

Regional Operational Plan No. ROP.CF.1J.2023.02

**Juvenile Abundance and Harvest of Unuk River
Chinook Salmon, 2022–2024**

by

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and

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March 2023

Alaska Department of Fish and Game

Divisions of Commercial Fisheries and Sport Fish



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Weights and measures (metric)		General		Mathematics, statistics	
centimeter	cm	Alaska Administrative Code	AAC	<i>all standard mathematical signs, symbols and abbreviations</i>	
deciliter	dL	all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.	alternate hypothesis	H_A
gram	g			base of natural logarithm	e
hectare	ha			catch per unit effort	CPUE
kilogram	kg	all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.	coefficient of variation	CV
kilometer	km			common test statistics	(F, t, χ^2 , etc.)
liter	L	at	@	confidence interval	CI
meter	m	compass directions:		correlation coefficient (multiple)	R
milliliter	mL	east	E	correlation coefficient (simple)	r
millimeter	mm	north	N	covariance	cov
		south	S	degree (angular)	$^\circ$
		west	W	degrees of freedom	df
Weights and measures (English)		copyright	©	expected value	E
cubic feet per second	ft ³ /s	corporate suffixes:		greater than	>
foot	ft	Company	Co.	greater than or equal to	≥
gallon	gal	Corporation	Corp.	harvest per unit effort	HPUE
inch	in	Incorporated	Inc.	less than	<
mile	mi	Limited	Ltd.	less than or equal to	≤
nautical mile	nmi	District of Columbia	D.C.	logarithm (natural)	ln
ounce	oz	et alii (and others)	et al.	logarithm (base 10)	log
pound	lb	et cetera (and so forth)	etc.	logarithm (specify base)	log ₂ , etc.
quart	qt	exempli gratia (for example)	e.g.	minute (angular)	'
yard	yd	Federal Information Code	FIC	not significant	NS
		id est (that is)	i.e.	null hypothesis	H_0
Time and temperature		latitude or longitude	lat or long	percent	%
day	d	monetary symbols (U.S.)	\$, ¢	probability	P
degrees Celsius	°C	months (tables and figures): first three letters	Jan, ..., Dec	probability of a type I error (rejection of the null hypothesis when true)	α
degrees Fahrenheit	°F	registered trademark	®	probability of a type II error (acceptance of the null hypothesis when false)	β
degrees kelvin	K	trademark	™	second (angular)	"
hour	h	United States (adjective)	U.S.	standard deviation	SD
minute	min	United States of America (noun)	USA	standard error	SE
second	s	U.S.C.	United States Code	variance	
		U.S. state	use two-letter abbreviations (e.g., AK, WA)	population	Var
Physics and chemistry				sample	var
all atomic symbols					
alternating current	AC				
ampere	A				
calorie	cal				
direct current	DC				
hertz	Hz				
horsepower	hp				
hydrogen ion activity (negative log of)	pH				
parts per million	ppm				
parts per thousand	ppt, ‰				
volts	V				
watts	W				

REGIONAL OPERATIONAL PLAN NO. ROP.CF.1J.2023.02

**JUVENILE ABUNDANCE AND HARVEST OF UNUK RIVER CHINOOK
SALMON, 2022–2024**

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PURPOSE

This plan describes the coded-wire-tagging of juvenile Chinook salmon *Oncorhynchus tshawytscha* on the Unuk River for the 2021 and 2022 brood years, which covers the coded-wire-tagging of parr in fall of 2022 and 2023 and smolt in spring of 2023 and 2024, and sampling returning adults for age, sex, length, and coded wire tags in escapement from the 2024 through 2029 return years. This study provides estimates of smolt and parr abundance, overwinter (freshwater) survival, mean lengths of juveniles, and harvest information of Chinook salmon originating from the Unuk River in Southeast Alaska. A separate project will be conducted on the Unuk River that employs aerial and foot survey peak counts to estimate large (≥ 660 mm mid eye to fork of tail length) adult Chinook salmon returning to the river in 2022 and 2023. The primary goals of this and the companion study are to estimate inriver run size, total run size, marine harvest and exploitation rates, harvest distribution, smolt and parr abundance, marine survival (smolt to adult) and overwinter survival (parr to smolt). The Alaska Department of Fish and Game uses this information to make local and regional management decisions and to evaluate the Unuk River Chinook salmon escapement goal, and the Pacific Salmon Commission uses the data for coastwide management and stock assessment through the Chinook Technical Committee.

Keywords: Chinook Salmon, *Oncorhynchus tshawytscha*, escapement, Unuk River, Behm Canal, parr, smolt, harvest, age, sex, length, composition, mark tag fraction, coded wire tag, adipose fin, Southeast Alaska

BACKGROUND

The Unuk River produces the largest natural run of Chinook salmon *Oncorhynchus tshawytscha* in southern Southeast Alaska (SEAK) and flows into Behm Canal, a narrow saltwater passage northeast of Ketchikan (Pahlke 2010). Unuk River Chinook salmon is a Pacific Salmon Commission (PSC) exploitation rate and escapement indicator stock and contributes towards management of the SEAK sport fishery allocation in accordance with the Pacific Salmon Treaty (PST). Stock assessment of Unuk River Chinook salmon includes full production estimates; the Unuk River coded wire tag (CWT) project is an important component towards estimating smolt abundance, marine harvest in mixed-stock fisheries, and marine survival from smolt to adult. Coded wire tag studies have been conducted on the Unuk River consistently since 1994. Smolt abundance along with harvest contributions have been estimated for Unuk River Chinook salmon brood years (BY) 1992–2014, with BYs 2015–2019 in progress.

The information provided from these studies was used to establish the current biological escapement goal (BEG) for the Unuk River stock of Chinook salmon (Hendrich et al. 2008). The BEG also meets provisions of the 2020 PST which requires “*an abundance-based framework for managing all Chinook fisheries*”; the framework should involve “*harvest regimes based on annual estimates of abundance*” that are “*designed to meet maximum sustained yield (MSY) or other agreed upon biologically based escapement and/or harvest rate objectives.*” The results are also used by the Chinook Technical Committee (CTC) of the PSC for: (1) development of a model stock for SEAK, (2) exploitation rate analysis, and (3) improved escapement assessment for Behm Canal Chinook salmon stocks.

The Unuk River stock of Chinook salmon is 1 of 12 stocks used by the ADF&G as an indicator stock of statewide Chinook salmon production in the Chinook Salmon Research Initiative (CSRI) program (ADF&G 2013). The recent downturn in Chinook salmon production prompted a look at statewide production and identification of stock assessment information gaps. Juvenile information was identified as a knowledge gap and the Unuk River is 1 of only 2 projects statewide that provides information on parr and smolt abundance and freshwater survival from parr to smolt; the other system providing this information is the Chilkat River, also located in Southeast Alaska (Elliott and Peterson 2020).

The Unuk, Chickamin, Blossom, and Keta Rivers traverse the Misty Fjords National Monument and flow into Behm Canal, a narrow saltwater passage east of Ketchikan (Figure 1). The Unuk River is used as indicator stock by the PSC (PSC 2020). The escapements in these streams are indexed using standardized observer counts conducted by helicopter and foot. Concerns for Chinook salmon escapements in Behm Canal systems were raised in 1992 when escapement indices dropped in the Behm Canal stocks. As a result, all available historical harvest and escapement data for the Unuk and Chickamin Rivers were reviewed to evaluate the status of these stocks.

The evaluation resulted in the ADF&G Division of Sport Fish (DSF) initiating a research program in Behm Canal in 1993 and 1994. Total escapement had not been estimated in any Behm Canal Chinook salmon system prior to 1994. Mark–recapture experiments were used to estimate the escapement of large (≥ 660 mm mid-eye-to-fork of tail (METF)) Chinook salmon in the Unuk River in 1994 (Pahlke et al. 1996), 1997–2009, and 2011 (Jones et al. 1998; Jones and McPherson 1999, 2000, 2002; Weller and McPherson 2003a-b, 2004, 2006a-b; Weller and Evans 2009); the 2010, 2012–2014 mark–recapture estimates were considered untrustworthy, so aerial expansion estimates were used (Weller and Evans 2012; Weller et al. 2012; Richards et al. 2018). The mark–recapture experiment was discontinued in 2015 due to the loss of the set gillnet site and inability to capture enough Chinook salmon during event 1, budgetary reasons, and confidence in the observer count index expansion method to estimate drainage-wide escapement. The estimates of escapement for large Chinook salmon spawners in 1997–2021 ranged from 956 fish in 2012 to 10,541 fish in 2001 and averaged 3,649 fish. During years when escapements were estimated with mark–recapture, approximately 13% to 25% of all large Chinook spawners were counted in surveys, a much lower percentage than previously thought. Spawning distribution in the Unuk River was estimated using radiotelemetry studies 1994–2009 and these studies showed that the index counts occurred in tributaries containing at least 80% of the large Chinook salmon drainage-wide escapement. After meeting or exceeding the lower bound of the escapement goal for 35 consecutive years (1977–2011), the Unuk River stock of Chinook salmon failed to make the goal 2012–2014, 2016–2017, and 2020.

Earlier research (1983–1988) in Behm Canal included coded-wire-tagging wild juvenile (mostly smolt) Chinook salmon on the Unuk and Chickamin Rivers to estimate adult harvest, harvest and exploitation rates, harvest distribution, and rearing areas for juvenile fish (Kissner 1985; Pahlke 1995). This work showed the majority of CWTs were recovered in the SEAK marine commercial troll fishery and during spawning grounds sampling. Harvest estimates for Unuk River Chinook salmon ranged from 726 fish (1985 BY) to 3,039 fish (1983 BY), with 95% relative precision of harvest estimates ranging from 24% (1982 BY) to 78% (1985 By). Further indications suggested that these stocks were harvested as both immature and mature fish throughout SEAK. Harvests were most abundant in southern and central SEAK inside waters in 1986–1992 but ranged from outer coast waters near Yakutat in the north to northern British Columbia Canada in the south and have since been recovered in fisheries operating in the Bering Sea.

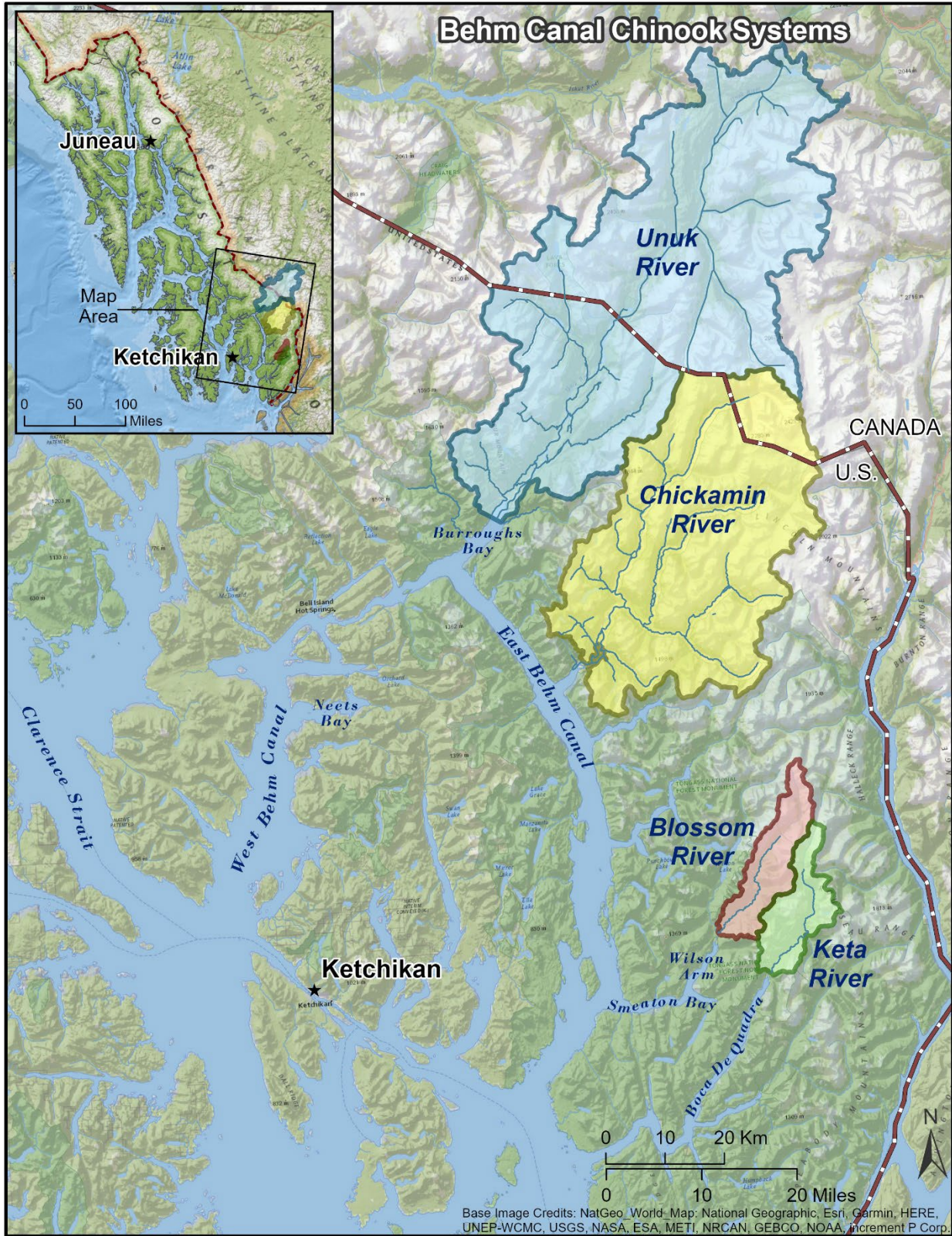


Figure 1.–Behm Canal area in Southern Southeast Alaska (inset), showing major Chinook salmon systems, including the Unuk River.

