Bull trout tagged in Yale Reservoir were potentially detected in Cougar Creek, and bull trout tagged in Swift Reservoir (and tributaries) were potentially detected in Pine Creek and/or Rush Creek (Table 1). Within each tributary, antenna were paired to increase detection probability and to determine direction of migration.

 Table 1. Summary of bull trout tagged and detected 2008–2015. Multiple antenna detections of a fish in the same year are counted as a single "detection".

Location	Number of distinct tagged fish	Number of detections
Yale Reservoir and Cougar Creek	187	312
Swift Reservoir, Pine Creek, and Rush Creek	373*	715
Includes 15 fish transmented from Vale Decomosin		

[†]Includes 15 fish transported from Yale Reservoir

2 Analysis

Program MARK (White and Burnham 1999) was used to estimate bull trout survival based on the available history of detections for each individual fish tagged and re-sighted during capture and detection efforts. All PIT tag and detection data was separated into two "capture periods" including:

- "Tagging periods" when fish were physically recovered (by a variety of methods) and (potentially) tagged, and
- "Antenna periods" when fish were detected at one of the stationary antennae, presumably on attempted spawning excursions.

There were a total of fourteen capture periods for the Yale group (includes Yale Reservoir and Cougar Creek), and ten for the Swift group (includes Swift Reservoir, and Pine, P8, Muddy, and Rush creeks) (Table 2). The objective of the analysis was to estimate survival between capture periods, and probability of detection within each period.

Capture Period	Method	Yale	Swift
June–August 2008	Reservoir Sampling	Х	
May–August 2009	Reservoir Sampling	Х	
June–August 2010	Reservoir Sampling	Х	
August–October 2010	Tributary Antennae	Х	
June–August 2011	Reservoir Sampling	Х	Х
August–October 2011	Tributary Antennae	X	X
May–August 2012	Reservoir Sampling	X	X

Table 2.	Capture	periods	2008-	-2015
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July–October 2012	Tributary Antennae	Х	Х
May–August 2013	Reservoir Sampling	Х	Х
July–October 2013	Tributary Antennae	Х	Х
June–August 2014	Reservoir Sampling	Х	Х
July–December 2014	Tributary Antennae	Х	Х
May–July 2015	Reservoir Sampling	Х	Х
July–October 2015	Tributary Antennae	Х	Х

The probability of detection within a capture period is interpreted as the product of the probability that a fish will migrate past the antenna during that period and the probability that it will be detected at the antenna if it does. Since there are two antennae at each location, and since a fish must pass both of them at least twice during migration, it was assumed that the detection probability for each capture period was close to 100%. Therefore the capture probabilities at the antennae can also be interpreted as the estimates that a fish will attempt to spawn in a given year.

3 Results

Four different models were fitted to the data using Program MARK (Figure 1). There are two kinds of parameters in these models: detection probabilities p_{\dots} , representing the probability that a tagged individual will be observed in a tagging or antenna survey if it is present, and survival probabilities ϕ_{\dots} representing the probability that a tagged fish present in one survey will still be present at the time of the next. The four models differ in how many distinct values these are assumed to take:

- Model 1, (the "parsimonious model") assumes that the detection probabilities have the same value p_t for all tagging periods and the same value p_a for all antenna periods, and that the survival probabilities have the same value ϕ_{ta} for all intervals between tagging and antenna periods of the same year, and the same value ϕ_{at} for all intervals between antenna periods of one year and the tagging period of the next.
- Model 4, (the "full model") has the maximum number of estimable parameters: a separate parameter for each detection period and a separate parameter for each survival interval, except that the final detection probability and final survival probability cannot be logically separated from each other.
- Models 2 and 3 (the "hybrid models") allow either the detection probabilities (Model 2) or the survival probabilities (Model 3) are allowed to vary as in the full model, while the other set of parameters is as in the parsimonious model.



Figure 1. Parameter structure for the mark-recapture models. Shaded survey periods and parameters apply only to Yale data. In Model 4, the parameters $\phi_{2015t,2015a}$ and p_{2015a} are not distinguishable, and so represent only one degree of freedom.

The relative performance of the models was assessed with the Akaike Information Criterion (AIC). Bayesian posterior-means and credibility intervals are often easier to interpret than maximum-likelihood estimates and confidence intervals. The various tables below include values for these generated by the Markov-chain Monte-Carlo option in MARK, using the default values for priors.

		Sw	vift				
model	df	AIC	ΔΑΙΟ	model	df	AIC	ΔΑΙΟ
1	3	702	35	1	4	1761	18
2	13	667	0	2	11	1748	5
3	12	726	59	3	10	1756	14
4	23	673	7	4	15	1743	0

Table 4. Comparison of models by Akaike Information Criteron (AIC; smaller values indicate better fits).

Although Model 1 is the poorest performing of the Swift models, and the second-poorest of the Yale models, it is still of interest because of its simplicity.

The estimated values for the parameters of these models are shown in Tables 5 and 6. These are generally consistent with those reported in previous years. In the case of Yale, the parameter ϕ_{at} is not well estimable by maximum likelihood, and is set to 1.0 by the MARK software; one way to interpret this is that only the product $\phi_{ta} \times \phi_{at}$ should be considered meaningful for this model.

	ML	estimates	95% Conf. Interval		Posterior statistics		95% Cred. Interval	
Parameter	Mean	Std. Dev.	Lower	Upper	Mean	Std. Dev.	Lower	Upper
ϕ_{ta}	0.622	0.033	0.555	0.684	0.644	0.040	0.572	0.727
ϕ_{at}	1.000	0.000	0.000	1.000	0.945	0.042	0.858	0.998
p_a	0.406	0.044	0.323	0.494	0.401	0.043	0.319	0.485
p_t	0.189	0.030	0.137	0.256	0.197	0.031	0.137	0.261

Table 5. Summary of results for Yale Reservoir, Model 1.

Table 6. Summary of results for Swift Reservoir, Model 1.

	ML	estimates	95% Conf. Interval		Posterior statistics		95% Cred. Interval	
Parameter	Mean	Std. Dev.	Lower	Upper	Mean	Std. Dev.	Lower	Upper
ϕ_{ta}	0.791	0.048	0.682	0.870	0.823	0.042	0.749	0.911
ϕ_{at}	0.969	0.074	0.198	1.000	0.920	0.052	0.816	0.999
p_a	0.357	0.026	0.308	0.409	0.350	0.026	0.300	0.403
p_t	0.175	0.020	0.140	0.217	0.180	0.019	0.143	0.215

Model 2 is currently the best performing of the Yale models, and the second-best performing of the Swift models. We interpret this as consistent with the idea that the "survival" parameters are fairly consistent from year to year (Table 7 and 8). As with Model 1, the MARK software is not able to estimate the parameter ϕ_{at} in the Yale data.

	ML	estimates	es 95% Conf. Interval Posterior statistics		erior statistics 95% Cred. Inter		d. Interval	
Parameter	Mean	Std. Dev.	Lower	Upper	Mean	Std. Dev.	Lower	Upper
ϕ_{ta}	0.590	0.035	0.520	0.656	0.613	0.044	0.531	0.703
ϕ_{at}	1.000	0.000	1.000	1.000	0.926	0.055	0.821	0.999
p_{2009t}	0.592	0.356	0.075	0.963	0.610	0.234	0.196	0.988
p_{2010t}	0.283	0.129	0.101	0.579	0.329	0.131	0.097	0.588
p_{2010a}	0.236	0.100	0.094	0.479	0.251	0.095	0.089	0.445
p_{2011t}	0.442	0.111	0.247	0.656	0.476	0.107	0.271	0.685
p_{2011a}	0.333	0.091	0.183	0.526	0.339	0.088	0.177	0.509
p_{2012t}	0.151	0.065	0.062	0.324	0.178	0.069	0.059	0.314
p_{2012a}	0.153	0.059	0.069	0.307	0.168	0.060	0.062	0.285
p_{2013t}	0.128	0.055	0.053	0.277	0.154	0.059	0.051	0.267
p_{2013a}	0.543	0.089	0.371	0.705	0.540	0.085	0.376	0.703
p_{2014t}	0.252	0.071	0.139	0.413	0.278	0.075	0.149	0.440
p_{2014a}	0.518	0.100	0.329	0.702	0.523	0.095	0.345	0.711
p_{2015t}	0.000	0.000	0.000	0.000	0.035	0.028	0.001	0.091
p_{2015a}	0.764	0.136	0.424	0.934	0.772	0.111	0.564	0.973

 Table 7. Summary of survival estimates for Yale Reservoir, Model 2.

