

**Report to the Alaska State Legislature on Status of
Cook Inlet Coho and Sockeye Salmon Genetic
Projects, 2015**

by

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Alaska Department of Fish and Game

Division of Commercial Fisheries



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

REGIONAL INFORMATION REPORT 5J16-02

**REPORT TO THE ALASKA STATE LEGISLATURE ON STATUS OF
COOK INLET COHO AND SOCKEYE SALMON GENETIC PROJECTS,
2015**

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March 2016

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ABSTRACT

This report summarizes the status of activities associated with legislative increments directed at Cook Inlet coho *Oncorhynchus kisutch* and sockeye *O. nerka* salmon genetic studies conducted by the Division of Commercial Fisheries Gene Conservation Laboratory and Central Region staff. The coho salmon study involved 3 investigative phases. In Phase I, analysis of existing samples indicated that sufficient population genetic structure exists among populations of Cook Inlet coho salmon to warrant construction of a full genetic baseline for genetic stock identification. In Phase II, development of the genetic baseline indicated 8 potential genetic reporting groups for genetic stock identification of Cook Inlet coho salmon fishery samples. The final report for Phase II will be published in the spring of 2016. In Phase III genetic stock identification was used to estimate the stock composition of harvests in test and commercial fisheries of Cook Inlet for the 2013–2015 seasons. Results from these analyses will be used to determine spatial and temporal distribution of coho salmon in the offshore test fishery and commercial harvest and to estimate the total harvest of selected stocks in the commercial salmon fisheries. During this period over 23,000 samples were collected for analysis from the Central District drift gill net fishery, Upper subdistrict set gillnet fishery, General and Eastern subdistrict set gillnet fisheries, and the northern and southern offshore test fisheries. The final report for Phase III is expected to be completed by the end of summer 2016. A fourth study, for sockeye salmon, will analyze the DNA from archived scales to retrospectively estimate historic stock compositions of Cook Inlet harvests. This is the third year of that 5 year project in which the laboratory will reconstruct escapement and total runs of sockeye salmon for Susitna River and the major systems in Upper Cook Inlet.

Key words: Coho salmon *Oncorhynchus kisutch*, sockeye salmon *Oncorhynchus nerka*, genetic stock identification, genetic baselines, mixed stock analysis, Cook Inlet.

INTRODUCTION

The Alaska State Legislature has requested annual status reports to the Finance Committees describing work by the Alaska Department of Fish and Game in Cook Inlet on escapement monitoring, genetics baseline data, mixed stock sampling, smolt outmigration, migratory studies and habitat improvements for Chinook *Oncorhynchus tshawytscha*, coho *O. kisutch*, and sockeye *O. nerka* salmon. This is the third report summarizing the status of activities associated with legislative increments directed at Cook Inlet coho and sockeye salmon genetic studies conducted by the Division of Commercial Fisheries Gene Conservation Laboratory and Central Region staff. The coho salmon study involved 3 investigative phases. Phase I was completed in 2013, and analyzed existing baseline samples to determine if sufficient population genetic structure exists among populations of Cook Inlet coho salmon to warrant construction of a full genetic baseline for genetic stock identification. In Phase II, genetic baseline tissue samples were collected in 2013 and 2014 from streams throughout Cook Inlet, to increase baseline representation. These samples were then genotyped in the laboratory and subsequently analyzed to produce a baseline dataset for use in the genetic stock identification of Cook Inlet coho salmon harvests. In Phase III of the coho salmon genetic study, the harvests of the Cook Inlet test and commercial fisheries of Cook Inlet were sampled in 2013–2015 to estimate stock composition of the harvest using the baseline developed in Phase II. In a separate study, a retrospective analysis is being used to estimate the stock composition of historic sockeye salmon harvests in Upper Cook Inlet. This study is based on analyzing DNA extracted from archived scales sampled from Cook Inlet harvests from 1986 to 2005. This is the third year of the 5 year study and the goal is to reconstruct escapement and total runs of sockeye salmon for Susitna River and the major systems in Upper Cook Inlet.

COOK INLET COHO SALMON GENETIC STOCK IDENTIFICATION PROJECT

Phase I: Feasibility Study

Phase I of the Cook Inlet coho salmon genetic stock identification project was completed in 2013 and the results were described in the previous report (DeCovich et al. 2013). For continuity, a brief description is provided here to help with understanding phases II and III.

The estimation of stock composition using genetic stock identification requires the existence of genetic differences among populations or groups of populations that can be detected by the technology available. Prior to spending state resources to collect samples and develop a baseline for Cook Inlet coho salmon, a skeleton baseline was developed using archived samples and existing genetic markers to ascertain whether sufficient population structure exists to warrant the construction of a full genetic baseline for genetic stock identification.

Tissues from 1,948 coho salmon collected from 22 locations within Cook Inlet (Figure 1) were obtained from tissue archives at the Alaska Department of Fish and Game (ADF&G) and U.S. Fish and Wildlife Service (USFWS) and analyzed for 12 microsatellite and 107 single nucleotide polymorphism (SNP) markers. Both marker types showed similar genetic structuring and levels of variation among collections. Clustering analyses showed that genetic similarities generally follow geographic characteristics (DeCovich et al. 2013). In addition, the magnitude of genetic differences among the coho salmon collections were similar to differences within Cook Inlet for sockeye salmon (Barclay et al. 2010b) and Chinook salmon (Barclay and Habicht 2015). Both sockeye and Chinook salmon currently have successful genetic stock identification programs within Cook Inlet.

