Regional Operational Plan No. ROP.SF.1J.2022.20

Operational Plan: Production and Harvest of Unuk River Chinook Salmon, 2020–2022

by

Nathan Frost

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and

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September 2022

Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

Symbols and Abbreviations

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

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

General

Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat or long
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	′
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	″
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

REGIONAL OPERATIONAL PLAN NO. ROP.SF.1J.2022.20

OPERATIONAL PLAN: PRODUCTION AND HARVEST OF UNUK RIVER CHINOOK SALMON, 2020-2022

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September 2022

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SIGNATURE/TITLE PAGE

Project Title:	Production and harvest of Unuk River Chinook salmon, 2020-2022.
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Approval

Title	Name	Signature	Date
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ABSTRACT

This plan describes the coded-wire tagging of juvenile Chinook salmon *Oncorhynchus tshawytscha* on the Unuk River for the 2019 and 2020 brood years, which covers the coded-wire tagging of parr in fall of 2020 and 2021 and smolt in spring of 2021 and 2022, and sampling returning adults for age, sex, length, and coded-wire tags in escapement from the 2022 through 2027 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 2020 and 2021. The primary goals of this and the companion study are to estimate inriver run size, total run size, marine harvest-exploitation rate and 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 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

PURPOSE

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) 1992–2012, with brood years 2013–2017 in progress.

The information provided from these studies was used to establish the current biological escapement goal (BEG) for the Unuk River (Hendrich et al. 2008). The BEG also meets provisions of the 2020 Pacific Salmon Treaty. This Treaty 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 is 1 of 12 stocks chosen by the ADF&G as an indicator stock for the Chinook Salmon Research Initiative (CSRI) program (ADF&G 2013). These rivers were chosen to help address issues of low production for Chinook salmon statewide. The recent downturn in Chinook salmon production initiated a look at production statewide and identification of gaps in our knowledge base. 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 Power 2016).

BACKGROUND

The Unuk, Chickamin, Blossom, and Keta rivers traverse the Misty Fjords National Monument (Figure 1). The Unuk and Chickamin rivers produce the largest natural runs of Chinook salmon *Oncorhynchus tshawytscha* in southern SEAK and flow into Behm Canal, a narrow saltwater passage east of Ketchikan. The Unuk River is used as indicator stock by the PSC (PSC 2020). The escapements in these streams are indexed using standardized surveys conducted by helicopter and foot. Concerns for Chinook salmon escapements in Behm Canal systems were raised in 1992 when escapement indices dropped in all 4 rivers. 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 (MEF)) Chinook salmon in the Unuk River in 1994 (Pahlke et al. 1996), from 1997 through 2009 and 2011; the 2010, 2012–2014 mark-recapture estimates were considered untrustworthy, so aerial expansion estimates were used (Jones et al. 1998; Jones and McPherson 1999, 2000, 2002; Weller and McPherson 2003a-b, 2004, 2006a-b; Weller and Evans 2009, 2012; Weller et al. 2012; Richards and Power 2017). The mark-recapture experiment was discontinued in 2015 due to the loss of the set gillnet site and inability to capture sufficient numbers of Chinook salmon during event 1. The estimates of escapement for large Chinook salmon spawners from 1997 to 2018 ranged from 956 in 2012 to 10,541 in 2001 and averaged 3,800. 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 radio telemetry studies in 1994 and 2009; these studies showed that the index surveys are conducted in tributaries on each river that contain over 80% of the large Chinook salmon escapement. After meeting or exceeding escapement for 35 consecutive years (1977–2011), the Unuk River stock of Chinook salmon has missed the lower bound of the escapement goal 5 out of the past 8 years (2012–2014, 2016–2017).

Earlier research (1983–1988) in Behm Canal systems included coded wire tagging wild juvenile (mostly smolt) Chinook salmon on the Unuk and Chickamin rivers to estimate adult harvest, harvest distribution, and rearing areas for juvenile fish (Kissner 1985; Pahlke 1995). The majority of recovered coded wire tags (CWTs) were made in troll fisheries and during escapement sampling. Harvest estimates for Unuk River Chinook salmon ranged from 726 fish (1985 brood) to 3,039 fish (1983 brood), with 95% relative precision of harvest estimates ranging from 24% (1982 brood) to 78% (1985 brood). 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 from 1986 to 1992 but ranged from outer coast waters near Yakutat in the north to northern British Columbia to the south and have since been documented to the southern Bering Sea.

