Regional Operational Plan No. ROP.SF.1J.2024.06

Estimation of Age, Sex, and Length Composition of Chinook Salmon in the Chickamin, Blossom, Keta and King Salmon Rivers, and Andrew Creek, 2020−2021

by

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and

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May 2024

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.SF1J.2024.06

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May 2024

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This document should be cited as follows:
Frost, N., P. Richards, and R. Peterson. 2024. Estimation of age, sex, and length composition of Chinook salmon in the Chickamin, Blossom, Keta, and King Salmon Rivers, and Andrew Creek, 2020−2021. Alaska Department of Fish and Game, Division of Sport Fish, Regional Operational Plan No. ROP.SF.1J.2024.06, Anchorage.

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SIGNATURE/TITLE PAGE

Project Title:	Estimation of age, sex, and length composition of Chinook Salmon in the Chickamin, Blossom, Keta and King Salmon Rivers, and Andrew Creek, 2020−2021
Project leader(s):	Nathan Frost, Fishery Biologist 2 Philip Richards, Fishery Biologist 3
Division, Region and Area	Sport Fish, Region I, Juneau/Ketchikan
Project Nomenclature:	NOAA PSC Base
Period Covered	August–September, 2020−2021
Field Dates:	August 1–September 25, 2020−2021
Plan Type:	Category II

Approval

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ABSTRACT

The goals of this project are to estimate the age-sex-length composition of the Chinook salmon *Oncorhynchus tshawytscha* escapement for the Chickamin, Blossom, Keta, King Salmon and Andrew Creek systems in Southeast Alaska and to expand peak survey counts on these systems to total escapement estimates. Sampled fish will also be examined for adipose clips and coded wire tags. A separate project, *Escapement of Chinook salmon in Southeast Alaska and transboundary rivers in 2020 and 2021*, will conduct standardized peak survey counts of these 5 systems. The age-sex composition of small (<400 mm mid eye to tail fork, medium (≥400 mm and <660 mm mid eye to tail fork), and large (≥660 mm mid eye to tail fork) Chinook salmon will be estimated.

Keywords: Chinook Salmon, *Oncorhynchus tshawytscha,* expansion factor, age-sex-length composition, Southeast Alaska, aerial surveys, Chickamin River, Keta River, Blossom River, King Salmon River, Andrew Creek

PURPOSE

The goals of this project are to 1) estimate adult age-sex-length composition for 5 Chinook salmon index systems in Southeast Alaska; and 2) expand index counts to provide estimates of total escapement in the 5 systems. Estimates generated from this project partially supplies the escapement data information needed by the Chinook Technical Committee of the Pacific Salmon Commission.

BACKGROUND

The Chickamin, Blossom, and Keta Rivers are on the mainland and traverse the Misty Fjords National Monument in southern Southeast Alaska (SEAK); these rivers support runs of Chinook salmon *Oncorhynchus tshawytscha* ranging from approximately 170 to 8,200 large fish (≥660 mm mid-eye to fork (METF), of which the Chickamin River represents the high end. The King Salmon River is located on Admiralty Island, south of Juneau, and supports a small run of Chinook salmon. Andrew Creek is a tributary of the lower Stikine River and supports a moderate run of Chinook salmon. Locations of the 5 rivers are shown in Figure 1.

These 5 stocks of Chinook salmon are all harvested in SEAK fisheries and the Behm Canal stocks (Chickamin, Keta and Blossom) are also harvested to a minor extent in northern British Columbia fisheries. The Chickamin River produces one of the largest wild runs of Chinook salmon in the Behm Canal and Ketchikan area. The 5 rivers are "index streams" for the Chinook salmon escapement estimation program in SEAK (Pahlke 1993). Indices of escapement (peak counts of large Chinook salmon) have been collected annually on the Chickamin, Blossom, Keta, and King Salmon rivers as well as on Andrew Creek using a standardized method described in Richards et al. (2022). The peak counts and resulting estimates of total escapement for these stocks are used by the Alaska Department of Fish and Game (ADF&G) and the Chinook Technical Committee (CTC) of the Pacific Salmon Commission (PSC) to evaluate stock status, and to implement abundance-based management.

Escapement indicator stocks are used by the CTC to judge stock status of naturally spawning Chinook salmon stocks coast wide, from SEAK through Oregon, and to judge performance of management actions designed to rebuild wild stocks, in accordance with the Pacific Salmon Treaty, Annex IV, Chapter 3 of the 2018 Agreement. The United States Section of the CTC (USCTC) developed data standards for stock specific assessments of escapement, terminal runs, and forecasts of abundance, against which existing stock assessment programs could be evaluated (USCTC 1997).

Figure 1.–Location of Chinook salmon systems in Southeast Alaska where age-sex-length information is collected.

The standard for escapement, developed by the USCTC, is as follows:

> **"*Escapement.*"** *Annual age and sex-specific estimates of total escapement should be available. Point estimates should be accompanied by variance estimates, and both should be based on annual sampling data. Factors used to expand the escapement from index areas (or counts of components of the escapement) should be initially verified a minimum of three times. Those expansion factors that have moderate to large amounts of interannual variability (a coefficient of variation of more than 20%) should be monitored annually."*

The USCTC (1997) report made specific findings for all U.S. escapement indicator stocks relative to these data standards.

The Keta, Blossom, and Chickamin Chinook salmon stock assessment programs failed to meet the minimum data standards developed by the USCTC because age and sex composition was not sampled on an annual basis, and index expansion factors specific to these rivers had not been estimated. The USCTC (1997) recommendations for SEAK included development of permanent, annual age and sex composition sampling of escapements for several river systems that were not sampled and development of expansion factors for these systems.

The expansion factor deficiency for the Keta River was addressed in 1998 to 2000 (Brownlee et al. 1999, Freeman et al. 2000, 2001) using paired peak survey count and mark-recapture studies to estimate the escapement of large fish. The expansion factor for the Keta River is 3.01 (SE = 0.56, CV = 18.6%) (Fleischman et al. 2011), and meets the USCTC standard for precision. Peak survey counts and annual escapement estimates from 1975 to 2019 of large Chinook salmon returning to the Keta River are summarized in Table 1.

The expansion factor for Blossom River was calculated using 4 paired peak survey count and mark-recapture studies (Brownlee et al. 1999, Pahlke and Magnus 2005, 2006, Weller et al. 2007a) that estimated the escapement of large fish in 1998 and 2004–2006. The expansion factors in 1998 and 2006 were 4.0 and 3.75, respectively, and they were estimated under normal survey conditions; the expansion factors of 2.20 in 2004 and 2.08 in 2005 were estimated under excellent conditions and during the lowest water levels seen by the surveyor (Keith Pahlke, Sport Fish Biologist—retired, ADF&G, Douglas, personal communication). The mean expansion factor for the 2 years with normal survey conditions is 3.87 (SE = 0.62, CV = 16.1%) and the overall mean for all 4 years is 3.01 (SE = 1.03, CV = 34.3%). Survey conditions have been recorded since 1991 and from 1991 through 2007, normal conditions were noted in 12 of 17 years. Although based on only 2 years of data, an expansion factor of 3.87 is therefore believed to be germane to most years and meets the USCTC standard for precision (Fleischman et al. 2011). Peak survey counts and annual escapement estimates from 1975 to 2019 of large Chinook salmon returning to the Blossom River are summarized in Table 2.

