Regional Operational Plan SF.2A.2016.12

Operational Plan: Upper Cook Inlet Commercial Eastside Set Gillnet Chinook Salmon Harvest Composition Study

by

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and

Andrew W. Barclay

July 2016

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.2016.12

OPERATIONAL PLAN: UPPER COOK INLET COMMERCIAL EASTSIDE SET GILLNET CHINOOK SALMON HARVEST COMPOSITION STUDY

by

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SIGNATURE/TITLE PAGE

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Approval

Title	Name	Signature	Date
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ABSTRACT

Genetic tissue and age, sex, and length composition information will be collected from harvested Chinook salmon in the Upper Cook Inlet Eastside set gillnet (ESSN) commercial fishery in 2016. The primary goals of the study are to estimate the proportion and harvest by genetic reporting group of Chinook salmon in the ESSN commercial fishery both within temporal and geographic strata and for the entire 2016 season. The harvest will be apportioned by 4 genetic reporting groups: Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries, and Cook Inlet other. Age, sex, and length composition will also be estimated for each temporal and geographic stratum and for the entire 2016 season.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, Kenai River, Eastside set gillnet, commercial fishery, ESSN, Upper Cook Inlet, mixed stock analysis, MSA, stock-specific harvest, Chinook Salmon Research Initiative, CSRI.

INTRODUCTION

PURPOSE

The Kenai River Chinook salmon stock has been chosen as 1 of 12 indicator stocks part of the Chinook Salmon Research Initiative (CSRI) (ADF&G Chinook Salmon Research Team 2013), and the lack of stock-specific harvest information from commercial harvests of Chinook salmon in Cook Inlet has been identified as an information gap. Stock-specific harvest and age, sex, and length (ASL) composition data are needed to more accurately represent harvest rates and production trends. Genetic samples are needed to estimate the relative proportions and, along with harvest data, the number of Chinook salmon harvested by genetic reporting group (including Kenai River mainstem and tributary populations) in the ESSN commercial fishery for particular temporal and geographic strata. This project will collect and analyze ASL and genetic tissue samples of Chinook salmon harvested in the Upper Cook Inlet (UCI) Eastside set gillnet (ESSN) commercial fishery. The Division of Sport Fish (SF) is responsible for the collection of genetic tissue samples and ASL data. Tissue samples will be sent to the Division of Commercial Fisheries (CF) Gene Conservation Lab (GCL), which will be responsible for mixed stock analysis (MSA).

BACKGROUND

All 5 species of Pacific salmon are harvested in UCI. Sockeye salmon (*Oncorhynchus nerka*) make up the majority of the harvest (Shields and Dupuis 2015) but Chinook salmon (*O. tshawytscha*) are also harvested. Recent low Chinook salmon runs in UCI have heightened interest in stock-specific harvest of Chinook salmon in these fisheries. A Chinook salmon genetic baseline that includes representative populations in UCI is available for MSA applications in fisheries using genetic stock identification (GSI) techniques (Barclay et al. 2012). Obtaining information about stock-specific harvest of Chinook salmon is needed to improve understanding of stock productivity, brood table development, and for setting and attaining escapement goals.

Most of the UCI commercial Chinook salmon harvest occurs in the Upper Subdistrict set gillnet fishery of the Central District. This fishery is commonly referred to as the Eastside set gillnet (ESSN) fishery and is located along the eastern shore of Cook Inlet between Ninilchik and Boulder Point (Figure 1). Since 1966, annually on average, the ESSN fishery has accounted for 65% of all Chinook salmon harvested in UCI commercial fisheries (Eskelin and Barclay 2016).

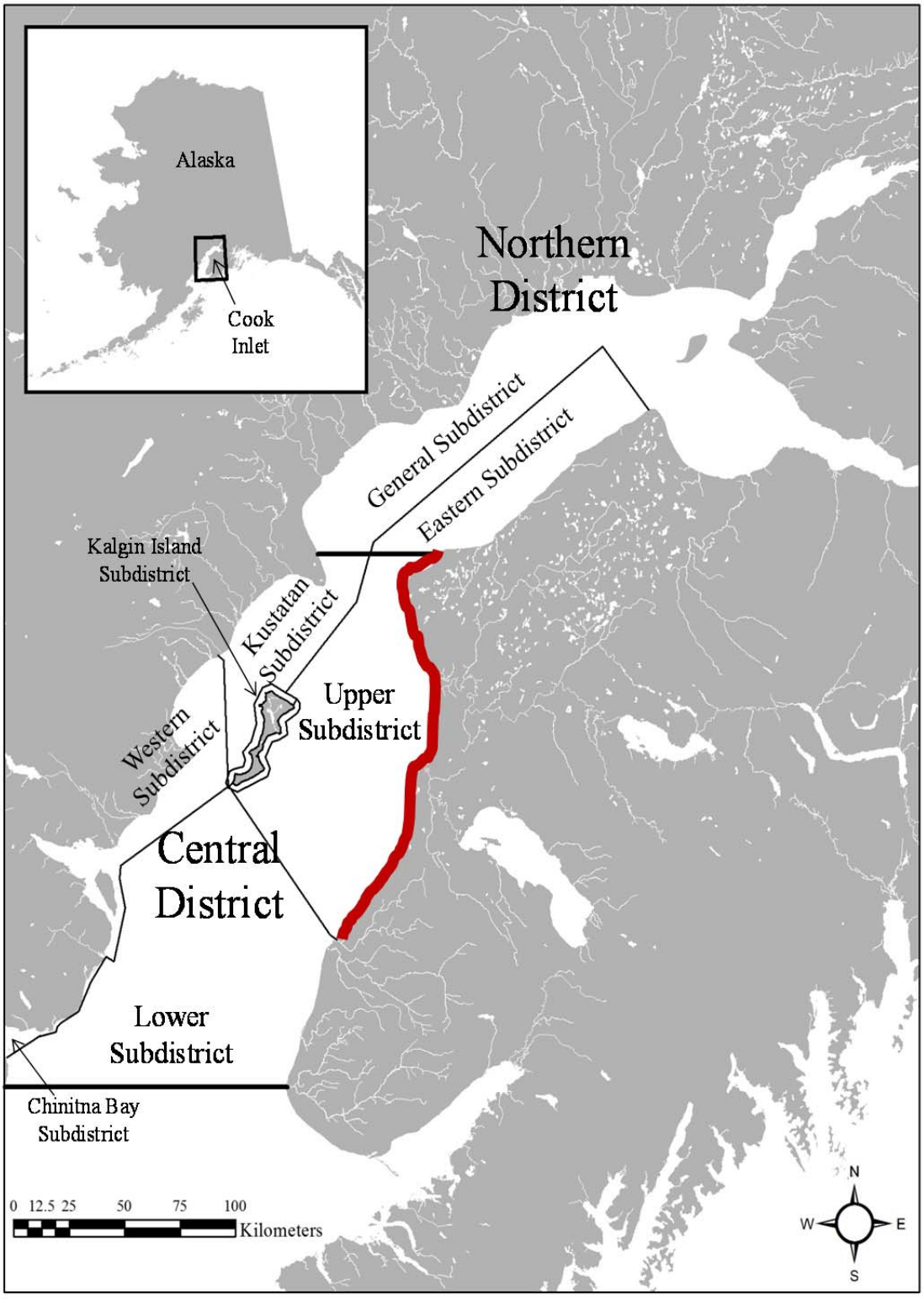

Figure 1.–Map of Upper Cook Inlet commercial fishing districts and subdistricts.