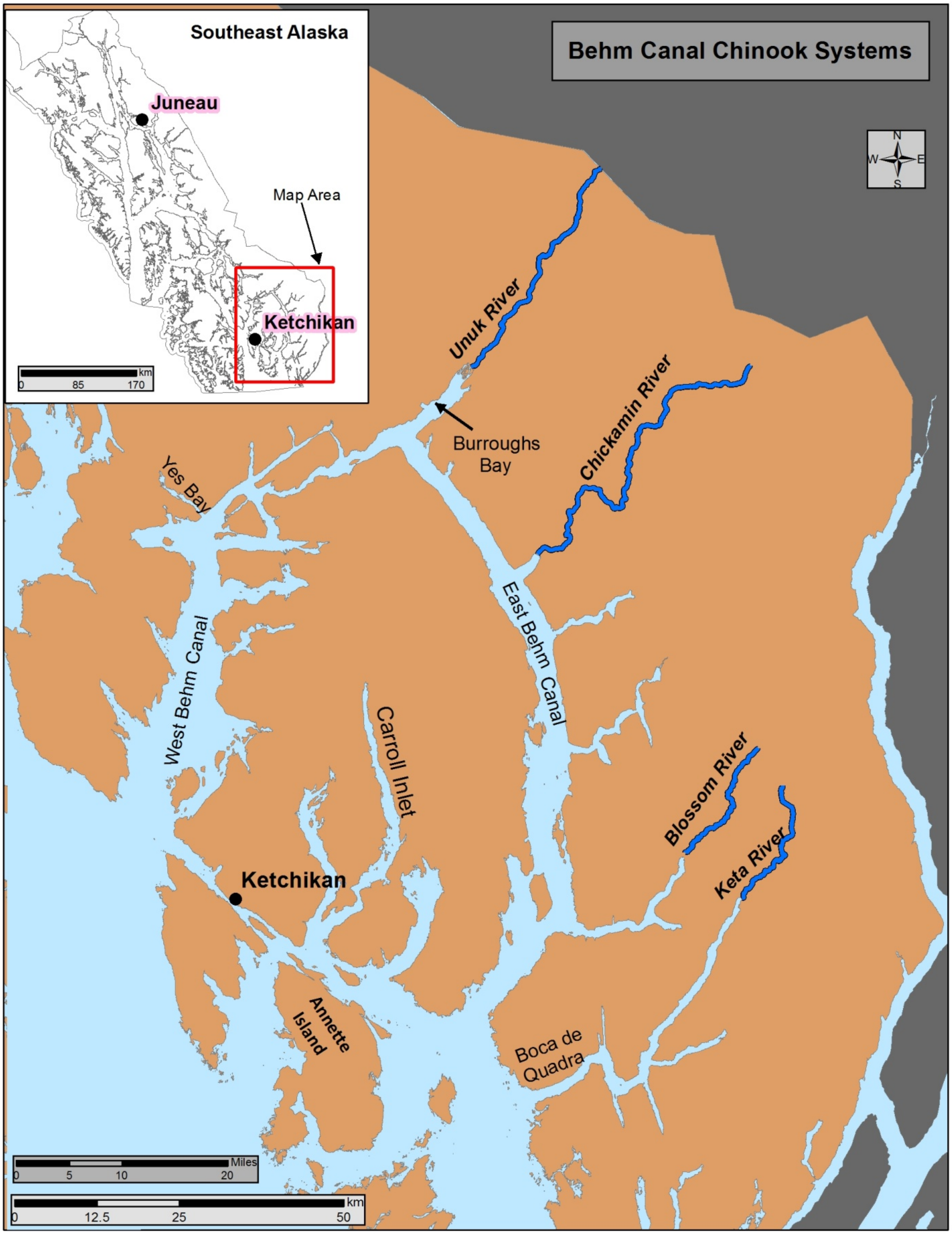

Figure 1.–Behm Canal area in Southern Southeast Alaska (inset), showing major Chinook salmon systems, including the Unuk River.

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 brood year 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 brood year (Appendix A1) and have resulted in CWT marked fractions as high as 10.7% (1996 brood year; Appendix A2). Recent tagging efforts have not been as successful, ranging from about 26,000 for the 2009 brood year to about 14,500 for the 2014 brood year. However, about 56,500 were tagged for the 2015 brood year, about 34,500 for the 2016 brood year, about 16,500 for the 2017 brood year, and just over 33,000 for the 2018 brood year. The marked fraction for the most recent complete brood year (2013) for which the 1.1 through 1.4 age classes have returned was 8.1%.

In 2020-2022, three studies will be conducted on the Unuk River: tagging brood year 2019 and 2020 juvenile Chinook salmon in freshwater in the fall (2020–2021) and spring (2021–2022) with CWTs, adult recovery of CWT fish on the spawning grounds, and aerial and foot surveys of large Chinook salmon (Richards 2016).

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

The research objectives for July 2020 through June 2022 are to:

1. Estimate smolt abundance for the 2021 and 2022 outmigration (2019 and 2020 brood years) 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 2020 and 2021) and smolt (spring 2021 and 2022) 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 MEF) 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 brood year marked with a CWT.
2. Estimate fall parr abundance in 2020 and 2021 (2019 and 2020 brood years).
3. Estimate the total harvest of Unuk River Chinook salmon, brood years 2019 and 2020, in sampled sport and commercial salmon fisheries from 2022 to 2027 via recovery of CWTs applied in the fall of 2020 and 2020 and spring of 2021 and 2022.
4. Estimate mean length-at-age and length-at-sex for the spawning population.
5. Estimate the age-sex composition of medium (≥400 to <660 mm MEF) and small (<400 mm MEF) 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, length sampling with the ultimate sampling goal being ≥ 325.

STUDY DESIGN

Age-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-sex composition and mark fraction data must come from spawning ground sampling. Samples used to estimate the marked fraction and age-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.

	Importance as	Historical survey dates			
Location	spawning site (rank)	Start	End	Peak	Index area
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	
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

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

Spawning ground sampling will begin approximately August 1st and continue as long as sampling is effective (approximately August 24–31). The goal of sampling is threefold: 1) to estimate the fraction of fish marked with adipose-finclips and CWTs; 2) to estimate age-sex and length (ASL) composition; 3) to report the numbers of fish seen.; and 4) collect genetic tissue samples.

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, Boundary creeks: live and dead large fish observed at each location will be counted while inspecting fish of all sizes for marks and collecting ASL samples.

All survey data will be recorded on the form described in Appendix B3.

In order 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 CWT's. 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 MEF). All male fish <660 mm MEF 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 ≥660 mm MEF 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 was 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, 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 given that the 5-year average of fish sampled on the spawning grounds is 600.

Smolt Abundance, Parr Abundance, and the Harvest of Chinook Salmon from the 2019 and 2020 Brood Years (Objective 1, Secondary Objectives 2, 3)

Smolt abundance, parr abundance, and the harvest of Unuk River Chinook salmon from the 2019 and 2020 brood years 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 CWT tagged fish in sampled marine commercial and recreational fisheries in 2022 through 2027.