Beginning in the fall of 1993, Chinook salmon parr rearing in the Unuk River were tagged with CWTs, and in the spring of 1994, smolt from the same BY were tagged. Beginning in 1999, all principal age classes of adult Chinook salmon returning to the Unuk River were tagged with CWTs in prior years as juveniles. As many as 79,000 Chinook salmon parr and smolt have been tagged during emigration per year since the 1996 BY (Appendix A) and have resulted in CWT marked fractions as high as 13% (2015 BY; Appendix B). Tagging efforts were not as successful for the 2009–2014 BYs, ranging from about 26,000 fish for the 2009 BY to about 14,500 fish for the 2014 BY. However, about 56,500 fish were tagged for the 2015 BY, about 34,500 fish for the 2016 BY, about 16,500 fish for the 2017 BY, just over 33,000 fish for the 2018 BY, and about 41,500 fish for the 2019 BY. The marked fraction for the most recent complete brood (2015 BY) for which the age-1.1 through age-1.4 fish have returned was 13%, which is the highest marked fraction seen for this stock.

In 2022–2024, three studies will be conducted on the Unuk River: tagging BY 2021 and BY 2022 juvenile Chinook salmon in freshwater in the fall (2022–2023) and spring (2023–2024) with CWTs, sampling of adults for age, sex, length (ASL) and tag information on the spawning grounds, and aerial and foot surveys of large Chinook salmon (Richards et al. 2022).

The data from these three Unuk River studies should enable us to estimate total harvest, harvest distribution, smolt abundance, and marine survival and exploitation rates for this stock.

OBJECTIVES

There are several research objectives:

1. Estimate smolt abundance for the 2023 and 2024 outmigration (2021 and 2022 BYs) such that the estimates are within 25% of the true value 95% of the time.
2. Estimate the mean length of Chinook salmon parr (fall 2022 and 2023) and smolt (spring 2023 and 2024) such that the estimates are within 1 mm of the true value 95% of the time.
3. Estimate the age and sex composition of large (≥ 660 mm METF) Chinook salmon in the Unuk River such that estimates are within 10 percentage points of the true value 95% of the time.

SECONDARY OBJECTIVES

1. Estimate the fraction of Chinook salmon from each BY marked with a CWT.
2. Estimate fall parr abundance in 2022 and 2023 (2021 and 2022 BYs).
3. Estimate the total harvest of Unuk River Chinook salmon, BYs 2021 and 2022, in sampled sport and commercial salmon fisheries from 2024 to 2029 via recovery of CWTs applied in the fall of 2022 and 2023 and spring of 2023 and 2024.
4. Estimate mean length-at-age and length-at-sex for the spawning population.
5. Estimate the age and sex composition of medium (≥ 400 to < 660 mm METF) and small (< 400 mm METF) Chinook salmon spawning in the Unuk River.
6. Estimate the abundance of small and medium Chinook salmon in the Unuk River based on the proportion of small and medium fish sampled on the spawning grounds.
7. Collect genetic tissue from all Chinook salmon captured during age, sex, and length sampling.

8. Collect genetic material using OmniSwabs (Appendix C) from juvenile Chinook salmon captured during the fall of 2022 with the ultimate sample size goal of 250 samples.

METHODS

STUDY DESIGN

Age and Sex Composition and Mark Fraction (Objective 3, Secondary Objectives 1, 4, 5, 6, 7)

With the loss of the adult mark–recapture project in 2015, all age and sex composition and mark fraction data must come from spawning ground sampling. Samples used to estimate the marked fraction and age and sex composition will be collected from index areas on select tributaries of the Unuk River (Table 1).

Table 1.–Unuk River tributary systems where spawning ground sampling occurs.

Location	Importance as spawning site (rank)	Historical survey dates			Index area
		Start	End	Peak	
Cripple Creek	1	8/3	8/9	8/6	Y
Clear Creek	2	8/7	8/14	8/10	Y
Kerr Creek	3	8/7	8/14	8/10	Y
Gene’s Lake Creek	4	8/15	8/27	8/27	Y
Lake Creek	5	8/7	8/14	8/10	Y
Eulachon River	6	8/14	8/21	8/18	Y
Boundary Creek	7				N

Note: In recent years, peak counts have occurred later than noted.

Spawning ground sampling will begin approximately 1 August and continue to approximately 31 August if sampling is effective. The goal of sampling is threefold: 1) to estimate the fraction of fish marked with adipose-finclips and CWTs; 2) to estimate ASL composition; 3) to report the numbers of fish seen. Genetic samples will be taken from adults to bolster the genetic baselines of the Unuk River tributaries.

Surveys will be conducted as follows:

Cripple, Clear, Kerr, and Gene’s Lake Creek: two surveys each of large live and dead fish approximately one week apart near the peak of spawning (Table 1). On both creeks, crews will walk upstream through the index area and count large fish (live and dead) throughout the established index area. Crews will then sample carcasses and live fish of all sizes as usual on the trip back downstream. Fish observed in the lake outlet will also be counted during the surveys.

Eulachon River and Lake Creek: live and dead large fish observed at each location will be counted while inspecting fish of all sizes for marks and collecting ASL samples.

Boundary Creek: not surveyed, but fish of all sizes will be collected for ASL sampling.

All survey data will be recorded on the form described in Appendix D.

To prevent double sampling of fish on the spawning grounds, every live and dead fish sampled will have its adipose fin cut and be given an operculum punch on the lower one-third (ventral side) of the left operculum (LLOP) for a secondary mark. Additionally, every dead fish sampled will be slashed through the preferred area on the left side using a knife. All previously unsampled Chinook salmon found or captured on the spawning grounds, regardless of size, will be counted and sampled for ASL, adipose-finclips, and CWTs. Note that any fish not suitable for sampling (head or tail missing, mangled to the point to preclude an accurate length measurement, etc.) will be ignored and not sampled. A variety of gear including dip nets, rod and reel snagging gear, short sections of netting, and spears (for dead fish) will be used to collect fish for sampling. Previous studies have shown this approach is effective for collecting age and sex composition samples and has little significant potential for bias. During studies on the Unuk River (Jones et al. 1998; Jones and McPherson 1999, 2000, and 2002), the Taku River (McPherson et al. 1997), and the Chickamin River (Freeman and McPherson 2003–2005), no significant size bias was detected for large Chinook salmon when these field procedures were carefully and diligently applied. Fish observed on the spawning grounds will be selected for sampling without conscious regard to their sex, size, or mark status. During each survey, all fish will be counted and previously unsampled fish will be inspected to identify marks and determine sex and measured to determine length (mm METF). All male fish < 660 mm METF found during sampling that are missing the adipose fin will be sacrificed for recovery of the CWT (See CWT sampling section), whether dead or alive. All fish \geq 660 mm METF missing the adipose fin and determined to be in a post spawn state will also be sacrificed for recovery of the CWT.

Sample Sizes–Age and Sex Composition

Operational plans prior to 2015 had more stringent objective criteria and therefore required greater sample sizes for estimating adult age and sex composition; however, recent poor runs and the loss of the adult mark–recapture project resulted in fewer fish being sampled and the criteria not being met. Production is anticipated to remain poor, and the adult mark recapture project discontinued. As a result, the criteria in Objective 3 were relaxed from 5 to 10 percentage points.

Based on the procedures in Thompson (1987) and assuming a scale regeneration rate of 17%, 153 fish need to be sampled to meet the criteria for Objective 3 for estimating age composition. Based on the procedures in Thompson (2002) and assuming no data loss and equal proportions of males and females, 96 fish need to be sampled to meet the criteria for Objective 2 for estimating sex composition. Sample size calculations assume no size or sex selectivity. Despite the recent poor returns, we anticipate meeting the criteria for Objective 3 since 743 fish have been sampled on the spawning grounds on average since 2017.

Smolt Abundance, Parr Abundance, and the Harvest of Chinook Salmon from the 2021 and 2022 Brood Years (Objective 1, Secondary Objectives 2, 3, 8)

Smolt and parr abundance and the harvest of Unuk River Chinook salmon from the 2021 and 2022 BYs will be estimated by marking and tagging juvenile salmon. Smolt and parr abundance will be estimated using a mark–recapture experiment. Harvest will be estimated from the recovery of marked and coded-wire-tagged fish in sampled marine commercial and recreational fisheries in 2024 through 2029.

Chinook salmon parr from the 2021 and 2022 BYs will be tagged with CWTs in the fall of 2022 and 2023, and smolt will be tagged in the spring of 2023 and 2024, respectively. Parr will be captured from late September through the end of October in the fall of 2022 and 2023, and smolt will be

captured from late March through late April in the spring of 2023 and 2024. Minnow traps will be set in the mainstem of the Unuk River between approximately river km 3 (just above the upper set net site) and river km 19 (just below lava falls; Figure 2). Approximately 150 traps baited with salmon eggs will be fished daily. These traps will be divided between 2 trap lines, each of which will be operated and checked by a 2-person crew. Tag codes used for parr and smolt will be unique and not mixed.

Almost all Chinook salmon smolt from the Unuk River spend 1 year in the freshwater as parr and then emigrate to marine waters as freshwater-age-1 (yearling) smolt. All tagged smolt are therefore primarily from a single BY. Chinook salmon mature and return over 5 years beginning with age-1.1 “jacks” and ending with age-1.5 fish.

Sample Sizes–Smolt Abundance

Smolt abundance for BY j will be estimated using a mark–recapture experiment. Average smolt abundance of Unuk River Chinook salmon is 309,112 fish (BY 1992–2015). Fall parr in year $j+1$ and smolt in year $j+2$ will be externally marked with an adipose-finclip and tagged with a CWT and returning adults in years $j+3, j+4, \dots, j+7$, will be inspected for marks and tags. Experience has shown that the proportion of adults from a given BY with an adipose-finclip or a CWT does not change appreciably over return years, and thus these data can be pooled. The average number of adults inspected for adipose-finclips is around 1,100 fish (BY 1992–2015). Using these averages and the methods described in Robson and Regier (1964), we need to tag approximately 19,000 Chinook smolt to meet the objective criteria for Objective 1; however, because both parr and smolt are tagged and not all parr survive to smolt, this sampling target needs to be adjusted to account for overwinter survival. Average overwinter survival is 0.50 (BY 1992–2016), so the number of parr that need to be tagged can be determined using the following equation: $M_f = (19,000 - M_s) / 0.50$, where M_f is the number of parr tagged and M_s is the number of smolt tagged. Though more effort is usually allocated to tagging parr because it is more cost-effective on a per smolt basis, enough of both parr and smolt need to be tagged to estimate overwinter survival and therefore smolt abundance. Past studies have shown that upwards to 87% of the tagging effort can be allocated towards fall parr tagging while still yielding reasonable estimates of smolt abundance.

We have met the precision goal in 2 of the past 5 complete broods (BY 2011–2015). Reduced funding, poor sampling conditions, and below average marine survival resulted in reduced numbers of parr and smolt being tagged and fewer adults being inspected for tags from these BYs. Budget constraints limited tagging efforts for the 2010 to 2014 BYs: it was reported that parr and smolt were present and had the resources been available more fish could have been tagged. More parr and smolt were tagged in 2016 to 2021 (BY 2015–2020) because additional funds were available. Assuming sufficient funds are again available, and that marine survival improves, we anticipate that we will meet the objective criteria for Objective 1.

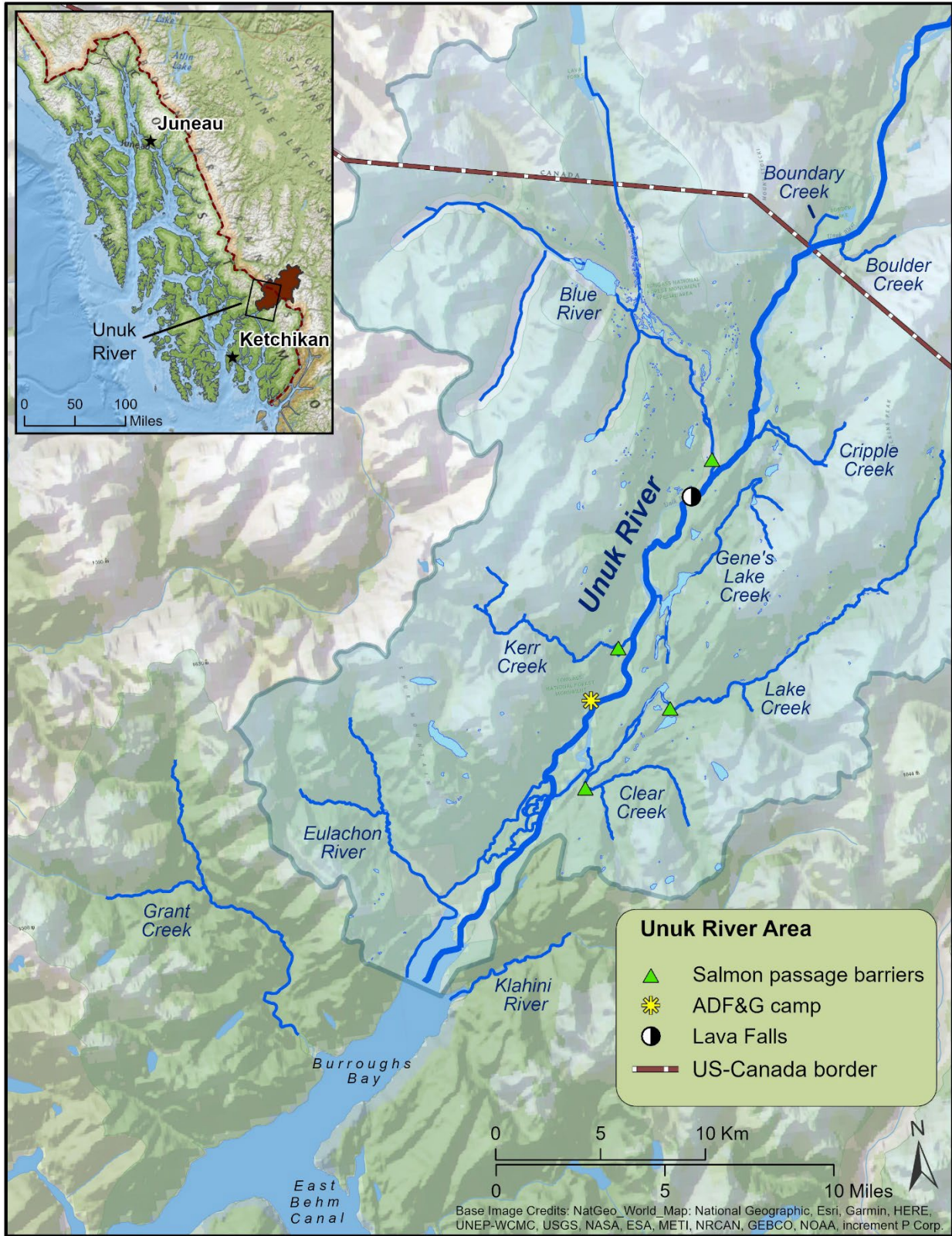


Figure 2.—Unuk River in Southeast Alaska, showing major tributaries, barriers to fish migration and location of research sites.

