Regional Operational Plan SF.2A.2018.08

Operational Plan: Susitna River Chinook Salmon Inriver Abundance, 2018

by

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and

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May 2018

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

Symbols and Abbreviations

The following symbols and abbreviations, and others approved for the Système International d'Unités (SI), are used without definition in the following reports by the Divisions of Sport Fish and of Commercial Fisheries: Fishery Manuscripts, Fishery Data Series Reports, Fishery Management Reports, and Special Publications. All others, including deviations from definitions listed below, are noted in the text at first mention, as well as in the titles or footnotes of tables, and in figure or figure captions.

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 SF.2A.2018.08

OPERATIONAL PLAN: SUSITNA RIVER CHINOOK SALMON INRIVER ABUNDANCE, 2018

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SIGNATURE/TITLE PAGE

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Period Covered	
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Approval

Title	Name	Signature	Date
Project leaders	Nick Decovich		
	Johnathon Campbell		
Gene Conservation Laboratory	Andrew Barclay		
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ABSTRACT

The goal of this study is to estimate the abundance of spawning Chinook salmon in the mainstem Susitna River in 2018 by conducting a 2-event, mark–recapture experiment. Fish wheels and gillnets will be operated at river mile (RM) 34 to capture Chinook salmon for marking with dart-PIT tags (a dart tag with an imbedded passive integrated transponder [PIT]). Recapture event sampling will occur at the Deshka River weir at RM 7 where a PIT detection array will be used. A concurrent genetics mark–recapture study will be performed using genetic samples taken from a systematic sample of all dart-PIT tagged fish. Radio tags will be applied to a subsample of Chinook salmon in the mainstem Susitna River to determine handling effects. The proportions of non-Deshka River Chinook salmon in the sport harvest taken in 2 sections of the Deshka River will also be estimated through harvest sampling of axillary processes and genetic stock identification.

Key words: Chinook salmon, abundance, mark–recapture, Susitna River, PIT tag, dart tag, gillnet, fish wheel, sport harvest, genetic stock identification

INTRODUCTION

Recent downturns in the productivity and abundance of Chinook salmon (*Oncorhynchus tshawtyshca*) stocks across Alaska have created social and economic hardships within many communities. There is a fundamental need to accurately describe productivity and abundance trends of Chinook salmon stocks across Alaska, gather essential information necessary to understand root causes of these widespread declines, and track population trends into the future (ADF&G Chinook Salmon Research Team 2013). The Susitna River was selected by the Alaska Department of Fish and Game (ADF&G) as a Chinook salmon indicator stock, and estimation of the inriver run size in the mainstem Susitna River was recommended as a stock assessment project.

In 2018, the ADF&G plans to estimate the inriver abundance for Chinook salmon in the mainstem Susitna River. Data collected from this study will supplement similar data collected in previous studies during 2012–2017 (Cleary et al. 2015; Cleary and Campbell 2016; Cleary et al. 2017; Yanusz et al. *In prep*). The 2017 mainstem Susitna River Chinook salmon abundance estimate upstream of the Yentna River confluence was 45,471 (95% CI 38,808–54,285).

Harvest, aerial survey, spawning distribution, and age composition data, along with abundance estimates, have been collected on Chinook salmon from the Susitna River drainage since the Susitna–Watana hydroelectric project study 1984. These data along with genetic sock identification and abundance estimates from this study will be used in a Bayesian state-space stock-specific abundance and run-timing model. Resulting estimates of abundance will help ADF&G determine the effectiveness of present and past stock assessments, choose future assessments that are efficient and effective, advise the Alaska Board of Fisheries regulatory process, and be useful in land use planning and permitting.

A separate component of the 2018 study is to estimate the proportion of non-Deshka River Chinook salmon in the Deshka River sport harvest. It is unknown at this time how many of the fish harvested in this fishery would have passed the Deshka River weir, and how many would have gone on to spawn in other tributaries had they not been harvested. Currently, the ADF&G statewide harvest survey (SWHS) partitions the harvest into 2 categories: above the weir and below the weir. Estimates of the Deshka River total run assume that all fish harvested below the weir are of Deshka River origin. A harvest sampling study would provide information regarding this assumption and is included in this operational plan. However, it will only be implemented in the event that harvest is allowed in the fishery.

OBJECTIVES

PRIMARY OBJECTIVES

1) Estimate the abundance of Chinook salmon greater than or equal to 500 mm mid eye to tail fork (METF) length in the mainstem Susitna River upstream of the mouth of the Yentna River at river mile (RM) 34[1], such that the estimate is within 20% of the true value 90% of the time.
2) If the sport fishery is opened to harvest, estimate the proportion of the non-Deshka River fish in the sport harvest from each of 2 sections of the Deshka River such that the estimated proportions are within 10% of the true values 95% of the time[2].

SECONDARY OBJECTIVES

1) Estimate the abundance of Chinook salmon greater than or equal to 500 mm METF in the mainstem Susitna River upstream of the mouth of the Yentna River at river mile (RM) 34 using genetic data in the event there is no sport harvest allowed on the Deshka River.
2) Incorporate temporal CPUE data, Deshka weir count, and GSI results from 2018 into the stock specific abundance and run timing (SSART) model (Reimer and Fleischman 2016).

METHODS

STUDY DESIGN

Abundance: Dart-PIT Tags

A 2-event, capture–recapture experiment will be used to estimate the inriver abundance of Chinook salmon in the mainstem Susitna River. Fish wheels and gillnets will be used at RM 34 of the mainstem Susitna River to capture Chinook salmon for marking with dart-PIT tags (PIT stands for passive integrated transponder; Appendix A1). Fish will be examined for tags at a weir on the Deshka River at RM 7 (the Deshka River mouth is at Susitna RM 38.8) where a PIT detection array will be used. Dart-PIT tags will be detected using swim-through PIT-tag antennas at the Deshka River weir (Appendix A1). The PIT tags will allow for automated sampling of all fish at the Deshka River weir; this set-up will maximize sample size while avoiding the labor and run disruption necessary when hand-sampling fish. Radio tags will also be deployed during dart-PIT-tagging and these will be used to quantify the proportion of tagged fish that drop out of the experiment, either through handling effects or switching drainages (i.e., swim up the Yentna River after swimming to the mainstem Sustinta River RM 34 location). GSI analysis of sampled dart-tagged fish will also provide information on fish that switch drainages. All tagged fish will also get a secondary mark consisting of a hole punch in the left operculum so that tag loss can be assessed. Examination of fish for secondary marks will occur for all fish that are sampled for biological data at the Deshka River weir.

[1] Defined by Alaska Energy Authority, Watana Hydroelectric Studies

[2] Within d% of the true value A% of the time implies $P(p - d/100 \leq \hat{p} \leq p + d/100) = A/100$ where p denotes the population proportion.

Abundance: Genetic Mixed Stock Analysis

Genetic mixed stock analysis will be used to produce a second mark–recapture estimate of Susitna River mainstem Chinook salmon inriver abundance in the event that there is no sport harvest of Deshka River fish. A subsample of 400 PIT–tagged fish will be analyzed genetically to estimate the proportions of Susitna River mainstem, Deshka River, and Yentna River fish passing RM 34 of the mainstem Sustina River. These stock proportions along with Chinook salmon counts from the Deshka River weir will then be used to estimate abundance of the mainstem Susitna River stock passing RM 34.

Proportion of Non-Deshka Chinook Salmon in the Deshka River Sport Fishery

If the sport fishery is opened to harvest on the Deshka River, the harvest will be sampled from 2 river sections; the first section will be from the confluence of the Deshka river and the mainstem Sustina River to an island approximately three-quarters of a mile from the confluence, and the second will be from the island to the weir. A genetic mixed stock analysis will be used to estimate the proportion of the harvest from both sections that is of non-Deshka River origin.

DATA COLLECTION

Marking with PIT- and Radio Tags

Chinook salmon tagging will occur approximately 21 May to 30 June 2018. Tagging will begin when water levels and debris loads allow for safe operations of fish wheels and gillnets. At each site, the field crew will consist of 6 people: 4 for each 2-person fish wheel shift and 1 crew of 2 people will sample with drift gillnets in a 7.5 h split shift. At the mainstem Susitna River tagging site (Figures 1 and 2), 2 fish wheels (1 on each bank) will be operated for 12 h/d each. A 2-person crew will operate both wheels for the first 6 h shift followed by a different 2-person crew operating both wheels for the second 6 h shift. The total shift time will be 7.5 h where 1.5 h will be used for crew organization prior to and after shifts. In addition, a total of 7.5 h/d will be spent gillnetting in shifts of 3¾ hours each.

Tag deployment data will be recorded on Rite-In-Rain[3] data sheets and entered in Excel spreadsheets at camp. Fish wheel and gillnet catch and effort data will be recorded on the 2018 "Catch and Effort" data forms (Appendices B1 and B2). The forms will be filled with date, crew initials, total fish wheel operation time (or gillnet soak time), shift, start and stop times, crew arrival and departure time, and the total number of Chinook salmon tagged and untagged. In addition, the total number of other species captured for the shift will be recorded.

[3] Product names used in the publication are included for completeness but do not constitute product endorsement.