The original King Salmon River and Andrew Creek Chinook salmon stock assessment programs failed to meet minimum data standards because, while expansion factors existed, age and sex composition of the annual escapements were not annually sampled. This deficiency was addressed through the annual collection of scale data. Peak survey counts, annual escapement estimates, and expansion factors for large Chinook salmon Andrew Creek and King Salmon River are summarized in Tables 3 and 4.

The expansion factor for the Chickamin River was calculated using 6 paired peak survey count and mark-recapture studies (Pahlke 1997, Freeman and McPherson 2003, 2004, 2005, Freeman et al 2007, Weller et al. 2007b) that estimated the escapement of large fish in 1996 and 2001–2005. A paired peak survey count and mark-recapture study conducted in 1995 (Pahlke 1996) was not used to calculate the expansion factor because the coefficient of variation of this estimate, 31%, was below the USCTC threshold. The expansion factor for the Chickamin River is 4.75 (SE = 0.70, CV = 14.7%), and meets the USCTC standard. Peak survey counts and annual escapement estimates from 1975 to 2019 of large Chinook salmon returning to the Chickamin River are summarized in Table 5.

Maintaining the stock assessment program for SEAK Chinook salmon at minimum USCTC standards is important for abundance-based management of PSC Chinook fisheries for 2 reasons. First, the CTC uses escapement data from six SEAK stocks, aggregated into a single stock group, in the Chinook salmon model for producing the annual preseason and postseason abundance indices, and other parameters. These 6 stocks include the 5 targeted in this operational plan (The sixth stock is the Unuk River stock and is covered by a separate operational plan). A second reason is that this work is important for stock specific, rather than coastwide, implementation of abundance-based management regimes. In the Pacific Salmon Treaty 2008 Revised Annexes, it states "SEAK fisheries will be managed to achieve escapement objectives for Southeast Alaska and Transboundary River Chinook stocks." (Chapter 3, footnote 16 to Attachment I). Data from this and other projects are essential for evaluation of escapement goals.

Table 1.–Escapement peak survey counts and escapement of large (≥660 mm METF) spawners for Keta River Chinook salmon from 1975 to 2019.

Year	Peak survey count	Spawning escapement
1975	203	611[a]
1976	84	253 [a]
1977	230	692 [a]
1978	392	1,180 [a]
1979	426	1,282 [a]
1980	192	578 [a]
1981	329	990 [a]
1982	754	2,270 [a]
1983	822	2,474 [a]
1984	610	1,836 [a]
1985	624	1,878 [a]
1986	690	2,077 [a]
1987	768	2,312 [a]
1988	575	1,731 [a]
1989	1,155	3,477 [a]
1990	606	1,824 [a]
1991	272	819 [a]
1992	217	653 [a]
1993	362	1,090 [a]
1994	306	921 [a]
1995	175	527 [a]
1996	297	894 [a]
1997	246	740 [a]
1998	180	446[b]
1999	276	968 [b]
2000	300	914 [b]
2001	343	1,032 [a]
2002	411	1,237 [a]
2003	322	969 [a]
2004	376	1,132 [a]
2005	497	1,496 [a]
2006	747	2,248[a]
2007	311	936 [a]
2008	363	1,093 [a]
2009	172	518 [a]
2010	475	1,430 [a]
2011	223	671 [a]
2012	241	725 [a]
2013	493	1,484 [a]
2014	439	1,321 [a]
2015	304	915 [a]
2016	446	1,342 [a]
2017	300	903 [a]
2018	552	1,662 [a]
2019	346	1,041 [a]

[a] Escapement estimated from expanded peak survey counts.

[b] Escapement estimated from mark-recapture studies.

Note: Escapement goal 550–1,300 large Chinook salmon.

Table 2.–Escapement peak survey counts and escapement of large (≥660 mm METF) spawners for Blossom River Chinook salmon from 1975 to 2019.

Year	Peak survey count	Spawning escapement
1975	146	565 [a]
1976	68	263 [a]
1977	112	433 [a]
1978	143	553 [a]
1979	54	209 [a]
1980	89	344 [a]
1981	159	615 [a]
1982	345	1,335 [a]
1983	589	2,279 [a]
1984	508	1,966 [a]
1985	709	2,744 [a]
1986	1,278	4,946 [a]
1987	1,349	5,221 [a]
1988	384	1,486 [a]
1989	344	1,331 [a]
1990	257	995 [a]
1991	239	925 [a]
1992	150	581 [a]
1993	303	1,173 [a]
1994	161	623 [a]
1995	217	840 [a]
1996	220	851 [a]
1997	132	511 [a]
1998	91	364 [b]
1999	212	820 [a]
2000	231	894 [a]
2001	204	789 [a]
2002	224	867 [a]
2003	203	786 [a]
2004	333	734 [b]
2005	445	926 [b]
2006	339	1,270 [b]
2007	135	522 [a]
2008	257	995 [a]
2009	123	476 [a]
2010	180	697 [a]
2011	147	569 [a]
2012	205	793 [a]
2013	255	987 [a]
2014	217	840 [a]
2015	166	642 [a]
2016	135	522 [a]
2017	88	341 [a]
2018	281	1,087 [a]
2019	144	557 [a]

[a] Escapement estimated from expanded peak survey counts.

[b] Escapement estimated from mark-recapture studies.

Note: Escapement goal 500–1,400 large Chinook salmon.

Table 3.–Escapement peak survey counts and escapement of large (≥660 mm METF) spawners for Andrew Creek Chinook salmon from 1975 to 2019.

Year	Peak survey count	Spawning escapement
1975	260	507 [a]
1976	ND	404 [b]
1977	ND	456 [b]
1978	ND	388 [b]
1979	221	327 [b]
1980	ND	282 [b]
1981	300	536 [b]
1982	332	672 [b]
1983	ND	366 [b]
1984	154	389 [b]
1985	320	624 [a]
1986	708	1,381 [a]
1987	788	1,537 [a]
1988	564	1,100 [a]
1989	530	1,034 [a]
1990	664	1,295 [a]
1991	400	780 [a]
1992	778	1,517 [a]
1993	1,060	2,067 [a]
1994	572	1,115 [a]
1995	343	669 [a]
1996	335	653 [a]
1997	293	571 [a]
1998	487	950 [a]
1999	605	1,180 [a]
2000	690	1,346 [a]
2001	1,054	2,055 [a]
2002	876	1,708 [a]
2003	153	1,160 [a]
2004	153	298 [a]
2005	1,015	1,979 [a]
2006	1,089	2,124 [a]
2007	890	1,736 [a]
2008	503	981 [a]
2009	322	628 [a]
2010	618	1,205 [a]
2011	480	936 [a]
2012	301	587 [a]
2013	472	920 [a]
2014	674	1261 [a]
2015	408	796 [a]
2016	206	402 [a]
2017	179	349 [a]
2018	247	482 [a]
2019	358	698 [a]

[a] Escapement estimated from expanded peak survey counts.

[b] Escapement enumerated using a weir.

Note: Escapement goal 650–1,500 large Chinook salmon.

Note: ND means no data was collected.

Table 4.–Escapement peak survey counts and escapement of large (≥660 mm METF) spawners for King Salmon River Chinook salmon from 1975 to 2019.