Note: Thick black lines indicate district borders and thin lines indicate subdistrict borders. The maroon line denotes the ESSN fishery.

The ESSN fishery is composed of 3 sections (Kasilof, Kenai, and East Foreland) and 7 statistical areas: Ninilchik Beach (244-22), Cohoe Beach (244-22), South K-Beach (244-31), North K-Beach (244-32), Salamatof Beach (244-41), East Foreland (244-42), and Kasilof River special harvest area (KRSHA, 244-25) (Figure 2). The recent 10-year (2006–2015) average ESSN Chinook salmon harvest is 6,394 fish and the historical (1966–2015) average is 9,418 fish. The 3 lowest documented harvests of Chinook salmon in the ESSN fishery were during 2012–2014 with 704, 2,988, and 2,301 fish in those years, respectively. While low Chinook salmon runs and subsequent reduced fishing time reduced Chinook salmon harvest substantially, in 2015 there was an increase in Chinook salmon abundance and, subsequently, more fishing time was given to the ESSN fishery, which resulted in an average harvest of 7,781 fish. In 2015, the Kasilof Section was fished on 28 days during 22 June–10 August including 1 day (18 July) that was restricted to fishing within one-half mile of the mean high tide line; the Kenai and East Foreland sections were fished on 20 days during 9 July–12 August. The KRSHA was fished 20 days during 7 July–2 August. In addition, there were 6 days during 15–31 July when the Kasilof Section was restricted to fishing within 600 ft of the mean high tide line.

The ESSN Chinook salmon harvest has been sampled by the Alaska Department of Fish and Game (ADF&G) for ASL composition information since 1986. In many years, 1 technician sampled harvested Chinook salmon at the receiving sites for fish processors both on regular period openings and opportunistically to collect ASL samples. Beginning in 2010, genetic tissue samples were added to the collection effort. The sampling effort has been increased since 2013 with funding from the CSRI to increase coverage and provide more informative temporally and geographically stratified estimates by reporting group. A sufficient number of representative samples were collected to allow for MSA in all years since 2010, except for 2012. Temporally and geographically stratified estimates have been produced since 2013 due to the increased funding and sampling effort whereas in 2010 and 2011, only seasonal MSA estimates were produced.

Reporting groups were defined based on 1 or more of the following criteria: 1) the genetic similarity among populations, 2) the expectation that proportional harvest would be greater than 5%, or 3) the applicability to answer fishery management questions. Reporting groups used in the MSA for each year were: "*Kenai River mainstem,*" "*Kasilof River mainstem,*" "*Kenai River tributaries,*" and "*Cook Inlet other*." The Kenai River supports 2 genetically divergent population aggregates (Barclay et al. 2012). Those that spawn in Kenai river tributaries enter the river prior to those that spawn in the mainstem Kenai River, although there is some overlap from late June to early July (Reimer 2013; Reimer et al. 2016). Results of genetic sampling thus far have shown that the ESSN Chinook salmon harvest is composed of almost entirely *Kenai River mainstem* and *Kasilof River mainstem* fish (Eskelin et al. 2013; Eskelin and Barclay 2015, 2016). MSA results by reporting group have been similar from year to year (Table 1), with the *Kenai River mainstem* reporting group having the greatest average proportional contribution (0.691), followed by *Kasilof River mainstem* (0.292), *Cook Inlet other* (0.014) and lastly, the *Kenai River tributaries* reporting group (0.008).

This project in 2016 will be the same as those in 2013–2015, which involved expanded sampling of the Chinook salmon harvest for ASL composition and genetic tissue. A total of 3 technicians will be assigned to sample the ESSN Chinook salmon harvest, providing coverage of the fishery during every regular period opening and also allowing for sampling of most fishing periods that may be opened by emergency order (EO).

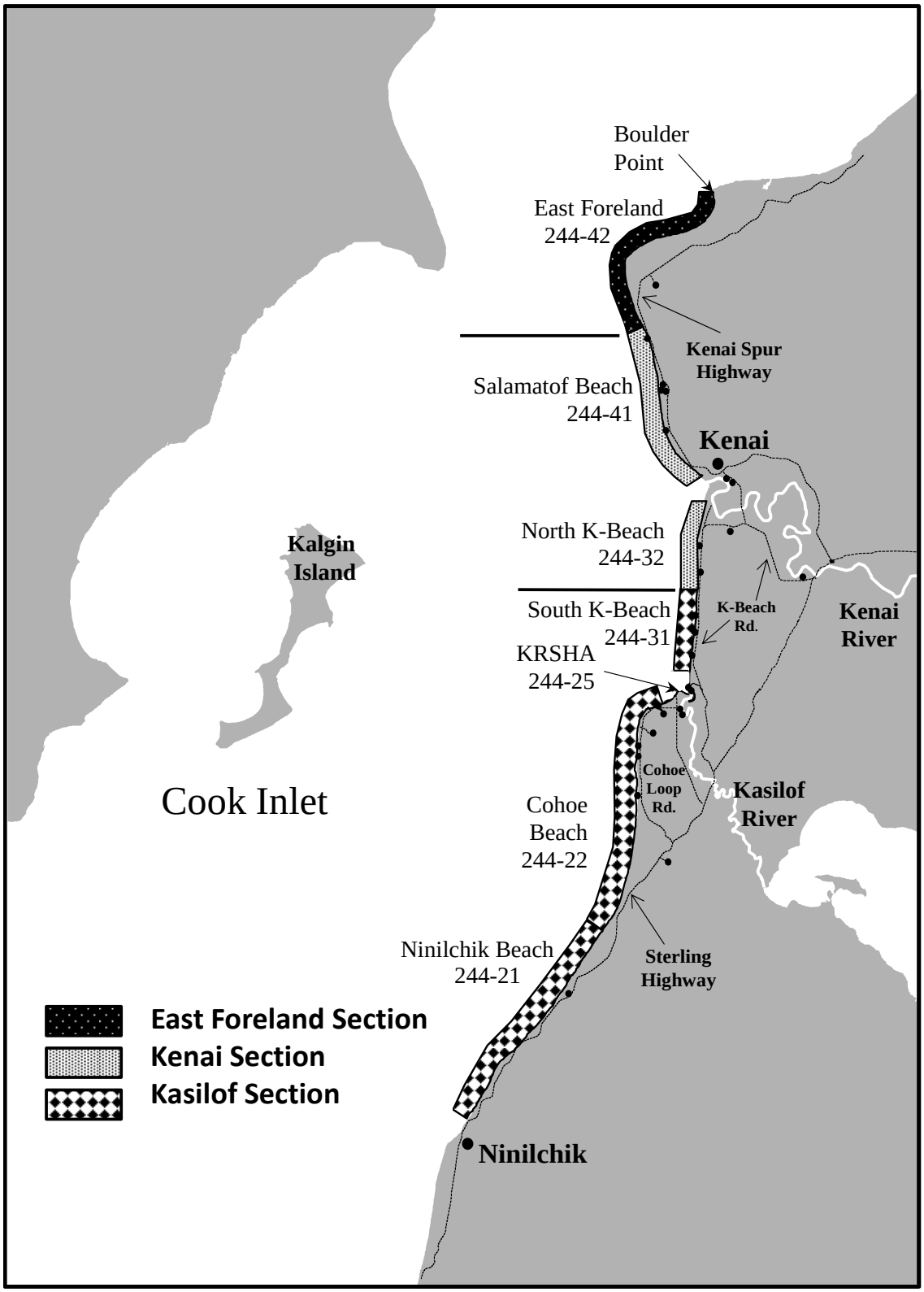

Figure 2.–Map of Upper Cook Inlet Eastside set gillnet commercial fishing statistical areas.