	ML	estimates	95% Conf. Interval		Posterior statistics		95% Cred. Interval	
Parameter	Mean	Std. Dev.	Lower	Upper	Mean	Std. Dev.	Lower	Upper
ϕ_{ta}	0.815	0.053	0.689	0.897	0.820	0.048	0.730	0.916
ϕ_{at}	0.895	0.072	0.654	0.974	0.884	0.059	0.769	0.992
p_{2011a}	0.248	0.047	0.168	0.350	0.251	0.046	0.161	0.341
p_{2012t}	0.182	0.043	0.112	0.280	0.188	0.042	0.115	0.278
p_{2012a}	0.217	0.038	0.152	0.301	0.220	0.037	0.146	0.290
p_{2013t}	0.209	0.039	0.143	0.296	0.215	0.039	0.143	0.295
p_{2013a}	0.394	0.045	0.310	0.486	0.396	0.045	0.310	0.483
p_{2014t}	0.218	0.038	0.152	0.301	0.224	0.038	0.155	0.300
p_{2015a}	0.465	0.050	0.371	0.563	0.469	0.049	0.381	0.567
p_{2015t}	0.149	0.032	0.096	0.223	0.156	0.032	0.095	0.216
p_{2015a}	0.432	0.052	0.335	0.536	0.437	0.051	0.341	0.539

Table 8. Summary of survival estimates for Swift Reservoir, Model 2.

Under the assumption that the probability that a migrating fish will be detected at least once by at least one antenna is close to 1, the parameter p_a can be interpreted as the probability that a random fish will make a spawning migration. The p_a estimates from Model 1 and the geometric mean of the $p_{20\cdots a}$ estimates from Model 2 are 0.41 and 0.37 for Yale, respectively. The corresponding estimates for Swift are 0.36 and 0.34, respectively.

The quantity $\phi_{ta} \times \phi_{at}$ has a natural interpretation as the probability that a fish will survive from one year to the next. For Yale, the product of the Bayesian estimates for these parameters is 0.61 for Model 1 and 0.57 for Model 2. The corresponding values for Swift are 0.76 and 0.72.

The new estimates are consistent with those from previous years, as illustrated by figures 2 and 3 below. The bounds on the estimates of the "survival" parameters ϕ_{ta} and ϕ_{at} continue to tighten a little as the amount of data increases. The "detection" parameters $p_{20 \cdot a}$ and $p_{20 \cdot t}$ benefit less from this effect because very few fish are detected more than twice.



Figure 2. Bayesian parameter estimates for Model 2 for Yale Reservoir system. The diamonds mark the posterior mean, and the vertical bars span 95% credibility intervals. In each pair of estimates, the one on the right is based on all the data through 2015; the others are the estimates for the same parameters from the previous reports.



Figure 3. Bayesian parameter estimates for Model 2 for Swift Reservoir system. The diamonds mark the posterior mean, and the vertical bars span 95% credibility intervals. In each pair of estimates, the one on the right is based on all the data through 2015; the others are the estimates for the same parameters from previous reports.

Because Model 4 has so many degrees of freedom, we have not reported details for this model in previous years. However, it does yield estimates of the "survival" parameters $\phi_{\cdot t \cdot a}$ and $\phi_{\cdot a \cdot t}$ for individual years, and in particular, year-specific estimates of the product $\phi_{\cdot t \cdot a} \times \phi_{\cdot a \cdot t}$.

3.1 Summary

A summary of the 2015 results is presented in Table 9. The estimates are posterior means, and the intervals are either 95% HPC intervals or (in the case of the derived annual survivals) 95% confidence intervals. The central challenge in summarizing results is that, as a matter of logic, a mark-recapture model cannot separate the capture probability at the final sample and the survival over the final interval between samples, without some additional constraints. To summarize the data in 2015, the two survival parameters are from a model in which the detection parameters are assumed to be the same in all years, and the two detection parameters are from a model in which the survival parameter, and can therefore be derived from the full model, in which all the survival and detection probabilities are unconstrained). Overall, despite challenges reliably separating survival and detection parameters there is a general trend of an increase in survival over time (figures 4 and 5).

Table 9. Summary of 2015 results.

Parameter	Interpretation	Estimate	95% Interval					
Yale Reservoir								
Model 4 $\phi_{2014t2014g} \times \phi_{2014g2015t}$	Survival from 2014 reservoir-sampling period to 2015 reservoir-sampling period	0.586	0.305-0.868					
Model 3 $\phi_{2014a2015t}$	Survival from 2014 antenna-detection period to 2015 reservoir-sampling period	0.794	0.560-0.996					
Model 3 $\phi_{2015t2015a}$	Survival from 2015 reservoir-sampling period to 2015 antenna-detection period	0.926	0.811-0.998					
$\begin{array}{c} \text{Model 2} \\ p_{2015a} \end{array}$	Probability of making a spawning excursion in 2015	0.772	0.564-0.993					
	Swift Reservoir							
Model 4 $\phi_{2014t2014a} \times \phi_{2014a2015t}$	Survival from 2014 reservoir-sampling period to 2015 reservoir-sampling period	0.841	0.696–0.986					
Model 3 $\phi_{2014a2015t}$	Survival from 2014 antenna-detection period to 2015 reservoir-sampling period	0.922	0.817-0.999					
Model 3 $\phi_{2015t2015a}$	Survival from 2015 reservoir-sampling period to 2015 antenna-detection period	0.891	0.754–0.997					
Model 2 <i>p</i> _{2015<i>a</i>}	Probability of making a spawning excursion in 2015	0.437	0.341-0.539					



Figure 4. Estimates of the "survival" parameters of Model 4 for Yale Reservoir system. The open diamonds mark the posterior means for the $\phi_{\cdot t \cdot a}$ and $\phi_{\cdot a \cdot t}$, and the vertical dotted bars span 95% credibility intervals. The filled diamonds mark the products $\phi_{\cdot t \cdot a} \times \phi_{\cdot a \cdot t}$, which can be interpreted as annual survivals, and the solid vertical bars extend to ± 1.96 °, where \hat{s} is an estimate of the standard deviation derived from the posterior standard deviations of the individual terms by ignoring covariance.



Figure 5. Estimates of the "survival" parameters of Model 4 for Swift Reservoir system. The open diamonds mark the posterior means for the $\phi_{.t\cdot a}$ and $\phi_{.a\cdot t}$, and the vertical dotted bars span 95% credibility intervals. The filled diamonds mark the products $\phi_{.t\cdot a} \times \phi_{.a\cdot t}$, which can be interpreted as annual survivals, and the solid vertical bars extend to $\pm 1.96\hat{s}$, where \hat{s} is an estimate of the standard deviation derived from the posterior standard deviations of the individual terms by ignoring covariance.

4 References

Burnham, K.P., and D. R. Anderson. 1998. *Model Selection and Inference: A practical information-theoretic approach*. Springer-Verlag, New York.

White, G. C., and K. P. Burnham. 1999. Program MARK: survival estimation from populations of marked animals. *Bird Study* 46 Supplement: 120-138.