Chinook salmon parr from the 2019 and 2020 brood years will be tagged with CWTs in the fall of 2020 and 2021, and smolt will be tagged in the spring of 2021 and 2022, respectively. Parr will be captured from late September through the end of October in the fall of 2020 and 2021, and smolt will be captured from late March through late April in the spring of 2021 and 2022. 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 brood year. 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 brood year *j* will be estimated using a mark-recapture experiment. Average smolt abundance of Unuk River Chinook salmon is 322,514 fish (BY 1992–2013). 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, …, *j*+7, will be inspected for marks and tags. Experience has shown that the proportion of adults from a given brood year 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 (BY 1992–2013). Using these averages and the methods described in Robson and Regier (1964), we need to tag approximately 20,000 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 0.57 (BY 1992–2013), so the number of parr that need to be tagged can be determined using the following equation: $M_f=(20{,}000-M_s)/0.57$, 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, a sufficient number 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 brood years (BY 2009–2013). 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 brood years. Budget constraints limited tagging efforts for the 2010 to 2014 brood years: 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 2019 (BY 2015–2019) because more funds were available. Assuming sufficient funds are available and that marine survival improves, we anticipate that we will meet the objective criteria for Objective 1.

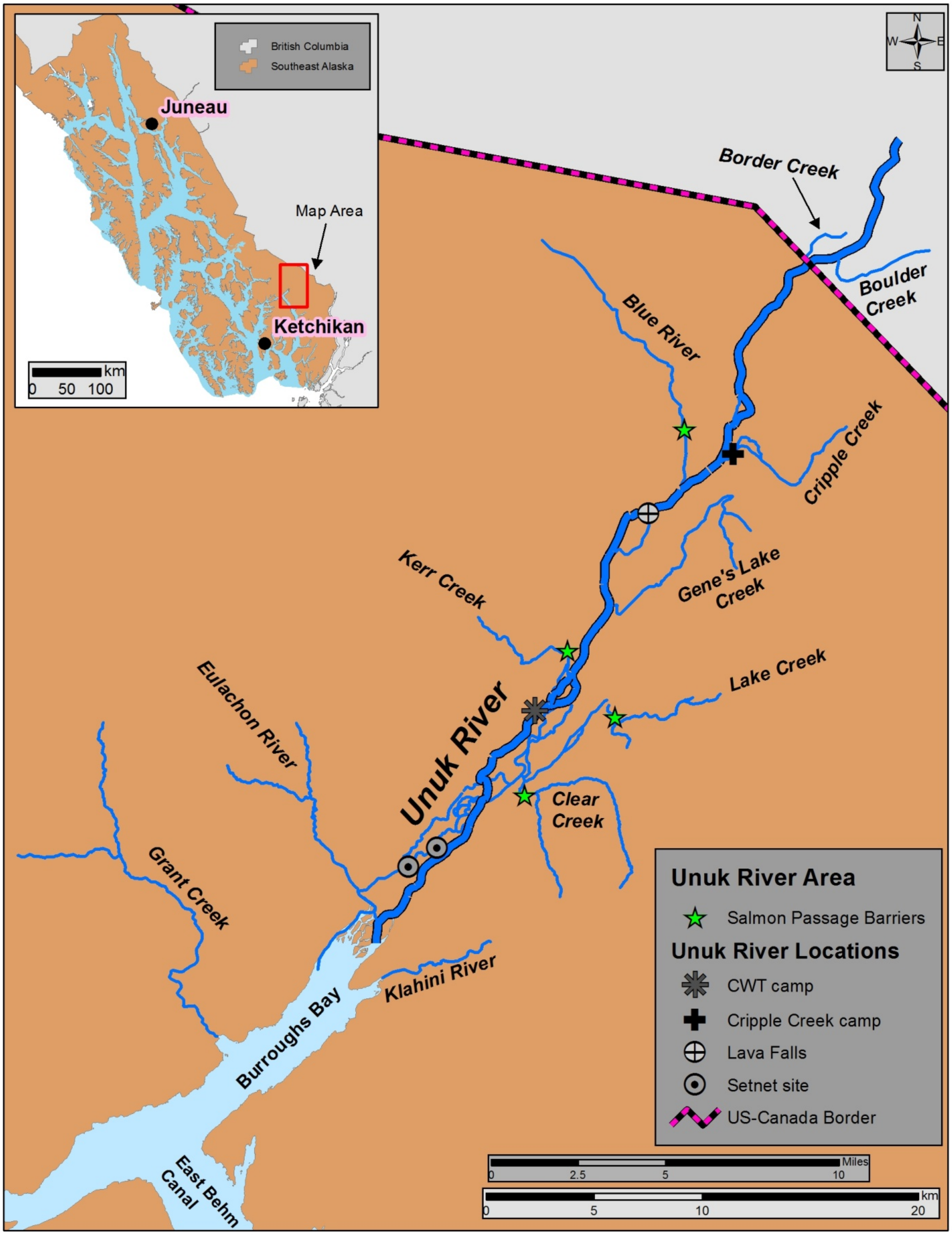

Figure 2.–Unuk River area in Southeast Alaska, showing major tributaries, barriers to fish migration and location of research sites.

Note: no setnet sites will be used in 2020—2022.