Mean Length of Chinook Salmon Juveniles (Objective 2)

Chinook salmon fall parr and spring smolt will be measured to the nearest 1 mm. Juvenile Chinook salmon measured for length will also be weighed to the nearest 1/10 g. There is no reason to collect scales on Unuk River Chinook salmon smolt for aging purposes as nearly all are age-1.0 smolt (Hendrich et al. 2008). Systematically drawn samples of captured juvenile Chinook salmon will be measured for length to estimate the mean length of the populations within 1 mm of the true value 95% of the time (Objective 2).

Sample Sizes–Mean Length

With simple random sampling, the sample size n needed to estimate the mean length of parr or smolt within d mm of the true value $(1-\alpha/2)\%$ of the time is given by (Cochran 1977):

$$n = \left(\frac{Z_{1-\alpha/2}S}{d} \right)^2 \quad (1)$$

where s is the standard deviation and Z is the value of a normal deviate corresponding to the desired confidence probability, α . The precision criteria of Objective 2 specifies an α of 0.05. For parr, for a standard normal variate $Z_{1-0.05/2} = 1.96$, $s = 6.5$, mm and $d = 1$ mm, the required sample size is $n = 162$. Based on a catch of 28,000 Chinook salmon parr (assumes 73% of fish tagged were parr), every 173rd parr should be measured. However, in case less than 28,000 parr are caught, every 100th parr will be measured. Similarly, for smolt, for a standard normal variate $Z_{1-0.05/2} = 1.96$, $s = 7.0$ mm and $d = 1$ mm, the required sample size is $n = 188$. Based on a catch of 5,100 smolt (assumes 27% of fish tagged were smolt), every 27th smolt should be measured. However, to be conservative, every 25th smolt will be measured.

DATA COLLECTION

Juvenile Tagging

All captured Chinook salmon parr and smolt with adipose fins intact will have their adipose fins removed, be tranquilized with a buffered MS 222 solution, and tagged with a CWT following procedures described in Koerner (1977). All coded-wire-tagged fish will be held overnight to test for mortality and tag retention prior to release. We assume that there is no impact on mortality from simply holding fish overnight and that any mortality observed the following day is due to tagging. All smolt captured that are missing an adipose fin will be passed through a magnetic tag detector, and the presence or absence of a CWT will be recorded.

All tagging, recapture, and retention data will be recorded daily on a *CWT Daily Log Form* (Appendix E). A separate *CWT Daily Log Form* will be filled out for each day of operation and a summary page will be updated periodically. A new form is also required upon initial use of each tag code, with a 1 mm length of wire taped to the form on the first day a new code is used. Daily procedures will be as follows:

1. Record tagging site, date, and species.
2. On the *Water Temperature and Depth Form* (Appendix F) record date, water temperature to the nearest 0.5°C, and water depth at the staff gauge to the nearest 0.5 inch. Data should be collected at approximately 0800 hrs each day.

3. At 0800–0900 hrs check 100 fish for tag retention in the sample of fish from the previous day’s tagging and record the results. If retention is less than 98 out of 100 fish, the entire batch will be rechecked and every fish that tests negative will be retagged. After all tag retention fish have been checked, count any mortalities, and then release all the live fish from the net pens into suitable habitat. Retag all fish that test negative if retention is less than 98 out of 100 fish. All retagged fish will be noted on the day they are retagged and subtracted from the day’s total to avoid double counting the fish.
4. Run the trap lines. Remove fish from the traps and transport them to the tagging station. Inspect each live fish and count the number missing adipose fins. Record this number under “Recaptures” on the *CWT Daily Log Form*. Check all recaptures for tags with the detector and record the number without CWTs. Release all recaptures after testing and retag any that test negative.
5. Give all live fish not previously tagged a CWT and pass each through the tag detector. If a fish tests negative for the presence of a CWT, retag the fish. Keep a count of all retagged fish on a hand counter. Write the beginning and ending machine numbers from the specific Northwest Marine Technology Mark IV tagging machine used on the *CWT Daily Log Form* and record the total number of retagged fish and erroneous tags (i.e., goofs, misses, tagged fingers, practice tags, etc.). Write out all hand calculations on the form so that these calculations can be checked and verified later.
6. Systematically select and measure to the nearest 1 mm FL every
 - a. 100th unmarked Chinook salmon parr (fall 2022 and 2023), and
 - b. 25th unmarked Chinook salmon smolt (spring 2023 and 2024).
7. All the fish in (6) will also be weighed to the nearest 1/10th g.
8. Systematically select and sample every 40th unmarked Chinook salmon parr (fall 2022 only) using the methods described in Appendix D.

Collecting Genetic Material from Juveniles

Juvenile Chinook salmon will be systematically sampled for genetic material. The minimum target sample size is 250 fish; however, because there are a lot of unknowns about sampling juveniles for genetics, the sample size target was increased to 700 fish. Assuming OmniSwabs are 90% effective (Kyle Shedd, *personal communication*), the 700 samples will result in a total of 630 viable samples, which will greatly exceed the minimum sample size goal. Assuming a catch of 28,000 parr, 1 in every 40 juveniles will need to be sampled for genetics.

Age, Sex, and Length Sampling

All adult Chinook salmon caught will be sampled for ASL and genetics. Age compositions for each escapement sampling location (tributary) will be tabulated using the *Spawning Grounds Age, Sex, and Length Form* (Appendix D). For age composition sampling, it is imperative that good scale samples be taken. Genetic samples for each escapement sampling location will be collected per the methods described in Appendix D.

Five scales will be removed from the preferred area on the left side accordingly: 3 scales from 2 to 3 rows above the lateral line taken 1 inch apart, and 2 scales 4 to 5 rows up and ½ inch from one of the lower 3 scales (Welanders 1940). In some cases, the preferred area on the left side of the fish

may be devoid of scales. In such instances, the preferred area on the right side of the fish should be sampled for scales and if this is devoid of adequate samples, then samples should be taken from the areas near the dorsal or anal fins on the left side of the fish. All scales will be carefully cleaned, mounted on scale gum cards, 5 per column, using methods described in ADF&G, *unpublished*¹. The gum cards will be labeled completely at the time of sampling. Scale cards are sequentially numbered by sampling location, beginning with 001 at each sampling location. The correct ASL stream code (Appendix H) should also be recorded on each card. Gender will be determined from secondary maturation characteristics and length will be taken to the nearest 5 mm METF. Secondary maturation characteristics can include predominant snouts and compressiform bodies for males, while females may display abraded caudal fins (i.e., “white tails”) and/or prominent bellies. Scales will be cleaned and mounted neatly, without excess water, sand, or mucus. If it is not possible to mount the scales in this manner on site, then the scales will be stored in numbered plastic slide pockets and then mounted later that evening at camp with care taken to clean them properly and to label the gum cards completely, including last names of all samplers for that location for that day. If scales are not collected from a fish for any reason, note that in the comment column on the ASL form and make sure to skip that column on the gum card.

MOST IMPORTANTLY:

- 1) sample every Chinook salmon encountered on the spawning grounds, regardless of size, and record all data for each fish on the appropriate form,
- 2) check every fish for the presence or absence of all marks (i.e., LLOP, LAA, adipose fin),
- 3) collect clean, readable scales from the preferred area (or other areas if necessary),
- 4) collect genetic tissue samples from every fish sampled for ASL, and
- 5) collect heads and scales from all adipose-finclipped fish that are dead, post spawn, or < 660 mm METF males

Coded Wire Tag Sampling

All fish sampled in the study will be inspected for adipose-finclips and sampled for ASL and the BY will therefore be known and estimation of BY-specific adipose-finclipped fractions will be possible. The high value of θ (~0.1) would lead to excessive mortality if all pre-spawn, adipose-finclipped fish were sacrificed to verify the presence of a valid Unuk River CWT. Therefore, only fish that are dead, post spawn, or < 660 mm METF males without adipose fins will be sacrificed to retrieve CWTs. This size limit for sampling live Chinook salmon will include almost all individuals through age-1.2 fish, a group that is almost exclusively male. All live, unspawned fish > 660 mm METF missing their adipose fin will be noted and released after sampling. Heads of all spawned-out fish alive or dead, will be taken if the adipose fin is missing and these heads will be given a uniquely numbered cinch strap obtained from the Division of Commercial Fisheries (DCF) Mark, Tag, and Age Laboratory (Tab Lab), and will be attached to each head. The head will then be sent with a completed CWT sampling form (Appendix I) to the lab for analysis. Results from the adipose-finclip, scale, and direct CWT sampling will be used to:

¹ ADF&G (Alaska Department of Fish and Game). *Unpublished*. Length, sex, and scale sampling procedure using the ADF&G adult salmon age-length mark-sense form version 3.0. Division of Commercial Fisheries, Douglas, AK.

- estimate the CWT marked fraction by BY, θ (using adipose-finclip, scale, and decoded CWT data); this fraction will be used to estimate marine harvest,
- compare ages derived from tags to ages determined from scales taken from the tagged fish (using scale and decoded CWT data),
- determine the incidence (if any) of strays from other tagged stocks (decoded CWT data),
- detect loss of CWTs (adipose-finclip and CWT data), and
- estimate abundance, return, and survival rates of smolts and juveniles when combined with other project data analyses (adipose-finclip, scale, and decoded CWT data).

DATA REDUCTION

It is the responsibility of the field crew leaders to ensure that all data are recorded daily. Data forms will always be kept up to date. Data will be transferred from field forms to EXCEL™ database spreadsheets after returning to camp in the afternoon. Field forms will be inspected for accuracy and compliance with sampling procedures, compared with the electronic database files, and error checked. Data forms will always be kept up to date and provided to the project leader as instructed.

The Tag Lab is the permanent repository for all information on CWTs in the state of Alaska. All tagging and release information will be reported to the Tag Lab through the MY FISH site (<https://mtalab.adfg.alaska.gov/FMPD/SignOn.aspx?ReturnURL=MyFISH.aspx>). Wire verification samples and forms from sequential wire tagging projects will be sent to the Tag Lab. The Alaskan CWT data is annually transferred to the Pacific States Marine Fisheries Commission, which stores coastwide CWT data in a permanent and standardized database.

Inspection for errors will follow; common issues include incorrect dates, transposed nonsensical lengths (i.e., 470 mm when the fish was 740 mm), incorrect length measurement method used (i.e., post orbit of eye-to-hypural (POH)), etc. Scale cards will be checked to ensure that scales are clean and mounted correctly, that the cards are correctly, completely labeled, and match up with the corresponding ASL data form. Data will be sent to the ADF&G office at regular intervals and inspected for accuracy and compliance with sampling procedures. Data will be transferred from field forms to EXCEL® spreadsheet files. Scales will be pressed, and ages estimated in the scale aging lab in Juneau or Ketchikan. Scale ages will be entered into the spreadsheet files. When input is complete, data lists will be obtained and checked against the original field data. This will be performed two times to ensure that data are error free.

A final, edited copy of the data, along with the metadata, will be sent to publication staff for electronic archiving when the report is completed and submitted.