Note: Small circles represent approximate locations of processing plants or receiving sites. KRSHA (244-25) is the Kasilof River special harvest area.

Table 1.–Proportion of ESSN Chinook salmon harvest by reporting group and year.

				Credibility interval				Credibility interval	
Reporting group	Year	Proportion	SD	5%	95%	Harvest	SD	5%	95%
Kenai River tributaries	2010	0.011	0.010	0.001	0.031	75	73	4	220
	2011	0.001	0.004	0.000	0.008	9	33	0	59
	2013	0.001	0.004	0.000	0.010	4	13	0	30
	2014	0.002	0.005	0.000	0.012	4	12	0	28
	2015	0.002	0.005	0.000	0.011	19	38	0	86
	Average	0.003				22			
	Range	0.001–0.011				4–75			
Kenai River mainstem	2010	0.643	0.037	0.581	0.703	4,536	263	4,100	4,963
	2011	0.667	0.040	0.601	0.733	5,135	309	4,624	5,641
	2013	0.766	0.023	0.727	0.804	2,289	69	2,173	2,401
	2014	0.609	0.033	0.555	0.664	1,401	76	1,276	1,527
	2015	0.770	0.032	0.709	0.814	5,988	248	5,519	6,330
	Average	0.691				3,870			
	Range	0.609–0.770				1,401–5,988			
Kasilof River. mainstem	2010	0.326	0.034	0.271	0.383	2,305	239	1,915	2,701
	2011	0.330	0.040	0.265	0.395	2,538	306	2,038	3,042
	2013	0.213	0.022	0.178	0.250	637	66	530	748
	2014	0.387	0.033	0.333	0.441	891	76	766	1,015
	2015	0.201	0.031	0.160	0.260	1,564	239	1,242	2,025
	Average	0.292				1,587			
	Range	0.201–0.387				637–2,538			
Cook Inlet other	2010	0.020	0.014	0.003	0.047	144	100	19	334
	2011	0.002	0.004	0.000	0.011	14	34	0	84
	2013	0.019	0.006	0.010	0.030	57	19	29	89
	2014	0.002	0.004	0.000	0.010	4	9	0	22
	2015	0.027	0.009	0.014	0.042	211	67	112	327
	Average	0.014				86			
	Range	0.002–0.027				4–211			

OBJECTIVES

PRIMARY OBJECTIVES

1) Estimate the proportion of Chinook salmon harvested in the UCI ESSN commercial fishery by reporting group (*Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries, and Cook Inlet other*) for each temporal and geographic stratum for the season such that the estimated proportions are within 13 percentage points of the true values 90% of the time.
2) Estimate the harvest of *Kenai River mainstem* and *Kasilof River mainstem* Chinook salmon in the UCI ESSN commercial fishery for each temporal and geographic stratum such that the estimates are within 30% of the true value 90% of the time.
3) Estimate the age composition of Chinook salmon harvested by the ESSN fishery such that the estimates are within 10 percentage points of the true values 95% of the time.

SECONDARY OBJECTIVES

1) Estimate the harvest of Chinook salmon for the reporting groups *Kenai River tributaries* and *Cook Inlet Other* in the UCI ESSN commercial fishery for each temporal and geographic stratum[1].
2) Sample 30% of the Chinook salmon harvested in the UCI ESSN commercial fishery for tissue, CWTs, scales, sex, and mid eye to tail fork (METF) length.
3) Estimate the sex and length compositions of Chinook salmon harvested in the UCI ESSN commercial fishery overall and for each temporal and geographic stratum.
4) Determine the sex of fish less than 750 METF length by internal examination.

METHODS

STUDY DESIGN

Regular period openings in the ESSN fishery are from 7:00 AM to 7:00 PM on Mondays and Thursdays. The first scheduled regular period in the Kasilof section (statistical areas 244-21, 244-22, and 244-31) for the 2016 season is Monday, June 27. The fishery could be opened as early as June 20 dependent on cumulative sockeye salmon passage in the Kasilof River. The first Kasilof section regular period or EO opening and all subsequent openings prior to the first opening of the Kenai section for the season will be sampled. The first scheduled regular period in the Kenai and East Foreland sections (statistical areas 244-32, 244-41, and 244-42) for the 2016 season is Monday, July 11. The Kenai and East Foreland sections will be sampled less vigorously than other area openings due to MSA results consistently showing that nearly all (>95%) of the harvest is *Kenai River mainstem* fish.

All regular fishing periods and up to 2 additional fishing periods opened by EO per week are budgeted to be sampled. If it is foreseen that there will be more than 2 openings by EO in a given week, which openings to sample will be chosen from recent harvests and insight from

[1] Based on previous MSA results, it is anticipated that Chinook salmon harvest of the reporting groups *Kenai River tributaries* and *Cook Inlet Other* will be low (<150 fish) so no precision criteria are set for estimation of these reporting groups. Sample size is driven by Primary Objectives 1 and 2.

commercial fishery managers based on likely scenarios of future openings. The fishery is scheduled to end August 15, with only regular fishing periods allowed after August 10. The regular period sampling schedule is shown in Appendix A1, but the sampling schedule will be modified inseason based on emergency openings.

During a fishing period, as many Chinook salmon as possible will be sampled, especially within the Kasilof section, while distributing sampling effort to allow for collection of a representative sample of the harvest. Each technician will be assigned an area to sample; however, overlap in sampling areas is likely among technicians, and modifications to assigned areas will probably occur during the season. Inseason analyses of the sampling rate by statistical area will be conducted and modifications will be made to the sampling strategy as necessary to ensure sampling rates are similar by statistical area. In past years, additional effort is needed at times to increase the sampling rate of Chinook salmon harvested from Ninilchik Beach and South K-Beach statistical areas.

Technicians will begin sampling on the southern end of their sampling area after the first round of deliveries to each buying station. Sampling at the southern end first and moving northward will follow the fish deliveries as they occur to maximize the number of samples collected. This sampling strategy should not introduce bias. If the technicians were to start at the northern beaches and move south, they would miss samples and have a lower sampling rate due to the later timing of northern deliveries. It is likely that Chinook salmon will be delivered to over 20 receiving sites spread throughout each statistical area. Technicians will sample at receiving sites during each opening until the fish are transported to processing plants. The day following each fishing period, additional Chinook salmon samples may be collected at fish processors if necessary. Most KRSHA openings will be sampled if opened by EO. If the Kasilof Section is open but restricted in area, such as within 600 ft or within one-half mile of the mean high tide line, all openings will be sampled.

Because the number and location of receiving sites changes each year, prior to the 2016 season, the project biologist will develop a list with contact information and a map showing locations to sample, which will be distributed to each technician. Technicians will be instructed to sample at receiving sites on their way north up the beach. There will be no set schedule for times to sample at each location. Schedules will depend on tides and the times of fishing periods.