APPENDIX B

2015 Lewis River Bull Trout Rapid Response Genetic Analysis and Genetic Estimation of Spawner Abundance



U.S. Fish and Wildlife Service

Rapid Response Genetic Analysis and Genetic Estimation of Spawner Abundance of Bull Trout Collected in the Lewis River, WA Final Report

January 2016 By Brice Adams Abernathy Fish Technology Center Longview, Washington Jeremiah Doyle

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Rapid Response Genetic Analysis and Genetic Estimation of Spawner Abundance of Bull Trout Collected in the Lewis River, WA

2015 Annual Report

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Background

The maintenance of migratory corridors and migratory life history type individuals has been recognized as an important factor for conserving bull trout populations (Rieman and Dunham 2000; Rieman and Allendorf 2001). Migratory individuals provide a means for recolonization of extirpated populations and gene flow among small populations, enabling persistence in dynamic landscapes and counteracting the loss of fitness caused by inbreeding (Northcote 1997; Reiman and Allendorf 2001). Migratory corridors utilized by bull trout have been extensively fragmented by the construction of dams that lack adequate fish passage facilities, and fragmentation of migratory corridors has been recognized as a threat to the persistence of many bull trout populations throughout the species range (Rieman et al. 1997; U.S. Fish and Wildlife Service [USFWS] 2002). Previous studies examining the effects of migratory barriers on bull trout populations have documented reduced genetic variation in populations isolated above barriers (Whiteley et al. 2006; DeHaan et al. 2011a) and entrainment of bull trout through dams (Neraas and Spruell 2001; Whiteley et al. 2006; DeHaan et al. 2011b).

The Lewis River is a Columbia River tributary in Washington which contains one of two bull trout populations in the USFWS Lower Columbia Critical Habitat Unit (USFWS 2010). Bull trout spawning has been documented in three main tributaries within the Lewis River system: Cougar Creek, Pine Creek, and Rush Creek (Figure 1). Four dams constructed on the mainstem Lewis River fragment bull trout habitat and prevent fish that migrate downstream through the dams from returning to spawning habitats. Cougar Creek is located above Yale Dam and is separated from Pine and Rush creeks by two dams; Swift No.1 and No. 2 (Figure 1). Each year bull trout are collected in the tailrace of Yale Dam and in the Swift Bypass Reach (the historic Lewis River channel) below Swift No. 1 Dam. The origins of these individuals are unknown but it is presumed that fish below Yale Dam originate in tributaries above the dam since spawning has not been observed below the dam, and it is presumed that some portion of the fish collected in the Swift Bypass Reach originate in Pine and Rush Creeks. Re-establishing migratory connectivity in the system is important for allowing highly fecund migratory fish to contribute to numerically depressed spawning populations and for maintaining gene flow among spawning populations and adequate effective population sizes.

Upstream transport of bull trout collected below Lewis River dams was suggested as a means to re-establish migratory connectivity in the system; however, there were concerns with simply passing all fish collected below the dams upstream. Cougar Creek is a relatively small population and passing fish from the Swift Bypass Reach to the area above Swift No. 1 Dam

may result in the transport of fish from Cougar Creek away from their natal spawning habitat. Additionally, fish collected below Yale Dam could have originated above Yale Dam in Cougar Creek or in tributaries above Swift No. 1 Dam (Pine and Rush creeks). It was recognized that information on the tributary of origin for fish collected below the dams would be helpful for guiding fish transport decisions. To help address this issue, the USFWS Abernathy Fish Technology Center (AFTC) conducted a genetic analysis of bull trout collected from Cougar, Pine, and Rush creeks as well as fish collected below Yale Dam and in the Swift Bypass Reach. Results of this analysis showed that genetically distinct local spawning populations exist in each of the three tributaries and that genetic population assignments could be used to identify the most likely local spawning population of origin for unknown individuals (DeHaan and Adams 2011).

Based on the results of these analyses, in 2011 PacifiCorp initiated an effort to transport bull trout collected below the Lewis River dams upstream. The goal of this program was to use real-time genetic assignment analysis (i.e. "rapid response") to determine the local spawning population of origin for bull trout collected below the dams and to use this information to help inform upstream transport decisions.

The number of bull trout spawning in the Swift Reservoir tributaries of Pine and Rush creeks each year is not well understood. These estimates of spawner abundance are important in developing effective conservation and management plans for Lewis River bull trout. Beginning in 1996 PacifiCorp and various state and federal partners (Doyle 2014) initiated annual surveys to track upstream passage of adult bull trout into Pine and Rush Creeks. They expanded this by adding annual bull trout redd surveys within P8, a tributary to Pine Creek, in 2010. In 2014 PacifiCorp contacted AFTC to provide a complementary genetic estimate of spawner abundance to current in-stream methods. Genetic monitoring to estimate spawner contribution can be a more effective way to look at the true reproductive contribution of individuals to a population of concern (Schwartz et al. 2007). This report summarizes this analysis of effective number of breeders (N_b) for bull trout in Cougar, Pine and Rush Creeks, as well as the fourth year of the rapid response genetic analysis conducted by AFTC, and the analysis of additional bull trout added to the population assignment baseline.

Materials and Methods

For rapid response analysis, PacifiCorp biologists collected adult bull trout below Yale Dam and in the Swift Bypass Reach on one or two days per week from May 27 through July 27, 2015. A small (approximately 1cm²) tissue sample was taken from all previously un-sampled

bull trout captured, and delivered to AFTC personnel, typically within 24 hours. Adult bull trout were held at the Washington Department of Fish and Wildlife's Merwin Fish Hatchery below Merwin Dam pending genetic results.

As soon as fin clips from adult bull trout captured below the Lewis River dams were delivered to AFTC, DNA was extracted using a modified Chelex extraction protocol (Miller and Kapuscinski 1996). All individuals were genotyped at the following 16 microsatellite loci: *Omm1128, Omm1130* (Rexroad et al. 2001), *Sco102, Sco105, Sco106, Sco107, Sco109,* (Washington Dept. of Fish and Wildlife *unpublished*), *Sco200, Sco202, Sco212, Sco215, Sco216, Sco218, Sco220* (DeHaan and Ardren 2005), *Sfo18* (Angers et al. 1995) and *Smm22* (Crane et al. 2004). Polymerase chain reactions (PCR) were conducted in 10µL volumes containing 2µL of template DNA, 5µL of 2X Qiagen multiplex PCR master mix (final concentration of 3mM MgCl₂), and 0.2µL of oligonucleotide PCR primer mix. PCR conditions were as follows: initial denaturation at 95°C for 15 minutes, then 29 cycles of 95°C for 30 seconds, 90 seconds at the multiplex specific annealing temperature, and 60 seconds primer extension at 72°C, followed by a final extension at 60°C for 20 minutes. Following PCR, capillary electrophoresis was conducted on an ABI 3130x1 Genetic Analyzer (Applied Biosystems Inc., Foster City, CA) following the manufacturer's protocols. All fish collected for rapid response analysis were genotyped two times to ensure consistency of results.

The baseline dataset used for genetic assignments consisted of fish from Cougar (n = 69), Pine (n=105), and Rush (n=72) creeks. The program GENECLASS2 (Piry et al. 2004) was used to assign unknown origin individuals collected below Lewis River Dams to their most likely population of origin. Each unknown origin individual was assigned to its first and second most likely local spawning population of origin, and the likelihood the individual originated in these two local populations and the probability of observing the individual's genotype in each local population were also reported. A description of the methods used for the likelihood and probability calculations can be found in Piry et al. (2004). Once genetic assignments were calculated, a report documenting the date and time samples were received at AFTC, the date and time results were sent, and for each individual, the individual's PIT (passive integrated transponder) tag number, collection location, first and second most likely local population of origin, the likelihood score and probability for each genetic assignment, and transport suggestions (Yale or Swift reservoir) was e-mailed to PacifiCorp biologists. An example report can be found in Appendix 1. Once PacifiCorp biologists received the genetic assignment data, this information was used to inform fish transport decisions. Bull trout that assigned to either the

Rush or Pine creek local population with a likelihood score greater than 99.0, or with a combined likelihood score for Pine and Rush creeks greater than 99.0, were transported upstream for release into Swift Reservoir. Bull trout that did not meet these criteria were transported and released into Yale Reservoir.