DATA ANALYSIS

Age and Sex Composition of Escapement

The proportion of the spawning population composed of a given age c within a size class k (large, medium, and small) will be estimated as a binomial variable:

$$\hat{p}_{kc} = \frac{n_{kc}}{n_k}, \quad (2)$$

$$\text{var}(\hat{p}_{kc}) = \frac{\hat{p}_{kc}(1 - \hat{p}_{kc})}{n_k - 1} \quad (3)$$

Where n_{kc} is the number of Chinook salmon of age c in size group k , and n_k is the number of Chinook salmon in the sample of size group k . Numbers of spawning fish by age will be estimated as the sum of the products of estimated age composition and estimated abundance within a size category:

$$\hat{N}_c = \sum_k (\hat{p}_{kc} \hat{N}_k) \quad (4)$$

Because the \hat{N}_k in Equation (4) are correlated (\hat{N}_S and \hat{N}_M are estimated from \hat{N}_L by Equation (6) and Equation (7), the $\text{var}(\hat{N}_c)$ will be estimated by simulation. The stochastic components in the simulation will be: the estimate of large fish as $\hat{N}_L^* \sim N(\hat{N}_L, \hat{\sigma}_{\hat{N}_L})$, the vector of estimated size proportions as $\hat{\phi}^* \sim \text{multinomial}(n_{sp}, \hat{\phi})/n_{sp}$, and the vector of estimated age and sex proportions for the k^{th} size group as $\hat{p}_k^* \sim \text{multinomial}(n_k, \hat{p}_k)/n_k$. Equations (2–4) and Equations (6–7) will be applied to each set of simulated values to produce a set of simulated numbers of spawning fish by age, \hat{N}_c^* . The simulated variance of \hat{N}_c will be taken as the sample variance of the \hat{N}_c^* 's. The stochastic process will be simulated 10,000 times.

The proportion of the spawning population composed of a given age will be estimated as :

$$\hat{p}_c = \frac{\hat{N}_c}{\hat{N}_{ALL}} \quad (5)$$

where \hat{N}_{ALL} is defined in Equation (13).

The $\text{var}(\hat{p}_c)$ will be estimated as the sample variance of the \hat{p}_c generated in the simulation described above.

Sex composition and age and sex composition for the entire spawning population and its associated variances will be estimated using the above equations by first redefining the binomial variables in samples to produce estimated proportions by sex \hat{p}_g , where g denotes gender (male or female), such that $\sum_g \hat{p}_g = 1$, and by age and sex \hat{p}_{cg} , such that $\sum_{cg} \hat{p}_{cg} = 1$.

Estimation of Adult Abundance

The estimated abundance of large Chinook salmon, \hat{N}_L , will be calculated as described in Appendix J, under the section “Systems where escapement is estimated”.

The abundance of small-sized fish \hat{N}_S and medium-sized fish \hat{N}_M will be estimated indirectly by expanding the estimate for large fish by the estimated size composition of the spawning escapement (McPherson et al. 1997):

$$\hat{N}_S = \hat{N}_L \frac{\hat{\phi}_S}{\hat{\phi}_L} \quad (6)$$

$$\hat{N}_M = \hat{N}_L \frac{\hat{\phi}_M}{\hat{\phi}_L} \quad (7)$$

Such that $\hat{\phi}_k$ is the estimated fraction of k -sized (small, medium, or large) fish in the Chinook salmon spawning population:

$$\hat{\phi}_k = \frac{n_k}{n_{sp}} \quad (8)$$

where,

n_{sp} = Number of fish sampled on the spawning grounds

n_k = Number of k -sized fish found in n_{sp} ,

with variance estimated as :

$$\text{var}(\hat{\phi}_k) = \frac{\hat{\phi}_k(1-\hat{\phi}_k)}{n_{sp}-1} \quad (9)$$

It is noted that the number of fish sampled for size is larger (includes all carcasses) than that sampled for age and that $\hat{\phi}_k$ are considered relatively unbiased.

The variance of the abundance of small fish will be estimated:

$$\text{var}(\hat{N}_S) = \hat{N}_L^2 \text{var}\left(\frac{\hat{\phi}_S}{\hat{\phi}_L}\right) + \left(\frac{\hat{\phi}_S}{\hat{\phi}_L}\right)^2 \text{var}(\hat{N}_L) - \text{var}\left(\frac{\hat{\phi}_S}{\hat{\phi}_L}\right) \text{var}(\hat{N}_L) \quad (10)$$

whereby the delta method (note that $\text{Cov}(\hat{\phi}_S, \hat{\phi}_L) = -\frac{\hat{\phi}_S \hat{\phi}_L}{n_{sp}}$),

$$\text{var}\left(\frac{\hat{\phi}_S}{\hat{\phi}_L}\right) \approx \left(\frac{\hat{\phi}_S}{\hat{\phi}_L}\right)^2 \left(\frac{\text{var}(\hat{\phi}_S)}{\hat{\phi}_S^2} + \frac{\text{var}(\hat{\phi}_L)}{\hat{\phi}_L^2} + \frac{2}{n_{sp}} \right) \quad (11)$$

Similarly,

$$\text{var}(\hat{N}_M) = \hat{N}_L^2 \text{var}\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right) + \left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right)^2 \text{var}(\hat{N}_L) - \text{var}\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right) \text{var}(\hat{N}_L) \quad (12)$$

The abundance of all fish will be estimated as:

$$\hat{N}_{ALL} = \frac{\hat{N}_L}{\hat{\phi}_L} \quad (13)$$

with variance estimated as:

$$\text{var}(\hat{N}_{ALL}) = \text{var}(\hat{N}_L) \left[\frac{1}{\hat{\phi}_L} \right]^2 + \hat{N}_L^2 \text{var} \left[\frac{1}{\hat{\phi}_L} \right] - \text{var}(\hat{N}_L) \text{var} \left[\frac{1}{\hat{\phi}_L} \right] \quad (14)$$

where

$$\text{var} \left(\frac{1}{\hat{\phi}_L} \right) \approx \left[\frac{1}{\hat{\phi}_L} \right]^4 \text{var}(\hat{\phi}_L) \quad (15)$$

Estimation of Fraction of Adults Bearing Coded Wire Tags

Experience has shown that estimates of the proportion of adults from a given BY with CWTs does not change appreciably over return years, and thus the fraction of adults from BY j that are marked with a CWT will be estimated from pooled data as:

$$\hat{\theta}_j = \frac{\sum_{i=1}^L a_{ij} \hat{\rho}_{ij}}{\sum_{i=1}^L n_{ij}} \quad (16)$$

where

n_{ij} = number of adults examined in year i from BY j for adipose-finclips;

a_{ij} = number of adipose-finclips observed in n_{ij} ;

ρ_{ij} = $\frac{t_{ij}}{a_{ij}}$, the proportion of sacrificed adults from BY j in year i that also possess a valid Unuk CWT; where

a'_{ij} = number of heads examined for CWTs from the a_{ij} fish with adipose-finclips;

t_{ij} = number of CWTs found in a'_{ij} ; and

L = number of years over which fish from a given brood return (maximum = 5 years, representing age-1.1 through age-1.5 fish).

The variance of $\hat{\theta}_j$ will be estimated using a parametric bootstrap simulation (e.g., Geiger 1990).

For each year of recovery i , adipose-finclips will be generated as $a_{ij}^* \sim \text{binomial} \left(n_{ij}, \frac{a_{ij}}{n_{ij}} \right)$, and

then CWTs will be generated as, $t_{ij}^* \sim \text{hypergeometric}$

($m = t_{ij} / a'_{ij} a_{ij}^*$, $n = a_{ij}^* - t_{ij} / a'_{ij} a_{ij}^*$, $k = a'_{ij} / a_{ij} a_{ij}^*$). Notation for hypergeometric parameters follows that of the R language (R Core Team 2021²). ρ_{ij}^* will then be calculated as $t_{ij}^* / (a_{ij}^* a'_{ij} / a_{ij})$, and $\hat{\theta}_j^*$ as:

$$\hat{\theta}_j^* = \frac{\sum_{i=1}^L a_{ij}^* \rho_{ij}^*}{\sum_{i=1}^L n_{ij}} \quad (17)$$

Many values of $\hat{\theta}_j^*$ will be simulated and the variance of $\hat{\theta}_j$ and $\frac{1}{\hat{\theta}_j}$ estimated as the sample variance of the simulated values.

Contributions to Fisheries

The contribution r_{ij} of a release group or brood of interest j to one fishery stratum i is

$$\hat{r}_{ij} = H_i \left[\frac{m_{ij}}{\lambda_i n_i} \right] \theta_j^{-1}; \quad \lambda_i = \frac{a'_i t'_i}{a_i t_i} \quad (18)$$

where H_i = total harvest in the stratum, n_i = number of fish inspected (the sample) from the stratum, a_i = number of fish in n_i that are missing an adipose fin, a'_i = number of heads from a_i that arrive at the Tag Lab, t_i = number of heads out of a'_i with CWTs detected, t'_i = number of CWTs out of t_i that are dissected and decoded, m_{ij} = number of CWTs with code of interest j (i.e., Unuk River, BY 2012), and θ_j = fraction of the cohort tagged with code of interest. In the sport fisheries, H_i is estimated with error and θ_j is estimated from sampling returning adults inriver. For these reasons, unbiased estimates of the variance of \hat{r}_{ij} will be obtained using equations in Table 2 of Bernard and Clark (1996), which show the formulations for large samples. The marked fraction θ will be based on the fraction of adults without adipose fins, adjusted for tag loss (see Johnson 2014). While an estimate of θ will be available at the end of 2019 (from age-1.1 fish returns), the final estimate for the 2016 BY of Chinook salmon will not be “complete” until the end of 2023. Numbers of recovered tags by age and numbers sampled by age will be summed across samples (years) to obtain the final estimate of θ (see Johnson 2014 for details). The total harvest for the 2016 BY will be calculated as the sum of harvests over sampled fishery strata.

Commercial catch data for the analysis will be summarized by ADF&G statistical week and district for gillnet and seine fisheries, or by period (e.g., winter, spring, or summer commercial troll) and quadrant for troll fisheries (Clark et al. 1985). Sport harvest estimates from ADF&G Statewide Harvest Survey reports (e.g., Jennings et al. 2015) will be apportioned using information from sampled marine sport fisheries to obtain estimates of total harvest by biweek and fishery. Sport fish CWT recovery data will be obtained from DCF Tag Lab reports and summarized by biweek and

² R Core Team. 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

fishery (e.g., biweek 16 during the Sitka Marine Creel Survey) to estimate contribution. In most cases, CWTs of interest may be recovered in only a few of the sport fish sampling strata that defined the fishery biweek. Assuming that the harvests of fish with CWTs of interest are independent of sampling strata within fishery biweeks, harvests and sampling information will be totaled over the fishery biweek to estimate contributions.

Estimates of Mean Length of Juveniles

Estimates of mean length and its variance will be calculated with standard sample summary statistics (Cochran 1977). Because size distributions of Chinook salmon parr and smolts are believed to be relatively narrow, any size-selective sampling with minnow traps should be negligible.

Smolt Abundance

Experience has shown that estimates of the proportion of adults from a given BY with adipose-finclips does not change appreciably over return years, and thus recovery data are pooled over the i years (5 maximum) in which fish from BY j return. Smolt abundance ($\hat{N}_{smolt,j}$) from BY j will be estimated using a version of the Chapman-modified Petersen formula:

$$\hat{N}_{smolt,j} = \frac{(\hat{M}_j + 1)(n_{\bullet,j} + 1)}{(a_{\bullet,j} + 1)} - 1 \quad (19)$$

where

$n_{\bullet,j} = \sum_{i=1}^L n_i$, where n_i is the number of adults examined in year i from BY j for missing adipose fins,

$L =$ number of years over which fish from a given brood return (maximum = 5),

$a_{\bullet,j} = \sum_{i=1}^L a_i$, where a_i is the number of adipose-finclips observed in n_i , and

$\hat{M}_j =$ estimated number of outmigrating smolt originating from BY j that bore an adipose-finclip and these fish may be from either the fall (f ; year $j+1$) or spring (s ; year $j+2$) tagging programs. \hat{M}_j is the sum of the estimated number of parr with adipose-finclips from BY j surviving to the spring ($\hat{M}_{f \rightarrow s,j}$) and the number of smolt with adipose-finclips from BY j ($M_{s,j}$), where:

$$\hat{M}_{f \rightarrow s,j} = M_{f,j} \hat{S}_j \quad (20)$$

and

$M_{f,j} =$ number of parr released with adipose-finclips in the fall of year $j+1$, and

$\hat{S}_j =$ estimated relative odds of $M_{f,j}$ that survived to the spring of $j+2$ against the survival of $M_{s,j}$ (overwinter survival) (see Weller and McPherson 2003a, Appendix A7), where:

$$\hat{S}_j = \frac{\hat{M}_{s,valid,j} v_{\bullet,f,j}}{\hat{M}_{f,valid,j} v_{\bullet,s,j}} \quad (21)$$

and

$\hat{M}_{s,valid,j} =$ estimated number of adipose-finclipped smolt released with valid CWTs in the spring of year $j+2$,

$\hat{M}_{f,valid,j} =$ estimated number of adipose-finclipped parr released with valid CWTs in the fall of year $j+1$,

$v_{\bullet,f,j} = \sum_{i=1}^L v_{i,f,j}$, where $v_{i,f,j}$ is the total number of fish from BY j implanted with valid CWTs in the fall of year $j+1$ that were subsequently recovered, regardless of recovery circumstances (for instance recovery location; marine fishery, escapement, etc, or sample type; random, select, or voluntary; see Harvest section below), and

$v_{\bullet,s,j} = \sum_{i=1}^L v_{i,s,j}$, where $v_{i,s,j}$ is the total number of fish from BY j implanted with valid CWTs in the spring of year $j+2$ that were subsequently recovered, regardless of recovery location or sample type.