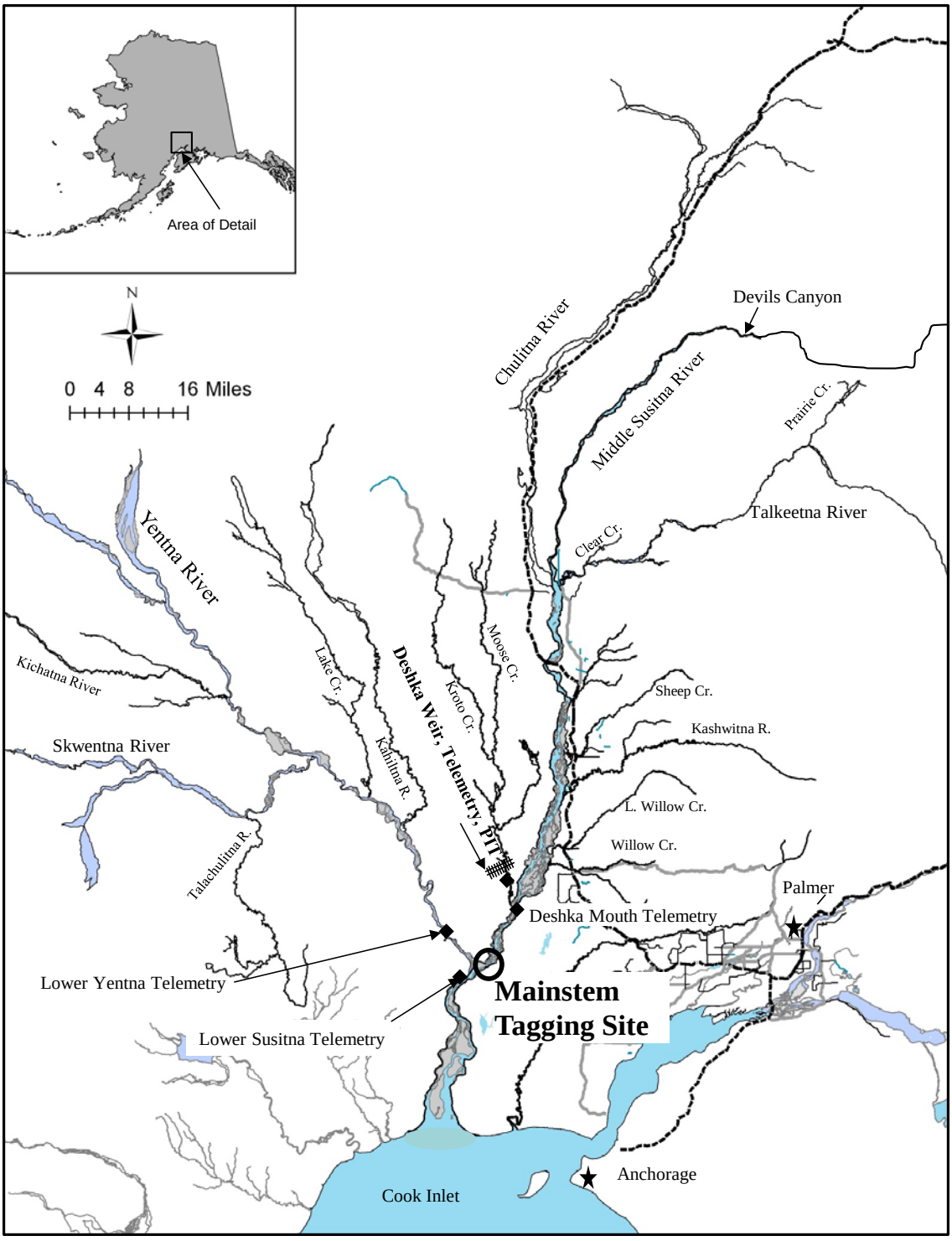

Figure 1.–Locations of fish wheels (open circle), fixed telemetry stations (diamonds), and Deshka weir site in the Susitna River drainage, Alaska.

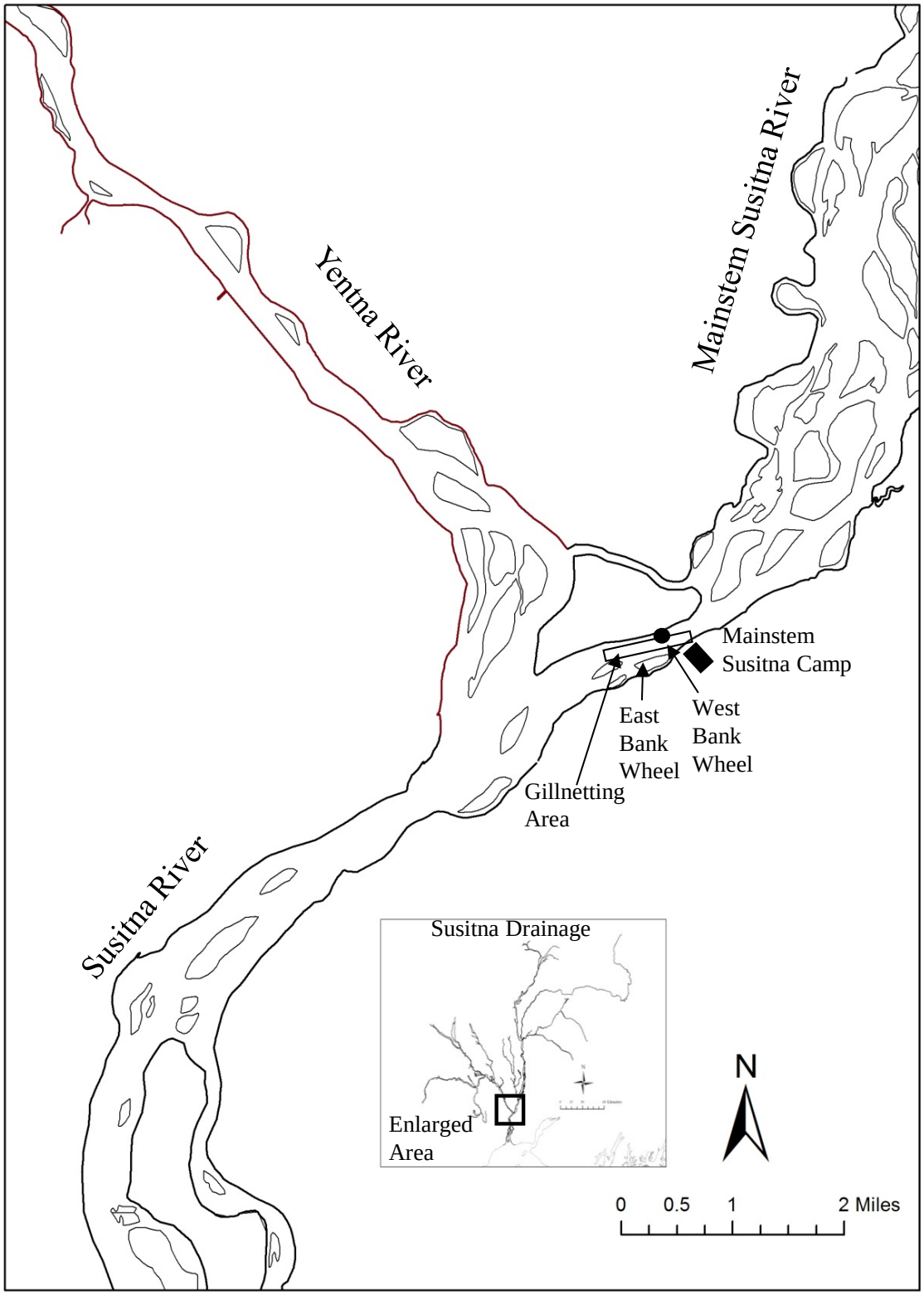

Figure 2.–Locations of fish wheels and gillnetting area at the RM 34 tagging site.

Fishwheel Operations

Both fish wheels will be operated every day of the season, except for flood events or when wheels need to be removed or repaired. Fish wheels will be aluminum, with three 6 ft wide or two 4 ft wide baskets webbed with knotless nylon 1.5-inch mesh netting (square measure). Captured fish will descend an aluminum basket chute to a fabric slide crossing above the float and exit into a live box. Live boxes will be 8 ft long, 2 ft wide, and 4 ft deep, with plywood sides with holes cut to allow water circulation. The configuration of the fish wheel axle, baskets, and floats make the fishing depth a maximum of 6.5 ft. Fish wheels will be tied to the river bank and braced offshore with poles to position the wheels in sufficient current to make them spin. The axle height will be adjusted so that the baskets sweep as close to the river bottom as possible. A picket weir with 1.5-inch gaps between pickets will be installed between shore and the fish wheel to direct migrating salmon towards the fish wheel baskets. In order to minimize fish wheel injuries, closed-cell foam padding will be placed where appropriate to prevent injuries as fish exit fish wheel basket chutes. The following is a set of guidelines used to operate the fish wheels at each site:

1) Each fish wheel will be visited by boat every 1 h or less. When a fish wheel has been untended for more than 1 h, all the fish in the live box shall be counted, measured, and released, but not tagged.
2) Fish with large, fresh injuries that are bleeding or fish that have been dropped in the boat will be measured and released without being tagged.
3) No tagging will occur without first placing the fish in a water-filled tote with a cradle.
4) An orange dart-PIT tag will be applied to every healthy Chinook salmon greater than or equal to 500 mm METF length. The left operculum of each dart-PIT-tagged fish will have a hole punched in it with a paper punch.
5) Every dart-PIT tagged Chinook salmon will have the distal 0.5 in of the left axillary process removed and preserved in a uniquely-numbered vial with ethanol (Appendix C1).
6) Scales will be collected from every dart-PIT tagged Chinook salmon. Additionally, 4 scales will be collected from every fifth Chinook salmon less than 500mm METF length.
7) All Chinook salmon (both tagged and not tagged) will be measured for METF length (Appendix C3), tallied on the data form (Appendix B1), and then released.
8) Other fish species will be tallied on the data form and then released.

Drift Gillnet Operations

In order to insure all lengths of Chinook salmon are represented in the sample of fish greater than or equal to 500 mm METF length, drift nets will be used to supplement the catches from fish wheels. In 2013 and 2014, Chinook salmon captured in gillnets were larger on average than those captured in fish wheels (LGL and ADFG 2014, 2015). It will be important to operate the drift gillnets as planned so that enough large fish can be tagged to provide a reasonably precise estimate of abundance in the larger size categories, should size stratification be required.

Prior to using new drift nets, old nets will be used to practice drift fishing and locate fishing sites that do not have snags. One drift gillnet mesh size (5.5 in, stretch measure) will be used. Nets will be 2 sizes: 10–12 feet deep and 15–17 feet deep. Drift locations, duration, and net depth will

be changed accordingly to productive fishing site location(s) and depths or when net snags are found. One crew of 2 technicians will make as many drifts as possible during a 7.5-hour split shift. Start times will rotate daily until a cycle is completed each week to reduce bias due to the run timing of any individual stock.