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

According to procedures in Cochran (1977, p. 77–78), the sample size *n* needed to estimate the mean length of parr or smolt within d mm for 100*(1-α)% relative precision under simple random sampling, with a standard deviation of lengths s, is given by:

$$n = (Z_{(1-\alpha/2)}\ s\ /\ d)^2 \tag{1}$$

For standard normal variate $Z_{(1-\alpha/2)}$ =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 captured should be measured. However, in case we capture less than 28,000 parr**,** we will measure every 100th Chinook salmon parr captured. Similarly for smolt, for a standard normal variate $Z_{(1-\alpha/2)}$ =1.96, s=7.0 mm and d=1 mm, the required sample size is *n*=188. Based on a catch of 5,400 smolt (assumes 27% of fish tagged were smolt), every 29th smolt should be measured. However, to be conservative, every 25th (4 in every 100) will be measured.

INJURED OR DEAD MARINE MAMMALS

Consistent with the terms and conditions of the Biological Opinion for Southeast Alaska, if during the course of the study injured or entangled marine mammals are observed, the following protocols will be implemented:

- 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 (e.g., line, gillnet, etc.) and how the animal is entangled, its relative degree of impairment, and direction of travel.
- As soon as possible, report to the 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).

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 CWT'd 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 B1). 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 Physical Data Form (Appendix B2) 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 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. 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[1] 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 at a later date.
6. Systematically select and measure to the nearest 1 mm FL every 100th unmarked Chinook salmon parr (fall 2020 and 2021) and every 25th unmarked Chinook salmon smolt (spring 2021 and 2022). All these fish will also be weighed to the nearest 1/10 g.

Age-Sex-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-Length Form (Appendix B3). <u>For age composition sampling, it is imperative that good scale samples be taken.</u> Genetic samples for each escapement sampling location will be collected per the methods described in Appendix D.

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[1] This and subsequent product names are included for a complete description of the process and do not constitute product endorsement.

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 (Welander 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*)[2]. 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 B4) 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 MEF. Secondary maturation characteristics can include predominant snouts and compressiform bodies for males, while females may display abraded caudal fins (i.e., white tails) and 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 MEF males

Coded Wire Tag Sampling

All adult fish sampled in the study will be inspected for adipose-finclips and sampled for ASL. The brood year of all fish sampled (with and without adipose fins) will therefore be known and estimation of brood-year 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 MEF 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 MEF 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. Heads so collected will be given a uniquely numbered cinch strap obtained from the Division of Commercial Fisheries (DCF) Mark, Tag, and Age Laboratory,

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[2] 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.

and will be attached to each head. The head will then be sent with a completed CWT sampling form (appendix B5) to the Mark, Tag, and Age Laboratory for dissection and decoding of tags. Results from the adipose-finclip, scale, and direct CWT sampling will be used to:

- estimate the CWT marked fraction by brood year, 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 in the office later. Field forms will be inspected for accuracy and compliance with sampling procedures, compared with the electronic database files, and error checked. Inspections for data entry errors will include looking for incorrect dates, transposed nonsensical lengths, incorrect length measurement method (i.e., FL), etc. Data forms will always be kept up to date.

The ADF&G Division of Commercial Fisheries (DCF) is the clearinghouse for all information on CWTs. Completed *CWT TAGGING SUMMARY AND RELEASE INFORMATION Form*s will be compiled using CWT Assist (Version 3.2.0) and sent to the DCF Mark, Tag, and Age Laboratory (Tag Lab). Note that the Tag Lab is the permanent repository for all CWT data for the State of Alaska. 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. An edited copy of the data, along with a data map, will be sent to Research and Technical Services (RTS) in Anchorage with the final report for archiving. All electronic files submitted with the final report will be archived in a report-specific folder on the Docushare system.

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., postorbit 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 a data map, will be sent to DSF Research and Technical Services in Anchorage for electronic archiving when the report is 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:

$$\hat{p}_{kc} = \frac{n_{kc}}{n_k}, \tag{2}$$

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

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:

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

Because the $\hat{N}_k$ in Eq. 4 are correlated ($\hat{N}_S$ and $\hat{N}_M$ are estimated from $\hat{N}_L$ by Eqs. 6 and 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 $\underline{\hat{\phi}}^* \sim multinomial\,(n_{sp}, \underline{\hat{\phi}})/n_{sp}$, and the vector of estimated age-sex proportions for the k^{th} size group as $\underline{\hat{p}}^*_k \sim multinomial\,(n_k, \underline{\hat{p}}_k)/n_k$. Equations 2-4 and 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 :

$$\hat{p}_c = \frac{\hat{N}_c}{\hat{N}_{ALL}} \tag{5}$$

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-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-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 C1, 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):

$$\hat{N}_S = \hat{N}_L \frac{\hat{\phi}_S}{\hat{\phi}_L} \tag{6}$$

$$\hat{N}_M = \hat{N}_L \frac{\hat{\phi}_M}{\hat{\phi}_L} \tag{7}$$

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

$$\hat{\phi}_k = \frac{n_k}{n_{sp}} \tag{8}$$

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 :

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

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

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

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

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

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

Similarly,

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

The abundance of all fish will be estimated as:

$$\hat{N}_{ALL} = \frac{\hat{N}_L}{\hat{\phi}_L} \tag{13}$$

with variance estimated as:

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

where,

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

Estimation of Fraction of Adults Bearing Coded Wire Tags

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

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

where

n_{ij} = number of adults examined in year i from brood year 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 brood year 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, representing ages 1.1 through 1.5).