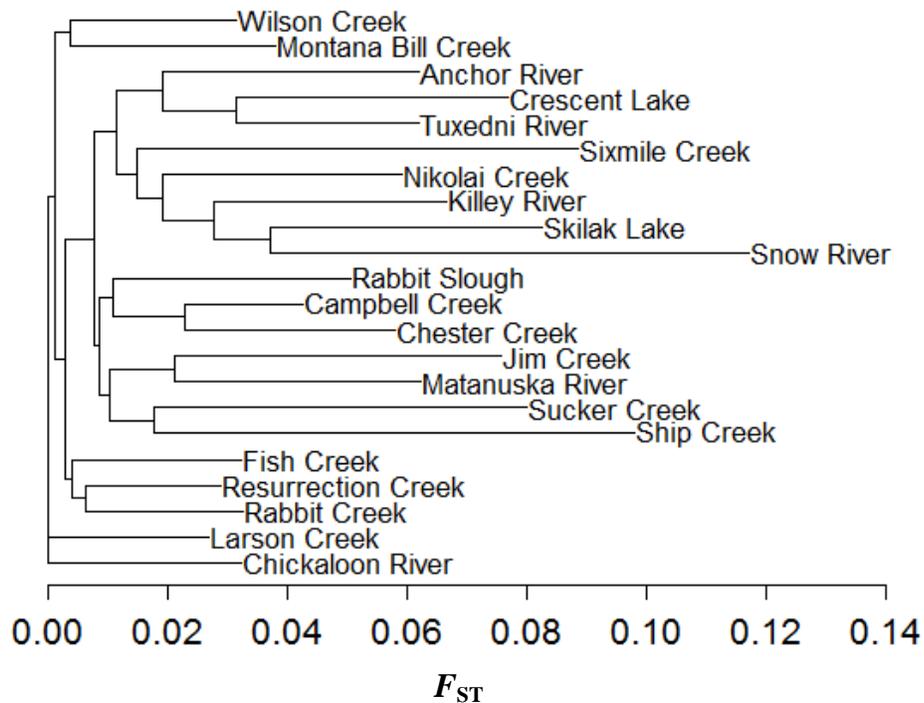


Figure 1.—Neighbor-joining genetic tree of F_{ST} (genetic distance) values among coho salmon populations based on 107 SNPs analyzed for Phase I of the Cook Inlet coho salmon genetic stock identification project.

The pattern of relationships among collections of coho salmon in Cook Inlet coupled with the level of genetic differences among those collections indicated that genetic stock identification would be possible for coho salmon in Cook Inlet (Figure 1). However, the incomplete correlation of genetic distance with geography in this initial study also indicated that the baseline needs to be comprehensive to provide an adequate understanding of population structure and accurate estimates for genetic stock identification. Therefore, we began the process of building a comprehensive baseline (Phase II) to be used for genetic stock identification of fishery samples collected during the 2013–2015 seasons (Phase III).

Phase II: Baseline Development

Phase II of the Cook Inlet coho salmon genetic stock identification project is complete and a final report is being prepared. This phase began after Phase I demonstrated that sufficient structure exists among Cook Inlet coho salmon populations to warrant construction of a genetic baseline. The objectives for this phase were 1) to collect tissues from coho salmon spawning locations in the Matanuska-Susitna drainages and other Cook Inlet drainages, and 2) to develop the genetic baseline necessary for stock composition analysis of fishery samples collected during the 2013–2015 seasons (Phase III). The baseline composed of genotypes from fish representing all spawning aggregates that might contribute to a fishery is complete and the final report will be available by Spring 2016.

Development of the comprehensive baseline necessary for this project in the short timespan available required a coordinated effort of multiple projects to collect samples of coho salmon (Table 1; Figure 2; Appendix A). Tissues were available from 12,942 coho salmon from various sources. Archived collections from the ADF&G Gene Conservation Laboratory and the USFWS provided the initial samples for this project. Since then, this project collected 5,875 samples from 60 locations during 2013–2014 (no samples were collected in 2015). These samples were collected by crews from the Gene Conservation Laboratory and regional offices. An additional 1,098 fish were sampled at 8 weirs in Northern Cook Inlet operated by ADF&G Division of Sport Fish, 121 fish were sampled from 2 radio-tagging projects operated by ADF&G Division of Sport Fish, 499 were collected by the Gene Conservation Laboratory under an Alaska Energy Authority project, 188 were collected by the National Park Service, and 100 fish were collected by Cook Inlet Aquaculture Association (Table 1).

Table 1.–Source of Cook Inlet coho salmon tissue samples currently available for the Cook Inlet coho salmon genetic stock identification project (details in Appendix A).

Source	Number	Percentage of samples
This project - Gene Conservation Laboratory	5,875	45%
Sport Fish weirs	1,098	8%
Sport Fish radio tag	121	1%
Gene Conservation Laboratory archive	2,813	22%
USFWS archive	2,248	17%
Alaska Energy Authority	499	4%
National Park Service	188	1%
Cook Inlet Aquaculture Association	100	1%
Total	12,942	100%

We previously reported the results of a preliminary analysis as part of Phase II in which a subset of collections representing 46 spawning aggregates were genotyped and analyzed using a subset of the most informative genetic markers evaluated during Phase I (Barclay et al. 2014a). The population structure revealed demonstrated potential to apportion fishery mixture samples into at least 5 reporting groups. This analysis also demonstrated that additional baseline collections would be necessary before genetic stock identification could be applied to Cook Inlet fishery samples.

In 2014, additional baseline samples were collected with the following priorities: 1) target spawning aggregates represented by fewer than 50 fish in the current baseline, and 2) target unsampled locations that represent significant spawning aggregates. In addition, the number of genetic markers assayed across this larger baseline was increased to 96. Based on these improvements, statistical analyses were conducted to further assess resolution of reporting groups and performance of genetic stock identification.

The baseline of genetic markers for coho salmon in Cook Inlet now contains representative samples from 89 populations from throughout Cook Inlet and the Kenai Peninsula (Figure 2; Appendix A). Patterns of genetic variation within these populations indicate population structure that is organized by geography, and influenced mainly, but not exclusively, by drainage (Figure 3). The greatest amount of diversity is found among populations spawning in southern portions of the inlet, mainly within the Kenai and Kasilof rivers. Conversely, populations in the northwestern portion of the inlet (*Northwest*, *Susitna* and *Yentna*) are less diverse both within and among drainages. This pattern is very similar to the structure among Chinook salmon populations within this region (Barclay and Habicht 2015).