Fin clips from age-0 bull trout were collected by PacifiCorp staff in 2015 from Cougar Creek (n=75), Pine Creek (n=33), P8 (a Pine Creek tributary, n=57), and Rush Creek (n=50) in order to estimate the effective number of breeders within those systems. Samples were genotyped using the methods described above except that DNA was extracted from fin clips using Qiagen DNeasy96 extraction kits (Qiagen Inc., Valencia, CA). Age-0 bull trout from Pine Creek and P8 genotyped in 2015 were combined for all analyses (DeHaan and Adams 2011). All local spawning populations were then tested for departures from Hardy-Weinberg equilibrium (HWE) expectations using exact tests implemented in the program GENEPOP v4.0.7 (Raymond and Rousset 1995). GENEPOP was also used to test populations for evidence of linkage disequilibrium (LD: non-random association among alleles). Populations were examined for number of full sibling families and number of individuals in each full sibling family using COLONY v2.0 (Wang 2004). Following protocols established in DeHaan and Adams (2011), we retained up to three full siblings from each family and removed all other siblings. Once full siblings had been removed, we conducted HWE and LD tests on the revised dataset.

We used the program NeEstimator v2 (Do et al. 2014) to estimate the effective population size (N_e) for age-0 samples from Pine and Rush Creeks based on linkage disequilibrium (Waples 2006). When this estimate is applied to individuals collected in a single cohort it allows us to estimate the effective number of breeders that produced the cohort (N_b ; Waples and Teel 1990). To minimize the effect of rare alleles on our estimates we selected P_{crit} =0.02 (Waples and Do 2010). Upper and lower 95% confidence intervals were estimated using the jackknife re-sampling method. To assess the role that large family groups within the dataset had on calculating N_b we made estimates with the original data set (including all age 0 fish) and with the reduced family data (removing all but three individuals assigned to a family group). Estimates of N_b were also obtained during the process of assigning individuals to family groups in Colony.

Genetic data from age-0 bull trout from Cougar, Pine and Rush Creeks were combined with previously genotyped samples from Cougar, Pine and Rush Creeks and added to the baseline dataset. We conducted leave-one-out assignment tests to examine the accuracy of the updated baseline for assigning unknown origin fish to their most likely local population of

origin. Each baseline individual was removed from the population it was collected from and treated as an unknown, the allele frequencies for all populations were then re-calculated, and the unknown fish was assigned to its most likely population. The number of individuals assigned to the local population they were collected from (presumably their natal tributary) provides a measure of assignment accuracy. Leave-one-out tests were conducted using GENECLASS2 and we determined the likelihood for each population assignment and the probability of observing that individual's genotype in the assigned population.

Results and Discussion

2015 Rapid Response Analysis

During 2015, 20 bull trout were collected for rapid response genetic analysis; all 20 in the Swift Bypass Reach. All samples were processed within 24 hours of receipt at AFTC. Of the 20 samples processed, 15 of them assigned to Cougar Creek as their most likely population of origin (Table 1). The remaining five samples assigned to Pine Creek as their most likely population of origin, however one fish did not meet the required likelihood score of 99.0 in order to be transported to Swift Reservoir. Likelihood values for population assignments ranged from 96.68 to 100.00 and probability scores for genetic assignments ranged from 0.061 to 0.996 (Table 1). Genotypes for all 20 rapid response bull trout analyzed in 2015 can be found in Appendix 2.

Previous genetic studies have documented entrainment of adult bull trout through mainstem dams (Neraas and Spruell 2001; DeHaan et al. 2011b) and data from this study show that entrainment of adult bull trout occurs at the Lewis River dams as well. Large migratory bull trout are highly fecund (Fraley and Shepard 1989; Al-Chokhachy and Budy 2008) and these fish can contribute significant numbers of offspring to demographically depressed populations. Prior to 2011, bull trout that migrated downstream through the Lewis River dams were lost from their natal spawning populations. Upstream transport of fish collected below the Lewis River dams greatly benefits populations above the dams by helping to maintain the number of spawning adults in these populations which in turn results in greater numbers of offspring produced.

All of the fish collected in 2015 were collected in the Swift Bypass Reach and genetic assignments showed that individuals originated from both above and below the two Swift dams. Simply passing all of these fish above Swift No. 1 Dam may have resulted in several fish from Cougar Creek potentially losing access to their natal spawning habitat. Cougar Creek is considered to be a relatively small local spawning population, and the loss of several spawning adults from Cougar Creek could have a negative effect on the long term persistence of this local

population. Clearly the use of genetic data to guide fish transport decisions benefits not only the Pine and Rush Creek local populations upstream of the dams that have lost migratory adults due to entrainment, but also benefits the local spawning population in Cougar Creek by helping to maintain the number of spawning adults.

COLONY Analysis

Two loci, Sco 215 and Sfo18, were fixed for a single allele in all Cougar, Pine, and Rush Creek age-0 bull trout. Cougar and Rush Creek samples deviated from Hardy-Weinberg equilibrium at Sco109; in addition Cougar Creek deviated at Omm1128, while Rush Creek deviated at Sco202. Ten pairs of loci (out of 91 total) exhibited evidence of linkage in Cougar Creek, four pairs showed evidence in Rush Creek, and four pairs of loci showed evidence in Pine Creek. Results of the linkage disequilibrium tests were consistent with collections of closely related individuals (i.e., full siblings). Results of the COLONY analysis indicated a large number of related individuals in the age-0 samples collected from Cougar and Pine creeks (Appendix 3). In Cougar Creek, there were two large full-sibling families with seven individuals, two full-sibling families with five individuals and several smaller families with three or four individuals. In Pine Creek there was one large full-sibling family with eight individuals, one full-sibling family with six individuals and one full-sibling family with four individuals. In Rush Creek there were no large full-sibling families detected in the collection. As indicated above, we removed all but three individuals from each full-sibling family prior to adding these individuals to the baseline dataset. After full-siblings were removed from the dataset, four pairs of loci (out of 91 total) exhibited linkage in Cougar Creek, three pairs of loci showed evidence in Rush Creek, and two pairs of loci showed evidence in Pine Creek.

Effective number of breeders - N_b

Estimates of effective number of breeders were greatest in Rush Creek ($N_b=23.0$; 95% C.I.=18.0-29.8 using the N_b estimator with reduced families), lower in Pine Creek ($N_b=19.5$; 95% C.I.=15.2-25.1), and lowest in Cougar Creek ($N_b=18.7$; 95% C.I.=15.2-23.2). Overlap in 95% C.I. indicated that these observed differences were not significant. Estimated values of N_b varied with estimation method and number of individuals used per family (Table 2), although they consistently estimated a smaller N_b for Cougar Creek when compared to Pine and Rush Creeks. These estimates provide a baseline to track how estimates of N_b fluctuate on an annual basis and can provide an indicator for the health of bull trout populations with long term

monitoring (Luikart et al 2010). In addition these data can provide a comparison with how redd counts and counts of spawning adults in these two tributaries relate to estimates of N_b . It is important to note that since these estimates of the effective number of breeders were generated using a single cohort of individuals, they are presumably lower than the true N_e (Luikart et al. 2010; Waples and Do 2010). General guidelines have been suggested for minimum viable levels of N_e with a minimum of 50 individuals suggested as necessary to avoid the short term effects of inbreeding and N_e of 500 to help ensure long-term population persistence (Franklin 1980). Although these are just general guidelines and true minimum N_e values vary among species and populations, the relatively low estimates observed for the two Lewis River bull trout populations suggest that these small populations may face increased risks from inbreeding and genetic drift in the short-term. It will be interesting to compare these initial estimates to estimates from future years to determine if N_b estimates for these two local populations are consistently low.

Baseline Analysis

Two loci, *Sco215* and *Sfo18*, were fixed for a single allele in all three baseline populations. These two loci were primarily included in genotyping efforts to identify hybrid individuals (no hybrid fish were observed in this study) and to facilitate comparisons with other studies. Cougar Creek and Rush Creek deviated from Hardy-Weinberg equilibrium expectations at the locus Sco109 due to a deficiency of heterozygotes. All other loci conformed to Hardy-Weinberg equilibrium expectations in all three populations. Four pairs of loci (out of 91 total) exhibited evidence of linkage in Cougar Creek, three pairs of loci showed evidence of linkage in Rush Creek, and four pairs of loci showed evidence of linkage in Pine Creek. Nearly all (99.3%) of the baseline fish were assigned to the local spawning population that they were collected from in the leave-one-out assignment tests. The exceptions were two fish collected in Cougar Creek one of which assigned to Pine Creek and the other to Rush Creek; and one fish that was collected in Pine Creek and assigned to Cougar Creek. Likelihood scores for the three incorrectly assigned fish were 85.179, 85.372 and 97.262, respectively (Figure 2a). Likelihood scores for the correctly assigned fish ranged from 75.664 to 100.0, and 97.4% of baseline individuals had a likelihood score greater than 95.0% (Figure 2a). Probability values for the incorrectly assigned fish were 0.090 and 0.795 (Figure 2b). Probability values for the correctly assigned fish ranged from 0.000 to 0.999 (Figure 2b).