Year	Peak survey count	Spawning escapement
1975	42	64 [a]
1976	65	99 [a]
1977	134	204 [a]
1978	57	87 [a]
1979	88	134 [a]
1980	70	106 [a]
1981	101	154 [a]
1982	259	394 [a]
1983	183	245 [b]
1984	184	265 [b]
1985	105	175 [b]
1986	190	255 [b]
1987	128	196 [b]
1988	94	208 [b]
1989	133	240 [b]
1990	98	179 [b]
1991	91	134 [b]
1992	58	99 [b]
1993	175	266 [a]
1994	140	213 [a]
1995	97	147 [a]
1996	192	292 [a]
1997	238	362 [a]
1998	88	134 [a]
1999	200	304 [a]
2000	91	138 [a]
2001	98	149 [a]
2002	102	155 [a]
2003	78	119 [a]
2004	89	135 [a]
2005	94	143 [a]
2006	99	150 [a]
2007	119	181 [a]
2008	79	120 [a]
2009	72	109 [a]
2010	104	158 [a]
2011	126	192 [a]
2012	102	155 [a]
2013	62	94 [a]
2014	45	68 [a]
2015	33	50 [a]
2016	98	149 [a]
2017	56	85 [a]
2018	20	30 [a]
2019	18	27 [a]

[a] Escapement estimated from expanded peak survey counts.

[b] Escapement estimated from mark-recapture studies.

Note: Escapement goal 120–240 large Chinook salmon.

Table 5.–Escapement peak survey counts and escapement of large (≥660 mm METF) spawners in the Chickamin River from 1975 to 2019.

Year	Peak survey count	Spawning escapement
1975	370	1,758 [a]
1976	157	746 [a]
1977	363	1,724 [a]
1978	308	1,463 [a]
1979	239	1,135 [a]
1980	445	2,114 [a]
1981	384	1,824 [a]
1982	571	2,712 [a]
1983	599	2,845 [a]
1984	1,102	5,235 [a]
1985	956	4,541 [a]
1986	1,745	8,289 [a]
1987	975	4,631 [a]
1988	786	3,734 [a]
1989	934	4,437 [a]
1990	564	2,679 [a]
1991	487	2,313 [a]
1992	346	1,644 [a]
1993	389	1,848 [a]
1994	388	1,843 [a]
1995	356	1,691 [a]
1996	422	1,587 [b]
1997	272	1,292 [a]
1998	391	1,857 [a]
1999	501	2,380 [a]
2000	801	3,805 [b]
2001	1,010	5,177 [b]
2002	1,013	5,007 [b]
2003	964	4,579 [b]
2004	798	4,268 [b]
2005	926	4,257 [b]
2006	1,330	6,318 [a]
2007	893	4,242 [a]
2008	1,111	5,277 [a]
2009	611	2,902 [a]
2010	1,156	5,491 [a]
2011	852	4,052 [a]
2012	444	2,109 [a]
2013	468	2,223 [a]
2014	652	3,097 [a]
2015	581	2,760 [a]
2016	203	964 [a]
2017	152	722 [a]
2018	432	2,052 [a]
2019	339	1,610 [a]

[a] Escapement estimated from expanded peak survey counts.

[b] Escapement estimated from mark-recapture studies.

Note: Escapement goal 2,140–4,300 large Chinook salmon.

OBJECTIVES

The research objectives[1] for 2020−2021 are to:

1. Estimate the age and sex composition of large (≥660 mm METF) Chinook salmon spawning in:
    a. the Chickamin River such that all estimated proportions are within 10% of the true values 95% of the time;
    b. the Keta River such that all estimated proportions are within 10% of the true values 95% of the time;
    c. the Blossom River such that all estimated proportions are within 10% of the true values 90% of the time;
    d. the King Salmon River such that all estimated proportions are within 15% of the true values 90% of the time; and
    e. Andrew Creek such that all estimated proportions are within 10% of the true values 95% of the time.
2. Estimate the escapements of large Chinook salmon in the systems outlined in Objective 1 such that the coefficient of variation of the expanded survey counts is <u>≤</u>20% for the Chickamin, Keta, Blossom and King Salmon river systems and ≤25% for Andrew Creek.

SECONDARY OBJECTIVES

1. Estimate mean length-at-age by sex and size class (small, medium, large) of Chinook salmon;
2. Estimate the escapement of medium (≥400 mm and <660 mm METF) Chinook salmon;
3. Estimate the age-sex composition of small (<400 mm METF) and medium (≥400 mm and <660 mm METF) Chinook salmon;
4. Count all large (≥660mm) Chinook salmon (live and dead) observed during age-sex-length sampling trips;
5. Examine all sampled Chinook salmon for a missing adipose fin; and
6. Opportunistically collect genetic tissue (Appendix C) from all Chinook salmon captured.

METHODS

STUDY DESIGN

Age, sex, and length data will be collected from all Chinook salmon sampled at upriver spawning locations, and all observed large Chinook salmon will be counted (Objective 1 a−e, Secondary Objectives 1–3). No coded-wire-tagging or clipping occurred in any of these systems during fingerling or smolt years corresponding to adult returns in 2020−2021. All Chinook salmon missing adipose fins will be sacrificed (Secondary Objective 5). Data collected from these CWT recoveries will be used to determine the number of strays in the escapement and the origins of the stray fish. Peak survey counts of large fish in the 5 rivers will be expanded to total escapements of large fish

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[1] Estimation of age, sex, and length composition and estimation of escapement for the Unuk River (1 of 6 index systems for SEAK) is described in separate operational plans: Juvenile abundance and harvest of Unuk River Chinook salmon, 2020-2022 (Frost et al. 2022) and Escapements of Chinook salmon in Southeast Alaska and transboundary rivers in 2020 and 2021 (e.g., Richards et al. 2022).

using established expansion factors (Objective 2); collection of peak survey data is described in a separate Regional Operational Plan (Richards et al. 2022). In 2020 and 2021, genetic tissue samples will be opportunistically collected per the direction of the ADF&G Gene Conservational Lab (Secondary Objective 6). These samples are used to refresh the baseline used in genetic mix stock analyses.

Effort Distribution

Effort will be distributed across known spawning areas and time of spawning for each system with the goal that every spawning Chinook salmon has a similar probability of being sampled.

Effort will be distributed among tributaries on the Chickamin River (Figure 2) based on a spawning distribution calculated from peak counts over a 19-year period 2001–2019. It is assumed that peak survey counts are a constant proportion of the spawning abundance in each area of the Chickamin River. The distribution of effort and estimates of spawning dates around which sampling should be concentrated are depicted in Table 6.