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, $t_{ij}^{*} \sim$ 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 Development Core Team 2005). ρ_{ij}^{*} will then be calculated as $t_{ij}^{*} /(a_{ij}^{*} a_{ij}^{'} / a_{ij})$, and $\hat{\theta}_j^{\,*}$ as:

$$\hat{\theta}_j^{\,*} = \frac{\sum_{i=1}^{L} a_{ij}^{\;*} \rho_{ij}^{\;*}}{\sum_{i=1}^{L} n_{ij}} \tag{17}$$

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

$$\hat{r}_{ij} = H_i \left[\frac{m_{ij}}{\lambda_i n_i} \right] \theta_j^{-1}; \qquad \lambda_i = \frac{a_i' t_i'}{a_i t_i} \tag{17}$$

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, brood year 2012), and θ_j = fraction of the cohort tagged with code of interest. H_i is estimated with error in sport fisheries, 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 returns), the final estimate for the 2016 brood year 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 brood year 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 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 brood year 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 brood year j return. Smolt abundance ($\hat{N}_{smolt,j}$) from brood year j will be estimated using a version of the Chapman-modified Petersen formula:

$$\hat{N}_{smolt,j} = \frac{\left(\hat{M}_j + 1\right)\left(n_{\bullet j} + 1\right)}{\left(a_{\bullet j} + 1\right)} - 1 \tag{18}$$

where

$n_{\bullet j}$ = $\sum_{i=1}^{L} n_i$, where n_i is the number of adults examined in year i from brood year 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 brood year j that bore an adipose-finclip; 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 brood year j surviving to the spring ($\hat{M}_{f\to s,j}$) and the number of smolt with adipose-finclips from brood year j ($M_{s,j}$), where:

$$\hat{M}_{f\to s,j} = M_{f,j}\hat{S}_j \tag{19}$$

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:

$$\hat{S}_j = \frac{\hat{M}_{s,valid,j} v_{\bullet,f,j}}{\hat{M}_{f,valid,j} v_{\bullet,s,j}} \tag{20}$$

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 brood year 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 brood year 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:

$$\operatorname{var}\left(\hat{N}_{smolt,j}\right) = \left(n_{\bullet j} + 1\right)^2 \operatorname{var}\left[\left(\hat{M}_{f\to s,j} + M_{s,j} + 1\right)\frac{1}{\left(a_{\bullet j} + 1\right)}\right] \tag{21}$$

where, by Goodman (1960) for independent variables:

$$\begin{aligned}\operatorname{var}\left[\left(\hat{M}_{f\to s,j} + M_{s,j} + 1\right)\frac{1}{\left(a_{\bullet,j} + 1\right)}\right] &= \left(M_{s,j} + \hat{M}_{f\to s,j} + 1\right)^2 \operatorname{var}\left[\frac{1}{a_{\bullet,j} + 1}\right] + \left[\frac{1}{a_{\bullet,j} + 1}\right]^2 \operatorname{var}\left(\hat{M}_{f\to s,j}\right) \\ &- \operatorname{var}\left[\frac{1}{a_{\bullet,j} + 1}\right] \operatorname{var}\left(\hat{M}_{f\to s,j}\right)\end{aligned} \tag{22}$$

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

According to the delta method:

$$\text{var}\left[\frac{1}{a_{\bullet}+1}\right]=\left[\frac{1}{a_{\bullet,j}+1}\right]^{4} n_{\bullet,j}\hat{p}_{a}\left(1-\hat{p}_{a}\right) \tag{23}$$

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

The two components in equation 23 are not independent, but a simulation using data from studies on 7 brood years 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 23) over the simulation.

Parr Abundance

Parr abundance $\hat{N}_{f}$ for brood year j will be estimated as:

$$\hat{N}_{f,j}=\hat{N}_{smolt,j}\frac{1}{\hat{S}_{j}} \tag{24}$$

$$\text{var}(\hat{N}_{f,j})\approx\hat{N}_{f,j}^{2}\left|cv^{2}\left(\hat{N}_{smolt,j}\right)+cv^{2}\left(\hat{S}_{j}\right)\right| \tag{25}$$

Equation 26 was derived using the delta method as described in Seber (1982), p. 8.

SCHEDULE AND DELIVERABLES

Parr tagging will begin approximately 24 September, 2020 and 2021 and span the month of October, after which inventory will be taken and gear will be stored for the winter. Spring tagging will run through approximately 24 March through April, 2021 and 2022. 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 the month of August 2020 and 2021. 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, 2020 and 2021 (Adult and parr data), and 1 June, 2021 and 2022 (spring smolt data).

An ADF&G Fishery Data Series report will be prepared by 1 June, 2029 summarizing brood years 2019 and 2020 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 II (Ketchikan)

Duties: 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. Responsible for daily radio call, arranging logistics with field crew, purchasing supplies, loading and unloading supply planes, proper conduct in the public's eye, and following department guidelines supplied by Richards. Responsible for supervising field crew, assists with field operations as necessary, makes recommendations on logistics to the project leader, adjusts personnel hours and schedules as appropriate. Enters field data into spreadsheets and edits and summarizes data. Adjusts field sampling priorities, as necessary. Responsible for tracking the budget, meeting reporting requirements, analysis, and publication of smolt and harvest contribution data.

Philip Richards, Fishery Biologist III

Duties: 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. Adjusts field sampling priorities, as necessary. With Frost, responsible for tracking the budget, meeting reporting requirements, analysis, and publication of smolt and harvest contribution data, may assist with work in the field and will arrange logistics with Frost and field crew. Conducts preseason startup meetings with field crew and Frost and follows departmental and state policy in all matters.

Randy Peterson, Biometrician III

Duties: Provides input to and approves sampling design. Reviews and provides biometric support for operational plan, data analysis, and final report.

Ed Jones, Salmon Research Coordinator

Duties: This position is the DSF Salmon Research Coordinator for salmon stock assessment and provides program and budget planning oversight. Also reviews the operational plan, data analysis, and final report.