The variance of the smolt estimate will be estimated as:

$$\text{var}(\hat{N}_{smolt,j}) = (n_{\bullet,j} + 1)^2 \text{var} \left[\left(\hat{M}_{f \rightarrow s,j} + M_{s,j} + 1 \right) \frac{1}{(a_{\bullet,j} + 1)} \right] \quad (22)$$

where, by Goodman (1960) for independent variables:

$$\begin{aligned} \text{var} \left[\left(\hat{M}_{f \rightarrow s,j} + M_{s,j} + 1 \right) \frac{1}{(a_{\bullet,j} + 1)} \right] &= (M_{s,j} + \hat{M}_{f \rightarrow s,j} + 1)^2 \text{var} \left[\frac{1}{a_{\bullet,j} + 1} \right] + \left[\frac{1}{a_{\bullet,j} + 1} \right]^2 \text{var}(\hat{M}_{f \rightarrow s,j}) \\ &- \text{var} \left[\frac{1}{a_{\bullet,j} + 1} \right] \text{var}(\hat{M}_{f \rightarrow s,j}) \end{aligned} \quad (23)$$

and $\text{var}(\hat{M}_{f \rightarrow s,j})$ is obtained as described in Weller and McPherson (2003a), Appendix A7.

According to the delta method:

$$\text{var}\left[\frac{1}{a_{\bullet} + 1}\right] = \left[\frac{1}{a_{\bullet,j} + 1}\right]^4 n_{\bullet,j} \hat{p}_a (1 - \hat{p}_a) \quad (24)$$

where $\hat{p}_{a,j} = \frac{a_{\bullet,j}}{n_{\bullet,j}}$ is the estimated proportion of inspected adults from BY j with an adipose-finclip.

The two components in Equation (24) are not independent, but a simulation using data from studies on seven BYs of Unuk River Chinook salmon to establish realistic population parameters showed the correlation to be negligible. The simulation showed the simulated variance of smolt abundance to be almost identical to that provided by the average of the Goodman-derived estimates (Equation (24)) over the simulation.

Parr Abundance

Parr abundance \hat{N}_f for BY j will be estimated as:

$$\hat{N}_{f,j} = \hat{N}_{smolt,j} \frac{1}{\hat{S}_j} \quad (25)$$

$$\text{var}(\hat{N}_{f,j}) \approx \hat{N}_{f,j}^2 \left[cv^2(\hat{N}_{smolt,j}) + cv^2(\hat{S}_j) \right] \quad (26)$$

Equation (27) was derived using the delta method (Seber 1982).

INJURED OR DEAD MARINE MAMMALS

- Document with photos/video (if possible, remain at least 100 yards from the animal) and record the date, time, and location (latitude/longitude, description of bay, point, island, etc.).
- If possible, record the species of marine mammal, age class, sex (for sea lions), type of gear, a description of the gear (i.e., line, gillnet, etc.) and how the animal is entangled, its relative degree of impairment, and direction of travel.
- As soon as possible, report to **ALASKA MARINE MAMMAL STRANDING NETWORK** (24-hr hotline 877-925-7773; 877-9-AKR-PRD) and include information gathered above. Ideally for dead animals, if communications allow, contact the hotline while near the carcass to determine if additional information/samples can be collected. Specifically for an observed live and entangled whale, immediately call the **U.S. Coast Guard** (VHF Channel 16).

SCHEDULE AND DELIVERABLES

Parr tagging will begin approximately 24 September 2022 and 2023 and span the month of October, afterwards inventory will be taken and gear will be stored for the winter. Spring tagging will run through approximately 24 March through April, 2023 and 2024. Following a preseason logistical startup meeting the crew will then depart Ketchikan for the Unuk River, camp will be setup, and soon thereafter traps will be set and smolt tagging will commence. Spawning grounds work is scheduled for August 2022 and 2023. All dates are subject to change and are weather dependent.

All field data will be entered in computer spreadsheets and checked for errors by 30 November 2022 and 2023 (Adult and parr data), and 1 June 2023 and 2024 (spring smolt data).

An ADF&G Fishery Data Series report will be prepared by 1 June 2029 summarizing BYs 2021 and 2022. Chinook salmon harvest contributions, associated data for estimating harvest by gear and time, marked fraction of returning adults, exploitation and survival rates, and all juvenile tagging data.

RESPONSIBILITIES

Nathan Frost, Fishery Biologist 2. This position serves as the project leader and is responsible for project activities from Ketchikan. With Richards, responsible for setting up all aspects of the project, including planning, budget, sample design, permits, equipment, personnel, and training. Conducts preseason startup meetings with field crew. Responsible for daily email, text message, or phone call, arranging logistics with field crew, purchasing supplies, loading, and unloading supply planes, proper conduct in the public's eye, and following department guidelines. Responsible for supervising field crew, tracking the budget, meeting reporting requirements, analysis, and publication of smolt and harvest contribution data. Assists with field operations as necessary.

Joseph Simonowicz, Fishery Biologist 1. This position serves as the crew leader and is responsible for supervising one portion of the field tagging program. Responsible for all aspects of field operations, including safe operation of riverboats, and other equipment, tagging, data collection, and general field camp duties. Has lead role in equipment and camp maintenance, makes recommendations on logistics to the project leader, adjusts personnel hours and schedules as appropriate. Edits, summarizes and error-checks field data daily and enters it into spreadsheets. Adjusts field sampling priorities, as necessary. Position is responsible for overseeing and directing juvenile coded-wire-tagging efforts. Position acts as lead tagger for juvenile tagging. This position is also responsible for reports to be submitted to the project leader weekly, and daily satellite communications to Frost while in the field. Follows departmental and state policy in all matters.

Kristian Larson, Fish and Wildlife Technician 3. This position is responsible for directing all field aspects of the project under directions from the project leader and crew leader. Will ensure that all crew members are trained in the proper operation of all aspects of the project including boating safety, fish handling, data collection and recording, conduct in the public's eye, and adherence to department policies. Position will be responsible for equipment maintenance and proper operation, fieldwork schedules, and scheduling of flights. Will attempt to resolve as many personnel and administrative items as is possible and is responsible for submitting inventories to the project leader at the end of the season. This position is also responsible for reports to be submitted to the project leader weekly, and daily satellite communications to Frost while in the field if the crew leader is absent. Follows departmental and state policy in all matters.

James Bryant, Fish and Wildlife Technician 3. This position is responsible for assisting in all aspects of escapement spawning grounds sampling including safe operation of riverboats and all other equipment and various data collection and conduct in the public's eye. Ensures all crew members are trained in data collection and recording and works with the project leader and crew leader on data recordkeeping responsibilities while in the field. Follows departmental and state policy in all matters.

Corbin Lind, Fish and Wildlife Technician 2. This position is responsible for assisting in all aspects of juvenile coded-wire-tagging and escapement spawning grounds sampling including safe

operation of riverboats and all other equipment and various data collection and conduct in the public's eye. Responsible for assisting in all equipment and camp maintenance. Follows departmental and state policy in all matters.

Vacant, Fish and Wildlife Technician 2. This position is responsible for assisting in all aspects of juvenile coded-wire-tagging and escapement spawning grounds sampling including safe operation of riverboats and all other equipment and various data collection and conduct in the public's eye. Follows departmental and state policy in all matters.

Philip Richards, Fishery Biologist 3. This position is responsible for supervising and assisting in setting up all aspects of the project, including planning, budget, sample design, permits, equipment, personnel, and training. With Frost, responsible for tracking the budget, meeting reporting requirements, analysis, and publication of smolt and harvest contribution data, may assist with field operations and will arrange logistics with Frost and field crew. Follows departmental and state policy in all matters.

Randy Peterson, Biometrician 3. Provides input to and approves sampling design. Reviews and provides biometric support for operational plan, data analysis, and final report.

Ed Jones, Fish & Game Coordinator. This position provides program and budget planning oversight. Also reviews the operational plan, data analyses, and final report.

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APPENDICES

Appendix A.—Numbers of Unuk River Chinook salmon fall parr and spring smolt captured and tagged with coded wire tags, BY 1992 to present.

BY	Year tagged	Fall/ spring	Tag code	Dates tagged	Released with adipose-finclips	Estimated released with valid CWTs and adipose-finclips
1992	1993	Fall	04-38-03	10/13–10/22/93	10,304	10,263
1992	1993	Fall	04-38-04	10/25/93	439	433
1992	1993	Fall	04-38-05	10/16–10/21/93	3,192	3,093
1992	1994	Spring	04-42-06	5/05–5/23/94	2,642	2,642
1992 total					16,577	16,431
1993	1994	Fall	04-33-49	10/07–10/24/94	1,706	1,700
1993	1994	Fall	04-33-50	10/07–10/22/94	11,152	11,139
1993	1994	Fall	04-35-57	10/22–11/01/94	7,688	7,687
1993	1995	Spring	04-42-13	4/10–5/05/95	3,227	3,227
1993 total					23,773	23,753
1994	1995	Fall	04-35-56	10/07–10/10/95	11,537	11,476
1994	1995	Fall	04-35-58	10/11–10/16/95	11,645	11,645
1994	1995	Fall	04-35-59	10/17–10/24/95	11,100	10,825
1994	1995	Fall	04-42-31	10/25–10/26/95	6,324	6,260
1994	1996	Spring	04-42-07	4/13–4/23/96	6,099	6,099
1994	1996	Spring	04-42-08	4/23–4/27/96	1,357	1,357
1994 total					48,062	47,662
1995	1996	Fall	04-47-12	9/30–9/15/96	24,224	24,224
1995	1996	Fall	04-42-36	10/16–10/19/96	11,200	11,200
1995	1996	Fall	04-42-18	10/20–10/21/96	3,753	3,753
1995	1997	Spring	04-38-29	3/31–4/18/97	12,517	12,517
1995 total					51,694	51,694
1996	1997	Fall	04-47-13	10/04–10/11/97	24,303	24,176
1996	1997	Fall	04-47-14	10/06–10/11/97	22,975	22,583
1996	1997	Fall	04-47-15	10/11–10/20/97	15,396	15,146
1996	1998	Spring	04-46-46	3/29–4/05/98	11,188	11,134
1996	1998	Spring	04-43-39	4/08–4/13/98	5,987	5,987
1996 total					79,849	79,026
1997	1998	Fall	04-01-39	10/04–10/13/98	22,374	22,366
1997	1998	Fall	04-01-40	10/13–10/23/98	11,640	11,522
1997	1999	Spring	04-01-44	4/08–5/01/99	7,948	7,948
1997 total					41,962	41,836
1998	1999	Fall	04-01-42	10/04–10/17/99	16,661	16,661
1998	2000	Spring	04-02-56	4/01–4/27/00	11,124	11,124
1998	2000	Spring	04-02-57	4/29–5/4/00	2,209	2,209
1998 total					29,994	29,994
1999	2000	Fall	04-03-74	10/06–10/20/00	21,853	21,853
1999	2000	Fall	04-02-88	10/20–10/29/00	10,072	10,072
1999	2001	Spring	04-01-45	4/2–4/23/01	16,561	16,561
1999 total					48,486	48,486

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Appendix A.–Page 2 of 4.

BY	Year tagged	Fall/ spring	Tag code	Dates tagged	Released with adipose-finclips	Estimated released with valid CWTs and adipose-finclips
2000	2001	Fall	04-02-92	9/29–10/05/01	10,950	10,950
2000	2001	Fall	04-04-57	10/05–10/09/01	11,231	11,231
2000	2001	Fall	04-04-58	10/09–10/14/01	11,223	11,200
2000	2001	Fall	04-04-60	10/14–10/23/01	10,990	10,990
2000	2002	Spring	04-05-38	4/4–4/24/02	10,904	10,904
2000	2002	Spring	04-05-39	4/25–4/26/02	1,067	1,067
2000 total					56,365	56,342
2001	2002	Fall	04-05-23	9/28–10/05/02	11,402	11,402
2001	2002	Fall	04-05-24	10/05–10/13/02	11,538	11,538
2001	2002	Fall	04-05-25	10/13–10/17/02	11,778	11,778
2001	2002	Fall	04-05-26	10/17–10/20/02	11,425	11,425
2001	2002	Fall	04-46-52	10/20–10/25/02	8,403	8,403
2001	2003	Spring	04-08-07	4/8–5/10/03	11,354	11,354
2001	2003	Spring	04-08-03	5/10/2003	483	483
2001 total					66,383	66,383
2002	2003	Fall	04-08-42	9/29–10/10/03	23,255	23,255
2002	2003	Fall	04-08-10	10/10–10/14/03	11,464	11,464
2002	2003	Fall	04-04-61	10/14–10/18/03	9,779	9,779
2002	2004	Spring	04-09-75	03/29–04/10/04	11,666	11,666
2002	2004	Spring	04-09-76	04/10–04/17/04	2,730	2,730
2002 total					58,894	58,894
2003	2004	Fall	04-09-77	9/19–10/03/04	11,789	11,789
2003	2004	Fall	04-09-78	10/03–10/19/04	11,417	11,417
2003	2004	Fall	04-09-81	10/19–10/21/04	3,923	3,923
2003	2005	Spring	04-09-80	4/10–4/28/05	8,618	8,585
2003 total					35,747	35,714
2004	2005	Fall	04-11-55	9/24–10/18/05	23,330	23,330
2004	2005	Fall	04-11-56	10/18/05	941	941
2004	2006	Spring	04-11-52	4/2–4/23/06	16,371	16,269
2004 total					40,642	40,540
2005	2006	Fall	04-13-05	10/3–10/12/06	23,406	23,406
2005	2006	Fall	04-11-51	10/12–10/19/06	9,393	9,393
2005	2007	Spring	04-12-81	4/9–4/27/07	4,731	4,721
2005 total					37,530	37,520
2006	2007	Fall	04-12-82	9/30–10/03/07	11,777	11,777
2006	2007	Fall	04-12-83	10/03–10/07/07	11,716	11,716
2006	2007	Fall	04-12-84	10/07–10/13/07	11,756	11,756
2006	2007	Fall	04-12-85	10/13–10/21/07	9,840	9,840
2006	2008	Spring	04-14-62	4/19–4/27/08	10,489	10,489
2006 total					55,578	55,578
2007	2008	Fall	04-14-65	10/03–10/21/08	16,595	16,595
2007	2009	Spring	04-14-63	4/17–5/02/09	5,578	5,573
2007 total					22,173	22,168

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Appendix A.–Page 3 of 4.