The desired capture technique will be to entangle fish by the snout to avoid injuries that gilling may cause. The net will be watched continuously until corks sink, then the net will be pulled in immediately. Chinook salmon captured in drift gillnets will be processed as described for fish wheels above, including measurement and tally (Appendix B2).

Marking Effort

At the fish wheels, sampling will begin when the live box door is installed to hold captured fish, approximately 1 h after the crew starts its shift. The 1 h delay, allows for sampling preparation and travel time. The first shift will begin at 0500 hours and will end at 1300 hours daily, and the second shift will be from 1400 to 2200 daily. After 6 h of effort during each shift, the live box door will be pulled so captured fish can escape. The fish wheel will be allowed to run in order to prevent debris from building up on the submerged basket. The crew will spend the remainder of its shift performing data compilation and equipment maintenance.

Dart-PIT tags

All captured healthy Chinook salmon greater than or equal to 500 mm METF length will receive an orange dart-PIT tag (passive integrated transponder embedded dart tag, Model PDAT-PIT [HPT-12] from Hallprint, Australia) as the primary mark and a lower left operculum hole punch as the secondary mark to allow assessment of tag loss. Each dart-PIT tag will be associated with a unique dart tag number and unique PIT-tag code.

To minimize handling stress, only Chinook salmon held in the live box less than 1 h will be tagged. Radiotelemetry data for coho salmon in the Kenai River (Carlon and Evans 2007) indicate that fish tagged immediately upon capture experience a mortality rate of 10% versus 20% for fish held for various times in a live box. Given that 1 crew (2 people) is tasked with operating 2 fish wheels simultaneously, sorting, dart-tagging, and measuring other fish, we feel a maximum 1 h holding time is a reasonable compromise. Live boxes will be checked at a maximum of 1 h intervals and the time of each check will be recorded.

Two-person crews will process selected salmon quickly to reduce handling time. Fish will be in a holding tank onboard a boat during tagging. A bucket will be used to frequently add water to the tank. A padded, aluminum cradle (Larson 1995) will be slipped around the fish to restrain it during tagging. One person will restrain the fish, and the second will insert a dart-PIT tag and record data. Dart-PIT tags will be inserted with stainless steel applicator needles immediately below the dorsal fin on the fish's left side, anchoring in the dorsal pterigiophores (bones). A paper punch will be used to punch a hole in the lower left operculum as a secondary mark to detect tag loss at the recapture site.

Radio Tags

One hundred of the dart-PIT-tagged Chinook salmon greater than or equal to 500 mm METF length will also be radiotagged; 33 will be tagged per fish wheel and 34 with gillnets. Radio tags will be deployed systematically, in proportion to the historical run timing of fish greater than or equal to 500 mm METF length (Table 1). The first available healthy fish ≥500 mm METF length will be radiotagged, thus avoiding selection bias by the crews. Methods for deploying leftover

tags, fish handling, and radiotagging are described below. When the scheduled number of radio tags has been deployed for a particular fish wheel shift, the wheels will still run for the duration of the shift to continue with dart-PIT tagging. Similarly, once the scheduled number of radio tags has been deployed for a particular gillnet shift, netting will continue for the full duration of the shift to maximize the number of dart-PIT tags deployed on Chinook salmon.

The number of radio tags to be deployed will be evenly split between the first and second shifts (AM vs. PM) and river bank (Fishwheel 1 vs. Fishwheel 2), with odd numbers of tags alternating between shifts and river banks (Table 1). If the scheduled number of radio tags cannot be deployed at a given wheel due to low catch during that shift, the leftover tags will be deployed by the next shift, even if it is the following day. The next shift will deploy its regularly scheduled tags first, then the leftover tags. This will continue until the leftover tags are deployed and the crew can get back on the original schedule. To enhance the chance that radio tags are deployed in proportion to the run, the number of tags deployed from each wheel may be adjusted depending on catch rates. Actual deployment of tags will be recorded in the "Catch and Effort" field data forms (Appendices B1 and B2).

Procedures to sample fish for radiotagging and to minimize handling stress will be identical to those described above for dart-PIT tagging. Radio tags will be inserted through the esophagus and into the upper stomach using a 0.38 inch (outside diameter), 12-inch long plastic tube. The antenna of the radio transmitter will be threaded through the tube and pinched by hand at the end of the tube such that the radio transmitter is held tightly against the opposite end of the tube. A paper punch will be used to punch a hole in the lower left operculum as a secondary mark. The crew will measure METF length and remove and preserve the distal 0.5 cm of the left axillary process of any radiotagged salmon.

Radio tag detection

Radio receivers (ATS^{TM} Model R4500C) at each stationary tracking site (Lower Yentna, Lower Susitna, and Deshka River mouth, Figure 1) will be visited and downloaded twice a month. Each record will contain the fields: year, Julian day, hour, minute, antenna, frequency, pulse code, signal strength, and duplicate counts, in ASCII text format. A laptop computer will be connected to the radio receiver with a serial cable and ATS software will be used to transfer the data file to the laptop. A logbook will be maintained at each station to note the date, staff, settings, and battery voltage for each visit. A checklist with radio receiver settings and the download steps will be at each site. Each downloaded file will be transferred to the Palmer local area network (LAN), uploaded to Docushare at the ADF&G Region II office (http://docushare.sf.adfg.state.ak.us/dsweb/Homepage) and eventually appended into a SQL telemetry database.

Recapture PIT Tags at Deshka River Weir

A resistance board, floating weir will be operated at RM 7 of the Deshka River from approximately 21 May to 3 September, 2018. Sampling at the Deshka River weir will be conducted by an independent project and will follow a separate operational plan (Lescanec and St. Saviour *In prep*). A dual-antenna, PIT-tag detection array will be attached to the upstream exit of the weir's sampling cage (Appendix A1). Crew members will regularly test the PIT array's detection rate. A biologist will be on call to troubleshoot issues over the phone and in person if required. The biologist will also make twice weekly visits to download the data file and make more in-depth checks of the system. System checks of the PIT-tag array are described in Appendix A1.

Table 1.–Radiotag deployment schedule for fish wheels and gillnet by date and shift (AM and PM), 2018.

	Fishwheel 1		Fishwheel 2		Gillnet	
Date	AM	PM	AM	PM	AM	PM
21 May	0	1	0	0	0	0
22 May	0	0	1	0	1	0
23 May	0	0	0	1	0	0
24 May	1	0	0	0	0	1
25 May	0	0	0	0	0	0
26 May	0	1	0	1	0	0
27 May	1	0	1	0	1	0
28 May	0	1	0	1	0	1
29 May	1	0	1	0	1	0
30 May	0	1	0	1	1	1
31 May	1	0	1	1	1	1
1 Jun	1	1	0	1	0	1
2 Jun	1	1	1	0	1	1
3 Jun	0	1	1	1	1	1
4 Jun	1	1	1	1	1	1
5 Jun	1	0	1	1	1	1
6 Jun	1	1	0	1	1	1
7 Jun	1	1	1	1	0	1
8 Jun	1	1	1	0	1	0
9 Jun	0	1	1	1	1	1
10 Jun	1	0	1	0	1	0
11 Jun	0	1	0	1	0	1
12 Jun	1	0	1	0	1	0
13 Jun	0	1	0	1	0	1
14 Jun	1	0	1	0	1	0
15 Jun	0	1	0	1	0	0
16 Jun	1	0	1	0	0	1
17 Jun	0	0	0	0	0	0
18 Jun	0	1	0	0	0	0
19 Jun	0	0	1	0	1	0
20 Jun	0	0	0	1	0	0
21 Jun	1	0	0	0	0	1
22 Jun	0	0	0	0	0	0
23 Jun	0	0	0	0	0	0
24 Jun	0	0	0	0	1	0
25 Jun	0	0	1	0	0	0
26 Jun	0	1	0	0	0	0
27 Jun	0	0	0	0	0	1
28 Jun	0	0	0	0	0	0
29 Jun	0	0	0	0	0	0
Total	16	17	17	16	17	17

Note: Deployment indicated by “1” and “0” means not deployed.

Tasks associated with the independent weir project will be as follows:

1) Clean and maintain the weir as needed to ensure its integrity.
2) Count and record all salmon, by species, through the weir.
3) For Chinook salmon, measure 350 representatively-sampled fish for METF length (to the nearest 5 mm).
4) Look for left operculum punch on all fish measured to assess any potential tag loss.
5) Opportunistically note dart-PIT tagged fish that are counted, and at what time they are counted. Capturing a tagged fish and reading the dart tag number may be done only if it does not disrupt movement of other fish.
6) Record water level and temperature.

The recapture technology involves a PIT-tag detection system deployed upstream of the weir trap to record dart-PIT-tagged fish as they swim through the antennas (Appendix A1). Two antennas will be operated to increase the probability of detection. Two tests will be run to verify proper operation of the PIT-tag detection array (Appendix A1).

A trap incorporated into the weir will allow capture of fish for sampling. METF length will be measured on a subsample of the Chinook salmon. Fish sampled for METF length will also be examined for secondary marks to assess tag loss, although the test will be very weak given only about 350 fish will be sampled for ASL at the weir. Other species counted through the weir will be tallied.

Tissue Sampling for Genetic Mixed Stock Analysis

A 1⅓-cm (half-inch) piece of the axillary process will be removed from each dart-PIT tagged Chinook salmon and placed in denatured ethanol in an individually labeled 2 ml vial (Appendix C1). All salmon samples and relevant collection data will be shipped to the ADF&G Division of Commercial Fisheries Gene Conservation Lab in Anchorage at the end of the season. All genetics sample processing, data storage, and data analysis will be the responsibility of the ADF&G Gene Conservation Lab.