The likelihood and probability values did not change considerably from the previous baseline dataset, therefore the likelihood score criteria developed for making transport decisions

should still be appropriate. Although probability values for some correctly assigned fish remained low, they were consistent with those in years past (DeHaan and Adams 2011; DeHaan and Adams 2012) and continued baseline collection efforts in the future may help to further improve the robustness of genetic assignments.

Data Management Plan

Raw (genotype) data generated in the course of the work described here have been archived in the U.S. Fish and Wildlife Service Abernathy Fish Technology Center Progeny Database.

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References

- Al-Chokhachy, R. and P. Budy. 2008. Demographic characteristics, population structure, and vital rates of a fluvial population of bull trout in Oregon. Transactions of the American Fisheries Society 137:1709–1722.
- Angers, B., L. Bernatchez, A. Angers, and L. Desgroseillers. 1995. Specific microsatellite loci for brook char reveal strong population subdivision on a microgeographic scale. Journal of Fish Biology 47(supplement A):177-185.
- Crane P. A., C. J. Lewis, E. J. Kretschmer, S. J. Miller, W. J. Spearman, A. L. DeCicco, M. J. Lisac, and J. K. Wenburg. 2004. Characterization and inheritance of seven microsatellite loci from Dolly Varden, *Salvelinus malma*, and cross-species amplification in Arctic Char, *S. Alpinus*. Conservation Genetics 5:737-741.
- DeHaan, P. W. and B. Adams. 2011. Analysis of genetic variation and assessment of population assignment methods for Lewis River bull trout. Final Report to the U.S. Fish and wildlife Service, Lacey, WA. June 28, 2011.
- DeHaan, P. W. and B. Adams. 2012. Rapid response genetic analysis of bull trout collected in the Lewis River, WA. Final Annual Report to PacifiCorp, February 13, 2013.
- DeHaan, P.W. and W.R. Ardren. 2005. Characterization of 20 highly variable tetranucleotide microsatellite loci for bull trout (*Salvelinus confluentus*) and cross-amplification in other *Salvelinus* species. Molecular Ecology Notes 5:582-585.
- DeHaan, P. W., S. J. Brenkman, B. Adams and P. Crain. 2011a. Genetic population structure of Olympic Peninsula bull trout populations and implications for Elwha Dam removal. Northwest Science 85:463-475.
- DeHaan, P. W, S. R. Bernall, J. M. DosSantos, L. L. Lockard, and W. R. Ardren. 2011b. Use of genetic markers to aid in re-establishing migratory connectivity in a fragmented metapopulation of bull trout (*Salvelinus confluentus*). Canadian Journal of Fisheries and Aquatic Science. 68: 1952–1969.
- Do, C., R.S. Waples, D. Peel, G.M. Macbeth, B.J. Tillet, and J.R. Ovenden. 2014. NeEstimator V2: re-implementation of software for the estimation of contemporary effective population size (Ne) from genetic data. Molecular Ecology Resources 14(1):209-214.
- Doyle, J. 2014. Lewis River Bull Trout (*Salvelinus confluentus*) Annual Operations Plan, PacifiCorp Energy 2014. January 2014.

- Fraley, J. J. and B. B. Shepard. 1989. Life history, ecology and population status of migratory bull trout (*Salvelinus confluentus*) in the Flathead Lake and River System, Montana. Northwest Science 63:133-143.
- Franklin, I. R. 1980. Evolutionary changes in small populations. Pages 135-149 in M. E. Soule, and B. A. Wilcox, editors. Conservation Biology: an Evolutionary-Ecological Perspective. Sinauer, Sunderland, MA.
- Luikart, G., N. Ryman, D.A. Tallmon, M.K. Schwartz, and F.W. Allendorf. 2010. Estimation of census and effective population sizes: the increasing usefulness of DNA-based approaches. Conservation Genetics 11:355-373.
- Miller, L. M. and A. R. Kapuscinski. 1996. Microsatellite DNA markers reveal new levels of variation in northern pike. Transactions of the American Fisheries Society 125:971-997.
- Neraas, L.P. and P. Spruell. 2001. Fragmentation of riverine systems: the genetic effects of dams on bull trout (*Salvelinus confluentus*) in the Clark Fork River system. Molecular Ecology 10:1153-1164.
- Northcote, T.G. 1997. Potamodromy in Salmonidae- living and moving in the fast lane. North American Journal of Fisheries Management 17:1029-1045.
- Piry, S., A. Alapetite, J.-M. Cornuet, D. Paetkau, L. Baudouin, and A. Estoup. 2004. GENECLASS2: a software for genetic assignment and first-generation migrant detection. Journal of Heredity. 95:536-539.
- Raymond, M., and F. Rousset. 1995. GENEPOP (Version-1.2) Population-genetics software for exact tests and ecumenicism. Journal of Heredity 86(3):248-249.
- Rexroad, C.E., R. L. Coleman, A.M. Martin, W.K. Hershberger, and J. Killefer. 2001. Thirtyfive polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). Animal Genetics 32:317-319.
- Rieman, B.E. and F.W. Allendorf. 2001. Effective population size and genetic conservation criteria for bull trout. North American Journal of Fisheries Management 21:756-764.
- Rieman, B.E. and J.B. Dunham. 2000. Metapopulations and salmonids: a synthesis of life history patterns and empirical observations. Ecology of Freshwater Fishes 9:51-64.
- Rieman, B. E., D. C. Lee, and R. F. Thurow. 1997. Distribution, status, and likely future trends of bull trout within the Columbia River and Klamath River basins. North American Journal of Fisheries Management 17:1111-1125.
- Schwartz, M.K., G. Luikart, and R.S. Waples. 2007. Genetic monitoring as a promising tool for conservation and management. Trends in Ecology and Evolution 22:25-33.