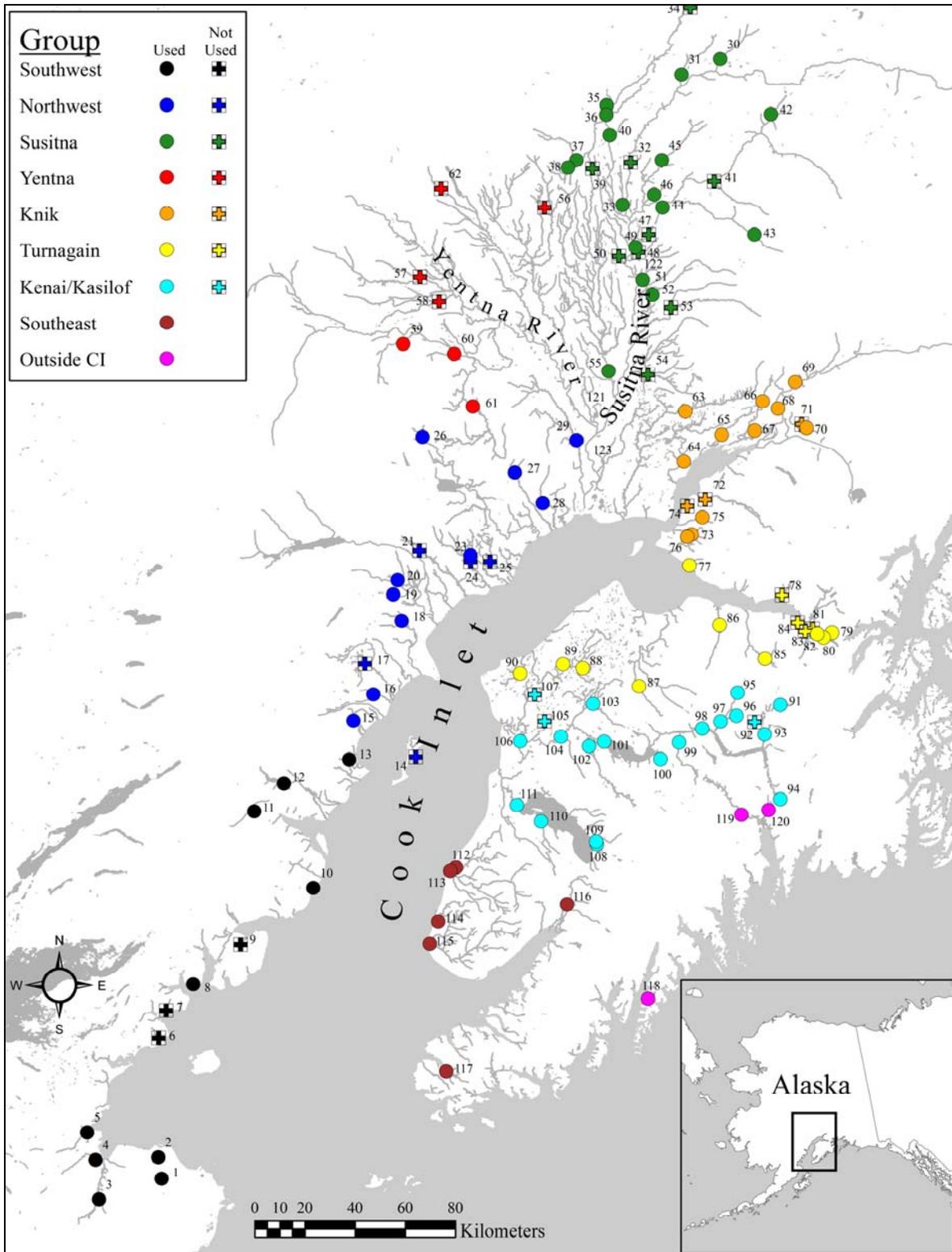


Figure 2.—Map representing 9 groups identified during baseline analysis in Phase II of the Cook Inlet coho salmon genetic stock identification project (details in Appendix A).