Geographic and Temporal Stratification

Proposed temporal and geographic stratification was determined by management criteria and past MSA results. Depending on how the fishery is prosecuted and how many samples are collected, temporal and geographic strata will likely be modified, but for planning purposes 5 strata were chosen (Table 2).

Table 2.–Proposed strata for ASL and MSA in 2016.

Stratum no.	Temporal stratum	Geographic area
1	25 June–10 July	Kasilof Section
2	11–31 July	Kasilof Section
3	Entire 2016 season	Kenai and East Forelands Sections
4	1–15 August	Kasilof Section
5	Entire 2016 season	KRSHA

Note: KRSHA is the Kasilof River special harvest area.

In 2016, Kasilof sections openings that are restricted in area, such as within 600 ft or one-half mile of the mean high tide line, will be considered individual strata if enough representative samples are collected to meet sample size requirements. All Kasilof section openings restricted in area will be rigorously sampled because MSA results for these openings would be new and very informative to managers in developing management strategies. Because past MSA results have shown that nearly all (>95%) of the harvest in the Kenai and East Foreland sections is composed of *Kenai River mainstem* fish, we may not analyze tissue samples collected in that stratum; the decision to analyze those samples will be dependent on how the fishery is prosecuted, the number of samples collected in other strata, and any budgetary constraints. However, a minimum of 2 fishing periods per week will be sampled in the Kenai and East Foreland sections and the ASL composition of those samples will be analyzed.

Sampling results and chosen temporal and geographic strata from 2015 were used to determine expected sampling and selection rates for 2016. Samples must be collected to represent the harvest, which is seldom possible, so subsampling of collections is required postseason to ensure the analyses accurately represent the harvest. In 2015, technicians were able to collect 2,241 tissue samples out of a harvest of 7,781 for a 29% sampling rate. After subsampling representatively when possible, 623 samples (8% of the harvest) were used in MSA. The goal for 2016 will be to sample at least 30% of the harvest and to select samples from 15% of the total harvest for MSA after subsampling representatively by date and statistical area. However, sampling goals will not drive the study design because the number of samples collected and the sampling rate is largely dependent on harvest. Strata used in the MSA will depend on the number of representative samples collected within each possible stratum. Length will be incorporated into the subsample selection criteria such that the length distribution of subsampled fish will be approximately equivalent to the length distribution of all fish sampled within each grouping. A grouping will usually be 1–2 fishing periods within each stratum.

Proof tests conducted by the GCL demonstrated that with a fishery mixture of 100 samples, we can estimate stock composition for the 4 reporting groups (*Kenai River tributaries, Kenai River mainstem, Kasilof River mainstem,* and *Cook Inlet other*) within 0.13 of the true values 90% of the time (Eskelin and Barclay 2014). These tests followed the same protocol as reported in Eskelin et al. (2013) for baseline evaluation tests; however, instead of using test mixtures with 100% of 1 reporting group, test mixtures were created with proportions from each reporting group that represented a realistic scenario for what might be expected in these fisheries. Taking into account the reporting group proportions from the analysis of the 2010, 2011, and 2013 ESSN harvests (Eskelin et al. 2013), tests were conducted under a realistic scenario for reporting group proportions in ESSN fishery mixtures: 0.02 for *Kenai River tributaries*, 0.58 for *Kenai River mainstem*, 0.38 for *Kasilof River mainstem*, and 0.02 for *Cook Inlet other*. With this precision of stock composition estimates and an anticipated sample size of 100 fish, we will be able to estimate the harvest of *Kenai River mainstem* and *Kasilof River mainstem* Chinook salmon in the UCI ESSN commercial fishery in each stratum within 30% of the true values 90% of the time.

All samples that are used in the MSA will be analyzed for ASL composition and reported by stratum and for the entire season. The objective criterion (± 0.10 with 95% confidence level) for estimating the age composition of Chinook salmon harvested in the ESSN fishery should be achieved with approximately 170 scale samples. To arrive at this sample size, we assumed a worst-case scenario of 25% scale regeneration rate with multinomial proportions of equality

among ages (Thompson 1987). Because we plan to collect and analyze substantially more samples in 2016 than previously, we are likely to achieve much higher precision for the age composition estimates than the objective states. New in 2016, technicians will verify sex of fish less than 750 mm METF by internal examination, granted permission is given from the processor. The primary goal will be to determine the minimum length of females in the sample.

DATA COLLECTION

Tissue Sampling for MSA

All fish sampled for ASL will also be sampled for tissue suitable for genetic analysis. A 1⅓-cm (half-inch) piece of the axillary process will be removed from each fish and placed on a Whatman[2] paper card in its own grid space and then stapled in place. Whatman cards with tissue samples will be placed in an airtight case with desiccant beads to preserve the tissue for DNA extraction. Sampling instructions are found in Appendix B1. Each Whatman card will have a unique barcode and a numbered grid. Card barcodes and grid position numbers will be recorded on data sheets for each sample (Appendix C1). All Whatman cards will be stored at the Soldotna office until the end of the season then sent to the GCL for analysis.

Age, Sex, and Length Sampling

Three scales will be removed from the preferred area of each fish and placed on an adhesive-coated card (Welander 1940; Clutter and Whitesel 1956). Acetate impressions will made of the scales on the card using a press under 25,000 pounds per square inch and the scale growth patterns viewed with a 40× power microfiche reader to determine freshwater and marine residence times. Sex will generally be identified from external morphometric characteristics (i.e., protruding ovipositor on females or a developing kype on males). METF length will be measured to the nearest half-centimeter. Fish less than 750 mm METF will be examined internally for positive sex identification by cutting a small slit in the anal opening using a plastic gut hook, if permission is granted by the processor or receiving site.

Chinook salmon will be sampled for ASL composition without regard to size, sex, length, or location. All ASL composition data and positive sex identification of smaller fish will be recorded on data sheets (Appendix C1).

CWT Sampling

All sampled Chinook salmon will be examined for an adipose finclip and if one is found, the technician will remove the head. A cinch strap will be attached to the head, which will be returned to the office for storage in a freezer. All data, including the number of Chinook salmon examined and the number observed missing the adipose fin, will be recorded on a tag recovery form (Appendix C2). The cinch strap number will also be recorded alongside ASL data (Appendix B1) to enable cross-referencing between datasets. Collected data will be returned to the Project Leader (Anthony Eskelin). CWT forms and heads of all adipose finclipped fish will be shipped at the end of the season to the ADF&G Mark, Tag, and Age Laboratory for CWT recovery, determination of stock of origin, and for archiving data.

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

Laboratory Analysis

Assaying Genotypes

DNA extraction and genotyping will generally follow the methods described in detail in Barclay and Habicht (2015). Briefly, genomic DNA will be extracted from tissue samples using a DNeasy 96 Tissue Kit by QIAGEN (Valencia, CA). Fluidigm 192.24 Dynamic Arrays (http://www.fluidigm.com) will be used to screen 40 SNP markers; this differs from the methods of Barclay et al. (2012) where 96.96 Dynamic Arrays were used. The Dynamic Arrays will be read on a Fluidigm EP1 System or BioMark System after amplification and scored using Fluidigm SNP Genotyping Analysis software. Assays that fail to amplify on the Fluidigm system will be reanalyzed on the Applied Biosystems platform. The plates will be scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software version 2.2.

Genotypes produced on both platforms will be imported and archived in the Gene Conservation Laboratory (GCL) 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 scored.

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 re-extracted and 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.