- U.S. Fish and Wildlife Service (USFWS). 2002. Bull trout (*Salvelinus confluentus*) draft recovery plan for the Columbia and Klamath River distinct population segments. Portland Oregon. Available on-line at: www.fws.gov/pacific/bulltrout/.
- U.S. Fish and Wildlife Service (USFWS). 2010. Revised designation of critical habitat for bull trout in the coterminous United States, Final Rule. Federal Register 75:210(18 October 2010):63898-64070.
- Wang, J.L. 2004. Sibship reconstruction from genetic data with typing errors. Genetics 166(4):1963-1979.
- Waples, R.S. 2006. A bias correction for estimates of effective population size based on linkage disequilibrium at unlinked loci. Conservation Genetics 7:167-184.
- Waples, R.S. and C. Do. 2010. Linkage disequilibrium estimates of contemporary Ne using highly variable genetic markers: a largely untapped resource for applied conservation and evolution. Evolutionary Applications 3:244-262.
- Waples, R.C. and D.J. Teel. 1990. Conservation Genetics of Pacific Salmon I. Temporal changes in allele frequency. Conservation Biology 4(2):144-156.
- Whiteley, A.R., P. Spruell, B.E. Rieman, and F.W. Allendorf. 2006. Fine-scale genetic structure of bull trout at the southern limit of their distribution. Transaction of the American Fisheries Society 135:1238-1253.
| PIT Tag # | Genetic
ID | Date
Sampled | Date
Received | Collection Location | Most Likely
Population #1 | Likelihood
Score | Probability | Most Likely
Population #2 | Likelihood
Score | Probability | Transport
Suggestions |
|-----------|---------------|-----------------|------------------|---------------------|------------------------------|---------------------|-------------|------------------------------|---------------------|-------------|--------------------------|
| AC7762E | 2966-001 | 5/27/2015 | 5/27/2015 | Swift Bypass Reach | Cougar Creek | 99.996 | 0.701 | Rush Creek | 0.004 | 0.109 | Yale |
| AC77630 | 2966-002 | 5/27/2015 | 5/27/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.615 | Rush Creek | 0.000 | 0.020 | Yale |
| AC7762D | 2966-003 | 5/27/2015 | 5/27/2015 | Swift Bypass Reach | Pine Creek | 99.999 | 0.670 | Cougar Creek | 0.001 | 0.025 | Swift |
| AC7762F | 2966-004 | 5/27/2015 | 5/27/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.713 | Rush Creek | 0.000 | 0.000 | Yale |
| AC77639 | 2966-005 | 6/1/2015 | 6/2/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.876 | Rush Creek | 0.000 | 0.001 | Yale |
| AC7763A | 2966-006 | 6/1/2015 | 6/2/2015 | Swift Bypass Reach | Cougar Creek | 99.997 | 0.750 | Rush Creek | 0.003 | 0.138 | Yale |
| AC7763B | 2966-007 | 6/1/2015 | 6/2/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.597 | Rush Creek | 0.000 | 0.000 | Yale |
| AC7763C | 2966-008 | 6/1/2015 | 6/2/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.518 | Rush Creek | 0.000 | 0.004 | Yale |
| AC77648 | 2966-009 | 6/8/2015 | 6/9/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.992 | Rush Creek | 0.000 | 0.034 | Yale |
| AC7764A | 2966-010 | 6/8/2015 | 6/9/2015 | Swift Bypass Reach | Cougar Creek | 99.977 | 0.170 | Rush Creek | 0.023 | 0.026 | Yale |
| AC7764C | 2966-011 | 6/15/2015 | 6/16/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.761 | Rush Creek | 0.000 | 0.014 | Yale |
| AC7764D | 2966-012 | 6/15/2015 | 6/16/2015 | Swift Bypass Reach | Cougar Creek | 99.979 | 0.267 | Rush Creek | 0.021 | 0.040 | Yale |
| AC77655 | 2966-013 | 6/22/2015 | 6/23/2015 | Swift Bypass Reach | Pine Creek | 100.000 | 0.382 | Cougar Creek | 0.000 | 0.003 | Swift |
| AC7765A | 2966-014 | 6/22/2015 | 6/23/2015 | Swift Bypass Reach | Pine Creek | 96.675 | 0.919 | Cougar Creek | 3.323 | 0.761 | Yale |
| AC77663 | 2966-015 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Pine Creek | 99.858 | 0.786 | Rush Creek | 0.086 | 0.484 | Swift |
| AC77664 | 2966-016 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.061 | Pine Creek | 0.000 | 0.000 | Yale |
| AC77665 | 2966-017 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.996 | Rush Creek | 0.000 | 0.008 | Yale |
| AC77666 | 2966-018 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Cougar Creek | 99.999 | 0.904 | Rush Creek | 0.001 | 0.176 | Yale |
| AC77667 | 2966-019 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Cougar Creek | 100.000 | 0.482 | Rush Creek | 0.000 | 0.017 | Yale |
| AC77668 | 2966-020 | 7/27/2015 | 7/28/2015 | Swift Bypass Reach | Pine Creek | 100.000 | 0.456 | Cougar Creek | 0.000 | 0.006 | Swift |

Table 1. Collection information and genetic population assignments for 20 adult bull trout collected below Lewis River dams in 2015.

Table 2. Estimates of effective number of breeders (N_b ; 95% CI) in three Lewis River tributaries for multiple N_b estimators in 2015 (minimum allele frequencies of 0.02).

Tributary	N _b Estimator All Individuals	N _b Estimator Reduced Families	Colony
Cougar Creek	18.6 (15.5-22.3)	18.7 (15.2-23.2)	26.5 (16.0-45.5)
Pine Creek	16.5 (13.1-20.8)	19.5 (15.2-25.1)	31.5 (20.0-52.5)
Rush Creek	23.0 (18.0-29.8)	23.0 (18.0-29.8)	28.5 (17.0-49.0)



Figure 1. Lewis River system in Washington. Cougar, Pine, and Rush creeks are the primary bull trout spawning tributaries and are the three populations in the baseline dataset. Bull trout for rapid response analysis were collected below Yale Dam and in the Swift Bypass Reach.



Figure 2. Range of likelihood scores (Figure 2a) and probability values (Figure 2b) for genetic assignments of Lewis River bull trout during leave-one-out assignment tests. Grey bars (correct assignments) represent individuals that were assigned to the tributary they were collected from and black bars (incorrect assignments) represent individuals assigned to a tributary other than the one they were collected from.

Appendix 1. Sample rapid response report sent by AFTC to PacifiCorp biologists.



2015 Lewis River Bull Trout Rapid Response Genetic Population ID

Date: May 28, 2015

- To: Jeremiah Doyle PacifiCorps Energy 105 Merwin Village Ct. Ariel, WA 98603 380-225-4448 (office) 360-608-2410 (cell) Jeremiah.Doyle@PacifiCorp.com
- From: Brice Adams brice_adams@fws.gov

Date and Time	Samples Received:	5/27/15 14:05			Date and Time	e Results Sent:	5/28/15 14:05	
Sample ID	Collection Location	Most Likely Population #1	Likelihood Score	Probability	Most Likely Population #2	Likelihood Score	Probability	Transport Suggestions
2966-001	Swift Bypass Reach	Cougar Creek	99,996	0.701	Rush Creek	0.004	0.109	Yale
2966-002	Swift Bypass Reach	Cougar Creek	100.000	0.615	Rush Creek	0.000	0.020	Yale
2966-003	Swift Bypass Reach	Pine Creek	99,999	0.670	Cougar Creek	0.001	0.025	Swift
2966-004	Swift Bypass Reach	Cougar Creek	100.000	0.713	Rush Creek	0.000	0.000	Yale

Appendix 2. Genotypes at 16 microsatellite loci for 20 bull trout collected below Lewis River Dams in 2015. Question marks represent genotypes that could not be determined due to failed PCR amplification.

PIT Tag																
Number	Omm	1128	Omn	า1130	Sco1	02	Sco1	05	Sco1	06	Sco1	07	Sco1	09	Sco2	200
AC7762E	281	351	298	302	169	169	154	190	208	208	285	297	296	360	142	142
AC77630	281	331	298	298	166	169	190	190	152	208	289	293	296	296	142	142
AC7762D	331	331	298	298	169	173	154	202	152	180	285	297	?	?	142	155
AC7762F	351	351	290	298	166	169	190	190	208	208	297	297	360	360	142	142
AC77639	351	351	302	302	166	169	154	190	180	208	285	293	360	360	142	142
AC7763A	281	281	298	298	169	173	154	194	152	208	285	293	360	360	142	155
AC7763B	351	351	290	302	169	169	190	190	208	208	285	297	360	360	142	142
AC7763C	351	351	298	302	166	173	154	190	180	208	297	297	360	360	142	142
AC77648	331	331	298	302	166	169	154	190	208	208	293	297	360	360	142	142
AC7764A	281	281	298	298	166	173	190	194	152	180	293	293	360	360	130	155
AC7764C	281	331	298	302	166	166	190	194	208	212	285	293	296	296	142	155
AC7764D	331	355	298	302	166	173	190	194	212	212	285	297	296	296	142	155
AC77655	331	351	302	302	169	169	194	194	152	152	293	297	296	296	155	155
AC7765A	331	351	298	298	169	169	190	194	180	208	285	297	296	296	142	142
AC77663	331	331	298	302	169	173	154	194	180	208	285	285	296	296	142	142
AC77664	351	351	302	302	166	169	154	194	180	180	289	297	296	296	142	142
AC77665	281	351	298	302	166	169	154	194	208	208	285	297	?	?	142	142
AC77666	281	331	298	298	166	173	154	190	208	212	297	297	296	296	142	142
AC77667	281	281	302	302	173	173	190	194	208	212	285	285	?	?	142	142
AC77668	351	351	298	298	169	169	194	194	180	180	293	297	296	300	142	142