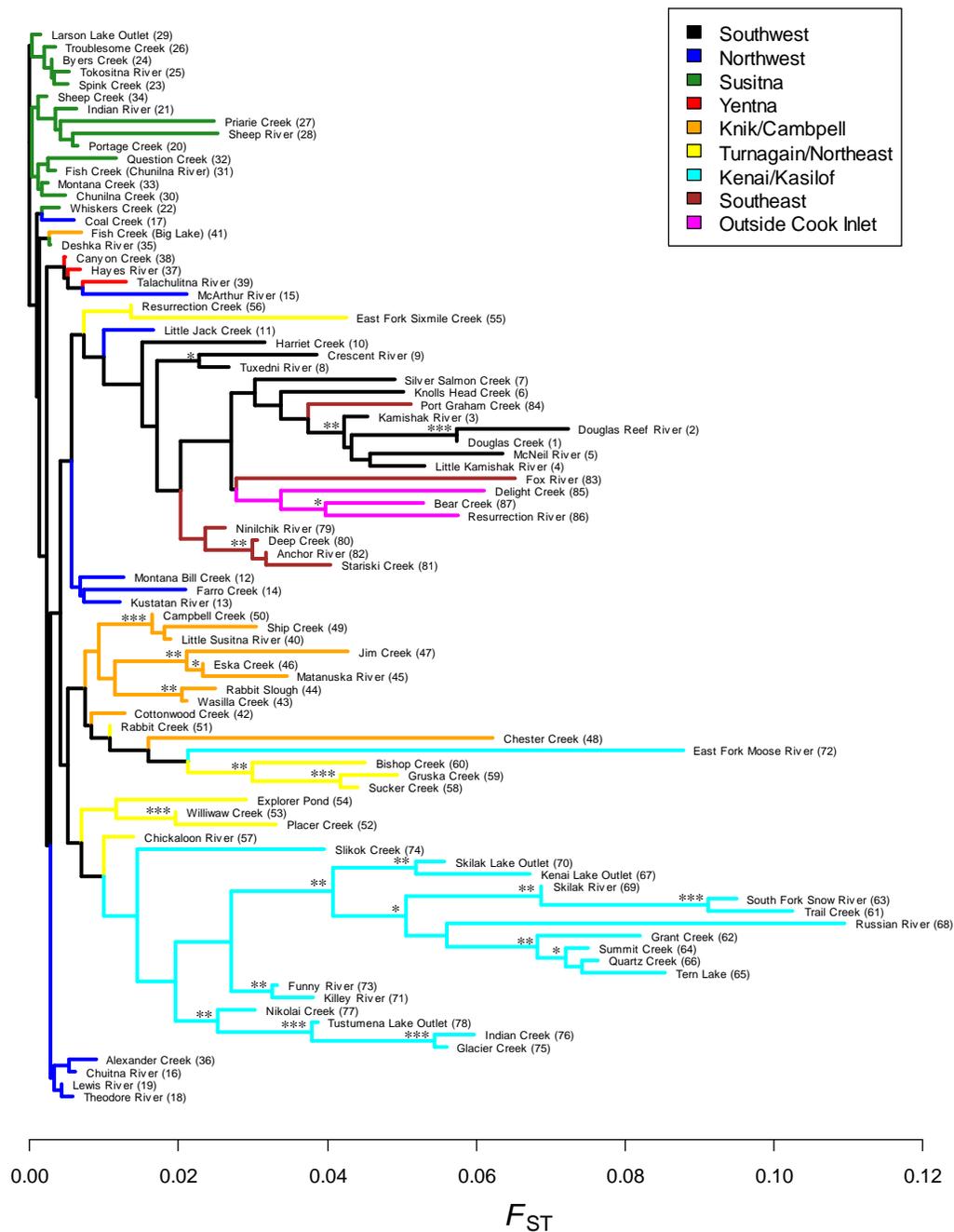


Figure 3.—NJ tree based on F_{ST} between coho salmon populations sampled from spawning areas in drainages of Upper Cook Inlet and the Kenai Peninsula, Alaska (see Appendix A for collection details).

Note: Colors denote groups as in Figure 2. Numbers in parentheses correspond to unique population numbers on Appendix A. Bootstrap consensus nodes occurring in >50% of trees are marked with an asterisk.

For mixed stock analysis applications, statistical analysis demonstrated high levels of identifiability among 6 Cook Inlet reporting groups (Figure 4). This analysis was accomplished by estimating the stock composition of 10 simulated mixtures of fish from a single reporting group. When greater than 90% of the mixture was consistently identified to the correct reporting group, the reporting group was designated as identifiable. The proportions correctly allocated for 2 additional reporting groups (*Northwest* and *Yentna*) were sufficient to indicate that they might be considered identifiable with additional work. To meet standards of accuracy and precision, these 2 groups will be initially combined pending further analysis that might support separating them. Genetic stock identification of the 2013–2015 fishery harvests in Phase III (see below) will provide the stock composition estimates for at least 7 reporting groups unless further analyses support separating *Northwest* and *Yentna*. In that case, 8 reporting groups will be used.

The laboratory and statistical analyses involved in this project were completed on schedule and within the original budget (Table 2). The final report is almost complete and will be published in the ADF&G Fishery Data Series and available to the public by June 30, 2016.

Table 2.–Schedule for completion of the genetic baseline for coho salmon in Cook Inlet.

Date	Activity	Status
Spring 2013	Develop plan to sample spawning coho salmon in Cook Inlet rivers in 2013.	Completed
Summer/Fall 2013	Sample coho salmon in Matanuska/Susitna drainages and Cook Inlet.	Completed
Winter 2013/2014	Extract DNA from available baseline samples.	Completed
Spring 2014	Develop plan to sample spawning coho salmon in Cook Inlet rivers in 2014.	Completed
Summer/Fall 2014	Sample coho salmon in Matanuska/Susitna drainages and Cook Inlet.	Completed
Winter 2014/2015	Extract DNA from available baseline samples and laboratory analysis of all baseline samples.	Completed
Spring/Fall 2015	Statistical analysis of genetic baseline.	Completed
June 2016	Final report of project results	In progress