DATA REDUCTION

Technicians will return their genetic cards, scale cards, and field data sheets to the Soldotna office daily and will be responsible for ensuring the recorded data are legible and accurate. The project biologist will ensure all data are returned, legible, and entered correctly. All data will be keypunched directly into a master electronic data file. Age data will be entered upon scale reading. CWT forms will be edited to ensure accuracy and mailed to Juneau ADF&G for data entry. A final edited copy of all data files along with a data map will be sent to the ADF&G Research and Technical Services (RTS) for archiving.

DATA ANALYSIS

Baseline and Reporting Groups

The current UCI Chinook salmon genetic baseline used for MSA applications is an update of the baseline reported in Barclay et al. (2012) and includes 62 additional collections and 25 new populations (Barclay and Habicht 2015; Table 3). The updated baseline includes the same set of SNP markers except that locus *Ots_FGF6B* was excluded because of its association with locus *Ots_FGF6A*.

Table 3.–Populations of Chinook salmon in the Upper Cook Inlet genetic baseline, including the sampling location, collection years, number of individuals sampled from each population (*n*), and the reporting groups used for mixed stock analysis of ESSN harvest.

Map no.	Reporting group	Location	Added after baseline[a]	Collection year(s)	*n*
1	*Cook Inlet other*	Straight Creek		2010	95
2		Chuitna River		2008, 2009	134
3		Coal Creek		2009, 2010, 2011	118
4		Theodore River	X	2010, 2011, 2012	190
5		Lewis River	X	2011, 2012	87
6		Red Creek	X	2012, 2013	111
7		Hayes River	X	2012, 2013	50
8		Canyon Creek	X	2012, 2013	91
9		Talachulitna River		1995, 2008, 2010	178
10		Sunflower Creek		2009, 2011	123
11		Peters Creek	X	2009, 2010, 2011, 2012	107
12		Portage Creek	X	2009, 2010, 2011, 2013	162
13		Indian River	X	2013	79
14		Middle Fork Chulitna R.		2009, 2010	169
15		East Fork Chulitna R.	X	2009, 2010, 2011, 2013	77
16		Byers Creek	X	2013	55
17		Spink Creek	X	2013	56
18		Troublesome Creek	X	2013	71
19		Bunco Creek	X	2013	98
20		Upper Talkeetna no name creek	X	2013	69
21		Prairie Creek		1995, 2008	161
22		East Fork Iron Creek	X	2013	57
23		Disappointment Creek	X	2013	64
24		Chunilna Creek		2009, 2012	123
25		Montana Creek		2008, 2009, 2010	213
26		Little Willow Creek	X	2013	54
27		Willow Creek		2005, 2009	170
28		Deshka River		1995, 2005, 2012	303
29		Sucker Creek	X	2011, 2012	143
30		Little Susitna River		2009, 2010	228
31		Moose Creek - Matanuska R.		1995, 2008, 2009, 2012	149
32		Eagle River	X	2009, 2011, 2012	77
33		Ship Creek		2009	261
34		Campbell Creek	X	2010	110
35		Carmen River	X	2011, 2012	50
36		Resurrection Creek	X	2010, 2011, 2012	98
37		Chickaloon River		2008, 2010, 2011	128

-continued-

Table 3.–Page 2 of 2.

Map no.	Reporting group	Location	Added after baseline[a]	Collection year(s)	*n*
38	*Kenai R. tributaries*	Grant Creek	X	2011, 2012	55
39		Quartz Creek		2006, 2007, 2008, 2009, 2010, 2011	131
40		Crescent Creek		2006	164
41		Russian River		2005, 2006, 2007, 2008	214
42		Benjamin Creek		2005, 2006	204
43		Killey River		2005, 2006	255
44		Funny River		2005, 2006	219
45	*Kenai R. mainstem*	Juneau Creek		2005, 2006, 2007	140
46		Upper Kenai R. mainstem		2009	191
47		Middle Kenai R. mainstem		2003, 2004, 2006	299
48		Lower Kenai R. mainstem	X	2010, 2011	118
49	*Kasilof R. mainstem*	Kasilof River mainstem		2005	321
50	*Cook Inlet other*	Crooked Creek		2005, 2011	306
51		Ninilchik River weir		2006, 2010	209
52		Deep Creek		2009, 2010	196
53		Stariski Creek	X	2011, 2012	104
54		Anchor River weir		2006, 2010	249

Note: Map numbers correspond to sampling sites in Figure 3.

[a] "X" indicates populations that have been added since the Barclay et al. (2012) baseline.

Reporting groups are defined based on 1 or more of the following criteria: 1) the genetic similarity among populations, 2) the expectation that proportional harvest would be greater than 5%, or 3) the applicability to answer fishery management questions. Based on these criteria, reporting groups chosen to apportion the harvest for this study are: "*Kenai River mainstem*," "*Kenai River tributaries*," "*Kasilof River mainstem*," and "*Cook Inlet other*." The *Cook Inlet other* reporting group represents all remaining Cook Inlet Chinook salmon baseline populations not included in the 3 other reporting groups (Table 3 and Figure 3)

To minimize misallocation between MSA reporting groups, the Slikok Creek (a Kenai River tributary) population was removed from the baseline because it is very small and is genetically similar to the Crooked Creek (a Kasilof River tributary) population (Barclay and Habicht 2015). In addition, Juneau Creek, a Kenai River tributary, was grouped with the *Kenai River mainstem* reporting group due to genetic similarity.