Tissue Sampling the Deshka River Sport Harvest

If harvest of Chinook salmon is allowed in the 2018 Deshka River sport fishery, a crew of 1 will be stationed at the Deshka Landing boat launch by 8:00 AM on days that are open to harvest of Chinook salmon. The majority of boats fishing the Deshka River launch from the Deshka Landing, and this strategy will provide the maximum opportunity for interaction with anglers. Anglers in each returning boat will be approached by project staff, and if it is determined they have harvested Chinook salmon from the Deshka River, they will be asked for permission to collect a tissue sample from each harvested fish. Each tissue sample will be stored according to whether the fish was harvested in the section from the Deshka River mouth to an island three-quarter miles upstream, or from the island to the Deshka River weir. A map of the area will be provided to each angler to help them accurately identify where their harvest occurred. In addition to ADF&G staff, 2 local fishing guides will also collect samples. Each guide will be supplied with 2 250 ml bottles filled with ethanol; one labeled “mouth to island” and one labeled “between island and weir.”

Subsampling for Genetic Mixed Stock Analysis

The genetic tissue samples collected throughout the season will be subsampled postseason to form a mixture of 400 Chinook salmon for genetic mixed stock analysis. Samples will be selected in proportion to the daily Chinook salmon counts at the fish wheels to represent the seasonal fish wheel catch.

Scale collection

Four scales from each sampled fish will be taken from the preferred location on the left side of the body at a point on a diagonal line from the posterior insertion of the dorsal fin to the anterior insertion of the anal fin and two rows above the lateral line (Welander 1940; Scarnecchia 1979). If the preferred scales cannot be obtained, another scale will be taken from as close to the preferred scale as possible, always from the first or second row above the lateral line, in order to capture the early life history portion of the age. If no scales are available in the preferred area on the left side of the fish, scales will be collected from the preferred area on the right side of the fish. If scales are not obtainable from a given fish, that fish will not be sampled at all and sampling will continue with the next available fish.

Subsampling scales for age assignment

The subsample of Chinook salmon selected for aging will mirror that of the genetics subsample described above. However, all scales collected from Chinook salmon under 500mm will be aged. The purpose of the less than 500mm sample is to verify that Chinook salmon in this size category are age 1.1.

Laboratory Analysis

Assaying Genotypes

Tissue samples will be genotyped following methods reported in Barclay and Habicht (*In prep*). Briefly, genomic DNA will be extracted from tissue samples using NucleoSpin 96 Tissue Kits by Macherey-Nagel (Düren, Germany). DNA will be screened for the 83 variant SNP markers reported in Barclay and Habicht (*In prep*) using Fluidigm 96.96 Integrated Fluidic Circuits. The Integrated Fluidic Circuits will be read on a Biomark or EP1 System (Fluidigm) after amplification and scored using Fluidigm SNP Genotyping Analysis software. Genotypes will be imported and archived in the Gene Conservation Laboratory Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Overall failure rate will be calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype will be considered a failure when a locus for a fish cannot be satisfactorily genotyped.

Quality control (QC) measures will be used to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8 of every 96 fish (1 row per 96-well plate) will be reanalyzed for all markers by staff not involved with the original analysis. Laboratory errors found during the QC process will be corrected, and genotypes will be corrected in the database. Inconsistencies not attributable to laboratory error will be recorded, but original genotype scores will be retained in the database.

Reporting Groups

Three reporting groups that perform adequately for MSA within the Susitna River drainage were chosen for this study:

1) *Yentna* (Yentna River populations)
2) *Susitna* (Susitna River mainstem populations excluding Alexander Creek and Deshka River)
3) *Deshka* (Deshka River population)

Genetic Baseline

To estimate the proportion of *Yentna*, *Susitna*, and *Deshka* reporting groups in the fish wheel mixture, a baseline will be used containing the 30 populations from the Susitna and Yentna rivers and 83 variant SNPs reported in Barclay and Habicht (*In prep*).

MARK–RECAPTURE ASSUMPTIONS

Chinook salmon abundance will be estimated with a Petersen-type estimator. For Petersen estimates of abundance to be unbiased, certain assumptions must be met (Seber 1982). These assumptions, expressed in the circumstances of this study, along with their respective design considerations and test procedures are as follows:

Assumption I: The population is closed to births, deaths, immigration, and emigration.

Considering the life history of Chinook salmon, there should be no recruitment (births, immigration) between sampling events. First event sampling (marking) will begin prior to any significant passage of fish past the tagging sites and will continue through the run until passage has dropped to near zero. With respect to emigration, some fish marked at the mainstem Susitna River marking sites will leave the system and migrate to the Yentna River. Also, some marked fish may fail to enter the experiment due to handling stress. Losses of fish due to either reason will be estimated from a sample of marked fish that are also instrumented with radio tags. Genetic analysis of sampled tagged fish will provide an additional estimate of the proportion of tagged fish that are Yentna-bound. Marked fish will be adjusted accordingly in the both the traditional and genetics-based mark–recapture estimates. Some fish may be harvested between the first and second events, but assuming the harvest rate on marked and unmarked fish is equal, then the dart-PIT abundance estimate at the marking site should remain unbiased. If there is harvest, then the genetics-based estimate will be biased low; the 'recaptures' ($\widehat{D}_i$ in Equation 7 below) will be biased high.

Assumption II: There is no trap induced behavior.

There is no explicit test for this assumption because the behavior of unhandled fish cannot be observed. We will attempt to meet this assumption by minimizing holding and handling time of all captured fish. Any obviously stressed or injured fish will not be tagged. Examples include fresh seal bites that penetrate into the muscle, capture injuries such as torn opercula, large skin wounds or broken snouts, or being dropped in the boat while tagging. This assumption does not apply to the genetics mark–recapture estimate; there are no physical 2nd event recaptures for this method.

Assumption III: Tagged fish will not lose their marks between sampling events and all marks are recognizable.

We have found little evidence of tag loss in similar experiments conducted on the mainstem Susitna and Yentna Rivers in past years (Cleary et al. 2016). We will continue to test this assumption by examining Chinook salmon sampled in the ASL sample at the Deshka River weir, although the test will be weak due to the small sample size. A fish with a secondary mark, but no dart-PIT tag will indicate the dart-PIT tag (primary mark) has been lost. This assumption does not apply to the genetics mark–recapture estimate.

Assumption IV: One of the following three conditions will be met:

1) Marked fish will mix completely with unmarked fish between samples.
2) All Chinook salmon will have the same probability of being captured in the second event.
3) All Chinook salmon will have the same probability of being caught in the first event.

With respect to the first condition, it is impossible that marked and unmarked fish will mix completely. Fish wheels and gillnets will be operated continuously during the run, with fish marked early in the run never having the opportunity to mix with unmarked fish from later stages of the run by the time they are sampled in the second event.

With respect to the second condition, the second event only consists of the weir at the Deshka River and therefore probability of capture cannot be uniform in the second event. All of the Deshka River population will be sampled at 100%, whereas none of the remaining stocks will be sampled in the second event.

With respect to the third condition, the marking event involves use of fish wheels and gillnets across the river and consistently through time. This design provides for the possibility that the population is sampled uniformly. However, fluctuations in water levels can affect the efficiency of fish wheels, resulting in variation in probability of capture over time. Also, the probabilities of capture by fish wheels may vary between banks due to differences in channel morphology and water flow (Yanusz et al. 2007). Further, uneven fishing efficiency and effort between gillnets and fish wheels may also result in uneven probability of capture between midriver and bank-oriented populations, and probability of capture may differ among size categories.

Unlike previous Susitna River mark–recapture studies, spatial diagnostic tests ("Equal Proportions Test;" Arnason et al. 1996) cannot be conducted for this study because there is only the single recapture event (Deshka weir). In addition, temporal tests of marked fractions in the recapture event are, and have been, considered unreliable due to the documented effects of tagging on sulking behavior of Chinook salmon (Bernard et al. 1999). Size-based tests of differential probability of capture are, however, still possible using length data of marked and captured and recaptured fish at the Deshka weir.

The accuracy of the final abundance estimate will depend on the partially untestable assumption that the probability of capture in the first event is spatially even. It is noted, however, that all three ADF&G mark–recapture estimates of Chinook salmon abundance at RM 34 of the Susitna River from 2015 through 2017 were analyzed as simple Petersen estimates within 2 size strata (unpublished analyses). The spatial test of probability of capture was only significant in 1 of 6 instances in these estimates. In the significant case, the "Mixing Test" (Arnason et al. 1996) allowed the Petersen estimate to be used. Given our ability to continue testing and correcting for size-related probability of capture failures (during first-event sampling) and our historical success of using the Petersen estimate, we believe it is likely that the mark–recapture experiment, with its consistent use of capture gear over the run, will yield unbiased results.

The procedures to analyze length data for statistical bias due to gear selectivity are described in (Appendix D1). If different probabilities of capture by size are indicated, data will be fully stratified into size groups where probability of capture is homogeneous within groups, and abundance estimates will be calculated for each size group and summed.

Contingency table analyses recommended by Seber (1982) and described in Appendix D2 will be used to determine if a Petersen estimate can be used. The "Mixing" and "Equal Proportions" tests (Tests I and II in Appendix D2) will not be performed. Test III in Appendix D2 will be performed. Based on experience from 2014 to 2015, it is anticipated that a pooled Petersen estimator will be used, possibly within each of 2 size strata.

SAMPLE SIZES

Abundance of Mainstem Susitna River Chinook Salmon (Objective 1)

Assessment of sampling effort necessary to achieve the precision criterion for Objective 1 will be based largely on experience gained during the 2015–2017 experiments (Cleary et al. 2015; Cleary and Campbell 2016; Cleary et al. 2017). We expect sampling rates (the proportions of the population passing each sampling site that are captured) will be similar in 2018 to that experienced in 2015–2017.

The approach of Robson and Regier (1964) was used to provide baseline sample sizes for a given population size and precision criterion under the assumption that a Petersen-type estimator will be used. These sample sizes are interpreted in the context of probable violations of assumptions required for the Petersen estimator.