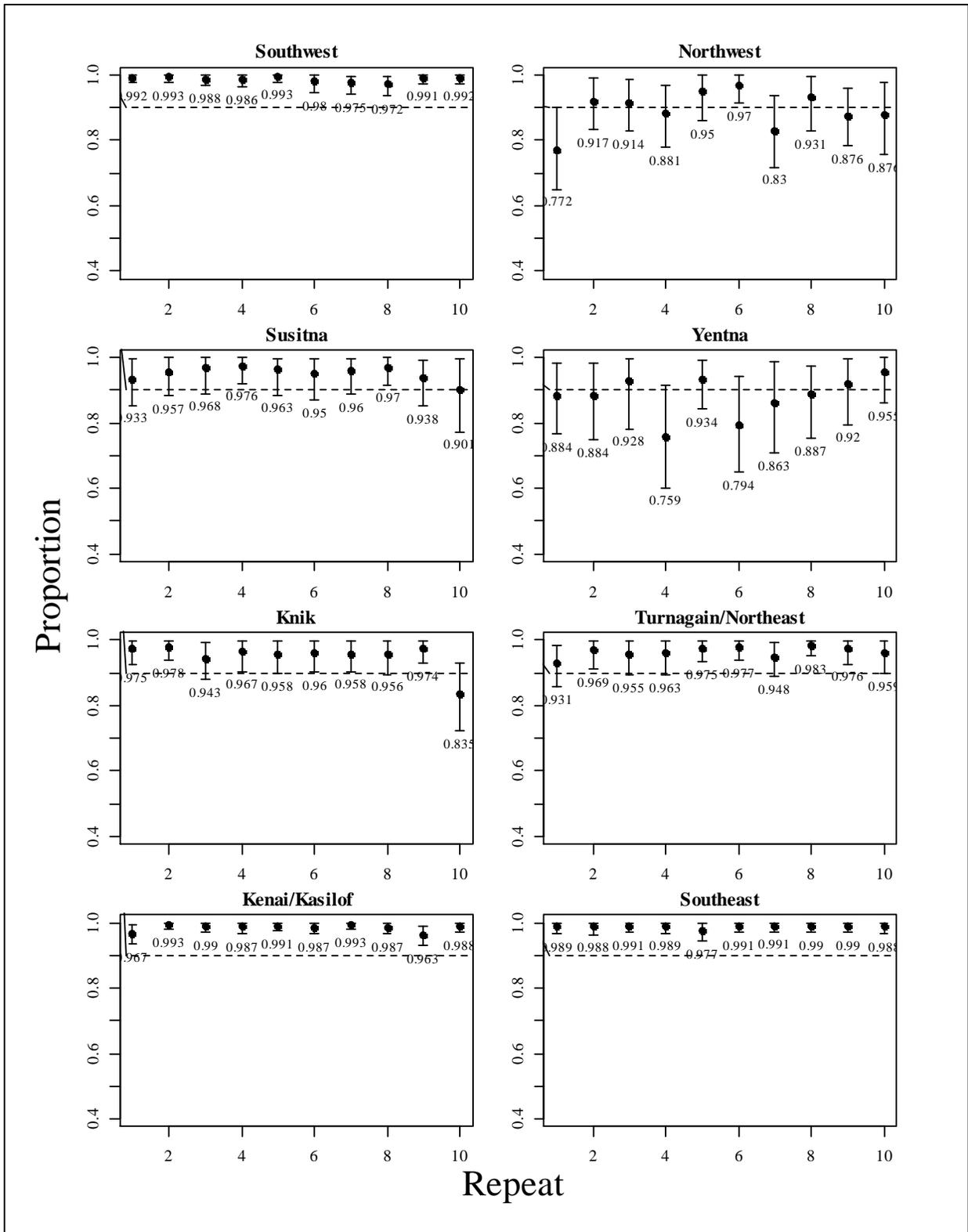


Figure 4.—Results of repeated proof testing for 8 Cook Inlet reporting groups. The points represent the correct allocation from each repeat with 95% credibility intervals for each point. Point estimates for each repeat are included below the lower credibility interval.

Phase III: Fishery Analysis

Phase III of the Cook Inlet coho salmon genetic stock identification project involves genetic stock identification of coho salmon harvested in the test and commercial fisheries of Cook Inlet during the 2013–2015 seasons. This analysis uses the genetic baseline developed and tested in Phase II.

Tissue samples were collected from coho salmon captured in the commercial fishery and offshore test fisheries in Cook Inlet from 2013 to 2015. A total of 23,386 fish were sampled over the 3 years of this project. The total number of samples available from the harvest by fishery is 1) Upper Subdistrict set gillnet fishery, 681, 2) Central District drift gillnet fishery, 8,857 fish, 3) General Subdistrict set gillnet fishery, 7,919 fish, and 4) Eastern Subdistrict set gillnet fishery, 3,143 fish. The offshore test fishery catch samples were successfully collected in 2013 and 2014 year from the Northern (883 fish) and each year in the Southern (1,903 fish) transects. The northern offshore test fishery was not operated in 2015; therefore, no samples were collected from that transect and, instead, samples were collected from the Upper Subdistrict set gillnet (East side set gillnet) fishery. Detailed sampling results by year from each fishery are available in Table 3. The locations of fishing districts in Cook Inlet are shown in Figure 5.

Table 3.–Number of coho salmon collected by fishery in 2013–2015 and the number selected to be genotyped for the Cook Inlet coho salmon genetic stock identification project.

Fishery	Number collected			Number selected to genotype		
	2013	2014	2015	2013	2014	2015
Commercial harvest						
Upper Subdistrict set gillnet	0	0	681	0	0	400
Central District drift gillnet	3,377	2,572	2,908	2,000	1,975	2,360
General Subdistrict set gillnet	3,998	1,959	1,962	1,095	1,103	1,287
Eastern Subdistrict set gillnet	1,251	804	1,088	505	434	564
Total commercial harvest	8,626	5,335	6,639	3,600	3,512	4,611
Offshore test fishery catches						
Northern	495	388	0	492	388	0
Southern	745	756	402	745	756	402
Total offshore test fishery catches	1,240	1,144	402	1,235	1,144	402
Grand total	9,866	6,479	7,041	4,835	4,656	5,013

Fish sampled from these harvests have been subsampled in proportion to harvest numbers so final numbers of fish analyzed are representative of the harvest in time/area strata for each fishery. All of the fish collected in the offshore test fisheries in 2013 and 2014 were selected for genotyping (Table 3). The fishery samples from each year were selected and extracted during the following spring for 2013 and 2014. In the winter of 2015, DNA extraction began on the fish sampled in 2015 (Table 4). After the baseline was completed (Phase II), the set of genetic markers to be used for genetic stock identification could be selected, and laboratory analysis of the fishery samples began in Summer/Fall of 2015 for the 2013 and 2014 samples. Samples from the 2015 fishery will be completed by winter of 2015/2016 and the final report will be available in spring of 2016.

Table 4.–Schedule for completion of genetic stock identification of the coho salmon harvest in Cook Inlet, 2013–2015.

Date	Activity	Status
Summer 2013	Collect samples from commercial and offshore test fisheries	Completed
Summer 2014	Collect samples from commercial and offshore test fisheries	Completed
	Extract DNA from 2013 commercial and offshore test fishery samples	Completed
Winter 2014/2015	Extract DNA from 2014 commercial and offshore test fish samples	Completed
	Genetic baseline completed (Phase II)	Completed
Summer/Fall 2015	Genotype 2013 and 2014 commercial and offshore test fish samples	Completed
Fall 2015	Extract DNA and genotype 2015 commercial and offshore test fishery samples	Completed
Winter 2015/2016	Genetic stock identification of fishery harvests	On schedule
Spring 2016	Final genetic stock identification report out for publication	On schedule