BY	Year tagged	Fall/ spring	Tag code	Dates tagged	Released with adipose-finclips	Estimated released with valid CWTs and adipose-finclips
2008	2009	Fall	04-13-87	9/28–10/01/09	10,963	10,933
2008	2009	Fall	04-13-88	10/02–10/05/09	11,289	11,289
2008	2009	Fall	04-13-89	10/05–10/09/09	11,556	11,556
2008	2009	Fall	04-13-85	10/09–10/14/09	11,149	11,149
2008	2010	Spring	04-13-86	4/9–4/24/10	8,190	8,190
2008 total					53,147	53,117
2009	2010	Fall	04-13-90	9/26–10/17/10	11,630	11,619
2009	2010	Fall	04-09-95	10/17–10/22/10	4,117	4,115
2009	2011	Spring	04-09-99	4/11–4/27/11	10,216	10,216
2009 total					25,963	25,950
2010	2011	Fall	04-09-93	10/05–10/09/09	11,466	11,466
2010	2011	Fall	04-09-94	10/09–10/14/09	2,211	2,211
2010	2012	Spring	04-14-66	4/16–4/28/12	3,942	3,942
2010 total					17,619	17,619
2011	2012	Fall	04-09-91	10/03–10/08/12	10,364	10,364
2011	2012	Fall	04-14-67	9/27–10/10/12	3,292	3,292
2011	2013	Spring	04-09-90	4/13–4/25/13	6,176	6,140
2011 total					19,832	17,796
2012	2013	Fall	04-15-35	9/30-10/3/13	12,070	12,070
2012	2013	Fall	04-09-92	10/3/2013	464	464
2012	2014	Spring	04-15-36	4/12-4/29/14	12,289	12,289
2012 total					24,823	24,823
2013	2014	Fall	04-15-38	10/8-10/24/14	4,218	4,218
2013	2015	Spring	04-15-37	4/1-4/28/15	10,817	10,817
2013 total					15,035	15,035
2014	2015	Fall	04-15-40	9/28-10/20/15	10,524	10,511
2014	2016	Spring	04-15-39	4/4-4/21/16	4,003	4,003
2014 total					14,527	14,514
2015	2016	Fall	04-15-41	9/30-10/4/16	10,342	10,342
2015	2016	Fall	04-38-98	10/4-10/9/16	11,306	11,306
2015	2016	Fall	04-38-96	10/8-10/14/16	10,905	10,905
2015	2016	Fall	04-38-99	10/14-10/22/16	10,484	10,484
2015	2017	Spring	04-35-78	4/3-4/19/17	11,464	11,441
2015	2017	Spring	04-35-79	4/19-4/22/17	2,112	2,108
2015 total					54,501	56,586
2016	2017	Fall	04-35-80	10/2-10/11/17	11,318	11,318
2016	2017	Fall	04-35-81	10/12-10/27/17	11,239	11,239
2016	2017	Fall	04-47-93	10/27/2017	449	449
2016	2017	Spring	04-48-82	4/3-4/23/2018	11,028	10,984
2016	2018	Spring	04-48-83	4/23/2018	436	436
2016 total					34,470	34,426
2017	2018	Fall	04-48-80	9/29-10/10/18	11,184	11,173
2017	2018	Fall	04-48-81	10/11-10/19/18	2,482	2,482
2017	2019	Spring	04-48-79	3/26-4/20/19	3,064	3,059
2017 total					16,730	16,714

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Appendix A.–Page 4 of 4.

BY	Year tagged	Fall/ spring	Tag code	Dates tagged	Released with adipose-finclips	Estimated released with valid CWTs and adipose- finclips
2018	2019	Fall	04-47-94	9/30-10/13/19	11,362	11,362
2018	2019	Fall	04-47-95	10/13-10/24/19	8,151	8,127
2018	2019	Fall	04-47-96	10/25-10/28/19	2,276	2,276
2018	2020	Spring	04-47-98	3/29 – 4/17/20	10,794	10,758
2018	2020	Spring	04-47-99	4/18 – 4/23/20	790	788
2018 total					33,373	33,311
2019	2020	Fall	04-54-03	9/27 - 10/11/20	10,487	10,485
2019	2020	Fall	04-54-04	10/11 - 10/17/20	11,671	11,671
2019	2020	Fall	04-54-05	10/17 - 10/23/20	11,495	11,495
2019	2020	Fall	04-54-06	10/23 - 10/25/20	1,950	1,950
2020	2021	Spring	04-55-61	3/25 - 4/21/21	6,182	6,179
2019 total					41,785	41,780
2020 total					39,938	39,919
2020	2021	Fall	04-55-57	10/5 - 10/10/21	11,402	11,402
2020	2021	Fall	04-55-58	10/10 - 10/20/21	11,619	11,612
2020	2021	Fall	04-55-59	10/21 - 10/27/21	7,870	7,870
2020	2022	Spring	04-15-03	3/30 - 4/25/22	9,047	9,035
2020 total					39,938	39,919

Appendix B.–Data pertaining to adipose-finclip and coded wire tag fractions by brood year (1992–2018) for Unuk River Chinook salmon.

Brood Year	Age	Year Sampled	Sampled	Adipose-Finclips	Sacrificed	CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs ^a
						Fall	Spring	Total			
1992	1.2	1996	33	0	0	0	0	0	–	0.0	–
1992	1.3	1997	436	11	11	10	1	11	100.0	2.5	2.5
1992	2.2	1997	1	0	0	0	0	0	–	0.0	–
1992	1.4	1998	324	15	11	4	4	8	72.7	4.6	3.4
1992	1.5	1999	1	0	0	0	0	0	–	0.0	–
1992 total			795	26	22	14	5	19	86.4	3.3	2.8
1993	1.1	1996	4	1	1	1	0	1	100.0	25.0	25.0
1993	1.2	1997	300	35	35	28	3	31	88.6	11.7	10.3
1993	1.3	1998	736	63	48	36	8	44	91.7	8.6	7.8
1993	2.2	1998	1	0	0	0	0	0	–	0.0	–
1993	1.4	1999	325	34	19	14	4	18	94.7	10.5	9.9%
1993	1.5	2000	9	0	0	0	0	0	–	0.0	–
1993 total			1,375	133	103	79	15	94	91.3	9.7	8.8
1994	1.1	1997	56	4	4	2	2	4	100.0	7.1	7.1
1994	1.2	1998	311	31	28	14	11	25	89.3	10.0	8.9
1994	2.1	1998	1	0	0	0	0	0	–	0.0	–
1994	1.3	1999	421	45	14	6	5	11	78.6	10.7	8.4
1994	1.4	2000	247	12	7	3	3	6	85.7	4.9	4.2
1994	1.5	2001	4	0	0	0	0	0	–	0.0	–
1994 total			1,040	92	53	25	21	46	86.8	8.8	7.7
1995	1.1	1998	81	15	14	8	5	13	92.9	18.0%	17.2
1995	0.2	1998	1	0	0	0	0	0	–	0.0	–
1995	1.2	1999	462	54	45	29	16	45	100.0	11.7	11.7
1995	1.3	2000	742	77	20	9	7	16	80.0	10.4	8.3%
1995	1.4	2001	512	53	19	12	7	19	100.0	10.4	10.4%
1995	1.5	2002	6	1	1	1	0	1	100.0	16.7	16.7
1995	2.4	2002	1	0	0	0	0	0	–	0.0	–
1995 total			1,805	200	99	59	35	94	94.9	11.1	10.5
1996	0.1	1998	2	0	0	0	0	0	–	0.0	–
1996	1.1	1999	65	6	6	4	1	5	83.3	9.2	7.7
1996	1.2	2000	541	69	49	33	14	47	95.9	12.8	12.2
1996	1.3	2001	1,177	137	43	27	11	38	88.4	11.6	10.3
1996	1.4	2002	551	58	15	11	4	15	100.0	10.5	10.5
1996	1.5	2003	7	1	0	0	0	0	–	14.3	–
1996 total			2,343	271	113	75	30	105	92.9	11.6	10.7

-continued-

Appendix B.–Page 2 of 5.

Brood Year	Year Age	Year Sampled	Adipose- Sampled	Finclips	Sacrificed	CWTs			% Clips w/CWTs	%Adipose- Finclips	% CWTs
						Fall	Spring	Total			
1997	1.1	2000	12	1	1	0	1	1	100.0	8.3	8.3
1997	1.2	2001	189	26	23	12	5	17	73.9	13.8	10.2
1997	0.4	2002	1	0	0	0	0	0	–	0.0	–
1997	1.3	2002	598	56	7	4	3	7	100.0	9.4	9.4
1997	2.2	2002	1	0	0	0	0	0	–	0.0	–
1997	1.4	2003	379	31	6	4	0	4	66.7	8.2	5.5
1997	1.5	2004	6	2	0	0	0	0	–	33.3	–
1997 total			1,186	116	37	20	9	29	78.4	9.8	7.7
1998	1.1	2001	31	3	3	0	3	3	100.0	9.7	9.7
1998	1.2	2002	419	26	21	12	9	21	100.0	6.2	6.2
1998	0.4	2003	1	0	0	0	0	0	–	0.0	–
1998	1.3	2003	1,112	117	28	11	17	28	100.0	10.5	10.5
1998	2.2	2003	1	0	0	0	0	0	–	0.0	–
1998	1.4	2004	542	51	1	1	0	1	100.0	9.4	9.4
1998	1.5	2005	6	1	0	0	0	0	–	16.7	–
1998 total			2,112	198	53	24	29	53	100.0	9.4	9.4
1999	0.2	2002	1	0	0	0	0	0	–	0.0	–
1999	1.1	2002	3	0	0	0	0	0	–	0.0	–
1999	1.2	2003	147	15	13	7	5	12	92.3	10.2	9.4
1999	1.3	2004	396	49	3	2	1	3	100.0	12.4	12.4
1999	2.3	2005	4	0	0	0	0	0	–	0.0	–
1999	1.4	2005	200	15	6	1	3	4	66.7	7.5	5.0
1999	1.5	2006	1	0	0	0	0	0	–	0.0	–
1999 total			752	79	22	10	9	19	86.4	10.5	9.1
2000	1.1	2003	72	4	4	2	2	4	100.0	5.6	5.6
2000	1.2	2004	804	62	52	29	22	51	98.1	7.7	7.6%
2000	2.2	2005	1	1	1	1	0	1	100.0	100.0	100.0
2000	1.3	2005	1,158	107	15	10	3	13	86.7	9.2	8.0
2000	1.4	2006	529	46	2	2	0	2	100.0	8.7	8.7
2000	2.3	2006	1	0	0	0	0	0	–	0.0	–
2000	1.5	2007	8	0	0	0	0	0	–	0.0	–
2000 total			2,573	220	74	44	27	71	95.9	8.6%	8.2%
2001	1.1	2004	36	7	7	5	2	7	100.0	19.4	19.4
2001	1.2	2005	186	20	17	11	5	16	94.1	10.8	10.1
2001	1.3	2006	618	57	7	5	1	6	85.7	9.2	7.9
2001	2.2	2006	1	0	0	0	0	0	–	0.0	–
2001	1.4	2007	272	29	4	2	2	4	100.0	10.7	10.7
2001	2.3	2007	2	0	0	0	0	0	–	0.0	–
2001	1.5	2008	4	1	1	0	0	0	0.0	25.0	0.0
2001 total			1,119	114	36	23	10	33	91.7	10.2	9.3

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Appendix B.–Page 3 of 5.