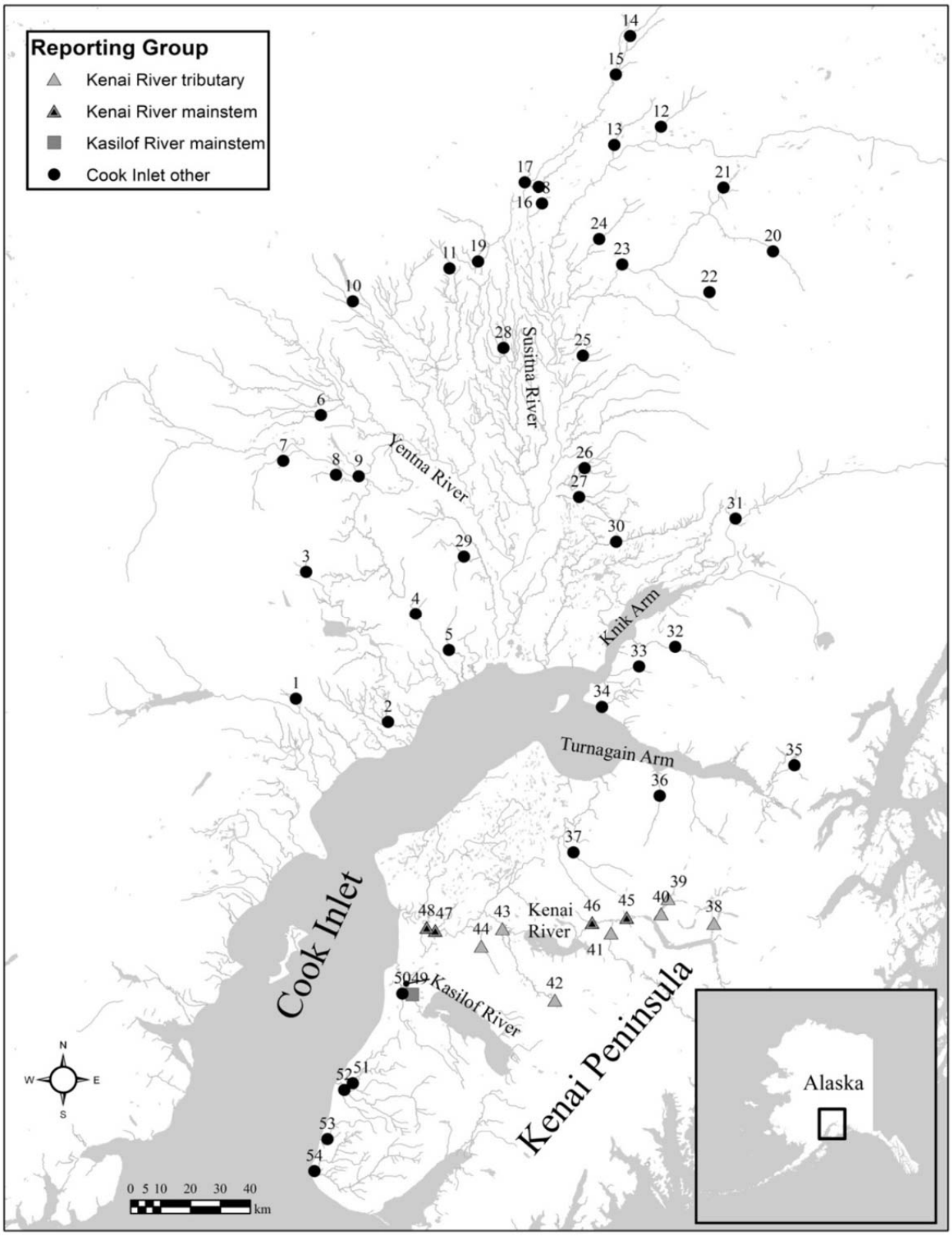

Figure 3.–Sampling locations for Chinook salmon populations included in the genetic baseline.

Note: Numbers correspond to map numbers on Table 3.

Mixed Stock Analysis

The stock composition of the commercial ESSN fishery harvest for each stratum will be estimated using the software package BAYES (Pella and Masuda 2001). BAYES employs a Bayesian algorithm to estimate the most probable contribution of the baseline populations to explain the combination of genotypes in the mixture sample. The final analysis will consist of the results from 5 separate Monte Carlo Markov chains where each chain will begin with different initial values. A random number generator will be used to create the initial values which will sum to 1 over all reporting groups. The Dirichlet prior distribution for the composition parameters in BAYES will be based upon the best available information for each mixture analysis. We believe the best available information for the prior to be the results of MSA of similar mixtures. For the 2016 ESSN mixtures, the best available information will be the stock proportions estimates from the analysis of the 2015 ESSN Chinook salmon samples. The sum of the Dirichlet prior parameters will equal 1, thus minimizing the overall influence of the prior distribution. The chains will be run until convergence is reached (shrink factor less than 1.2) for the 5 chains (Pella and Masuda 2001). The first half of each chain will be discarded in order to remove the influence of the initial values; the rest will be used to estimate the posterior distribution of stock composition proportions. The point estimates of stock composition and the variance of these estimates will be calculated from the mean and standard deviation of the posterior distributions.

Harvest of Chinook Salmon by Reporting Group

The number ($\hat{H}^g$) of Chinook salmon from reporting group *g* harvested in the commercial ESSN fishery between the first opening as early as late June and the last opening on or before August 15 will be estimated as follows:

$$\hat{H}^g = \sum_{i=1}^{T} \sum_{j=1}^{S} H_{i,j}\, \hat{p}_{i,j}^{g} \tag{1}$$

where

$\hat{p}_{i,j}^{g}$ = estimated proportion of ESSN harvest in time stratum *i* and geographic stratum *j* comprising Chinook salmon from reporting group *g* (*Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries,* or *Cook Inlet other*) and based on Bayesian mixed stock analysis as described in the previous section,

$H_{i,j}$ = ESSN Chinook salmon harvest in time stratum *i* and area stratum *j* obtained from fish ticket data,

T = number of time strata (prior to 8 July, 8–31 July, and after 31 July), and

S = number of geographic strata (Kenai–East Foreland and Kasilof sections)

The variance of $\hat{H}^g$ will be estimated as follows:

$$\text{var}(\hat{H}^g) = \sum_{i} \sum_{j} (H_{i,j})^2 \,\text{var}(\hat{p}_{i,j}^{g}) \tag{2}$$

where $\text{var}(\hat{p}^{g}_{i,j})$ will be available from the Bayesian mixed stock analysis (Pella and Masuda 2001).

Age and Sex Composition of Chinook Salmon in the ESSN Harvest

The age (or sex) proportions of Chinook salmon harvested in the commercial ESSN fishery by sampling stratum will be estimated as follows:

$$\hat{p}^{z}_{i,j} = \frac{n^{z}_{i,j}}{n_{i,j}} \tag{3}$$

where

$\hat{p}^{z}_{i,j}$ = the estimated proportion of salmon of age (or sex) category *z* from sampling stratum (*i*, *j*),

$n^{z}_{i,j}$ = the number of fish sampled from sampling stratum (*i*, *j*) that were classified as age (or sex) category *z*,

$n_{i,j}$ = the number of Chinook salmon sampled for age (or sex) determination from sampling stratum (*i*, *j*).

The variance of $\hat{p}^{z}_{i,j}$ will be estimated by

$$\text{var}\left[\hat{p}^{z}_{i,j}\right] = \left(1 - \frac{n_{i,j}}{H_{i,j}}\right)\frac{\hat{p}^{z}_{i,j}\left(1-\hat{p}^{z}_{i,j}\right)}{n_{i,j}-1} \tag{4}$$

where $H_{i,j}$ is the number of Chinook salmon harvested in a sampling stratum (*i*, *j*).

The estimates of harvest by age (or sex) categories in each sampling stratum will be calculated by

$$\hat{H}^{z}_{i,j} = H_{i,j}\hat{p}^{z}_{i,j} \tag{5}$$

with variance estimated as

$$\text{var}\left[\hat{H}^{z}_{i,j}\right] = H^{2}_{i,j} * \text{var}\left[\hat{p}^{z}_{i,j}\right] \tag{6}$$

The total harvest by age (or sex) category and its variance will then be estimated by summation:

$$\hat{H}^{z} = \sum_{i=1}^{T}\sum_{j=1}^{S}\hat{H}^{z}_{i.j} \tag{7}$$

and

$$\text{var}\left[\hat{H}^{z}\right] = \sum_{i=1}^{T}\sum_{j=1}^{S}\text{var}\left[\hat{H}^{z}_{i,j}\right] \tag{8}$$

where *T* and *S* are the number of time and geographic strata, respectively.

Finally, the total proportion of the ESSN harvest by age (or sex) category and its variance will be estimated by the following:

$$\hat{p}^{z} = \frac{\hat{H}^{z}}{H} \tag{9}$$

and

$$\mathrm{var}\left[\hat{p}^{z}\right] = \frac{\mathrm{var}\left[\hat{H}^{z}\right]}{H^{2}}. \tag{10}$$

CWT Recoveries

With the low numbers of CWT recoveries expected, no direct estimates of CWT recoveries by stock will be made, but the data will be archived with Mark, Tag, and Age Laboratory in Juneau.