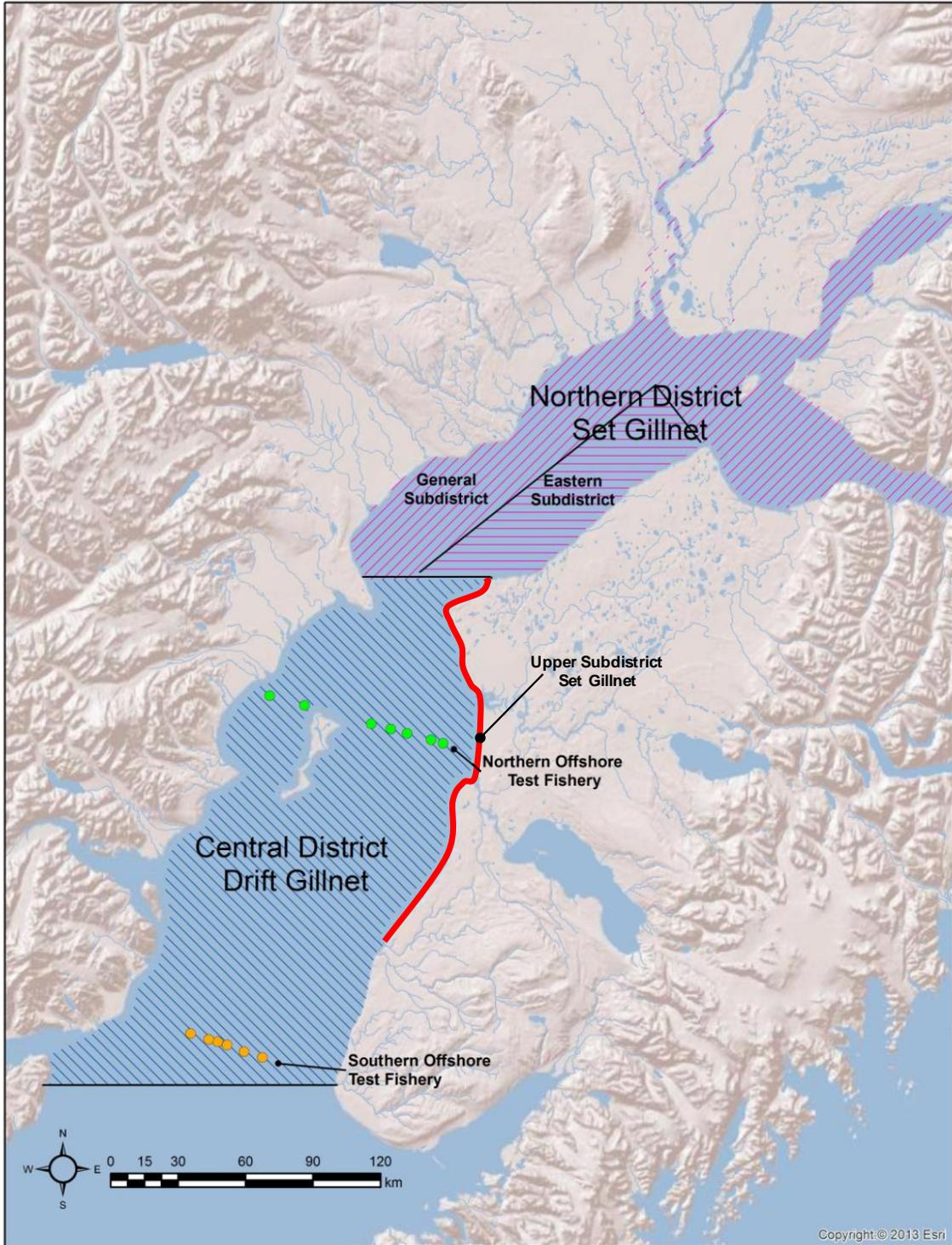


Figure 5.—Map of Cook Inlet showing locations of commercial and test fisheries sampled for coho salmon in for the Cook Inlet coho salmon genetic stock identification project.

COOK INLET SOCKEYE SALMON RETROSPECTIVE ANALYSIS, 2014

This is the third year of a 5 year retrospective analysis by ADF&G that uses recently developed genetic technologies to extract DNA from archived scales sampled from sockeye salmon captured in selected Upper Cook Inlet commercial fisheries from 1986 to 2005. The DNA will then be used to estimate stock composition of historic harvests with genetic stock identification in the same way that has been used annually with contemporary harvests since 2006 (Barclay et al. 2010a, 2010b, 2013, and 2014b). These stock composition estimate will use the Barclay and Habicht (2012) baseline. This information can be used to achieve 2 objectives:

1. Reconstruct Susitna River escapement. Sonar estimates of sockeye salmon escapement in the Yentna River go back to 1981 but appear to be a poor indicator of escapement (Fair et al. 2009). Sporadic weir counts also exist for select systems within the Susitna drainage beginning in the 1970s, 3 of which now have sustainable escapement goals. However, it is only since 2006 that ADF&G has estimates of total drainagewide escapement. Susitna River escapements from 1986 to 2005 will be reconstructed by first estimating the proportion of Susitna River-bound fish from historical catches in the Central District drift gillnet, Eastside set gillnet, and Northern District set gillnet fisheries, since these harvest areas intercept the vast majority (98%) of Susitna River sockeye salmon harvested in Upper Cook Inlet (Table 5; Barclay et al. 2010a). DNA will be extracted from historical scales collected from harvests in these 3 areas using standard methods similar to a recent Bristol Bay study (Smith 2010). Escapement to the Susitna River drainage will then be estimated using annual harvest rates in historic commercial fisheries estimated using data collected since 2006.
2. Reconstruct Upper Cook Inlet total runs for the major systems. The harvest of sockeye salmon in Cook Inlet can be separated into 4 large-scale stocks: Kenai River, Kasilof River, Susitna River, and Other. This objective will use a modified version of the Bristol Bay run reconstruction model (Cunningham et al. 2012) that accounts for the unique characteristics of Upper Cook Inlet fisheries and escapements and will tie in the critical components from Objective 1.

Initial planning for this project was based on target sample sizes of 400 fish per fishery stratum for each year from 1986 to 2005 (Table 6). This was a good starting point, but necessary sample sizes have changed as a result of success rates for extracting usable DNA from archived scales.