Given results from the 2015–2017 mainstem Susitna River Chinook salmon studies, we expect that size-stratified Petersen models will be needed rather than on overall Petersen model based on pooled data. The following sample size calculations consider a size-stratified model. With respect to size-stratification, the 2015–2017 mainstem Chinook salmon estimates had to be stratified; the costs of the stratification in increased CV of the abundance estimate were 1.5, 1.2, and 1.2 times, respectively.

For these experiments, we assume that the CVs of our final estimates of abundance using size stratification will be 1.25 times as large as we would see if no stratification was necessary and a pooled Petersen-type model was appropriate. The methods of Robson and Regier (1964) were used to calculate the necessary sample sizes to estimate the abundance of Chinook salmon in the Susitna River drainage upstream of the mouth of the Yentna River within 16% (0.8 of specified relative precision of 20% for Objective 1) of the true values 90% of the time. We expect that these same sample sizes will allow us to estimate abundances of Chinook salmon within 20% of the true values 90% of the time under size stratification.

In the 2015–2017 radiotagging experiments, the proportion of radio tags deployed at RM 34 that remained in the experiment (were not censored because of handling stress or because the fish left the drainage) averaged 0.75, and ranged from 0.6 to 0.85. For 2018, we will assume we will censor 25% of our tags due to drop-outs and drainage switches.

During 2015–2017, 1,596 (2015), 948 (2016), and 624 (2017) Chinook salmon greater than or equal to 500 mm were caught in fishwheels and drift gillnets from estimated populations of about 89,000, 66,000, and 45,000, respectively. These marking efforts correspond to 1.8%, 1.4%,

and 1.4% of the population, respectively. We will conservatively assume that we will catch 1% of the Chinook salmon population greater than or equal to 500 mm at the mainstem marking site.

Using the assumptions outlined above, the expected number of Chinook salmon marked in the first event and the minimum sample size needed in the second event for estimation of population sizes between 20,000 and 80,000 were calculated (Appendix D3). The range of population sizes examined spans the 95% confidence intervals of the 2015–2017 mainstem Chinook salmon estimates. About 32% of the population needs to be sampled in the worst case (population of 30,000) in the second event to meet objective criteria (Appendix D3). In 2015–2017, an average of about 25% of the population of Chinook salmon greater than or equal to 500 mm passed through the Deshka weir. Given that the second event samples comprise all Deshka weir fish greater than or equal to 500 mm, we are confident that for all but one of the scenarios presented in Appendix D3 sufficient sampling will occur to meet the Objective 1 criterion.

Proportion of Non-Deshka River Fish in Sport Harvest

It will be assumed that sampling from each section of Deshka River (confluence to island or island to weir) will be done in a random manner. A minimum sample size of 100 fish from each river section will allow estimates of the proportion of non-Deshka River fish in the harvest to meet the Objective 2 precision criterion. At this time, we do not know if harvest will be allowed in 2018, and if allowed, how much effort will be permitted. It is difficult, therefore, to predict how many fish will be sampled from the harvest using our methods. Over the last 5 years, harvest from the Deshka River below the weir has averaged 1,335 and ranged from 934 to 2,115 when permitted. We are confident that we can sample 100 fish from such harvests. Should the fishery be severely curtailed, then fewer than 100 fish may be sampled; mitigating such a lower sample size is the fact that the required sample size for Objective 2 will be lower due to the finite population correction factor.

DATA REDUCTION

Each sampling site will provide a daily summary of catch, effort, tags deployed or recovered, weather and water data, and any operational changes to a biologist at the Palmer Division of Sport Fish office via telephone 5 days per week.

All data collected by tagging crews (Appendices B1–B2) will be entered into Excel spreadsheets as they become available inseason and consolidated into a master Excel workbook file (Master_Susitna_2018_Chinook_ Abundance_mm_dd_yy.xlsx) with separate worksheets for each data type (e.g., tagging, recovery, fishing effort, etc.), and then stored in a dedicated subdirectory on the Palmer ADF&G LAN and uploaded to Docushare at the ADF&G Region II office (http://docushare.sf.adfg.state.ak.us/ dsweb/HomePage). A documentation spreadsheet will also be incorporated into the workbook that describes the variables in each sheet. Only the project leader (N. Decovich) will have editing rights to the master workbook. All data files (.csv format) that are used in analyses by the R software package (R Core Team 2017) will be directly created from the latest master Excel file.

The master Excel file will serve as the basis for all data analysis required to achieve the study objectives. After all data are edited and analyzed, a final copy of the master Excel workbook and R analysis code will be e-mailed, along with a data map, to Research and Technical Services (RTS) in the Anchorage ADF&G office for archiving on the SF intranet site.

DATA ANALYSIS

PIT Tag Abundance Estimates

A 2-sample mark–recapture model will be used to estimate the number of Chinook salmon passing by the first event sampling sites. The appropriate abundance estimator will depend on the results of tests. If stratification is not needed, Chapman's (1951) version of Petersen's abundance estimator for closed populations (see Seber 1982) will be used:

$$\hat{N} = \frac{(\hat{M}_U + 1)(\hat{C} + 1)}{(R + 1)} - 1, \quad (1)$$

where

$\hat{N}$ = estimated number Chinook salmon at RM 34,

$\hat{M}_U$ = the estimated number of marked Chinook salmon moving upstream of the Susitna River mainstem tagging site and remaining in the mainstem river,

$\hat{C}$ = the estimated number of Chinook salmon greater than or equal to 500 mm that are inspected for marks at the second event sampling site, and

R = number of marked Chinook salmon recaptured during second event sampling.

For Chinook salmon, we will estimate $\hat{M}_U$ as follows:

$$\hat{M}_U = \hat{p}_{UP} M , \quad (2)$$

where M is the total number of marked Chinook salmon, and

$$\hat{p}_{UP} = \frac{r_{up}}{r} , \quad (3)$$

where r is the number of radio tags applied and r_{up} is the number of r that entered the mark–recapture experiment.

We will estimate $\hat{C}$ as follows:

$$\hat{C} = C_T \, \hat{p}_{500+} , \quad (4)$$

where

C_T = total number of Chinook salmon counted past the Deshka River weir and

$\hat{p}_{500+}$ = estimated proportion of Chinook salmon at the Deshka River weir that were greater than or equal to 500 mm METF.

The proportion $\hat{p}_{500+}$ is estimated from length composition data at the Deshka River weir:

$$\hat{p}_{500+} = n_{500+} / n , \quad (5)$$

where

n = total number of Chinook salmon sampled for length at the Deshka River weir, and

n_{500+} = those members of n that were greater than or equal to 500 mm METF.

If stratification by size or sex is required (Appendix D1), the data will be fully stratified and estimates for each stratum will be generated using Equations 1–5. Stratum estimates of abundance and variance (see below) will be summed over size strata for estimates pertinent to the entire population.

An estimate of the variance for $\hat{N}$ within a size stratum will be obtained through simulation. The estimated number of marks continuing upstream will be simulated as a binomial variable [$\hat{M}_U^*$ ~bin(M, $\hat{p}_{Up}$)], and the number of recaptures R will be modeled as a binomial variable [R^*~ bin($\hat{C}$, $\hat{M}_u / \hat{N}$)]. The number of Chinook salmon greater than or equal to 500 mm METF length at the Deshka River weir will be modeled as binomial variables bin(C_T, $\hat{p}_{500+}$), and simulated values $\hat{C}^*$ will be calculated using Equation 4. A large number of simulated values R^*, $\hat{M}_U^*$, and $\hat{C}^*$ will be generated, and simulated samples of the abundance estimate $\hat{N}^*$ will be calculated using Equation 1.

A minimum of 1,000,000 simulations (B) will be drawn. The approximate variance of $\hat{N}$ will be calculated as follows:

$$\text{var}(\hat{N}) = \frac{\sum_{b=1}^{B} (\hat{N}_b^* - \bar{\hat{N}}^*)^2}{B-1} \tag{6}$$

where $\bar{\hat{N}}^*$ is the average of the $\hat{N}_b^*$. Confidence intervals will be calculated from the B simulations using the percentile method.

Size stratification tests will be conducted first and the data partitioned into appropriate size classes. Test III in Appendix D2 will be conducted within each size stratum. A nonsignificant result of this test may indicate that the Chapman–Petersen model is adequate, without the need for assumptions relating to even probability of capture in the marking event. A significant result means the assumption of even marking is required.

Genetic Abundance Estimates

The following abundance estimate will be calculated in the absence of sport harvest on the Deshka River. The stock composition of the fish wheel mixture will be estimated using the software package *BAYES* (Pella and Masuda 2001). *BAYES* employs a Bayesian algorithm to analyze the combination of genotypes in a mixture sample and to estimate the most probable contribution of the baseline populations to the sample. A total of 4 Markov Chain Monte Carlo (MCMC) chains will be run with 40,000 iterations each and the first 20,000 iterations will be discarded to remove the influence of starting values. The prior parameters for each reporting group will be defined to be equal (i.e., a flat prior). Within each reporting group, the population prior parameters will be divided equally among the populations within that reporting group. Stock proportion estimates and the 90% credibility intervals will be calculated by taking the

mean and 5% and 95% quantiles of the posterior distribution from the single chain output. The BAYES posterior output of stock composition estimates from the genetic mixed-stock analysis of a mixture of 400 PIT-tagged fish will be used to estimate the number of Susitna River mainstem Chinook salmon passing RM 34. Abundance estimates will be produced for each iteration i of the posterior using a modified Chapman's estimator (Seber 1982):

$$\widehat{N}_i = \frac{(W+1)(\hat{S}_i+1)}{\widehat{D}_i+1} - 1, \tag{7}$$

where

$\widehat{N}_i$ = estimated number Susitna River mainstem Chinook salmon in MCMC iteration *i*,

W = the number of Chinook salmon passing the Deshka River weir site,

$\hat{S}_i$ = the estimated number of Chinook salmon of Susitna River mainstem origin in the 400 sample mixture, and

$\widehat{D}_i$ = the estimated number of Chinook salmon of Deshka River origin in the 400 sample mixture.