Brood Year	Year Age	Year Sampled	Adipose-Sampled	Adipose-Finclips	Sacrificed	CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs
						Fall	Spring	Total			
2002	1.1	2005	70	5	5	1	1	2	40.0	7.1	2.9
2002	1.2	2006	794	58	46	21	14	35	76.1	7.3	5.6
2002	1.3	2007	1,266	120	19	10	4	14	73.7	9.5	7.0
2002	1.4	2008	423	48	4	3	0	3	75.0	11.3	8.5
2002	1.5	2009	4	1	0	0	0	0	–	25.0	–
2002 total			2,557	232	74	35	19	54	73.0	9.1	6.6
2003	1.1	2006	28	2	2	1	1	2	100.0	7.1	7.1
2003	1.2	2007	218	22	21	8	10	18	85.7	10.1	8.7
2003	2.1	2007	1	0	0	0	0	0	–	0.0	–
2003	1.3	2008	324	30	2	1	1	2	100.0	9.3	9.3
2003	1.4	2009	151	14	3	1	2	3	100.0	9.3	9.3
2003	2.3	2009	1	0	0	0	0	0	–	0.0	–
2003	1.5	2010	3	0	0	0	0	0	–	0.0	–
2003 total			726	68	28	11	14	25	89.3	9.4	8.4
2004	0.2	2007	1	0	0	0	0	0	–	0.0	–
2004	0.2	2007	1	0	0	0	0	0	–	0.0%	–
2004	1.1	2007	38	5	5	2	3	5	100.0	13.2	13.2%
2004	0.3	2008	1	0	0	0	0	0	–	0.0	–
2004	1.2	2008	216	18	14	4	4	8	57.1	8.3	4.8
2004	1.3	2009	581	57	15	4	5	9	60.0	9.8	5.9
2004	2.3	2010	1	0	0	0	0	0	–	0.0	–
2004	1.4	2010	161	7	2	1	1	2	100.0	4.3	4.3
2004	1.5	2011	1	0	0	0	0	0	–	0.0	–
2004 total			1,000	87	36	11	13	24	66.7	8.7	5.8
2005	0.1	2007	1	0	0	0	0	0	–	0.0	–
2005	1.1	2008	25	2	2	2	0	2	100.0	8.0	8.0
2005	1.2	2009	582	44	43	20	16	36	83.7	7.6	6.3
2005	2.2	2010	1	0	0	0	0	0	–	0.0	–
2005	1.3	2010	663	51	7	5	1	6	85.7	7.7	6.6
2005	1.4	2011	143	16	2	2	0	2	100.0	11.2	11.2
2005	1.5	2012	0	0	0	0	0	0	–	–	–
2005 total			1,415	113	54	29	17	46	85.2	8.0	6.8
2006	1.1	2009	20	2	2	1	0	1	50.0	10.0	5.0
2006	0.3	2010	1	0	0	0	0	0	–	0.0	–
2006	1.2	2010	222	13	12	7	3	10	83.3	5.9	4.9
2006	1.3	2011	354	17	5	5	0	5	100.0	4.8	4.8
2006	1.4	2012	44	4	3	2	1	3	100.0	9.1	9.1
2006	1.5	2013	–	–	–	–	–	–	–	–	–
2006 total			641	36	22	15	4	19	86.4	5.6	4.9
2007	1.1	2010	23	1	1	1	0	1	100.0	4.3	4.3
2007	1.2	2011	172	5	5	3	1	4	80.0	2.9	2.3
2007	1.3	2012	199	8	2	1	1	2	100.0	4.0	4.0
2007	1.4	2013	44	3	1	0	0	0	–	6.8	–
2007	1.5	2014	–	–	–	–	–	–	–	–	–
2007 total			438	17	9	5	2	7	77.8	3.9	3.0

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Appendix B.–Page 4 of 5.

Brood Year	Age	Year Sampled	Sampled	Adipose-			CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs
				Finclips	Sacrificed	Fall	Spring	Total				
2008	1.1	2011	11	0	0	0	0	0	–	–	–	
2008	1.2	2012	117	16	16	5	10	15	93.8	13.7	12.8	
2008	1.3	2013	152	16	4	3	1	4	100	10.5	10.5	
2008	1.4	2014	47	3	1	0	0	0	–	6.4	–	
2008	1.5	2015	0	0	0	0	0	0	–	–	–	
2008 total			327	35	21	8	11	19	90.5	10.7	9.7	
2009	1.1	2012	23	1	1	0	1	1	100.0	4.3	4.3	
2009	1.2	2013	90	3	2	0	1	1	50.0	3.3	1.7	
2009	1.3	2014	173	12	5	2	3	5	100.0	6.9	6.9	
2009	1.4	2015	35	0	0	0	0	0	–	–	–	
2009	1.5	2016	–	–	–	–	–	–	–	–	–	
2009 total			321	16	8	2	5	7	87.5	5.0	4.4	
2010	1.1	2013	10	0	0	0	0	0	–	0.0	–	
2010	1.2	2014	119	5	5	2	3	5	100.0	4.2	4.2	
2010	1.3	2015	258	8	1	1	0	1	100.0	3.1	3.1	
2010	1.4	2016	47	1	1	1	0	1	100.0	2.1	2.1	
2010	1.5	2017	1	–	–	–	–	–	–	–	–	
2010 total			435	14	7	4	3	7	100.0	3.2	3.2	
2011	1.1	2014	9	4	3	2	1	3	75	44.4	33.3	
2011	1.2	2015	146	6	4	1	2	3	75	4.1	3.1	
2011	1.3	2016	225	9	9	2	6	8	88.9	4.0	3.6	
2011	1.4	2017	51	1	0	0	0	0	–	2	–	
2011	1.5	2018	–	–	–	–	–	–	–	–	–	
2011 total			155	10	8	3	3	6	82.4	4.6	3.8	
2012	1.1	2015	4	1	1	0	1	1	100	25	25	
2012	1.2	2016	63	3	2	1	1	2	100	4.8	54.5	
2012	1.3	2017	155	6	1	1	0	1	100	3.9	3.9	
2012	1.4	2018	39	2	2	0	2	2	100	5.1	5.1	
2012	1.5	2019	–	–	–	–	–	–	–	–	–	
2012 total			261	12	6	2	4	6	100	4.6	4.6	
2013	1.1	2016	38	7	3	0	3	3	100	18.4	18.4	
2013	1.2	2017	145	16	15	7	5	12	80	11	8.8	
2013	1.3	2018	282	24	2	0	2	2	100	8.5	8.5	
2013	1.4	2019	40	2	1	0	1	1	100	5	5	
2013	1.5	2020	–	–	–	–	–	–	–	–	–	
2013 total			506	50	22	7	11	18	81.8	9.9	8.1	

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Appendix B.–Page 5 of 5.

Brood Year	Age	Year Sampled	Sampled	Adipose-		CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs
				Finclips	Sacrificed	Fall	Spring	Total			
2014	1.1	2017	51	5	4	2	2	4	100	9.8	9.8
2014	1.2	2018	346	18	11	3	6	9	81.8	5.2	4.3
2014	1.3	2019	694	46	15	10	3	13	86.7	6.6	5.7
2014	1.4	2020	27	4	0	0	0	0	-	14.8	-
2014	1.5	2021	-	-	-	-	-	-	-	-	-
2014 total			1,119	73	30	15	11	26	86.7	6.5	5.7
2015	1.1	2018	10	2	2	1	1	2	100	20	20
2015	1.2	2019	214	26	24	14	7	21	87.5	12.1	10.6
2015	1.3	2020	302	48	25	14	8	22	88	15.9	14
2015	1.4	2021	49	9	0	0	0	0	-	18.4	-
2015	1.5	2022	-	-	-	-	-	-	-	-	-
2015 total			xxx	xx	x	x	x	x	xx	xx	xx
2016	1.1	2019	169	36	36	16	19	35	97.2	21.3	20.7
2016	1.2	2020	234	38	33	19	14	33	100	16.2	16.2
2016	1.3	2021	445	79	7	0	7	7	100	17.8	17.8
2016	1.4	2022	-	-	-	-	-	-	-	-	-
2016	1.5	2023	-	-	-	-	-	-	-	-	-
2016 total			xxx	xx	x	x	x	x	xx	xx	xx
2017	1.1	2020	44	7	7	4	3	7	100	15.9	15.9
2017	1.2	2021	271	15	11	5	6	11	100	5.5	5.5
2017	1.3	2022	-	-	-	-	-	-	-	-	-
2017	1.4	2023	-	-	-	-	-	-	-	-	-
2017	1.5	2024	-	-	-	-	-	-	-	-	-
2017 total			xxx	xx	x	x	x	x	xx	xx	xx
2018	1.1	2021	134	10	10	7	2	9	90%	7.5%	6.7%
2018	1.2	2022	-	-	-	-	-	-	-	-	-
2018	1.3	2023	-	-	-	-	-	-	-	-	-
2018	1.4	2024	-	-	-	-	-	-	-	-	-
2018	1.5	2025	-	-	-	-	-	-	-	-	-
2018 total			xxx	xx	x	x	x	x	xx	xx	xx

^a $\hat{\theta}_i$ in Equation (16)

Note: An en-dash (–) either indicates that the quantity could not be calculated (division by zero), or the data have not been collected.

Appendix C.–Juvenile Finfish Tissue Sampling for DNA Analysis.

The following appendix was provided by the Genetics Lab (Kyle Shedd, *personal communication*).

I. General Information

We use the mucus samples from juvenile fish using OmniSwab to determine the genetic characteristics and profile of a particular run or stock of fish. The most important thing to remember in collecting sample is that only quality tissue samples give quality results. If sampling from carcasses: tissues need to be as “fresh” and as cold as possible and recently moribund, do not sample from fungal fish.

II. Sampling Method



Figure 1



Figure 2

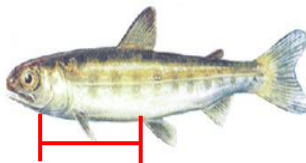


Figure 3

-continued-

III. Sampling Instructions

Steps for taking mucus samples in 2.0 ml vials:

- Organize work area prior to sampling.
- Hinged plastic box will hold up to 50 silica pre-filled vials. Works best with 40 vials or less so hinged lid can close easily between sampling events.
- Lift lid on white box, should be marker line upper left edge of box bottom; starting vial #1,2,3 ... left to right.
- Load plastic box with vial #s 1,2,3 ... in consecutive order. All vials remain capped until sampling each fish. Do not uncapped vials ahead of time since silica will begin absorbing moisture. Want to minimize exposure time to moisture.
- Cover work area (cooler, tarp, raincoat, backpack, under tree) to protect samples from rain and/or direct sunlight.
- Wipe right hand dry before opening each OmniSwab to reduce excess water dripping on swab pad applicator.
- Dry hands, open OmniSwab by peeling package open at the handle end of swab and remove carefully.
- Pick up one fish and hold in palm of left hand with belly side up (Figure 1).
- Do not touch swab pad applicator (Figure 2).
- Sample location on fish is located between lower jaw and front of pelvic fin (Figure 3).
- Hold OmniSwab handle in right hand, gently rub the swab pad serrated edge against preferred area (Figure 3 and below):
 - Rub swab pad back/forth 8-10 times (back and forth, one time).
 - Very important to complete total 10 swab cycles!
- Be careful not to depress ejector tip while swabbing fish.
- Once sampling is complete, release fish back to the local stream or waterway.
- Uncap vial with dry hand after sample is taken. Tilt vial on slight angle making room for swab pad in silica beads and eject swab pad (using release button at tip) into one vial. Cap and swiftly shake capped vial to distribute silica beads around applicator pad to enhance drying process.
- Place only one swab pad per vial!
- Record metadata (vial #, date, location, lat/long, etc...) electronic copy preferred.
- Place each individual vial back into white storage box, working from vial #s 1,2,3 ... 100 consecutively until the entire box of 100 vials are full.

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- Swab pads will slowly dry inside capped vials and be dry by the end of the day.
- In field: store vial collection at room temperature away from heat and/or place in dry cooler or tote.

IV. Supplies included in sampling kit

1. OmniSwab – plastic applicator swab for collecting mucus from fish.
2. 2.0 ml vials – pre-labeled individual vial and cap for sample storage.
3. Silica beads – vial pre-filled ½ silica beads/capped prior to sampling.
4. White boxes – storage for individual capped vials with silica beads.
5. Hinged plastic box – used while sampling, protects vials from rain.
6. Sampling instructions.

V. Shipping

No special paperwork required for return shipment of these samples. Address the sealed mailer box for return shipment to ADF&G Genetics lab:

Return to ADF&G Anchorage Genetics Lab:	ADF&G – Genetics 333 Raspberry Road Anchorage, Alaska 99518	Lab staff: 907-267-2247 Judy Berger: 907-267-2175 Freight code: _____
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Appendix D.—Unuk River spawning grounds age, sex, and length form, 2022.

Location: _____
 Stream code: _____
 Species: _____

Year: 2022

Fish #	Date	Sex	Length			FW	SW	AEC	LAA	UOP	Ad Clip Cinch #	Gear type	Fish condition	Comments
			METF (mm)	Card #	Scale #									
1	8/3	M	860	1	1				N	N	YES	Lure	Pre	Adclip released
2	8/4	F	720	1	2				N	N		Lure	Pre	
3	8/4	F	865	1	3				N	N		Lure	Active	
4	8/4	M	585	1	4				Y	Y		Lure	Active	Spag tag
5	8/4	F	720	1	5				N	N		Snag	Pre	
6	8/4	M	655	1	6				N	N	433110	Lure	Active	Adclip sacrificed (adsac)
7	8/19	F	945	1	7				N	N		Snag	Active	
8	8/19	M	880	1	8				N	N		Dipnet	Active	
9	8/19	M	725	1	9				Y	Y	YES	Snag	Active	Adclip released, spag tag
10	8/19	M	1005	1	10				N	N		Carcass	Dead	
11	8/19	F	820	2	11				N	N		Snag	Post	
12	8/19	F	785	2	12				N	N		Snag	Post	
13	8/24	F	820	2	13				N	N	433111	Snag	Post	Adsac
14	8/24	M	345	2	14				N	N		Carcass	Dead	
15	8/24	M	785	2	15				N	U		Carcass	Dead	Opercle plate missing
16	8/26	M	865	2	16				N	N	433126	Carcass	Dead	Adsac, SELECT, LLOP

Commercial Fisheries Division CWT Daily Log Form

Date _____

Tagging Site: _____

Species: _____

Machine Serial #: _____

Today's Tag Code: _____

a	Machine ending number	_____
b	Machine beginning number	_____
c	# of Injections (a-b)	_____
d	Retags/Morts/Etc.	_____
e	# tagged fish for this day (c-d)	_____
f	Overnight mortality	_____
g	Total tagged fish (e-f)	_____

Recaptures from Minnow Traps:

h	# with CWTs	_____
i	# without CWTs	_____
j	Total # recaptures (h+i)	_____

24-Hour Retention:

k	# with CWTs	_____
l	# without CWTs	_____
m	Total # tested (k+l)	_____
n	Short-term retention % (k/m)	_____
o	Valid tagged and released (n x g)	_____

Cumulative Tagged and Released (code specific) _____

Appendix G.–Adult Finfish Tissue Sampling for DNA Analysis.