Appendix 2. Continued

PIT Tag																
Number	Sco2	202	Sco2	212	Sco2	215	Sco2	16	Sco2	218	Sco2	220	Sfo1	8	Smm	122
AC7762E	122	122	273	277	289	289	209	213	213	233	294	342	151	151	226	226
AC77630	122	130	273	300	289	289	213	213	209	233	294	294	151	151	222	246
AC7762D	130	130	273	300	289	289	213	213	197	233	342	394	151	151	222	226
AC7762F	122	130	273	273	289	289	213	213	197	213	294	294	151	151	226	246
AC77639	122	122	273	273	289	289	213	269	209	209	294	347	151	151	210	226
AC7763A	122	130	273	273	289	289	213	213	209	213	294	342	151	151	222	226
AC7763B	122	122	261	273	289	289	213	229	209	209	294	294	151	151	210	210
AC7763C	122	126	273	300	289	289	213	221	209	233	294	342	151	151	222	246
AC77648	122	122	273	273	289	289	213	213	209	209	294	342	151	151	210	246
AC7764A	122	122	273	277	289	289	209	213	209	213	294	294	151	151	222	226
AC7764C	122	126	273	273	289	289	213	213	209	233	294	294	151	151	210	222
AC7764D	122	122	273	273	289	289	213	213	213	233	294	294	151	151	218	222
AC77655	122	130	230	300	289	289	213	221	209	213	294	294	151	151	218	242
AC7765A	130	130	273	273	289	289	213	213	197	209	294	294	151	151	222	226
AC77663	126	130	273	300	289	289	213	213	197	209	294	342	151	151	222	242
AC77664	122	130	261	273	289	289	213	229	197	209	294	294	151	151	222	238
AC77665	122	122	273	273	289	289	213	213	209	213	294	294	151	151	210	222
AC77666	122	130	273	273	289	289	213	213	209	209	294	342	151	151	222	246
AC77667	122	122	273	273	289	289	213	213	209	233	294	294	151	151	218	246
AC77668	130	130	273	300	289	289	213	221	197	197	294	294	151	151	218	226

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Cougar	1	0.989	2966-061	2966-066	2966-081	2966-086	2966-088	2966-096	2967-041	
Cougar	2	1	2966-062							
Cougar	3	1	2966-063	2966-078	2966-089	2966-090	2967-040	2967-044	2968-084	
Cougar	4	1	2966-064							
Cougar	5	1	2966-065							
Cougar	6	1	2966-067	2966-069	2966-071	2966-082	2966-085			
Cougar	7	0.7468	2966-068	2968-083	2968-092	2968-093				
Cougar	8	1	2966-070							
Cougar	9	1	2966-072							
Cougar	10	0.7502	2966-073	2966-080	2967-036	2967-038	2967-039			
Cougar	11	1	2966-074							
Cougar	12	1	2966-075							
Cougar	13	1	2966-076							
Cougar	14	1	2966-077							
Cougar	15	1	2966-079							
Cougar	16	1	2966-083	2967-046	2968-091					
Cougar	17	0.989	2966-084	2966-095	2967-037					
Cougar	18	1	2966-087							
Cougar	19	0.6266	2966-091	2968-078						
Cougar	20	1	2966-092							
Cougar	21	1	2966-094	2968-071	2968-085					
Cougar	22	1	2966-097	2966-099	2968-100					
Cougar	23	0.932	2967-042	2967-045						
Cougar	24	1	2967-043							

Appendix 3. Results of COLONY analysis for age-0 bull trout collected from Cougar, Pine and Rush Creeks. Individuals assigned to each full sibling family are listed in the rows of the table.

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Cougar	25	1	2967-047							
Cougar	26	1	2968-069							
Cougar	27	0.9995	2968-070	2968-077						
Cougar	28	1	2968-072							
Cougar	29	1	2968-073							
Cougar	30	1	2968-074							
Cougar	31	1	2968-075							
Cougar	32	1	2968-076							
Cougar	33	1	2968-079							
Cougar	34	1	2968-080							
Cougar	35	1	2968-081							
Cougar	36	1	2968-082							
Cougar	37	1	2968-086							
Cougar	38	1	2968-087							
Cougar	39	1	2968-088							
Cougar	40	1	2968-089							
Cougar	41	1	2968-090							
Pine	1	0.9994	2967-007	2967-009	2967-019	2967-021	2967-022	2967-023	2968-033	2968-037
Pine	2	0.9947	2967-008	2967-013	2967-029	2967-033	2968-050	2968-055		
Pine	3	1	2967-010	2968-041	2968-049					
Pine	4	1	2967-011							
Pine	5	1	2967-012	2967-032	2967-035	2968-022				
Pine	6	1	2967-014							
Pine	7	1	2967-015							
Pine	8	1	2967-016							
Pine	9	1	2967-017							
Pine	10	1	2967-018							

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Pine	11	1	2967-020							
Pine	12	1	2967-024							
Pine	13	1	2967-025							
Pine	14	1	2967-026							
Pine	15	1	2967-027							
Pine	16	0.7595	2967-028	2968-001						
Pine	17	1	2967-030							
Pine	18	1	2967-031							
Pine	19	1	2967-034							
Pine	20	1	2968-002							
Pine	21	1	2968-003							
Pine	22	1	2968-004							
Pine	23	1	2968-005							
Pine	24	1	2968-006							
Pine	25	1	2968-007							
Pine	26	1	2968-008							
Pine	27	1	2968-009							
Pine	28	1	2968-010							
Pine	29	1	2968-011							
Pine	30	1	2968-012							
Pine	31	1	2968-013							
Pine	32	1	2968-014							
Pine	33	1	2968-015							
Pine	34	1	2968-016							
Pine	35	1	2968-017							
Pine	36	1	2968-018							
Pine	37	1	2968-020							

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Pine	38	1	2968-021							
Pine	39	1	2968-023							
Pine	40	1	2968-024							
Pine	41	1	2968-025							
Pine	42	1	2968-026							
Pine	43	1	2968-027							
Pine	44	1	2968-028							
Pine	45	1	2968-031							
Pine	46	1	2968-035							
Pine	47	1	2968-036							
Pine	48	1	2968-038							
Pine	49	1	2968-039							
Pine	50	1	2968-040							
Pine	51	1	2968-042							
Pine	52	1	2968-043							
Pine	53	1	2968-044							
Pine	54	1	2968-045							
Pine	55	1	2968-046							
Pine	56	1	2968-047							
Pine	57	1	2968-048							
Pine	58	1	2968-051							
Pine	59	1	2968-052							
Pine	60	1	2968-053							
Pine	61	1	2968-054							
Pine	62	1	2968-056							
Pine	63	1	2968-057							
Pine	64	1	2968-058							

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Pine	65	1	2968-059							
Pine	66	1	2968-060							
Pine	67	1	2968-061							
Pine	68	1	2968-062							
Pine	69	1	2968-063							
Pine	70	1	2968-064							
Pine	71	1	2968-065							
Pine	72	1	2968-066							
Rush	1	0.8419	2967-001	2967-086						
Rush	2	1	2967-002	2967-053						
Rush	3	1	2967-003							
Rush	4	0.9993	2967-004	2967-063	2967-087					
Rush	5	1	2967-049							
Rush	6	1	2967-050							
Rush	7	1	2967-051	2967-076						
Rush	8	1	2967-052							
Rush	9	1	2967-054							
Rush	10	1	2967-055							
Rush	11	1	2967-057							
Rush	12	1	2967-058							
Rush	13	1	2967-059							
Rush	14	1	2967-060							
Rush	15	1	2967-061							
Rush	16	1	2967-062							
Rush	17	1	2967-064							
Rush	18	1	2967-065							
Rush	19	1	2967-066							