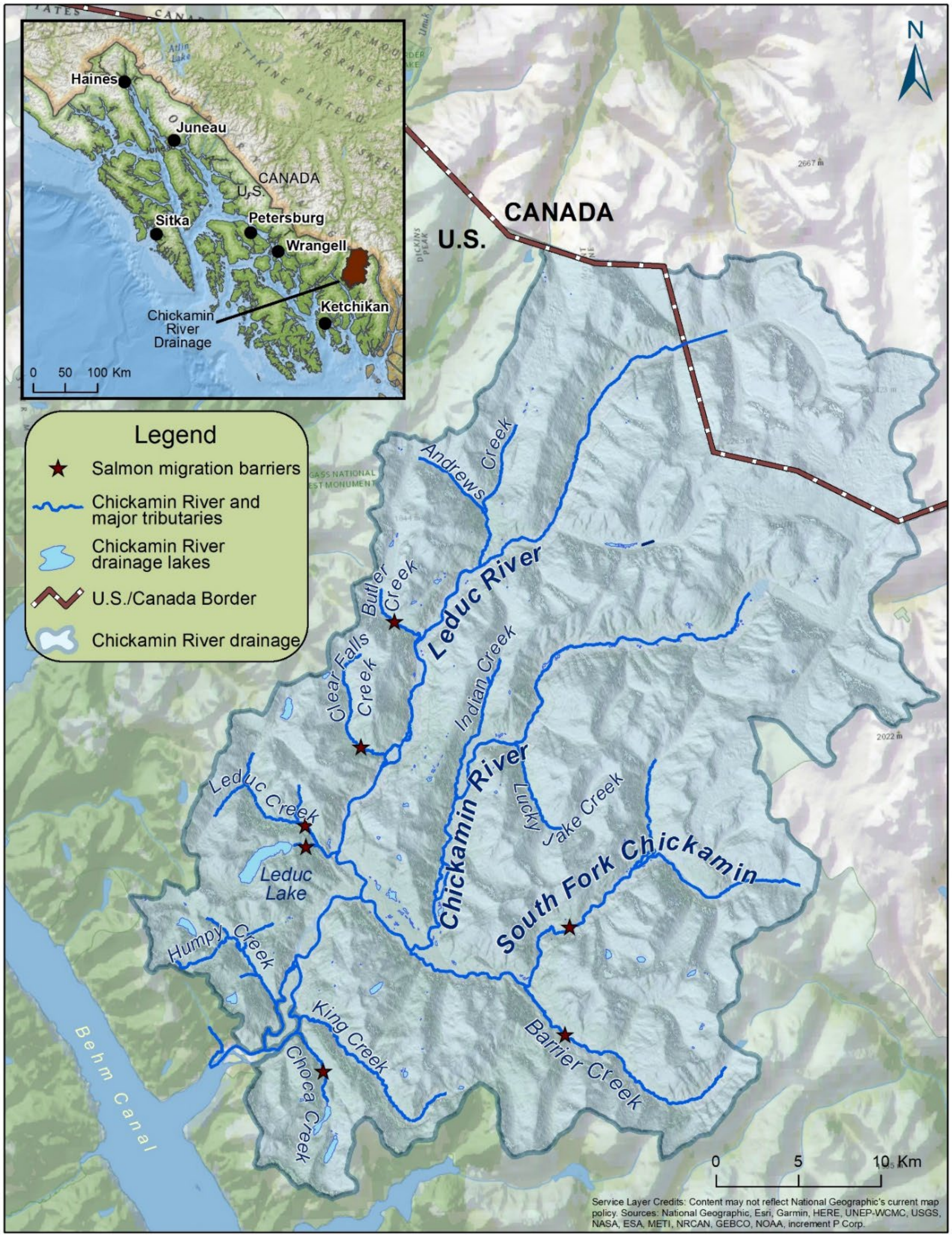
Table 6.-Summary information necessary to identify sampling schedules and sampling effort on the tributaries of the Chickamin River, Southeast Alaska.

Tributary	Range of prime sampling dates	Estimated date of peak spawning	% Effort
King Creek	24 Aug – 6 Sept	1 Sept	36
South Fork Creek	20 Aug – 10 Sept	25 Aug	19
Butler Creek	3 Aug – 17 Aug	10 Aug	20
Humpy Creek	24 Aug – 6 Sept	1 Sept	8
Indian Creek	1 Aug – 20 Aug	10 Aug	7
Clear Falls Creek	1 Aug – 20 Aug	10 Aug	3
Leduc Creek	10 Aug – 24 Aug	17 Aug	5
Barrier Creek	10 Aug – 24 Aug	17 Aug	3

Note: Percent effort is based on the 19-year average of survey counts.

Actual sampling dates will be adjusted to coincide with observed abundances and water conditions. Roughly 50% of sampling effort should be spent on South Fork and King creeks and roughly 50% on Butler and Humpy, Indian, Lucky Jake, Clear Falls, Barrier, and Leduc Creeks.

In 2016, the North Fork of the Chickamin River cut into the Indian Creek clearwater about halfway up the tributary. Since then, Chinook counts have dropped in Indian Creek and there has been increased spawning activity at Lucky Jake Creek just upstream from Indian Creek. With very small counts at Indian Creek, sampling effort has shifted to Lucky Jake Creek in lieu of Indian Creek. Lucky Jake Creek is not in Table 6 as it is not surveyed.



Service Layer Credits: Content may not reflect National Geographic's current map policy. Sources: National Geographic, Esri, Garmin, HERE, UNEP-WCMC, USGS, NASA, ESA, METI, NRCAN, GEBCO, NOAA, increment P Corp.

Figure 2.–Chickamin River drainage showing major tributaries and salmon migration barriers in Southeast Alaska.

Samplers will sample each Chickamin River tributary on at least 2 different days across the range of sampling dates. Tributaries with fewer fish (Barrier, Leduc, Indian, Lucky Jake, and Clear Falls) may be thoroughly sampled in a day, while those with many fish (King Creek, Butler, and South Fork) may take more to sample thoroughly. An initial trip into Indian, Lucky Jake, and Butler Creeks should occur on or about 3 August, based on historically low catches on these systems after 15 August. Sampling data will be collected as described in the Data Collection section: Age-Sex-Length and Coded Wire Tag Sampling of this plan.

The Blossom and Keta rivers are too big, and the spawning areas too widely dispersed to conduct foot surveys without helicopter assistance. Crews from Ketchikan or the Chickamin and Unuk River base camps must fly in by helicopter and have the aircraft standby all day to move the crew from one spawning area to the next. Two to four trips to each system are required and each trip may take as much as 6 hours of flight time and up to 14 hours on the spawning grounds to maximize efficiency of helicopter and fishing time. It is noted that unlike the Chickamin River, the Blossom and Keta rivers do not have substantial spawning tributaries.

To sample the King Salmon River, a crew from Juneau will be dropped off by helicopter at the upper end of the spawning area, work their way downstream to the mouth and be picked up again by helicopter. Flight time per trip is variable and 3 or 4 trips may be necessary to collect enough samples because of the small run size and dispersed spawning.

To sample Andrew Creek a crew must fly to Wrangell, travel by boat to a camp on the lower Stikine River and boat from there to the spawning area.

The project leader will adjust the actual sampling schedule in concert with the crew leader as needed; the goal is to sample as many fish as possible while attempting to sample a constant fraction of the escapement from every major spawning area.

Age-Sex-Length, Coded Wire Tag, and Genetic Tissue Sampling

Spawning ground sampling will begin approximately 1 August and continue <u>as long as sampling is effective</u> (ending approximately 15 September). The goal of sampling is 2-fold: 1) to estimate ASL compositions; and 2) to report the numbers of large Chinook salmon observed.

To prevent double sampling of Chinook salmon on the spawning grounds, every live and dead fish sampled will be given an operculum punch on the lower one-third (ventral side) of the left operculum (LLOP). Additionally, every dead fish sampled will be slashed several times 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 and adipose clips. 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 or size. 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 Chinook salmon missing adipose fins will be sacrificed. Data collected from these CWT recoveries will be used to determine straying rates and origins.