Kristian Larson, Fish and Wildlife Technician III (Ketchikan)

Duties: This position is responsible for directing all field aspects of the project under directions from the project 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, scheduling of flights with Frost. With Frost, will attempt to resolve as many personnel and administrative items as is possible and is responsible for submitting inventories at the end of the season to Frost. This position is also responsible for reports to be submitted to the project leader weekly, and daily satellite phone calls, inreach messages, or emails to Frost while in the field. Follows departmental and state policy in all matters.

Mackenzie Oliver, Fish and Wildlife Technician III

Duties: 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. Position will be responsible for overseeing and directing juvenile coded wire tagging efforts in the tag shack and submitting data accurately and timely. Position acts as lead tagger for juvenile tagging. With Frost and Larson, will ensure all crew members are trained in data collection and recording. Will work with Frost and Larson on data recordkeeping responsibilities while in the field. Follows departmental and state policy in all matters.

Vacant, Fish and Wildlife Technician II.

Duties: 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.

Vacant, Fish and Wildlife Technician II.

Duties: 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.

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APPENDIX A: HISTORIC ACCOUNTING OF CWT OPERATIONS

Appendix A1.–Numbers of Unuk River Chinook salmon fall parr and spring smolt captured and tagged with coded wire tags, 1992 brood year to present.

Brood year	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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year total					48,486	48,486

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Brood year	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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year total					22,173	22,168

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Brood year	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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year total					16,730	16,714

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Brood year	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 brood year total					33,373	33,311

Appendix A2.–Data pertaining to adipose-finclip and coded wire tag fractions by brood year (1992-2015) 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 brood year 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 brood year 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 brood year 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.%	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 brood year 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 brood year total			2,343	271	113	75	30	105	92.9	11.6	10.7

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Appendix A2.–Page 2 of 5.

Brood Year	Age	Year Sampled	Sampled	Adipose-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 brood year 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 brood year 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 brood year 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 brood year 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 brood year total			1,119	114	36	23	10	33	91.7	10.2	9.3

-continued-

Appendix A2.–Page 3 of 5.

Brood Year	Age	Year Sampled	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 brood year 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 brood year 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 brood year 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 brood year 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 brood year 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 brood year total			438	17	9	5	2	7	77.8	3.9	3.0

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Appendix A2.–Page 4 of 5.

Brood Year	Age	Year Sampled	Sampled	Adipose-Finclips	Sacrificed	CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs
						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 brood year 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 Brood year 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 Brood year 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 Brood year 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 Brood year 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 Brood year total			xxx	xx	x	x	x	x	xx	xx	xx

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Appendix A2.–Page 5 of 5.

Brood Year	Age	Year Sampled	Sampled	Adipose-Finclips	Sacrificed	CWTs			% Clips w/CWTs	%Adipose-Finclips	% CWTs
						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	-	-	-	-	-	-	-	-	-
2014	1.5	2021	-	-	-	-	-	-	-	-	-
2014 Brood year total			xxx	xx	x	x	x	x	xx	xx	xx
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.	10.6
2015	1.3	2020	-	-	-	-	-	-	-	-	-
2015	1.4	2021	-	-	-	-	-	-	-	-	-
2015	1.5	2022	-	-	-	-	-	-	-	-	-
2015 Brood year 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	-	-	-	-	-	-	-	-	-
2016	1.3	2021	-	-	-	-	-	-	-	-	-
2016	1.4	2022	-	-	-	-	-	-	-	-	-
2016	1.5	2023	-	-	-	-	-	-	-	-	-
2016 Brood year total			xxx	xx	x	x	x	x	xx	xx	xx

[a] $\hat{\theta}_i$ in Equation 17

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

APPENDIX B: PROJECT DATA FORMS

Appendix B1.–Division of Sport Fish coded wire tag daily log form.

Sport Fish 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 B2.–Physical data form.

Date	Water temp °C	Water depth (inches)

Appendix B3.–Unuk River spawning grounds age-sex-length form, 2020.