Tributary	Full Sib Family #	Prob(Inc.)	Member-1	Member-2	Member-3	Member-4	Member-5	Member-6	Member-7	Member-8
Rush	20	1	2967-067							
Rush	21	1	2967-068							
Rush	22	1	2967-069							
Rush	23	1	2967-070							
Rush	24	1	2967-071							
Rush	25	1	2967-072							
Rush	26	1	2967-075							
Rush	27	1	2967-077							
Rush	28	1	2967-078							
Rush	29	1	2967-079							
Rush	30	1	2967-080							
Rush	31	1	2967-081							
Rush	32	1	2967-082							
Rush	33	1	2967-083							
Rush	34	1	2967-084							
Rush	35	1	2967-085							
Rush	36	1	2967-088							
Rush	37	1	2967-089							
Rush	38	1	2967-090							
Rush	39	1	2967-091							
Rush	40	1	2967-092							
Rush	41	1	2967-093							
Rush	42	1	2967-094							
Rush	43	1	2967-095							
Rush	44	1	2967-096							

U.S. Fish & Wildlife Service Abernathy Fish Technology Center Longview, Washington, 98632 Phone:360-425-6072 http://www.fws.gov/aftc/index.html



APPENDIX C

ACC Comments received by the due date of April 1, 2016 $\,$

Agency	Comment	Utility Response
WDFW	I suggest including Appendices (i.e., tables) with raw PIT tagging and recapture data (tag/recapture date, code, length, weight) and PIT array detections (Array Name, Code, Detection Date-Time). (pg 1 of Report)	Comment noted and changes will be incorporated into 2016 Annual Report
WDFW	The primary purpose of quantifying tag loss for mark- recapture estimators is to test one of the assumptions of the estimator (fish do not lose their marks) and to make adjustments in the number of marks available for recapture (or, in this case, resight) if necessary. So, the main interest is to determine the probability that a fish has lost both tags- the fish has lost it's mark. The probability that a fish has lost both floy tags is (# of single tagged fish observed/# of marked fish observed) squared. Using the 2015 as an example - the probability that a fish lost both tags using the Aug 27 data is $(1/7)^2 = 2.0\%$). For the entire data set, this number is 0.1%. No issues with tag loss. (pg 3)	Comment Noted
WDFW	Should include a statement that says assumptions of the estimator were most likely violated and this estimate is unreliable. (pg 4)	See Discussion Section within Report, violations of estimate are discussed in detail.
WDFW	USFWS calculates Nb (effective number of breeders) not Ne (Effective population size). From what I understand from USFWS geneticists, Ne can only be calculated after several years of data have been collected. In any event, Nb is reported in this section, not Ne. See my additional comment in Appendix B. (pg 8)	This is true in 2016 and for the interim until Ne can be calculated, at which time USFWS geneticists will in fact calculate Ne

WDFW	Include standard error (error bars). (pg 12)	SE will be included within these graphs in 2016
WDFW	We do not know detection efficiencies of these arrays. In 2014, P-Corp and WDFW ran arrays in Rush Creek. P-Corp array was only 22% as effective as WDFW's at detecting HDx tags and can not detect any FDX tags. Just how much can we trust these detections? (pg 13)	The Antenna at Rush Creek in 2014 experienced an unusually high level of power loss as well as unforeseen technical difficulties with the motherboard within the antenna itself, which led to very few days of operation and extremely low detection efficiencies, all of which was documented in the 2014 Annual Report. Head to head tests were also conducted at this same site the year prior in 2013 and both the antenna operated by WDFW and the HDX antenna interrogated the same tags throughout the season, all of which was also documented in the 2013 Annual Report.
WDFW	This assumes fish growth is a steady state. We know this is not true as fish growth is dependant on fish age and food supply. (pg 15)	Being that it is derived from linear regression based off of measured fish lengths during recapture from one year to the next, it is not assuming nor taking into consideration ideal or difficult growing seasons. It simply is plotting growth from one year to the next from measured recaptures. Empirical growth from one year to the next is plotted to give an expected average size-class increase based off of recapture iterations so as to estimate growth for fish previously handled and later interrogated at a PIT antenna.

WDFW	What do these #'s in yellow really mean. Ranges are pretty extensive. They do not take into account good and bad prey production years. Also a 600mm fish will grow much less than a 350mm fish during the same year. (pg 16)	Ranges are size-class and are extensive based off of low confidence in predicting exact growth from one year to the next. The estimator is simply meant to be a rough guide to what range of growth may have been expected from the previously handled fish. The numbers in yellow represent last empirical measurement and then estimated growth based off of last year encountered (1-3 years previous).
WDFW	Are these upstream detections or upstream and downstream detections? This question applies to all the "PIT Antenna Detections" graphs. Please include graphs for upstream movement timing (moving to the redd site) and downstream movement timing (finished spawning). (pg 18)	Graphs depict all unique detections on a given day. It would be difficult to infer what is simply an upstream migration to the spawning site, and what is simply a downstream migration after spawning has concluded. Bull trout do not make nice clean migrations such as salmon; many times an individual will make numerous migrations up to the spawning site and then back down again in very short periods of time throughout the spawning season. Trying to infer when migration spawning actually occurred would be impossible. Thus we have decided to simply show all migrations during each day. For many PIT antenna wired streams there is delineated an obvious peak upstream flux and peak downstream flux from which one could infer timing of pre and post spawn movement.
WDFW	Concerning Yale Tailrace Collection and Transport I think we are reaching a point of diminishing returns on this phase. I would favor putting the time into something more useful juvenile scale and genetic collections or redd surveys. (pg 26)	Agreed and comment noted. Unfortunately this activity is a currently a compliance obligation and as such some version of it needs to be performed annually. Per consultation with USFWS, it is being tapered back for 2016.

WDFW	I think this assumption needs to be validated as it effects the interpretation of the results (e.g., probability a fish will attempt to spawn in a given year). I looked at Pine detection efficiency by comparing individual detections in Pine and P8 between 2012 and 2015. The assumption of the comparison is that fish detected in P8 passed the Pine array and should have been detected. For example, if all fish detected in P8 were detected in Pine, the Pine array efficiency would be 100%. Pine array efficiency for each year was $2012 = 37.5\%$, $2013 = 53.1\%$, $2014 = 77.8\%$ and $2015 = 83.3\%$. First, in some years detection efficiency can be extremely low for this antenna (and possibly other antennae). Second, it is interesting that the pattern of increasing efficiency of the Pine array over time is very similar to the pattern of Pa in Figure 3. (pg 48)	Agreed, assumption needs to be validated. Care will be taken in 2016 to document and analyze capture efficiency. Array efficiency as you have attempted to analyze it does not work though for multiple reasons. We know that every year fish are upstream of our antenna within Pine and P8 creeks before we are physically able to install the antennas (due to high water). We know this because we get first detections from those fish moving in a downstream direction before we ever had any upstream detection from these same fish, so the direct comparison of Pine detections to P8 detections at this time will not work. We also have periods that are well documented within annual Reports of unexpected periodic power loss, at which time fish may transit past an antenna and not be detected. Efficiency has in fact increased since 2014 when we moved away from an antenna design of looping the wire only along the stream bottom, to one of looping the wire in a way that forces the fish to swim thru the loop and we've found it to be much higher in detection efficiency is by using raw redundant detections from the two synchronized antennae. Analyzing if one antenna detected a fish but the other at the same site did not. This would give a true measurement. This will indeed be done in 2016.
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WDFW	The link between Pa and the probability that a random fish will make a spawning migration needs to be further investigated. The result here, as I interpret it, suggests that 65% of mature bull trout (the vast majority of PIT tagged bull trout are mature) do not make a spawning run. This is contradictorily to data from the Lewis River and multiple published research papers. (pg 51)	This in fact is not contradictory to data from the Lewis River. In 2015, only 12 of 64 (19%) bull trout PIT tagged at Eagle Cliffs migrated past a PIT antenna in a spawning tributary to make a presumed spawning migration.
WDFW	Over the study period, detection effort (increases in PIT tags out and increases in array effort) and, potentially, dectection efficiency has increased. Is this coincidental, or does increased effort and detection efficiency effect the results. In either case, the author needs to address that effort has increased and how this may or may not effect the results. (pg 52)	Agreed, and comment noted. Care will be taken during 2016 Annual Report construction to take this into consideration.