In 2020 and 2021, live and dead fish encountered on the spawning grounds will be sampled for genetic tissue per the direction of the ADF&G Gene Conservation Lab.

SAMPLE SIZES

Age and Sex Composition Estimation

Sample sizes needed to meet the objective criteria of Objective 1 are presented in Table 7. The sample size calculations assume no size or sex selectivity and are based on the methods of Thompson (1987). A finite population correction factor is used, based on the recent five-year average escapement estimate, and a scale regeneration rate of 17% for the Chickamin, Blossom, Keta, and Andrew Creek and one of 30% for the King Salmon River.

Table 7.–Required sample sizes and associated parameters for estimation of age composition of large Chinook salmon on selected index systems in Southeast Alaska in 2020−2021.

	Objective criteria					
System	Relative precision	α	5-yr average escapement	Scale regeneration rate	Sample size	Historic average sample size (year range)
Chickamin	10	95	1,622	17%	143	321 (2006–2019)
Blossom	10	90	630	17%	105	81 (2001–2019)[a]
Keta	10	95	1,173	17%	139	139 (2001–2019)[b]
Andrew	10	95	506	17%	123	158 (2001–2014)[c]
King Salmon	15	90	75	30%	35	33 (2001–2013)[d]

[a] Not sampled in 2010 and 2011 due to budget constraints and inclement weather; 15 fish sampled in 2012 due to inclement weather; Not sampled in 2016 due to inclement weather.

[b] Not sampled in 2010 and 2011 due to budget constraints and inclement weather; 61 and 63 fish sampled in 2012 due to inclement weather.

[c] Not sampled in 2011 due to inclement weather; Not sampled from 2015-2019 due to low abundance.

[d] Not sampled in 2011 due to inclement weather; 2 fish sampled in 2012 and not sampled 2014–2019 due to low abundance.

Planned effort on the Chickamin, Keta, and Blossom Rivers will be commensurate with the levels associated with historic sampling, and we believe prescribed sample sizes will be met under typical sampling conditions and run size (i.e., moderate weather conditions and escapement within or above the goal range). With the current trend in effort and population size, we are not confident in being able to meet sampling goals for King Salmon River and Andrew Creek. The King Salmon River has not been sampled in recent years due to extremely low abundance; however, if fish are available, it is possible that 30 to 60 samples could be collected in a day, and we consider it worthwhile trying to sample this system again, if the population is within or above the escapement goal. Evaluation will take place after the first and second surveys in 2020−2021. If there are enough fish present, the Juneau staff will attempt to collect samples; if the count is low, sampling will not take place. The cost-benefit equation of sampling King Salmon River and Andrew Creek will be addressed both in-season and after the 2020−2021 field seasons. For example, Considerations include how many fish are observed relative to the escapement goal as obtaining the required sample size would mean handling a substantial component of the total escapement (i.e., for the King Salmon River, approximately 50%, or 35/75 would need to be sampled according to Table 7), which is not desirable during periods of low abundance. Another consideration is whether obtaining the required number samples is achievable.

Peak Survey Count Expansions

Chickamin

The mean expansion factor for the Chickamin River is 4.75 (SE = 0.7, CV = 14.7%). From Eq.'s 19 and 20 in Appendix B1, the expected coefficient of variation of a new peak survey count, C, is then,

$$\sqrt{C^{2}0.7^{2}}\Big/_{\bar{\pi}C} = 0.7/4.75 \approx 0.15$$

so the objective criterion of Objective 2 should be achieved.

Blossom

The mean expansion factor for the 2 years with normal survey conditions is 3.87 (SE = 0.62, CV = 16.1%) and meets the USCTC standard for precision (Objective 2, Weller et al. 2007a).

Keta

The expansion factor for the Keta River is 3.01 (SE = 0.56, CV = 18.6%), and meets the USCTC standard for precision (Objective 2; Der Hovanisian et. al 2011).

King Salmon

The expansion factor for the King Salmon River is 1.52 (SE = 0.27, CV = 17.8%), and meets the USCTC standard for precision (Objective 2; Der Hovanisian et. al 2011).

Andrew Creek

The expansion factor for the Andrew Creek is 1.95 (SE = 0.45, CV = 23.1%), and meets the USCTC standard for precision. (Objective 2; Der Hovanisian et. al 2011).

DATA COLLECTION

Age-Sex-Length and Coded Wire Tag Sampling

All Chinook salmon caught on the spawning grounds will be sampled for ASL. Data from fish sampled on the spawning grounds will be recorded on the Spawning Grounds Age-Sex-Length Form (Appendix A1). For age composition sampling, it is imperative that good scale samples be taken. 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 0.5 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 scale gum cards will be labeled with a scale card number, date, initials of samplers and location at the start of sampling. Scale cards are sequentially numbered by sampling location, beginning with 001 (or 00A if multiple crews are sampling the same system, on the same day). The ASL stream code (Table 8) will be recorded on each card upon returning to camp. Sex will be determined from secondary maturation characteristics, and length will be measured to the nearest 5 mm METF. Secondary maturation characteristics can include predominant snouts and compressiformed bodies for males, and abraded caudal fins (i.e., white tails) and prominent bellies for females. 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 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, a note in the comment column on the ASL form will be placed and that column will be skipped on the gum card.

Table 8.–Alaska Department of Fish and Game stream codes for Chinook salmon index areas in the Chickamin River drainage and Blossom, Keta and King Salmon rivers and Andrew Creek.

Location	Stream number	Coded wire tag sample number	Age-sex-length number
Chickamin River	101-71-10040	46000X	101-71-004
Humpy Creek	101-71-10040-2005	46300X	101-71-04H
Choca Creek	101-71-10040-2004	46100X	101-71-04E
King Creek	101-71-10040-2006	46200X	101-71-04K
LeDuc Creek	101-71-10040-2015-3003	46400X	101-71-04L
Clear Falls Creek	101-71-10010-2015-3009	46600X	101-71-04C
South Fork	101-71-10040-2018	46900X	101-71-04S
Barrier Creek	101-71-10040-2018-3010	46700X	101-71-04A
Indian Creek	101-71-10040-2025	46800X	101-71-04I
Lucky Jake Creek	101-71-10040-2034	46950X	101-71-04LJ
Butler Creek	101-71-10040-2015-3011	46750X	101-71-04B
Clear Creek	101-70-10060	46350X	101-70-060
Pond Slough	101-71-10060	46450X	101-71-060
Blossom River	101-55-10400	DQ000x	101-55-040
Keta River	101-30-10300	DQ000x	101-55-020
Andrew Creek	108-40-10150-2008	16741001	108-40-020
King Salmon River	111-17-10100	16AJ1001	111-17-010

A Coded Wire Tag Sampling Form (Appendix A3) will also be filled out for each day's spawning grounds sampling at each location. Any fish sampled on the spawning grounds, live or dead, missing an adipose fin will be noted. Furthermore, heads and scales will be removed from all adipose-finclipped Chinook salmon encountered on the spawning grounds. These heads will then be sent to the ADF&G Mark, Tag, and Age Laboratory (Tag Lab) along with the CWT form. In systems with no active CWT program (every system except Andrew Creek), ALL Chinook

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

salmon, missing adipose fins will be sacrificed. A uniquely numbered cinch tag from the escapement sampling packet provided by the Tag Lab will be attached to each head.