Location: ______________________ Year: 2020

Stream code: ___________________

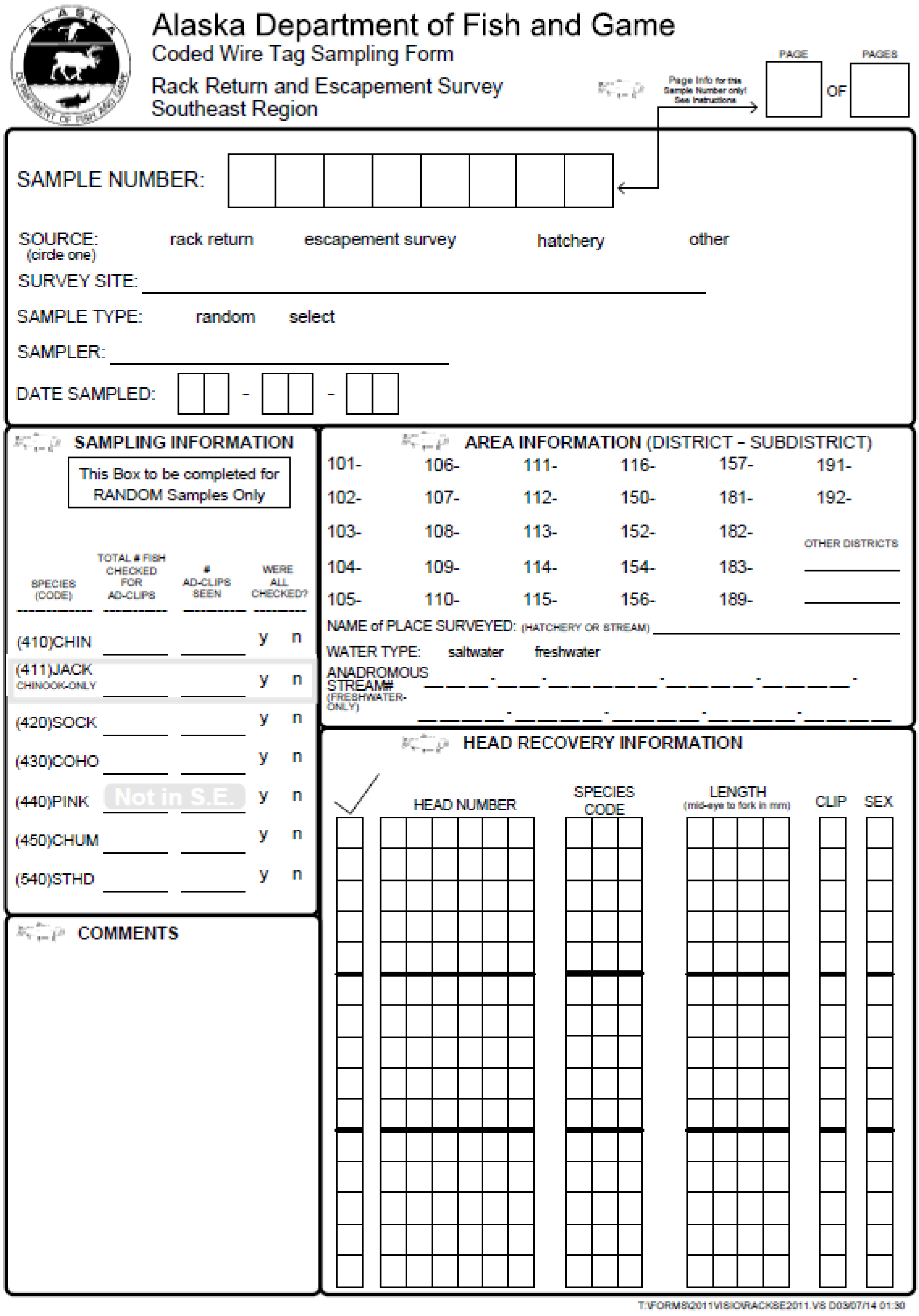
Species: ________________________

Fish #	Date	Sex	Length MEF (mm)	Card #	Scale #	Age FW	Age MW	AEC	Spaghetti tag #	LAA	UOP	Ad Clip Cinch #	Gear type	Fish condition	Comments
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				9321	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				9123	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

Appendix B4.–Coded wire tag (CWT) anadromous stream numbers, coded wire tag sample numbers, and age-sex-length (ASL) stream codes for the Unuk River and its tributaries.

Location	CWT Anadromous Stream #	Sample numbers	ASL 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

Appendix B5.–Coded wire tag sampling form.



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

This Box to be completed for RANDOM Samples Only

SPECIES (CODE)	TOTAL # FISH CHECKED FOR AD-CLIPS	# AD-CLIPS SEEN	WERE ALL CHECKED?	
(410)CHIN	______	______	y	n
(411)JACK CHINOOK-ONLY	______	______	y	n
(420)SOCK	______	______	y	n
(430)COHO	______	______	y	n
(440)PINK	Not in S.E.	______	y	n
(450)CHUM	______	______	y	n
(540)STHD	______	______	y	n

AREA INFORMATION (DISTRICT - SUBDISTRICT)

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) ___-___-_____-_____-_____-
_____-_____-_____-_____-_____

HEAD RECOVERY INFORMATION

✓	HEAD NUMBER	SPECIES CODE	LENGTH (mid-eye to fork in mm)	CLIP	SEX

COMMENTS

T:\FORMS\2011VISIO\RACKSE2011.VS D09/07/14 01:30

APPENDIX C: EXPANSION FACTOR TECHNIQUES FOR INDEX SYSTEMS

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:

$$\bar{\pi} = \frac{\sum_{y=1}^{k} \pi_y}{k} \tag{1}$$

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*(π)-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):

$$v\hat{a}r(\pi_p) = v\hat{a}r(\pi) + v\hat{a}r(\bar{\pi}) \tag{2}$$

where

$$v\hat{a}r(\pi) = \frac{\sum_{y=1}^{k} (\pi_y - \bar{\pi})^2}{k-1} \tag{3}$$

and

$$v\hat{a}r(\bar{\pi}) = \frac{\sum_{y=1}^{k} (\pi_y - \bar{\pi})^2}{k(k-1)} \tag{4}$$

such that

$$v\hat{a}r(\pi_p) = \frac{\sum_{y=1}^{k} (\pi_y - \bar{\pi})^2}{k-1} + \frac{\sum_{y=1}^{k} (\pi_y - \bar{\pi})^2}{k(k-1)} \tag{5}$$

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-

$$\overline{\pi} = \frac{\sum_{y=1}^{k} \hat{\pi}_y}{k} \tag{6}$$

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 other terms are as described above.

The variance for prediction will again be estimated:

$$v\hat{a}r(\pi_p) = v\hat{a}r(\pi) + v\hat{a}r(\overline{\pi}) \tag{7}$$

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):

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

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

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

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

$$v\hat{a}r(\pi) = v\hat{a}r(\hat{\pi}) - \frac{\sum_{y=1}^{k} v\hat{a}r(\hat{\pi}_y)}{k} \tag{10}$$

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

We can calculate:

$$v\hat{a}r(\hat{\pi}) = \frac{\sum_{y=1}^{k} (\hat{\pi}_y - \overline{\pi})^2}{k-1} \tag{11}$$

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

$$v\hat{a}r(\overline{\pi}) = \frac{\sum_{y=1}^{k} (\hat{\pi}_y - \overline{\pi})^2}{k(k-1)} \tag{12}$$

where both process and measurement errors need to be included.