The Central District drift gillnet fishery is the highest priority for analysis because most Susitna-bound fish are harvested in this fishery (Table 6). For this reason, samples from the Central District drift gillnet fishery for all years will be analyzed prior to analysis of the Eastside set gillnet and Northern District set gillnet fishery samples. Using this method, sample sizes from the Eastside set gillnet or Northern District set gillnet harvests will be adjusted to account for changes required by success rates with archived DNA or reduction in future funding for the project.

During the winter of 2013/2014, 6,000 individual scale samples were identified from the archived scale cards collected from the Central District drift gillnet fishery harvests from 1986 to 2001. During the spring and summer of 2014, DNA extraction and genotyping began on the first 190 samples from the 1986 drift fishery to optimize laboratory methods. Initial analyses failed to produce genotypes. We suspected that this failure was due to a combination of low DNA yield that failed to amplify and fish-to-fish contamination. We then applied a series of methods

designed to increase DNA amplification, and we identified methods that yielded high amplification success (99% of the samples amplified). However, these amplifications produced genotypes that documented high DNA concentrations from multiple fish per sample (contamination) in 45% of the samples. Excluding these contaminated samples allowed for genotyping of the remaining samples.

Based on these 190 samples from a single year, we estimate that this project will need to analyze 2 fish for every 1 fish successfully genotyped. These dropouts should not affect the stock composition estimates because fish-to-fish contamination is not stock associated. However, these dropouts will add cost. This increased cost can be absorbed by excluding lower-priority samples from the project or by extending the project for additional years using general funds from the Cook Inlet sockeye salmon genetics project.

After estimating the average dropout rate, the next step was to determine the dropout rate by year so that we could calculate how many fish from each year should be analyzed to yield 400 successfully genotyped individuals. DNA yield and contamination rates are affected by sampling methods: given that scales were not originally intended for DNA analysis, slight deviations in methods across years result in different levels of DNA yield and contamination. For example, some technicians cleaned scales more thoroughly than others before placing them on scale cards (most of the DNA is in the mucus around the scale, not in the scale itself) or some scale cards were dried more quickly than others (fast drying preserves DNA better). To investigate DNA yield and contamination across years, a quarter ($N = 100$) of the selected ($N = 400$) drift gillnet fishery scales from each year were analyzed to estimate the level of oversampling needed to meet the target of 400 fish per year.

In the Winter 2014/2015 we analyzed the samples to investigate DNA yield and contamination rates across years. Dropout rates varied drastically across years ranging from 19% to 73% and averaging 50%. These data were then used to select an appropriate sample size per year to yield approximately 400 successfully genotyped individuals. These selected samples for the Central District drift gillnet fishery have been selected and extracted. Extracted samples are ready for contamination analysis followed by genotyping of uncontaminated individuals.

This project is on schedule and will be completed in 5 years, 2018.

Table 5.—Proportion of total Susitna River sockeye salmon harvest in Upper Cook Inlet gillnet fishery strata, 2006–2012 (calculated from Barclay et al. 2010a, 2010b, 2013, 2014b, and *In prep*).

Fishery stratum	Mean	Min	Max
Central District drift	0.706	0.459	0.839
Eastside (Upper Subdistrict) set			
Kasilof Section set	0.051	0.001	0.146
Kenai/East Forelands sections set	0.056	0.009	0.140
Kalgin Island Subdistrict set	0.015	0.002	0.075
Western Subdistrict set	0.001	0.000	0.003
Northern District set	0.042	0.005	0.089

Table 6.—Number of samples initially extracted/analyzed to determine contamination rates, the percent of samples that can successfully used in the final analysis (success rate), and the number of additional samples extracted accounting for success rates from the Drift Gillnet fishery and target sample sizes to estimate stock composition of sockeye salmon from each gillnet fishery by year in Upper Cook Inlet. Shaded cells indicate the samples to be analyzed by spring 2016. No drift fishery occurred in 1989.

Year	Central District drift			Eastside set	Northern District set
	Target	Extracted/Analyzed	Success Rate	Additional Extracted	Target
1986	400	190	55%	492	400
1987	400	100	34%	1,212	400
1988	400	100	43%	912	400
1989	—	—	—	—	400
1990	400	101	51%	741	400
1991	400	100	57%	641	400
1992	400	100	42%	943	400
1993	400	100	81%	392	400
1994	400	99	76%	431	400
1995	400	100	64%	549	400
1996	400	100	63%	562	400
1997	400	100	34%	1,211	400
1998	400	100	40%	1,002	400
1999	400	100	27%	1,573	400
2000	400	100	35%	1,169	400
2001	400	99	57%	642	400
2002	400	100	52%	718	400
2003	400	100	50%	760	400
2004	400	100	37%	1,094	400
2005	400	0	NA	9 ^a	400
Total	7,600	1,889	50%	15,053	8,000

^a Genetic tissue samples were collected and analyzed from gillnet fisheries in Upper Cook Inlet in 2005; additional scale samples were needed for a harvest proportional sample.

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APPENDIX A

Appendix A.—Genetic tissue collections from Cook Inlet coho salmon currently available for the Cook Inlet coho salmon genetic stock identification project. Map numbers correspond to location numbers on Figure 2.