Most importantly:

- every Chinook salmon encountered must be sampled on the spawning grounds, regardless of size, and all data for each fish will be recorded on the appropriate form;
- every fish must be checked for the presence or absence of an adipose fin and LLOP;
- clean, readable scales must be collected from the preferred area (or other areas if necessary); and
- heads and scales from all adipose-clipped fish will be collected

Survey Counts

A count will be made of the total number of large fish seen by observers traversing a tributary on a single day; this count will be recorded on the Spawning Grounds Survey Form (Appendix A2) each day a survey count is made (see Study Design section for more details). The location, date, stream code (Table 8, survey number, surveyors, all water and weather conditions, total number of large fish, and predators will be recorded on this form. The percentage of large fish the observer(s) believed were counted, and why they thought so, will also be recorded.

Genetic Tissue (Secondary Objectives 6, 7)

Genetic tissue data will be collected using the methods described in Appendix C.

DATA REDUCTION

It is the responsibility of the field crew leader to record and error-check all data. Data forms are to be filled out daily and always kept up to date. Data forms should be error free, legible, and complete. Scales on gum cards should be clean and cards must be labeled completely and stored flat and dry. Data will be transferred from field books or forms to Excel spreadsheet files. When input is complete, data lists will be obtained and checked against the original field data.

The Tag Lab in Juneau is the clearinghouse for all information on CWTs. Completed CWT sampling summary information will be sent to the Tag Lab, after first being given to the project leader and error checked using computer software. All CWT data (sampled fish, decoded tags, location, data type, samplers, etc.) are archived and accessible on a permanent ADF&G statewide database, and once per year are provided to the permanent coast wide database at the Pacific States Marine Fisheries Commission.

Data files will be stored in a DSF network shared drive. For this project, all recovery data is recorded by hand on specialized field forms, transcribed into Excel workbooks and analyzed in Excel and other commercial and custom software. The original hard copies of all tagging and recovery forms, scale gum cards and acetates will be logged and stored in the Region 1 ASL data archives, located in file cabinets in the Douglas regional office.

DATA ANALYSIS

Age and Sex Composition of Large (Objective 1) and Medium Fish (Secondary Objective 3)

The proportion of the spawning population of age *c* within a size class k (large or medium) for each system will be estimated as a binomial variable:

$$\hat{p}_{k,c} = \frac{n_{k,c}}{n_k} \tag{1}$$

$$var\left(\hat{p}_{k,c}\right) = \frac{\hat{p}_{k,c}\left(1 - \hat{p}_{k,c}\right)}{n_k - 1} \tag{2}$$

where n_k is the number of Chinook salmon in the sample of size group k and $n_{k,c}$ is the number of Chinook salmon of age *c* in n_k.

Adult Escapement of Large Fish (Objective 2)

The estimated abundance of large Chinook salmon, $\widehat{N}_L$, will be calculated as described in Appendix B1, under the section "Systems where escapement is estimated".

Mean Length at Age (Secondary Objective 1)

Mean length at age and sex will be calculated using standard summary statistics (Cochran 1977).

Abundance and Age Sex Composition of Fish ≥ 400 mm METF (Secondary Objectives 2, 3)

The abundance of all fish ≥ 400 mm METF will be estimated as:

$$\widehat{N}_{\geq 400} = \frac{\widehat{N}_L}{\hat{\phi}_L} \tag{3}$$

where $\hat{\phi}_L$ is the estimated fraction of large fish in the Chinook salmon spawning population ≥ 400 mm METF:

$$\hat{\phi}_L = \frac{n_L}{n_{\geq 400}} \tag{4}$$

where,

$n_{>400}$ = Number of fish sampled on the spawning grounds ≥ 400 mm METF

n_L = Number of large fish found in $n_{\geq 400}$,

with variance estimated as :

$$var\left(\hat{\phi}_L\right) = \frac{\hat{\phi}_L\left(1 - \hat{\phi}_L\right)}{n_{\geq 400} - 1} \tag{5}$$

Variance of $\widehat{N}_{\geq 400}$ will be estimated as:

$$var\left(\widehat{N}_{\geq 400}\right) = var\left(\widehat{N}_L\right)\left(\frac{1}{\hat{\phi}_L}\right)^2 + \widehat{N}_L^2 var\left(\frac{1}{\hat{\phi}_L}\right) - var\left(\widehat{N}_L\right) var\left(\frac{1}{\hat{\phi}_L}\right) \tag{6}$$

where,

$$var\left(\frac{1}{\hat{\phi}_L}\right) \approx \left(\frac{1}{\hat{\phi}_L}\right)^4 var(\hat{\phi}_L) \tag{7}$$

It is noted that the number of fish sampled for size (≥ 400 mm METF) is larger (includes all carcasses) than that sampled for age and that the $\hat{\phi}_k$ are considered relatively unbiased.

The abundance of medium-sized fish $\hat{N}_M$ (≥400 mm and <660 mm METF) will be estimated indirectly by expanding the estimate for large fish by the estimated size composition of the spawning escapement ≥ 400 mm METF (McPherson et al. 1997):

$$\hat{N}_{\mathrm{M}} = \frac{\hat{N}_L\hat{\phi}_M}{\hat{\phi}_L} \tag{8}$$

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

$$var(\hat{N}_{\mathrm{M}}) = var(\hat{N}_L)\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right)^2 + \hat{N}_L^2 var\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right) - var(\hat{N}_L)var\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right) \tag{9}$$

whereby the delta method (note that $Cov(\hat{\phi}_M, \hat{\phi}_L) = -\frac{\hat{\phi}_M\hat{\phi}_L}{n_{\geq 400}}$),

$$var\left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right) \approx \left(\frac{\hat{\phi}_M}{\hat{\phi}_L}\right)^2 \left(\frac{var(\hat{\phi}_M)}{\hat{\phi}_M^2} + \frac{var(\hat{\phi}_L)}{\hat{\phi}_L^2} + \frac{2}{n_{\geq 400}}\right) \tag{10}$$

Numbers of spawning fish by age in the spawning population ≥ 400 mm METF will be estimated as the sum of the products of estimated age composition and estimated abundance within a size category:

$$\hat{N}_c = \sum_k \hat{p}_{k,c}\hat{N}_k \tag{11}$$

Because the $\hat{N}_k$ in Equation 11 are correlated ($\hat{N}_M$ is estimated from $\hat{N}_L$ by Eq. 8), the $var(\hat{N}_c)$ will be estimated by simulation. The stochastic components in the simulation will be: the estimate of large fish as $\hat{N}_L^* \sim normal(\hat{N}_L, \hat{\sigma}_{\hat{N}_L})$, the vector of estimated size proportions as $\hat{\phi}^* \sim \mathrm{multinomial}(n_{\geq 400}, \hat{\phi})/n_{\geq 400}$, and the vector of estimated age and sex proportions for the k^{th} size group as $\hat{p}_k^* \sim \mathrm{multinomial}(n_k, \hat{p}_k)/n_k$. Equations 8 and 11 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 ≥ 400 mm METF composed of a given age will be estimated as :

$$\hat{p}_c = \frac{\hat{N}_c}{\hat{N}_{\geq 400}} \tag{12}$$

The $var(\hat{p}_c)$ 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 sex (male or female), such that $\sum_g \hat{p}_g = 1$, and by age-sex $\hat{p}_{c,g}$, such that $\sum_g \sum_c \hat{p}_{c,g} = 1$.