For large *k* (*k* > 30), equations (11) and (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 $var(\overline{\pi})$ 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 $v\hat{a}r(\hat{\pi}_y)$. 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 $\overline{\pi}_{(b)}$. This procedure is repeated B = 1,000,000 times. We can then estimate $var(\hat{\pi})$ using:

$$v\hat{a}r_B(\hat{\pi}) = \frac{\sum_{b=1}^{B}(\hat{\pi}_{(b)} - \overline{\hat{\pi}_{(b)}})^2}{B-1} \tag{13}$$

where

$$\overline{\hat{\pi}_{(b)}} = \frac{\sum_{b=1}^{B}\hat{\pi}_{(b)}}{B} \tag{14}$$

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

$$v\hat{a}r(\pi_p) = v\hat{a}r_B(\hat{\pi}) - \frac{\sum_{y=1}^{k}\mathrm{v\hat{a}r}(\hat{\pi}_y)}{k} + v\hat{a}r_B(\overline{\pi}) \tag{15}$$

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 $var(\overline{\pi})$ 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:

$$\hat{N}_p = \overline{\pi}\, C_p \tag{16}$$

and

$$v\hat{a}r(\hat{N}_p) = C_p^2 v\hat{a}r(\pi_p) \tag{17}$$

APPENDIX D: GENETIC DNA SAMPLING GUIDANCE

Appendix D1.–Adult Finfish Tissue Sampling for DNA Analysis.

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

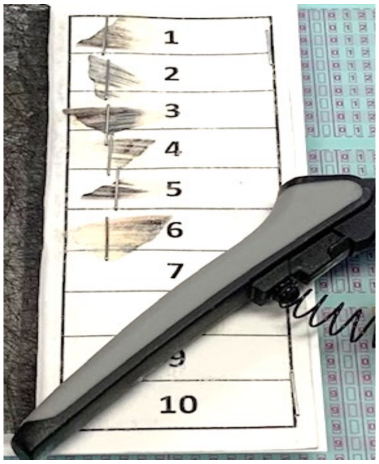
I. General Information

We use fin tissues as a source of DNA to genotype fish. Genotyped fish are used to determine the genetic characteristics of fish stocks or to determine stock compositions of fishery mixtures. 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.

Preservative used: Silica desiccant bead packet dries and preserves tissues for later DNA extraction. Quality DNA preservation requires **dry storage** (with desiccant packs) in Pelican box or watertight file box.

II. Sampling Method

Pelvic fin located below axillary spine.



III. Sampling Instructions

- Prior to sampling:
  - Set up workspace, fill out required collection information (upper left-hand corner only).

- Place Whatman genetic card (10WGC) on mini clipboard flat for easy access. One Whatman card per scale card. Same card can be used throughout same day.

- Sampling:
    - Wipe excess water and/or slime off the pelvic fin prior to sampling to avoid getting excess water or fish slime.
    - Fin clip will be taken from lower portion of the pelvic fin.
    - Cut off a portion of the fin clip using Fiskar scissors to get roughly a **¾ - 1" inch maximum** piece and/or about the size of a small fingernail (see cutting line to left in orange).
    - Place one clipped fin tissue onto appropriate grid space. Follow sampling order printed on card - do not deviate. If large tissue sample, center tissue diagonally on grid space.
    - **Only one fin clip per fish into each numbered grid space.**
    - Fin clips will stick to the 10WGC grid card (see photo).
    - **Staple** fin clip to card; this secures the fin for handling in lab.
    - **DO NOT** staple landscape cloth to paper edge.
    - Sampling complete.
    - Periodically, wipe or rinse the scissors with water so not to cross contaminate samples.
    - Insert the 10WGC card inside Pelican case and layer with blotter cards and desiccant packs.
    - Close and secure the lid of Pelican box so drying begins.
    - Data to record: Record **each fin clip number to paired data** information (i.e. location, lat./long., sample date(s), etc.). Electronic version preferred.
- Loading the Pelican Case:
    - First card: Remove blotter papers and desiccant packs (remove vacuum pack plastic) from Pelican Case. Place first card in Pelican Case with tissues facing up. Next, place blotter paper directly over card and place 2 desiccant packs on top. Close and secure lid so drying begins.
    - Up to 4 cards can be added per case. Add them so the **tissue samples always face the desiccant pack** through blotter paper: 2nd card facing down between desiccant packs; 3rd card facing up between desiccant packs; and 4th card facing down on top of second desiccant pack. Close and secure Pelican Case after inserting each card.
    - All Whatman cards **must remain in Pelican 1400 case at all times** to dry cards flat.

- Post-sampling storage:
    - Store dried 10WGC tissue cards in Pelican box at room temperature or below. Two-four desiccant packs fit inside Pelican 1400 case. This helps flatten the cards as they dry out over time.

- Shipping at end of the season:
    - Keep all **dried** cards layered inside Pelican box with secured lid until preparing for shipment. Pack all dry cards into photo pages and inside priority mailing box with returning sampling supplies. Tape box shut and tape return address on box.

IV. Supplies included in sampling kit:

1. Scissors - for cutting a portion of selected fin.
2. Whatman genetics card (10WGC) – holds 10 fish/card.
3. Bostitch stapler – staple secures fin clip to card.
4. Pelican Case - 1st stage of drying/holding card with samples.
5. Pelican 1400 case – long term dry storage for all cards
6. Desiccant packs – removes moisture from samples.
7. Pre-cut blotter paper – covers full sample card for drying.
8. Shipping box – put sealed Pelican case inside a box.
9. Clipboard – holds Whatman genetics card while sampling.
10. Zip ties – to secure the Pelican case for return shipment.
11. Laminated “return address” labels.
12. Sampling instructions.
13. Pencil

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:___________