We will estimate $\hat{S}_i$ as follows:

$$\hat{S}_i = M\ (\hat{s}_i + \hat{d}_i), \tag{8}$$

where M is the number of fish in the mixture sample, $\hat{s}_i$ is the estimated proportion of the *Susitna* reporting group in the mixture, and $\hat{d}_i$ is the estimated proportion of the *Deshka* reporting group in the mixture.

We will estimate $\widehat{D}_i$ as follows:

$$\widehat{D}_i = M\ (\hat{d}_i). \tag{9}$$

The variability of the $\widehat{D}_i$and $\hat{S}_i$ over MCMC iterations incorporates both uncertainty from the mixture model estimation and sampling variability. The mean Susitna River mainstem abundance estimate and 90% credibility intervals will be calculated by taking the mean and 5% and 95% quantiles of the posterior distribution of abundance estimates.

Proportion of non-Deshka River Chinook Salmon in Harvest

If there is a sport fishery, the estimated proportion of non-Deshka River Chinook salmon in the sport harvest from section *s* of the Deshka River will be calculated as follows:

$$\hat{p}_{NDs} = \frac{n_{ND}}{n_s}, \tag{10}$$

where

n_{ND} = number of Chinook salmon of non-Deshka River origin in n_s

n_s = number of Chinook salmon sampled from the harvest from section *s* of the Deshka River.

The estimated variance of $\hat{p}_{NDs}$ will be calculated as follows:

$$\text{var}(\hat{p}_{NDs}) = \frac{\hat{p}_{NDs}(1-\hat{p}_{NDs})}{n_s - 1}. \quad (11)$$

SSART Model

The procedures outlined in Reimer and Fleischman (2016) will be followed using the temporal CPUE data, harvest, Deshka River weir count, and GSI results.

SCHEDULE AND DELIVERABLES

Dates	Activity
Approximately 22 May–30 June 2018	Marking operations at RM 34 mainstem Susitna River site
Approximately 19 May–15 July 2018	Weir sampling at Deshka River
15 September–31 December 2018	Data reduction and analysis
30 March 2019	Finalized 2018 Fishery Data Series Report. Genetics results will be reported separately, to be determined by ADF&G Gene Conservation Lab

RESPONSIBILITIES

John Campbell, Fishery Biologist II
Duties: Lead all radiotelemetry and PIT data recovery and tracking portions of project, and supervise project FB I. Coordinate data collection, data analysis, purchasing, reporting, crew training, radiotracking station setup and downloads. Assist with hiring and writing the operational plan. Coauthor on report.

David Evans, Biometrician III
Duties: Advise all portions of the biometrics including planning, sample sizes, statistical methods, and data analysis. Perform data analysis and produce final estimates. Coauthor on report.

Andy Barclay, Fishery Biologist III
Duties: Advise portions of the genetics: planning, sample sizes, statistical methods, data analysis, and reporting. Supply tissue collection materials and instructions.

Nick Decovich, Fishery Biologist III
Duties: Supervise all aspects of project (excluding data analysis): planning, budget, data collection, and reporting. Lead author on operational plan and report.

Steve Dotomain, Fishery Biologist I
Duties: Supervise the mainstem Susitna River site and assist with planning, hiring and training field staff, data collection, data analysis, supervision, and purchasing. Assist with writing the operational plan and final report.

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APPENDIX A: PIT TAG METHODS

All healthy Chinook salmon greater than or equal to 500 mm mideye to tail fork (METF) length captured at the mainstem Susitna River site (RM 34) will be tagged with an orange, 14 cm long, vinyl, dart-PIT tag (model PDAT-PIT [HPT-12] from Hallprint, Australia). Each dart-PIT tag (Figure A1-1) is associated with a unique number (10,000–25,000) printed on the tag twice (bottom and top portions), contact information for the researchers, and an embedded Biomark (Biomark Inc.) high performance FDX-B glass PIT tag (HPT-12).

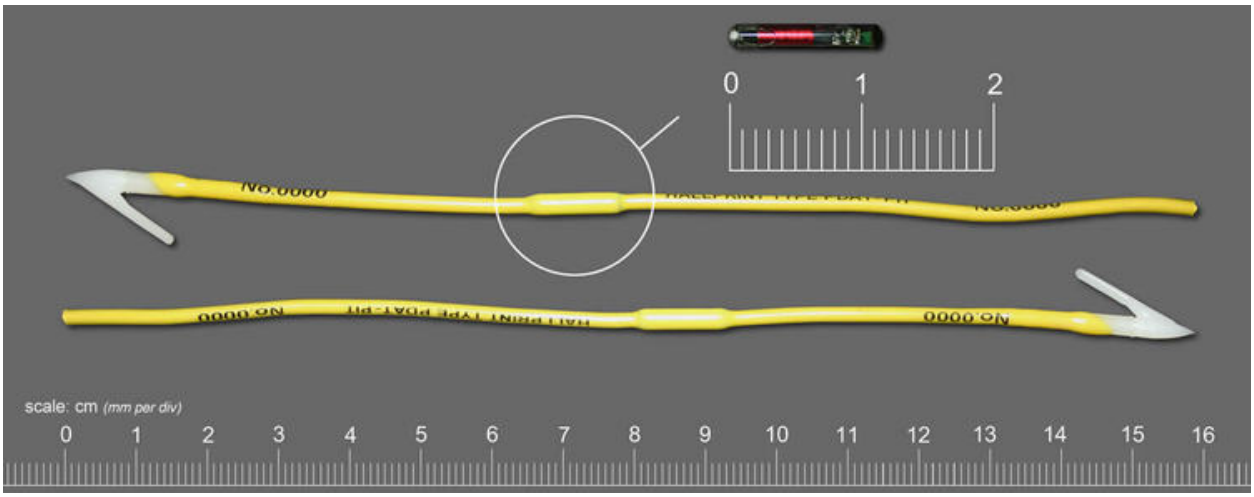


Figure A1-1.–Example of Hallprint PDAT-PIT tag.

Each tag will be applied beneath the dorsal fin with a hollow 8-gauge stainless steel applicator needle. In addition to the dart tag, each fish will also receive a left operculum hole punch to estimate tag loss at the recapture sites. Instructions from the tag manufacturer are quoted as follows:

HALLPRINT TECHNICAL NOTES 2
APPLICATION INSTRUCTIONS FOR PLASTIC TIPPED DART TAGS - TUNA

This information is for guidance to the first-time user. Procedures will vary, depending on the species to be tagged, size of tag, fish and field conditions.

Always check correct location of the dart head etc. before engaging in actual tagging operations (see over).

Tag description

Plastic tipped dart tags are constructed from a cylindrical printed and numbered marker, moulded to a plastic barbed head. Several sizes/shapes of dart head are used in combination with various length/diameter markers.

-continued-

(quoted instructions continued)

Loading of applicator

It is a good idea to keep a pre-loaded one, with the tags, your measure, notes and a pen, in a handy place so that the fish does not have to wait too long for you to find them.

Load tag with only the barb exposed at the pointed end.

If the tag does not slide easily out of applicator then it is either choked with debris or bent. This must be rectified otherwise you will probably get a hung-up tag.

Loosely fitting tags can be secured by making a slight bend in the printed marker—do not alter the applicator.

Some researchers prefer to use a handle which can be made from a short length of 20 mm diameter dowel with a hole drilled in one end. Retractable and non-retractable fabricated handles are available (other than for PDX/PDXL needles) from Hallprint if needed.

Insertion of tags into fish

Minimize trauma and damage to fish. Keep it under control. If it has noticeably suffered by capture do not waste time tagging it. Release gently, or keep if legal and you intend to eat.

1) Remove a scale with the applicator point just below the base of a dorsal spine on the second dorsal fin (see over). Avoid placing the tag too deeply into muscle.

2) Hold needle with exposed tag barb in line with fish, with barb facing head. Turn needle so barb is on the fish side.

3) Start inserting the needle at a shallow angle under the scales until you feel it pierce the skin, then raise the needle to an angle of 45 degrees so making clearance for the barb.

4) When barb is below skin, return to a shallow angle and insert until the barb is just beyond the fin spine. A slight "click" can be felt as the barb slides over the bone and locks behind it.

5) Pause for a second then withdraw the needle smoothly. A slight tug will help "set" the tag. Particularly with small tags/small fish do not place any undue strain on either tag or fish after insertion.

6) The fish should then be gently released. Fish showing undue stress, damage or inability to swim should not be released if tagged.

(end quote)

Prior to deployment, all dart-PIT tags will be scanned with a 134.2 kHz signal from a Biomark 601 hand-held reader to ensure that the PIT tag is operating properly and to determine its unique code. The code will be recorded along with the corresponding dart tag number. The same process will be performed independently by a different person to insure that each code and corresponding dart tag number is correct.

-continued-

Antenna Set-Up

A double antenna, Biomark PIT detection system will be installed immediately upstream of the fish cage at the Deshka River floating weir (Figure A1-2). The system will consist of a 2 m long, 1 m wide, and 1.5 m tall U-shaped chute, constructed of 2.5 cm size mesh polyethylene netting, that will force fish that have passed through the weir cage to swim through two 1.2 m × 1.5 m Biomark antennas located 1 m and 2 m upstream of the weir.

Figure A1-2.–PIT detection antennas above the Deshka River floating weir and cage, 2015.

Chest Enclosure

Antennas will have 30 m Biomark antenna exciter cables attached to them and will be routed along the stream bed to the stream bank where they will be connected to a Biomark IS1001 chest enclosure (Figure A1-3), which will contain 2 Biomark IS1001 24V control nodes, a Biomark IS1001 data logger, a Biomark IS1001 data logger board, and two 12V, 75AH, maintenance-free batteries. The system will be kept charged by a 200 W solar panel mounted 1 to 2 m above the chest enclosure in an area that receives direct sunlight. A 24 V charge controller will be used to control the voltage being supplied to the batteries and prevent the batteries from being drained during low light periods.

-continued-

Figure A1-3.–Biomark IS 1001 chest enclosure showing the components and the 2 antenna exciter cables.

System Checks

In order to ensure that the system is operational and the antennas are working properly, 2 tests will be performed daily. In addition to daily checks of the battery voltage, tests will be performed to ensure that any PIT tags passing through the antennas are being recorded.