SCHEDULE AND DELIVERABLES

The crews will begin work on or around 1 August 2020−2021. Spawning ground sampling will begin approximately 1 August and continue as long as sampling is effective (approximately 15 September). Raw field data will be entered and error checked by 30 November. An ADF&G Fishery Data Series report will be prepared in draft form by 1 July 2025 summarizing the results of this project.

RESPONSIBILITIES

Nathan Frost, Fishery Biologist 2 (project leader)

Duties: This position is responsible for supervision of all project activities, including administrative, field, personnel, and other activities. Maintains daily contact with crew leader and tracks sampling effort, logistics, personnel, etc. Will edit, error-check, analyze, and report data for project under supervision of Richards. Will track budget and stay within allocations. Ensures project follows operational plan and actively participates in field operations. Will conduct or assist Richards with aerial Chinook salmon index surveys. Will conduct start-of-project meetings with field crew. Follows Departmental and State policy.

Randy Peterson, Biometrician 3

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

Philip Richards, Fishery Biologist 3

Duties: Supervises project. Will oversee or assign aerial Chinook salmon index surveys and may assist with field work.

Ed Jones, Chinook Salmon Research Coordinator

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

Joseph Simonowicz, Fishery Biologist 1 (crew leader)

Duties: This position is the primary crew leader. Responsible for assisting in all aspects of field operations, including safe operation of riverboats and motors and all other equipment, training of lower-level technicians, data collection and editing, maintenance of jet outboard and skiff, general camp maintenance and duties, and daily contacts with project leader. Responsible for leading spawning grounds team, and for inventorying equipment and supplies at end of the project. Larson will work in consultation with the project leader on personnel and administrative issues, as encountered. Responsible for daily safety checks with town via email or satellite phone. Follows Departmental and State policy in all matters.

Kristian Larson, Fish & Wildlife Technician 3

Duties: This position is responsible for assisting in all aspects of field operations including data collection and editing, maintenance of jet outboard and skiff, and general camp duties. Responsible for daily cleaning and maintenance of equipment as assigned by the crew leader. Follows Departmental and State policy in all matters.

James Bryant, Fish & Wildlife Technician 3

Duties: This position is responsible for assisting in all aspects of field operations including data collection and editing, maintenance of jet outboard and skiff, and general camp duties. Responsible for daily cleaning and maintenance of equipment as assigned by the crew leader. Follows Departmental and State policy in all matters.

Corbin Lind, Fish & Wildlife Technician 2

Duties: This position is responsible for assisting in all aspects of field operations including data collection and editing, maintenance of jet outboard and skiff, and general camp duties. Responsible for daily cleaning and maintenance of equipment as assigned by the crew leader. Follows Departmental and State policy in all matters.

Vacant, Fish & Wildlife Technician 2

Duties: This position is responsible for assisting in all aspects of field operations including data collection and editing, maintenance of jet outboard and skiff, and general camp duties. Responsible for daily cleaning and maintenance of equipment as assigned by the crew leader. Follows Departmental and State policy in all matters.

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APPENDIX A

Appendix A1.–Spawning grounds age-sex-length form, 2020−2021.

Location: Year:2020
Stream code:
Species:Chinook

Fish #	Date	Sex	Length METF (mm)	Card #	Scale #	Age FW	Age SW	AEC	Ad Clip / Cinch #	Gear type	Fish condition	Comments
1	8/9		805	1	1							
2	8/9	F	800	1	2					Lure	Pre	
3	8/9	M	760	1	3					Lure	Active	
4	8/9	M	675	1	4				433110	Snag	Active	Adclip sacrificed (adsac)
5	8/9	M	350	1	5					Lure	Pre	
6	8/9	F	900	1	6					Dip net	Pre	
7	8/9	F	925	1	7					Gillnet	Post	
8	8/9	F	780	1	8					Gillnet	Active	
9	8/9	M	850	1	9					Carcass	Dead	
10	8/9	M	875	1	10					Snag	Active	

11	8/9	M	1005	2	1					Snag	Pre	
12	8/9	M	750	2	2				433111	Snag	Post	Adsac
13	8/9	M	675	2	3					Carcass	Dead	
14	8/9	F	845	2	4					Carcass	Dead	
15	8/9	F	810	2	5					Lure	Post	
16	8/9	F	940	2	6					Lure	Post	
17	8/9	F	705	2	7					Snag	Post	

Appendix A2.–Spawning grounds survey form, 2020−2021.

SPAWNING GROUNDS SURVEY FORM

(please be as detailed as possible)

Location: ________________________ Date: _______/________/______
(River, stream name)

Survey no. ____________ Surveyors______________________________
(1st, 2nd, etc.)

Water Conditions (water level, clarity, flow, temp, etc.): __________________________