Map No.	Population No.	Reporting Group	Location	Collection Year(s)	N	Analyzed
Southwest						
1	1		Douglas River	2013, 2014	256	92
2	2		Douglas Reef River	2013, 2014	241	94
3	3		Kamishak River	2013, 2014	217	92
4	4		Little Kamishak River	2013, 2014	271	90
5	5		McNeil River	2013, 2014	53	53
6			Sunday Creek	2012	7	—
7			Brown's Peak Creek	2013, 2014	13	—
8	6		Knolls Head Creek	2014	200	150
9			Fitz Creek	2013	3	—
10	7		Silver Salmon Creek	2013	160	93
11	8		Tuxedni River	2012	86	81
12	9		Crescent River	1998, 2013	326	184
13	10		Harriet Creek	2014	63	63
Northwest						
14			Packers Creek	2013, 2014	40	—
15	11		Little Jack Creek	2013	104	95
16	12		Montana Bill Creek	2012	101	95
17			Big River	2009	19	—
18	13		Kustatan River	2013	119	95
19	14		Farro Creek	2013, 2014	127	95
20	15		McArthur River	2014	100	95
21			Straight Creek	2014	15	—
22	16		Chuitna River	1992	54	53
23	16		Wilson Creek	2010	223	94
24			Middle Creek	2008	40	—
25			Lone Creek	2008	35	—
26	17		Coal Creek	2013, 2014	88	86
27	18		Theodore River	2012, 2013	79	77
28	19		Lewis River	2013	57	56
29	20		Alexander Creek ^a	2014	100	92
Susitna						
30	21		Portage Creek	2014	61	59
31	22		Indian River	2013, 2014	157	144
32			Lane Creek	2014	10	—
33	23		Whiskers Creek	2013, 2014	81	79
34			Honolulu Creek	2013	4	—
35	24		Spink Creek	2008, 2014		94
36	25		Byers Creek	2014	56	55
37	26		Tokositna River ^b	2008, 2009–2012	62	62
38	26		Bunco Creek	2013, 2014	65	55
39			Swan Lake	2009	20	—
40	27		Troublesome Creek	2014	107	88
41			Iron Creek	2013, 2014	40	—
42	28		Prairie Creek	2014	53	51
43	29		Sheep River	2013	113	95
44	30		Larson Lake outlet	2011, 2014	132	132
45	31		Chunilna Creek	2013	135	94
46	32		Fish Creek	2014	65	65

-continued-

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Map No.	Population No.	Reporting Group	Location	Collection Year(s)	N	Analyzed
47			Birch Creek	2014	2	–
48			Answer Creek	2013	7	–
49	33		Question Creek	2013, 2014	153	126
50			Rabideux Creek	2014	1	–
51	34		Montana Creek	2013, 2014	404	87
52	35		Sheep Creek	2014	47	47
53			Kashwitna River	2014	24	–
54			Willow Creek	2014	27	–
55	36		Deshka River ^c	2009, 2010, 2011, 2012	59	59
		Yentna				
56			Martin Creek	2013	36	–
57			Nakochna River	2014	8	–
58			Red Creek	2014	26	–
59	37		Hayes River	2014	87	84
60	38		Canyon Creek	2008, 2013, 2014	160	105
61	39		Talachulitna River	2013, 2014	158	122
62			Sunflower Creek	2014	8	–
		Knik				
63	40		Little Susitna River	2013, 2014	197	144
64	41		Fish Creek	2009, 2013, 2014	397	185
65	42		Cottonwood Creek	2014	125	73
66	43		Wasilla Creek	2013, 2014	100	100
67	44		Rabbit Slough	2011	95	95
68	45		Matanuska River	2009	94	94
69	46		Eska Creek	2013, 2014	96	94
70	47		Jim Creek	2009, 2014	208	117
71			Jim Lake	2011	7	–
72			Eagle River	2014	24	–
73	48		Chester Creek	2011, 2013, 2014	80	77
74			Sixmile Creek	2009, 2014	89	–
75	49		Ship Creek	1991, 2012, 2013, 2014	797	93
76	50		Campbell Creek ^d	2009, 1010	134	94
		Turnagain/Northeast				
77	51		Rabbit Creek	2011, 2013, 2014	63	62
78			California Creek	2014	9	–
79	52		Placer Creek	2014	75	71
80	53		Williwaw Creek	2013, 2014	72	71
81			Portage Creek	2014	17	–
82	54		Explorer Pond	2013, 2014	164	139
83			Placer River	2014	6	–
84			Ingram Creek	2013, 2014	14	–
85	55		East Fork Sixmile Creek	2014	90	90
86	56		Resurrection Creek	2010	96	93
87	57		Chickaloon River	2010	104	100
88	58		Sucker Creek	1997	94	91
89	59		Gruska Creek	2013, 2014	108	103
90	60		Bishop Creek	2014	62	57
		Kenai/Kasilof				
91	61		Trail Creek	2006	134	108
92			Moose Creek	1993	150	---

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Map No.	Population No.	Reporting Group	Location	Collection Year(s)	N	Analyzed
93	62		Grant Creek	2013	100	95
94	63		South Fork Snow River	1998, 2002	123	95
95	64		Summit Creek	2002	50	50
96	65		Tern Lake	2002	96	95
97	66		Quartz Creek	1998	75	73
98	67		Kenai Lake outlet	2014	108	95
99	68		Russian River	2013, 2014	154	140
100	69		Skilak River	2003	100	94
101	70		Skilak Lake outlet	1999, 2014	183	173
102	71		Killey River	2000, 2002	117	92
103	72		East Fork Moose River	2002	96	93
104	73		Funny River	2006	150	92
105			Soldotna Creek	2013	13	–
106	74		Slikok Creek	2008	67	65
107			Beaver Creek	2013	12	–
		Kenai/Kasilof				
108	75		Glacier Creek	2009	68	65
109	76		Indian Creek	2009	55	55
110	77		Nikolai Creek	2009	92	88
111	78		Tustumena Lake outlet	2009	100	90
		Southeast				
112	79		Ninilchik River	2013, 2014	202	94
113	80		Deep Creek	2013, 2014	201	89
114	81		Stariski Creek	2013, 2014	161	87
115	82		Anchor River	2006, 2009	204	95
116	83		Fox River	2013, 2014	228	109
117	84		Port Graham River	2014	113	95
		Outside Cook Inlet				
118	85		Delight Creek	2014	261	111
119	86		Resurrection River	2014	100	95
120	87		Bear Creek	2009, 2012	453	97

^a Alexander Creek is more genetically similar to northwest populations than Susitna River populations so it was grouped with Northwest populations.

^b Radiotagged coho salmon samples from Sunshine fish wheels (2008) and Flathorn fish wheels (2009–2012).

^c Radiotagged coho salmon samples from Flathorn fish wheels (2009–2012).

^d Campbell Creek is genetically similar to Ship Creek stock so it was grouped with Knik Arm populations.