The first test will be performed every morning and afternoon. It will consist of testing the antennas by using a test PIT tag mounted to a 2 m long, 2 cm diameter wooden dowel. During periods of time when the trap door is closed on the weir (no fish passing) the PIT tag will be moved through all areas of each antenna to ensure that there are no "dead spots" where the tag is not being detected. If dead spots are detected, the systems will be configured until there are no dead spots.

The second test will also take place as conditions allow. As the weir crews are passing fish, they will record the time they observe an orange dart-tagged fish passing through the weir. Twice per week, the PIT detection data will be downloaded and the crew will assess whether a PIT tag was detected during the time period that the dart-tagged fish was observed passing through the weir. The system has real time indicators for when a tag is detected, and if circumstances allow, this test can be used to provide immediate evaluation of the system.

APPENDIX B: FIELD DATA FORMS

Appendix B1.–Fish wheel catch and effort field data form.

MAINSTEM FISH WHEEL CATCH - EFFORT AND TAGGING

Fish Wheel: 1 2 Date:_____/2018

Shift: 1 2 Scale Start Card_____End Card_____ Samplers:_____

Operation Shift Times

Start:	Stop:	Start:	Stop:	Start:	Stop:	Start:	Stop:	Total Min:

CHINOOK TAGS

#	START TIME	END TIME	MEF	DART #	PUNCH (✓)	RADIO FREQUECNY	PULSE CODE	VIAL	Scale #	RELEASE TIME	UN-TAGGED (circle one)	RECAP/NO TAG (CIRCLE ONE)	OTHER SALMON	NON SALMON
1	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
2	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
3	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
4	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
5	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
6	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
7	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
8	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
9	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
10	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
11	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
12	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		
20	:	:				.				:	INJ ESC REC >1HR <500	AD LO UC		

Total Chinook:	Total Darts:	Total Radios:	Total Recaps:		Other Salmon:	Total Others:

* AD, LO, UC = Adipose, left operculum, upper caudal

* **Salmon: Chinook=King=KS, Sockeye=SO, Coho=CO, Chum=CU, Pink=P.** NP=Northern Pike, B=Burbot, AG=Arctic Grayling, RT=Rainbow Trout, BC=Bering Cisco, HWF=Humpback Whitefish, RWF=Round Whitefish, LNS=Longnose Sucker, AC=Arctic Char. INJ=Injured, ESC=Escaped, REC=Recaptured

Comments:

Appendix B2.–Gillnet catch and effort field data form.

MAINSTEM GILL NET CATCH - EFFORT - TAGGING

GPS #: ______ Date:________________________/2018

SHIFT: 1 2 Scale Start Card_______End Card______ Samplers:_________________________

Gill Net Sets Gill Net Catch - Enter every fish in its own row

EFFORT					CHINOOK	TAGS									
SET	START TIME	END TIME	MIN	WAY POINT	MEF	DART #	PUNCH (✓)	RADIO FREQUECNY	PULSE CODE	VIAL	Scale #	RELEASE TIME	UN-TAGGED (circle one)	RECAP (CIRCLE ONE)	OTHER
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	
	:	:						.				:	INJ ESC REC >1HR <500	AD LO UC	

Total Min:	Total Chinook:	Total Darts:	Total Radios:	Total Recaps:	Total Others:

* **AD, LO, UC** = Adipose, left operculum, upper caudal

* **Salmon:** Chinook=King=**KS**, Sockeye=**SO**, Coho=**CO**, Chum=**CU**, Pink=**P**. **Others: NP**=Northern Pike, **B**=Burbot, **AG**=Arctic Grayling, **RT**=Rainbow Trout, **BC**=Bering Cisco, **HWF**=Humpback Whitefish, **RWF**=Round Whitefish, **LNS**=Longnose Sucker, **AC**=Arctic Char. **INJ**=Injured, **ESC**=Escaped, **REC**=Recaptured

APPENDIX C: BIOLOGICAL SAMPLING PROCEDURES

Appendix C1.–Genetic tissue sample collection procedures.

Non-lethal Sampling of Finfish Tissue for DNA Analysis

ADF&G Gene Conservation Lab, Anchorage

I. General Information

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

Sample preservative: Ethanol (ETOH) preserves tissues for later DNA extraction without having to store frozen tissues. Avoid extended contact with skin.

II. Sample procedure:

1. Tissue type: Axillary process, clip axillary process from each fish (Appendix C2).
2. Data to record: Record each vial number to paired data information.
3. Prior to sampling, fill the tubes half way with ETOH from the squirt bottle. Fill only the tubes that you will use for a particular sampling period.
4. To avoid any excess water or fish slime in the vial, wipe the axillary process dry prior to sampling. Using the dog toe nail clipper or scissors, clip off axillary process (**1/2 -1" max**) to fit into the cryovial.
5. Place axillary process into ETOH. The tissue/ethanol ratio should be **slightly less than 1:3** to thoroughly soak the tissue in the buffer.
6. Top up tubes with ETOH and screw cap on securely. Invert tube twice to mix ETOH and tissue. Periodically, wipe the dog toe nail clippers or scissor blade so not to cross contaminate samples.
7. Discard remaining ethanol from the 500ml bottle before returning samples. **Tissue samples must remain in 2ml ethanol** after sampling. HAZ-MAT paperwork will be required for return shipment. Store vials containing tissues at cool or room temperature, away from heat in the white sample boxes provided. In the field: keep samples out of direct sun, rain and store capped vials in a dry, cool location. Freezing not required.

III. Supplies included with sampling kit:

1. (1) – Dog toe nail clipper - used for cutting the axillary process
2. (1) – Scissors can be used to cut a portion axillary process – if clippers don't work for your crew
3. Cryovial- a small (2ml) plastic vial, pre-labeled.
4. Caps – with or without gasket to prevent evaporation of ETOH.
5. Cryovial rack- white plastic rack with holes for holding cryovials while sampling
6. Ethanol (ETOH) – in (2) 500 ml plus (1) – 125 ml Nalgene bottle
7. Squirt bottle – to fill or "top off" each cryovial with ETOH
8. Paper towels – use to blot any excess water or fish slime off axillary process
9. Printout of sampling instructions
10. (3) – three pair of lab gloves (size large)
11. Laminated "return address" label

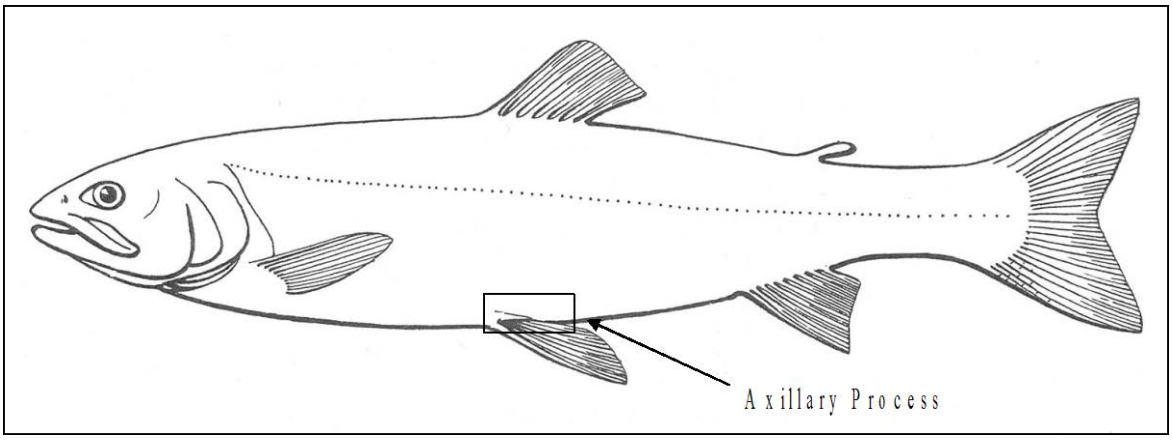
IV. Shipping: HAZMAT paperwork is required for return shipment of these samples and is included in the kit.

Ship samples to: ADF&G – Genetics

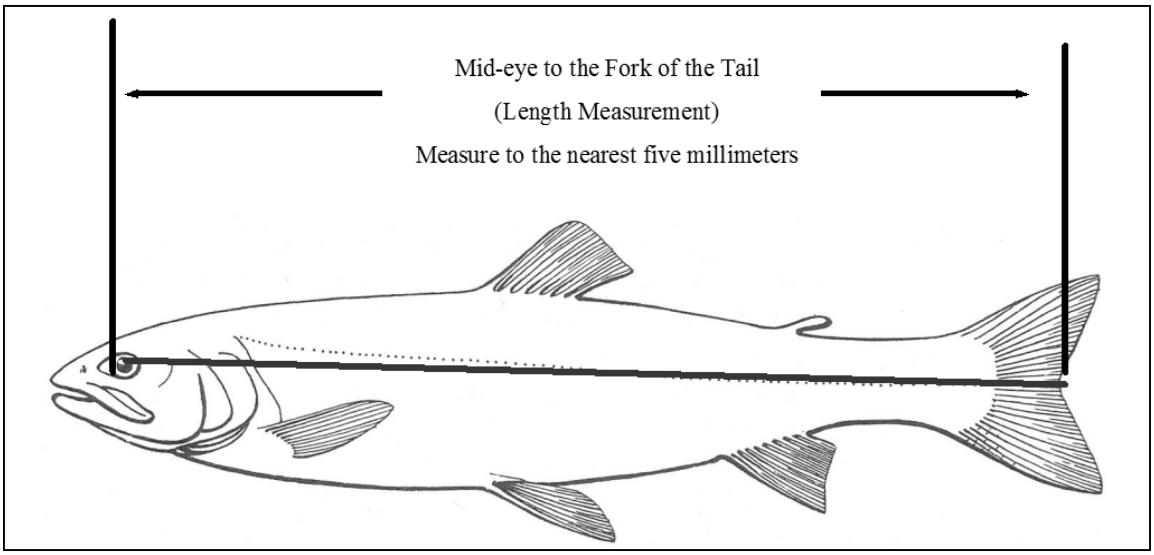
333 Raspberry Road

Lab staff: 1-907-267-2247

Judy Berger: 1-907-267-2175



Appendix C2.–Location of axillary process.