____

Weather conditions: ____

A. Total number of large-sized fish counted __________

B. Rate survey conditions on a scale of 1-10 (10 = best) __________

C. What % of the fish present do you think you counted? __________

Why? ____

____

D. % of fish counted that were *fresh*: _______________

E. % of fish counted that were *spawned out*: _______________

F. % of fish counted that were *dead*: _______________

G. Signs of predation: ____

____

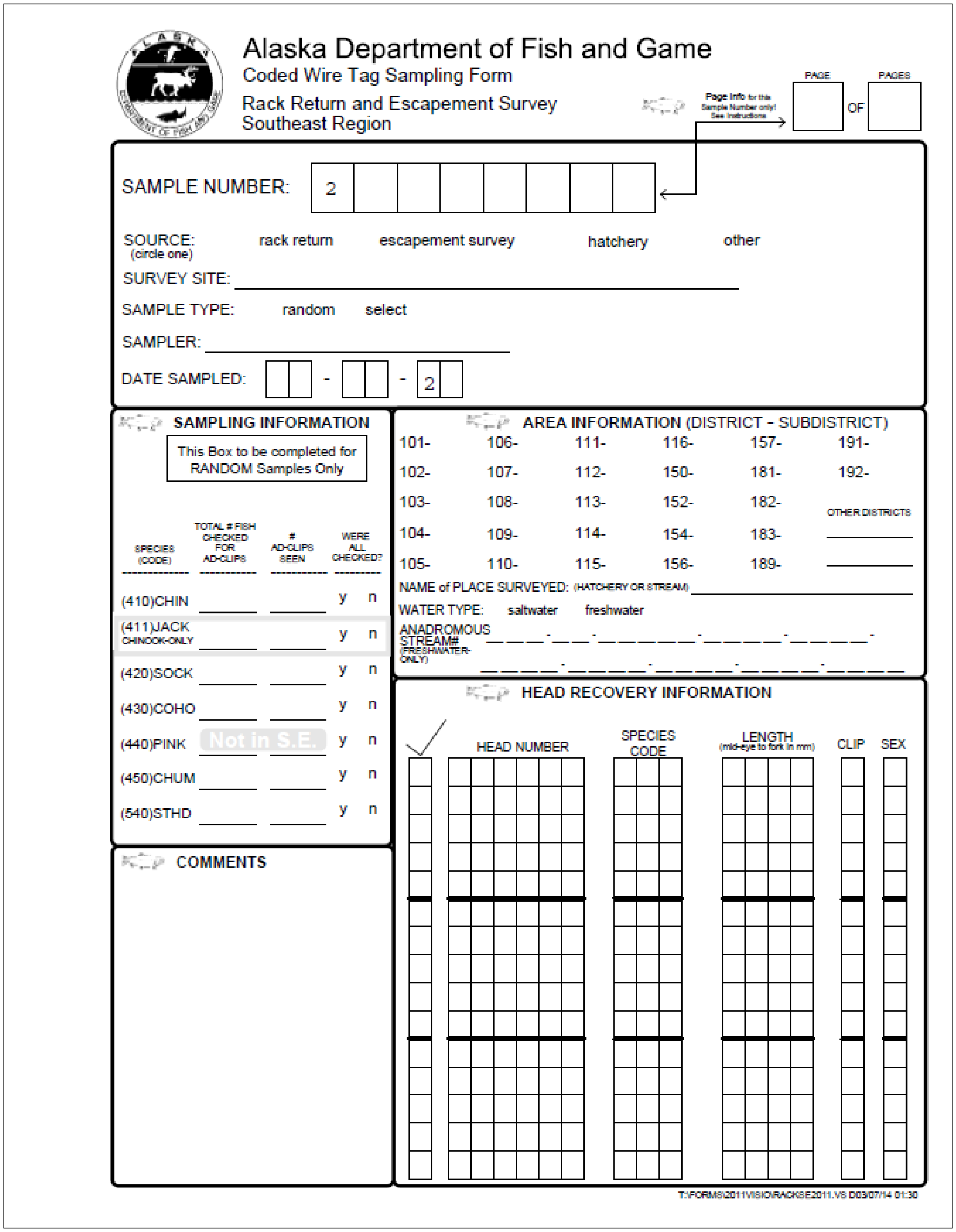
____

Other notes and comments: ____

____

____

Appendix A3.–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: 2 ☐☐☐☐☐☐☐

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

SURVEY SITE: ____________________

SAMPLE TYPE: random select

SAMPLER: ____________________

DATE SAMPLED: ☐☐ - ☐☐ - 2☐

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 D03/07/14 01:30

APPENDIX B

Appendix B1.–Predicting escapement from index counts using an expansion factor.

Expansion factors provide a means of predicting escapement in years where only an index count of escapement is available (i.e., no weir count or mark–recapture study was conducted). An expansion factor is the average ratio of escapement (as estimated by a mark–recapture experiment or known through a weir count) to the index count over several years.

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_y'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 2 sources of uncertainty for any predicted value of π, (π_{pred}). 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 with additional escapement estimates. The variance for prediction will be estimated (Kutner et al. 2005):

$$var(\pi_{pred}) = var(\pi) + var(\bar{\pi}) \tag{2}$$

where

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

and

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

such that

$$var(\pi_{pred}) = \frac{\sum_{y=1}^{k} (\pi_y - \bar{\pi})^2}{k-1} \left(1 + \frac{1}{k}\right) \tag{5}$$

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 ($\hat{\pi}_y's$) for that system:

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

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 the other terms are as described as above. The variance for prediction will be estimated similar as before (see Eq. 2):

$$var\left(\pi_{pred}\right) = \widehat{var}(\pi) + var(\bar{\pi}) \tag{7}$$

The estimate of process error, $var(\bar{\pi})$, should reflect only process error; however, since the π_y's are estimated ($\hat{\pi}_y$), these estimates represent process error plus measurement error (e.g., the mark–recapture induced error in escapement estimation), which can be expressed as (Mood et al. 1974):

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

Equation 8 can be rearranged to isolate process error, that is:

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

Therefore, an estimate of $var(\pi)$, ($\widehat{var}(\pi)$), representing only process error is:

$$\widehat{var}(\pi) = var(\hat{\pi}) - \frac{\sum_{y=1}^{k} var\left(\hat{\pi}_y\right)}{k} \tag{10}$$

where $var\left(\hat{\rho}_y\right)$ is the variance of the estimated escapement in year y, which is calculated as:

$$var\left(\hat{\pi}_y\right) = var\left(\hat{\pi}_y\right) / C_y^2 \tag{11}$$

Both $var(\hat{\pi})$ and $var(\bar{\pi})$ are computed similar as before (see Eq. 3 and 4), except $\hat{\pi}_y$ is substituted for π_y:

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

and

$$var(\bar{\pi}) = \frac{\sum_{y=1}^{k}\left(\hat{\pi}_y - \bar{\pi}\right)^2}{k(k-1)} \tag{13}$$

such that

$$var\left(\pi_{pred}\right) = \frac{\sum_{y=1}^{k}\left(\hat{\pi}_y - \bar{\pi}\right)^2}{k-1}\left(1 + \frac{1}{k}\right) - \frac{\sum_{y=1}^{k} var\left(\hat{\pi}_y\right)}{k} \tag{14}$$

Bootstrap

For large k (k > 30), Eq. 14 should provide reasonable estimates of the prediction variance; however, for small k the estimates may be imprecise and could result in negative estimates. Because k is typically small (k< 10), we will estimate $var(\pi)$ 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 $var(\hat{\pi}_y)$. 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 many times. We then estimate $var(\pi)$ as:

$$var_B(\pi) = \frac{\sum_{b=1}^{B}\left(\hat{\pi}_{(b)} - \overline{\hat{\pi}_{y(b)}}\right)^2}{B-1} \tag{15}$$

where

$$\overline{\hat{\pi}_{y(b)}} = \frac{\sum_{b=1}^{B}\hat{\pi}_{y(b)}}{B} \tag{16}$$

Similarly, we estimate $var(\bar{\pi})$ as:

$$var_B(\bar{\pi}) = \frac{\sum_{b=1}^{B}\left(\bar{\pi}_{(b)} - \overline{\bar{\pi}_{(b)}}\right)^2}{B-1} \tag{17}$$

where

$$\overline{\bar{\pi}_{(b)}} = \frac{\sum_{b=1}^{B}\bar{\pi}_{(b)}}{B} \tag{18}$$

The prediction variance is then estimated using Eq. 7 with the appropriate substitutions. 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 applications indicated that the bias is < 1%.

Estimating Escapement

In years when an index count, C_y, is available but escapement, N_y, is not known, it can be estimated as:

$$\hat{N}_y = \bar{\pi}C_y^2 \tag{19}$$

with variance:

$$var(\hat{N}_y) = C_y^2 var(\pi_{pred}) \tag{20}$$

APPENDIX C

Appendix C1.–Adult Finfish Tissue Sampling for DNA Analysis.

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

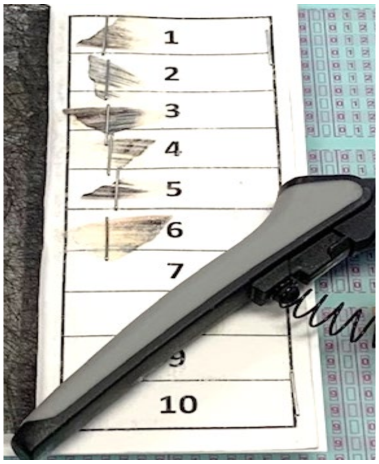
I. General Information

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.

-continued-

- 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.

-continued-

- 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:___________