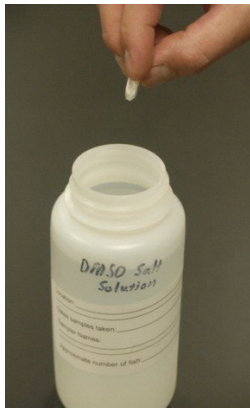
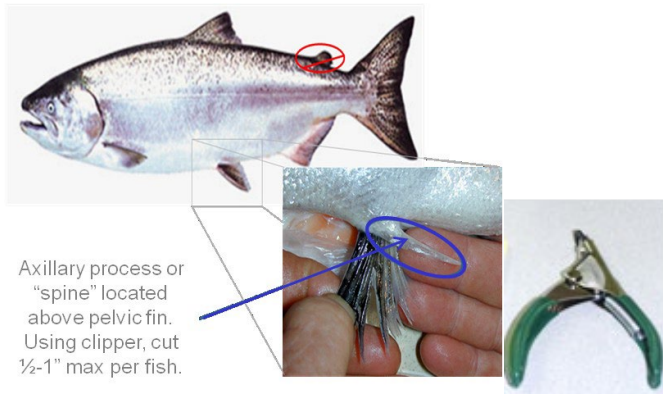
The following appendix was provided by the ADF&G Gene Conservation Lab (Genetics Lab), Anchorage (Kyle Shedd, *personal communication*).

I. General Information

We use axillary process samples from individual fish to determine the genetic characteristics and profile of a particular run or stock of fish. This is a non-lethal method of collecting tissue samples from adult fish for genetic analysis. The most important thing to remember in collecting samples is that only quality tissue samples give quality results. If sampling from carcasses: tissues need to be as “fresh” and as cold as possible and recently moribund, do not sample from fungal fins.

Preservative used: Isopropanol/Methanol/Ethanol (EtOH) preserves tissues for later DNA extraction. Avoid extended contact with skin.

II. Sampling Method



SILLY: _____
Location: _____
Sample Date(s): ___/___/___
Sampler's name: _____
Total # fish sampled: _____
Latitude: _____
Longitude: _____
Species: _____
Comments: _____
ADF&G: Preserved in EtOH

-continued-

III. Sampling Instructions

Sampling instructions are written for (N = 100 fish / 125 ml) bulk bottle. Steps for collecting axillary process tissues:

- Wipe dry the axillary process “spine” prior to sampling to avoid getting excess water or fish slime into the 125 ml bottle (see diagram).
- Clip off the axillary “spine” using dog nail clippers or scissors to get roughly a ½ - 1” inch maximum piece and/or about the size of a small fingernail.
- Place each tissue piece into bulk bottle (place only one piece of axillary from each fish).
- Repeat: up to 100 fish / 125 ml bulk bottle (into same bottle). If you don’t reach this number of fish per location, that’s ok. Maximum storage capacity 125 ml bulk for proper preservation of axillary tissue is (N = 100).
- Record on each label: Location, sampling date (mm/dd/yyyy), sampler’s name(s), total number of fish sampled, latitude/longitude, and field notes (if any). Use pencil. This insures correct data with each collection bottle.
- If collection occurs over 4~5-day period, “refresh” EtOH at end of the collection.
- After the collection is complete and 24 hours have passed, “refresh” the axillary tissues as follows: carefully pour off ¾ EtOH and then pour fresh EtOH into sample bottle containing axillary clips. Cap and invert bottle twice mixing EtOH and tissue.
- Freezing not required, store sample bottle in upright cool location for good tissue quality.

IV. Supplies included in sampling kit

1. Clipper- used to cut a portion of **one** axillary process per fish.
2. Sample target: 100 axillary clips / 125 ml bulk bottle.
3. Labels on bulk sample bottles: Location, Sample date, Sampler, Total # fish sampled and comments (if any).
4. 1:125 ml wide mouth bottle(s) for EtOH “refresh” step.
5. Sampling instructions.

V. Shipping

Address the sealed mailer box for return shipment to ADF&G Genetics lab:

Return to ADF&G Anchorage Genetics Lab:	ADF&G – Genetics 333 Raspberry Road Anchorage, Alaska 99518	Lab staff: 907-267-2247 Judy Berger: 907-267-2175 Freight code: _____
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Appendix H.—Coded wire tag anadromous stream numbers, sample numbers, and stream codes for the Unuk River and its tributaries.

Location	Anadromous Stream #	Sample numbers	Stream code
Unuk River	101-75-10300	06930xxx	101-75-030
Boulder Creek	101-75-10300-BOULDER	0693975x	101-75-030-BOULDER
Boundary Creek	101-75-10300-2999	06939xxx	101-75-30B
Chum Creek	101-75-10300-CHUM	069305xx	101-75-030-CHUM
Clear Creek	101-75-10300-2014-3004	06933xxx	101-75-30C
Cripple Creek	101-75-10300-2030	06938xxx	101-75-30Q
Cutthroat Slough	101-75-10300-CUTTHROAT	069325xx	101-75-030-CUTTHROAT
Eulachon River	101-75-10150	06932xxx	101-75-015
Genes Lake Creek	101-75-10300-2022	06937xxx	101-75-30G
Grizzly Slough	101-75-10300-GRIZZLY	069315xx	101-75-030-GRIZZLY
Hell Roaring Creek	101-75-10300-HELLROARING	069395xx	101-75-030-HELLROARING
Kerr Creek	101-75-10300-2019	06936xxx	101-75-30K
Lake Creek	101-75-10300-2014	06934xxx	101-75-30L
Rockface	101-75-10300-ROCKFACE	069335xx	101-75-030-ROCKFACE



Alaska Department of Fish and Game
Coded Wire Tag Sampling Form
Rack Return and Escapement Survey
Southeast Region

Page Info for this Sample Number only! See instructions → PAGE OF PAGES

SAMPLE NUMBER:

SOURCE: (circle one) rack return escapement survey hatchery other

SURVEY SITE: _____

SAMPLE TYPE: random select

SAMPLER: _____

DATE SAMPLED: - -

SAMPLING INFORMATION				AREA INFORMATION (DISTRICT - SUBDISTRICT)							
This Box to be completed for RANDOM Samples Only				101-	106-	111-	116-	157-	191-		
				102-	107-	112-	150-	181-	192-		
				103-	108-	113-	152-	182-	OTHER DISTRICTS		
				104-	109-	114-	154-	183-			
				105-	110-	115-	156-	189-			
				NAME of PLACE SURVEYED: (HATCHERY OR STREAM) _____							
				WATER TYPE: saltwater freshwater							
				ANADROMOUS STREAM# (FRESHWATER-ONLY) _____							
SAMPLING INFORMATION				HEAD RECOVERY INFORMATION							
SPECIES (CODE)	TOTAL # FISH CHECKED FOR AD-CLIPS	# AD-CLIPS SEEN	WERE ALL CHECKED?	HEAD NUMBER	SPECIES CODE	LENGTH (mid-eye to fork in mm)	CLIP	SEX			
(410)CHIN	_____	_____	y n	<input checked="" type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(411)JACK CHINOOK-ONLY	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(420)SOCK	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(430)COHO	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(440)PINK	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(450)CHUM	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		
(540)STHD	_____	_____	y n	<input type="checkbox"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>		

COMMENTS

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Appendix J.–Predicting escapement from index counts using an expansion factor.

The expansion factor provides a means of predicting escapement in years where only an index count of the escapement is available, i.e., no weir counts or mark–recapture experiments were conducted. The expansion factor is the average over several years of the ratio of the escapement estimate (or weir count) to the index count.

Systems where escapement is known

On systems where escapement can be completely enumerated with weirs or other complete counting methods, the expansion factor is an estimate of the expected value of the “population” of annual expansion factors (π 's) for that system:

$$\bar{\pi} = \frac{\sum_{y=1}^k \pi_y}{k} \quad (1)$$

where $\pi_y = N_y / C_y$ is the observed expansion factor in year y , N_y is the known escapement in year y , C_y is the index count in year y , and k is the number of years for which these data are available to calculate an annual expansion factor.

The estimated variance for expansion of index counts needs to reflect two sources of uncertainty for any predicted value of π , (π_p). First is an estimate of the process error ($var(\pi)$ –the variation across years in the π 's, reflecting, for example, weather or observer-induced effects on how many fish are counted in a survey for a given escapement), and second is the sampling variance of $\bar{\pi}$ ($var(\bar{\pi})$), which will decline as we collect more data pairs.

The variance for prediction will be estimated (Neter et al. 1990):

$$\hat{var}(\pi_p) = \hat{var}(\pi) + \hat{var}(\bar{\pi}) \quad (2)$$

where

$$\hat{var}(\pi) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k - 1} \quad (3)$$

and

$$\hat{var}(\bar{\pi}) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k(k - 1)} \quad (4)$$

such that

$$\hat{var}(\pi_p) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k - 1} + \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k(k - 1)} \quad (5)$$

Systems where escapement is estimated

On systems where escapement is estimated, the expansion factor is an estimate of the expected value of the “population” of annual expansion factors (π 's) for that system:

-continued-

$$\bar{\pi} = \frac{\sum_{y=1}^k \hat{\pi}_y}{k} \quad (6)$$

where $\hat{\pi}_y = \hat{N}_y / C_y$ is the estimate of the expansion factor in year y , \hat{N}_y is the estimated escapement in year y , and C_y is the index count in year y .

The variance for prediction will again be estimated:

$$\hat{var}(\pi_p) = \hat{var}(\pi) + \hat{var}(\bar{\pi}) \quad (7)$$

The estimate of $var(\pi)$ should again reflect only process error. Variation in $\hat{\pi}$ across years, however, represents process error plus measurement error within years (e.g. the mark–recapture induced error in escapement estimation) and is described by the relationship (Mood et al. 1974):

$$V(\hat{\pi}) = V[E(\hat{\pi})] + E[V(\hat{\pi})] \quad (8)$$

This relationship can be rearranged to isolate process error, that is:

$$V[E(\hat{\pi})] = V[\hat{\pi}] - E[V(\hat{\pi})] \quad (9)$$

An estimate of $var(\pi)$ representing only process error therefore is:

$$\hat{var}(\pi) = \hat{var}(\hat{\pi}) - \frac{\sum_{y=1}^k \hat{var}(\hat{\pi}_y)}{k} \quad (10)$$

where $\hat{var}(\hat{\pi}_y) = \hat{var}(\hat{N}_y) / C_y^2$ and $\hat{var}(\hat{N}_y)$ is obtained during the experiment when N_y is estimated.

We can calculate:

$$\hat{var}(\hat{\pi}) = \frac{\sum_{y=1}^k (\hat{\pi}_y - \bar{\pi})^2}{k - 1} \quad (11)$$

and we can estimate $var(\bar{\pi})$ similarly to as we did above:

$$\hat{var}(\bar{\pi}) = \frac{\sum_{y=1}^k (\hat{\pi}_y - \bar{\pi})^2}{k(k - 1)} \quad (12)$$

where both process and measurement errors need to be included.

For large k ($k > 30$), Equation (11) and Equation (12) provide reasonable parameter estimates, however for small k the estimates are imprecise and may result in negative estimates of variance when the results are applied as in Equation (7).

-continued-

Because k is typically < 10 , we will estimate $var(\hat{\pi})$ and $var(\bar{\pi})$ using parametric bootstrap techniques Efron and Tibshirani (1993). The sampling distributions for each of the $\hat{\pi}_y$ are modeled using Normal distributions with means $\hat{\pi}_y$ and variances $\hat{var}(\hat{\pi}_y)$. At each bootstrap iteration, a bootstrap value $\hat{\pi}_{y(b)}$ is drawn from each of these Normal distributions and the bootstrap value $\hat{\pi}_{(b)}$ is randomly chosen from the k values of $\hat{\pi}_{y(b)}$. Then, a bootstrap sample of size k is drawn from the k values of $\hat{\pi}_{y(b)}$ by sampling with replacement, and the mean of this bootstrap is the bootstrap value $\bar{\pi}_{(b)}$. This procedure is repeated $B = 1,000,000$ times. We can then estimate $var(\hat{\pi})$ using:

$$\hat{var}_B(\hat{\pi}) = \frac{\sum_{b=1}^B (\hat{\pi}_{(b)} - \bar{\pi}_{(b)})^2}{B-1} \quad (13)$$

where

$$\bar{\pi}_{(b)} = \frac{\sum_{y=1}^k \hat{\pi}_{y(b)}}{B} \quad (14)$$

and we can calculate $var_B(\bar{\pi})$ using Equation (13) and Equation (14) with appropriate substitutions. The variance for prediction is then estimated:

$$\hat{var}(\pi_p) = \hat{var}_B(\hat{\pi}) - \frac{\sum_{y=1}^k \hat{var}(\hat{\pi}_y)}{k} + \hat{var}_B(\bar{\pi}) \quad (15)$$

As the true sampling distributions for the $\hat{\pi}_y$ are typically skewed right, using a Normal distribution to approximate these distributions in the bootstrap process will result in estimates of $var(\hat{\pi})$ and $var(\bar{\pi})$ that are biased slightly high, but simulation studies using values similar to those realized for this application indicated that the bias in Equation (15) is $< 1\%$.

Predicting Escapement

In years when an index count (C_p) is available, but escapement (N_p) is not known, it can be predicted:

$$\hat{N}_p = \bar{\pi} C_p \quad (16)$$

and

$$\hat{var}(\hat{N}_p) = C_p^2 \hat{var}(\pi_p). \quad (17)$$