SCHEDULE AND DELIVERABLES

Dates	Activity
Mid to late June 2016	Hiring and preseason training (Eskelin)
Late June to mid-August	ESSN Chinook salmon harvest sampling (3 FWT II)
September 2016	Data edited, tissue collection transferred to GCL (Eskelin)
September 2016	Tissue, age, sex, and length subsamples selected and scales aged (Eskelin)
October 2016	Draft ASL composition estimates completed (Eskelin and Huang)
December 2016 [a]	Tissues analyzed by GCL (Barclay)
January 2017 [a]	Draft MSA and harvest estimates complete by temporal and geographic strata, and reporting group (Barclay, Eskelin, and Huang)
February 2017 [a]	Memo summarizing draft results disseminated to regional staff (Eskelin and Barclay
	Final report completed (Eskelin and Barclay)

[a] Due to multiple projects associated with upcoming Alaska Board of Fisheries meetings, MSA analyses for ESSN Chinook salmon reporting group compositional estimates may not be provided as early as detailed in this schedule but will be completed and disseminated as soon as possible thereafter.

RESPONSIBILITIES

Principle Investigator
Tony Eskelin, Project Leader, Fishery Biologist II

Duties: The project leader is responsible for writing the operational plan, hiring and training personnel, and supervising data collection. The project biologist will be responsible for collating data and transferring tissue samples to Anchorage for MSA and associated data, and any CWT heads and data forms to the Mark, Tag and Age Lab in Juneau. This position will be responsible for all scale aging. This position will also ensure all data are in proper format and archived with RTS at the completion of the field season and will be primary author on any reporting.

Coprincipal Investigator
Andy Barclay, Fishery Biologist III

Duties: This position is the Gene Conservation Lab representative and is responsible for the analysis of tissue samples for MSA and providing estimates to the project biologist and biometrician. This position will be co-author on FDS reports and memos.

Consulting Biometrician
Jiaqi Huang, Biometrician III

Duties: This position will provide guidance on sampling design and data analysis, prepare estimates of harvest of Chinook salmon by reporting group, and assist with preparation of the operational plan and any reports.

Sampling Crew
Madeline Fox, Fish and Wildlife Technician II, 20 June–16 August
Fish and Wildlife Technician II (non-perm), 20 June–16 August
Fish and Wildlife Technician II (non-perm), 20 June–16 August

Duties: These positions are responsible for operating state of Alaska vehicles, adhering to the sampling schedule, sampling harvested Chinook salmon for ASL and tissue, recording data accurately, and entering data into a computerized database in a timely manner.

BUDGET SUMMARY

Budget for FY16 and FY17

Line item	Category	FY16 Budget ($K)	FY17 Budget ($K)
100	Personal Services	8.5	25.3
200	Travel	–	–
300	Contractual	3.0	26.4
400	Commodities	1.0	2.0
500	Equipment	–	–
Total		8.7	53.7

Funded personnel

PCN	Name	Level	Funded man months (2016 field season)
NP	Vacant	FWT II	1.8
NP	Vacant	FWT II	1.8
11-4062	Fox, Madeline	FWT II	1.8
Total			5.4

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APPENDIX A: PRELIMINARY 2016 ESSN CHINOOK SALMON SAMPLING SCHEDULE

Appendix A1.–Preliminary 2016 ESSN Chinook salmon sampling schedule.

Sunday	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
26-Jun	27-Jun	28-Jun	29-Jun	30-Jun	1-Jul	2-Jul
	Regular Period Kasilof section			Regular Period Kasilof section		
3-Jul	4-Jul	5-Jul	6-Jul	7-Jul	8-Jul	9-Jul
	Regular Period Kasilof section			Regular Period Kasilof section		
10-Jul	11-Jul	12-Jul	13-Jul	14-Jul	15-Jul	16-Jul
	Regular Period All section			Regular Period All Sections		
17-Jul	18-Jul	19-Jul	20-Jul	21-Jul	22-Jul	23-Jul
	Regular Period All sections			Regular Period All Sections		
24-Jul	25-Jul	26-Jul	27-Jul	28-Jul	29-Jul	30-Jul
	Regular Period All sections			Regular Period All Sections		
31-Jul	1-Aug	2-Aug	3-Aug	4-Aug	5-Aug	6-Aug
	Regular Period All sections			Regular Period All Sections		
7-Aug	8-Aug	9-Aug	10-Aug	11-Aug	12-Aug	13-Aug
	Regular Period All sections			Regular Period All Sections		
14-Aug	15-Aug					
	Regular Period All sections					

Note: Schedule is subject to change during the season as fishery openings occur.

APPENDIX B: INSTRUCTIONS FOR TISSUE SAMPLING

Appendix B1.–Instructions for tissue sampling.

Adult Finfish Tissue Sampling for DNA Analysis

ADF&G Gene Conservation Lab, Anchorage

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 and salt dries and preserves tissues for later DNA extraction. Quality DNA preservation requires **Fast drying** (under 5 hours at 65°F); **Dry storage** (with 2 desiccant packs) in weathertight file box.

II. Sampling Method

III. Sampling Instructions

- **Every morning**: before sampling, rotate 3 desiccant packs (2-Pelican micro, 1-file box) into dehydrator @ **160° F** for 12 hrs. (NOT SAMPLES)!
- **Prior to sampling**: Set up work space, fill out required collection information (upper left hand corner only) and place Whatman genetics card (10WGC) flat for easy access; ready to sample.
- **Sampling**:
  - Wipe fin prior to sampling.
  - Briefly wipe or rinse clippers with water between samples to reduce cross contaminating.
  - Using clippers, cut one axillary fin per fish.
  - 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.**
  - Staple each sample to 10WGC (see photo).
  - Sampling complete, dust tissues with **1 tsp. non-iodized salt** to promote the preservation process.
  - Staple landscape cloth "rain fly" to paper edge (2 staples max).
- **Loading Pelican Case**:
  - 1st card: Remove blotter papers and desiccant packs from Pelican case. Place first card in Pelican case with tissues facing up. Next, place blotter paper directly over card and place one desiccant pack on top. Close and secure lid so drying begins.
  - Up to 4 cards can be added per case. Add them so **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 **remain in Pelican overnight** to dry flat.
- **Post-sampling storage**: Every morning, store dried tissue cards in weathertight file box at room temperature. Two desiccant packs are allocated for file box: every morning rotate 3 desiccant packs (2-Pelican, 1-file box) into dehydrator @ **160° F** for 12 hours. (NOT SAMPLES)!
- **Shipping at end of the season**: Pack 10 **dried cards** per plastic photo page, slide in manila envelope, pack inside priority mailing box. Tape box shut and tape return address on box.

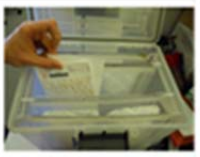
IV. Supplies included in sampling kit:

1. Clippers - for cutting a portion of selected fin.
2. Whatman genetics card – holds 10 fish/card.
3. Pelican case - 1st stage of drying and holding card samples.
4. Non-iodized salt – distribute 1 tsp. non-iodized salt over each card.
5. Silica packs – desiccant removes moisture from samples.
6. Blotter paper – covers full sample card for drying; multiple use.
7. Watertight file box – dry storage prior to return shipment.
8. Plastic photo page – 10 cards per page for return shipment.
9. Manila envelope – pack dried cards in manila envelope.
10. Shipping box – put sealed manila envelope inside box.
11. Stapler – extra protection, secure sample to numbered grid.
12. Staples – only use staples provided, specific for stapler.
13. Dehydrator – oven-dry desiccant packs overnight (share w/CF).
14. Laminated "return address" labels.
15. Sampling instructions.
16. Pencil

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

Return to ADF&G Anchorage lab: ADF&G – Genetics
333 Raspberry Road
Anchorage, Alaska 99518

Lab staff: 907-267-2247
Judy Berger: 907-267-2175
Freight code: _____



APPENDIX C: SAMPLING FORMS

Appendix C1.–2016 ESSN Chinook salmon sampling form.