Appendix C3.–Measuring salmon for length (mid eye to tail fork).

APPENDIX D: TESTS OF MARK–RECAPTURE ASSUMPTIONS AND SAMPLE SIZES

Appendix D1.–Detection and mitigation of selective sampling during a 2-event mark–recapture experiment.

Size- and sex-selective sampling may cause bias in 2-event mark–recapture estimates of abundance and size and sex composition. Kolmogorov–Smirnov (KS) 2 sample tests are used to detect size-selective sampling, and contingency table analyses (chi-square tests of independence) are used to detect evidence of sex-selective sampling.

Results of the KS and chi-square tests will dictate whether the data need to be stratified to obtain an unbiased estimate of abundance. The nature of the detected selectivity will also determine whether the first, second, or both event samples are used for estimating size and sex compositions.

Definitions

M = Lengths or sex of fish marked in the first event

C = Lengths or sex of fish inspected for marks in the second event

R = Lengths or sex of fish marked in the first event and recaptured in the second event

Size-selective sampling: KS tests

Three KS tests are used to test for size-selective sampling:

Test 1	C vs R	Used to detect size selectivity during the 1st sampling event. H_o: Length distributions of populations associated with C and R are equal.
Test 2	M vs R	Used to detect size selectivity during the 2nd sampling event. H_o: Length distributions of populations associated with M and R are equal.
Test 3	M vs C	Used to corroborate the results of the first two tests. H_o: Length distributions of populations associated with M and C are equal.

Sex-selective sampling: chi-square tests

Three contingency table analyses (chi-square tests on 2 × 2 tables) are used to test for sex-selective sampling:

Test 1	C vs R	Used to detect sex selectivity during the 1st sampling event. H_o: Sex is independent of the C–R classification.
Test 2	M vs R	Used to detect sex selectivity during the 2nd sampling event. H_o: Sex is independent of the M–R classification.
Test 3	M vs C	Used to corroborate the results of the first two tests. H_o: Sex is independent of the M–C classification.

-continued-

There are several possible results of selectivity testing, interpretation, and prescribed action (Table D1-1).

Table D1-1.–Possible results of selectivity testing, interpretation, and action.

Case	KS or chi-square test: M vs R (2nd event test)	KS or chi-square test: C vs. R (1st event test)	KS or chi-square test: M vs. C (1st vs 2nd event)	Interpretation and action	
I	Fail to reject H_o	Fail to reject H_o	Fail to reject H_o	**Interpretation**:	No selectivity during either sampling event.
				Action:	
				Abundance:	Use a Petersen-type model without stratification.
				Composition:	Use all data from both sampling events.
II	Reject H_o	Fail to reject H_o	Reject H_o	**Interpretation:**	No selectivity during the 1st event but there is selectivity during the 2nd event.
				Action:	
				Abundance:	Use a Petersen-type model without stratification.
				Composition:	Use data from the 1st sampling event without stratification. 2nd event data only used if stratification of the abundance estimate is performed, with weighting according to Equations 1–3 below.
III	Fail to reject H_o	Reject H_o	Reject H_o	**Interpretation:**	No selectivity during the 2nd event but there is selectivity during the 1st event.
				Action:	
				Abundance:	Use a Petersen-type model without stratification.
				Composition:	Use data from the 2nd sampling event without stratification. 1st event data may be incorporated into composition estimation only after stratification of the abundance estimate and appropriate weighting according to Equations 1–3 below.
IV	Reject H_o	Reject H_o	Either result	**Interpretation:**	Selectivity during both 1st and 2nd events.
				Action:	
				Abundance:	Use a stratified Petersen-type model, with estimates calculated separately for each stratum. Sum stratum estimates for overall abundance.
				Composition:	Combine stratum estimates according to Equations 1-3 below.
V	Fail to reject H_o	Fail to reject H_o	Reject H_o	**Interpretation:**	The results of the 3 tests are inconsistent.
				Action:	Need to determine which of Cases I–IV best fits the data. Inconsistency can arise from high power of the M vs C test or low power of the tests involving R. Examine sample sizes (generally M or C from <100 fish and R from <30 are considered small), magnitude of the test statistics (D_{max}), and the *P*-values of the 3 tests to determine which of which of Cases I–IV best fits the data.

-continued-

Composition estimation for stratified estimates

An estimate of the proportion of the population in the *k*th size or sex category for stratified data with *I* strata is calculated as follows:

$$\hat{p}_k = \sum_{i=1}^{I} \frac{\hat{N}_i}{\hat{N}} \hat{p}_{ik} \tag{1}$$

with variance estimated as

$$var[\hat{p}_k] \approx \frac{1}{\hat{N}^2} \sum_{i=1}^{I} \left(\hat{N}_i^2 var[\hat{p}_{ik}] + \left(\hat{p}_{ik} - \hat{p}_k \right)^2 var[\hat{N}_i] \right) \tag{2}$$

where

$\hat{p}_{ik}$ = estimated proportion of fish belonging to category *k* in stratum *i*;

$\hat{N}_i$ = estimated abundance in stratum *i*,

and the estimated total abundance is

$$\hat{N} = \sum_{i=1}^{I} \hat{N}_i \ . \tag{3}$$

Tests of consistency for Petersen Estimator

Three contingency table analyses are used to determine if the Petersen estimate can be used (Seber 1982). If any of the null hypotheses are not rejected, then a Petersen estimator may be used. If all three of the null hypotheses are rejected, a temporally or spatially-stratified estimator (Darroch 1961) should be used to estimate abundance.

Seber (1982) describes 4 conditions that lead to an unbiased Petersen estimate, some of which can be tested directly:

1) Marked fish mix completely with unmarked fish between events.
2) Equal probability of capture in event 1 and equal movement patterns of marked and unmarked fish.
3) Equal probability of capture in event 2.
4) The expected number of marked fish in recapture strata is proportional to the number of unmarked fish.

In the following tables, the terminology of Seber (1982) is followed, where a represents fish marked in the first event, n fish are captured in the second event, and m marked fish are recaptured; $m_{\bullet j}$ and $m_{i\bullet}$ represent summation over the ith and jth indices, respectively.

I. Mixing Test

Tests the hypothesis (condition 1) that movement probabilities (θ_{ij}), describing the probability that a fish moves from marking stratum i to recapture stratum j, are independent of marking stratum: H_0: $\theta_{ij} = \theta_j$ for all i and j.

Area–time marking stratum (i)	Area–time recapture stratum (j)				Not recaptured
	1	2	…	t	$a_i - m_{i\bullet}$
1	m_{11}	m_{12}	…	m_{1t}	$a_1 - m_{1\bullet}$
2	m_{21}	m_{22}	…	m_{2t}	$a_2 - m_{2\bullet}$
…	…	…	…	…	…
s	m_{s1}	m_{s2}	…	m_{st}	$a_s - m_{s\bullet}$

-continued-

II. Equal Proportions Test[4] (SPAS[5] terminology)

Tests the hypothesis (condition 4) that the marked to unmarked ratio among recapture strata is constant: H_0: $\Sigma_i a_i \theta_{ij} / U_j = k$, where k is a constant, U_j is unmarked fish in stratum j at the time of 2nd event sampling, and a_i is the number of marked fish released in stratum i. Failure to reject H_0 means the Petersen estimator should be used only if the degree of closure among tagging strata is constant; i.e., $\Sigma_j \theta_{ij} = \lambda$ (Schwarz and Taylor 1998: page 289). A special case of closure is when all recapture strata are sampled, such as in a fishwheel-to-fishwheel experiment, where $\Sigma_j \theta_{ij} = 1.0$; otherwise biological and experimental design information should be used to assess the degree of closure.

	Area–time recapture stratum (j)			
	1	2	…	t
Recaptured ($m_{\cdot j}$)	$m_{\cdot 1}$	$m_{\cdot 2}$	…	$m_{\cdot t}$
Unmarked ($n_j - m_{\cdot j}$)	$n_1 - m_{\cdot 1}$	$n_2 - m_{\cdot 2}$	…	$n_t - m_{\cdot t}$

III. Complete Mixing Test[6] (SPAS terminology)

Tests the hypothesis that the probability of re-sighting a released animal is independent of its stratum of origin: H_0: $\Sigma_j \theta_{ij} p_j = d$, where p_j is the probability of capturing a fish in recapture stratum j during the second event, and d is a constant.

	Area–time marking stratum (i)			
	1	2	…	s
Recaptured (m_i)	$m_{1\cdot}$	$m_{2\cdot}$	…	$m_{s\cdot}$
Not recaptured ($a_i - m_{i\cdot}$)	$a_1 - m_{1\cdot}$	$a_2 - m_{2\cdot}$	…	$a_s - m_{s\cdot}$

4 There is no 1:1 correspondence between Tests II and III and conditions 2–3 above. It is pointed out that equal probability of capture in event 1 will lead to (expected) nonsignificant Test II results, as will mixing, and that equal probability of capture in event 2 along with equal closure ($\Sigma j \theta i j = \lambda$) will also lead to (expected) nonsignificant Test III results.

5 Stratified Population Analysis System (Arnason et al. 1996).

Appendix D3.–Anticipated sampling rates and sample sizes necessary to estimate mainstem Chinook salmon abundance within 20%, 90% of the time using a size-stratified Petersen model and adjusting for 25% loss of marked fish.

				2nd Event	
Population size (*N*)	Marks deployed	Mark loss	Valid marks	Sample size needed	Sample % of N
110,000	1,100	25%	825	12,635	11.5
90,000	900	25%	675	12,321	13.7
70,000	700	25%	525	11,857	16.9
50,000	500	25%	375	11,105	22.2
30,000	300	25%	225	9,673	32.2

Note: Marks deployed based on average estimated capture rate in 2015 and 2017 (0.01).