2016 ESSN Chinook salmon sampling form

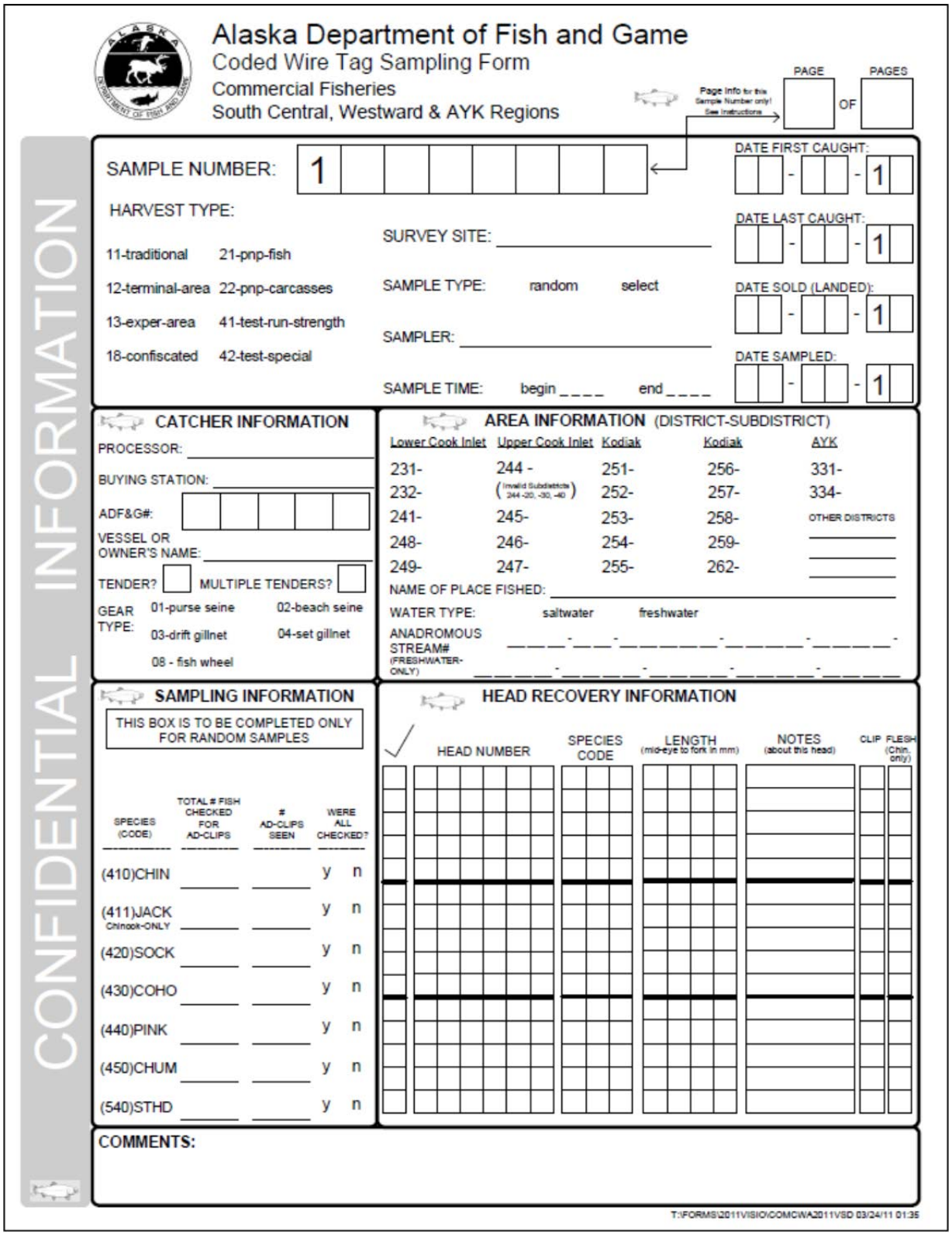
Date:___________ **Sampler(s):** _______________

Start Time: _________ **End Time:**________

Scale		METF		Sex	Genetics		Sample	Stat	
Card#	Scale#	Length	Sex	Verify?	Card#	Box#	Location	Area	CWT #
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								

Sex: 1-male 2-female, verify sex for fish less than 750 mm METF (if granted permission)
Length: mid eye to fork-of-tail in nearest 5 mm.

Appendix C2.–Coded wire tag sampling form.



Alaska Department of Fish and Game

Coded Wire Tag Sampling Form

Commercial Fisheries

South Central, Westward & AYK Regions

PAGE ____ OF PAGES ____

Page info for this Sample Number only! See instructions

CONFIDENTIAL INFORMATION

SAMPLE NUMBER: 1 _____

DATE FIRST CAUGHT: __ - __ - 1_

DATE LAST CAUGHT: __ - __ - 1_

DATE SOLD (LANDED): __ - __ - 1_

DATE SAMPLED: __ - __ - 1_

HARVEST TYPE:

11-traditional 21-pnp-fish

12-terminal-area 22-pnp-carcasses

13-exper-area 41-test-run-strength

18-confiscated 42-test-special

SURVEY SITE: _____

SAMPLE TYPE: random select

SAMPLER: _____

SAMPLE TIME: begin ____ end ____

CATCHER INFORMATION

PROCESSOR: _____

BUYING STATION: _____

ADF&G#: _____

VESSEL OR OWNER'S NAME: _____

TENDER? ☐ MULTIPLE TENDERS? ☐

GEAR TYPE: 01-purse seine 02-beach seine 03-drift gillnet 04-set gillnet 08 - fish wheel

AREA INFORMATION (DISTRICT-SUBDISTRICT)

Lower Cook Inlet	Upper Cook Inlet	Kodiak	Kodiak	AYK
231-	244 -	251-	256-	331-
232-	(Invalid Subdistricts 244 -20, -30, -40)	252-	257-	334-
241-	245-	253-	258-	OTHER DISTRICTS
248-	246-	254-	259-	_____
249-	247-	255-	262-	_____

NAME OF PLACE FISHED: _____

WATER TYPE: saltwater freshwater

ANADROMOUS STREAM# (FRESHWATER-ONLY) ____-___-_____-_____-_____-_____-_____-_____

SAMPLING INFORMATION

THIS BOX IS TO BE COMPLETED ONLY FOR RANDOM SAMPLES

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	_____	_____	y n
(450)CHUM	_____	_____	y n
(540)STHD	_____	_____	y n

HEAD RECOVERY INFORMATION

✓	HEAD NUMBER	SPECIES CODE	LENGTH (mid-eye to fork in mm)	NOTES (about this head)	CLIP	FLESH (Chin only)

COMMENTS:

T:\FORMS\2011VISIO\COMCWA2011VSD 03/24/11 01:35