

**Report to Yukon River Panel: Project No. URE-01-15**

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**Genetic stock identification of fall chum salmon in  
commercial harvests, Yukon River, 2012–2015.**

by

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and

**Bonnie M. Borba**

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June 2016

Alaska Department of Fish and Game

Divisions of Commercial Fisheries



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

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*This document should be cited as:*

*DeCovich, N. A. and B. M. Borba. 2016. Genetic stock identification of fall chum salmon in commercial harvests, Yukon River, 2012–2015. Alaska Department of Fish and Game, Report to Yukon River Panel Project No. URE-01-15, Anchorage.*

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## ABSTRACT

Chum salmon (*Oncorhynchus keta*) genetics samples were collected from the commercial fishery conducted in District 1 of the Lower Yukon Area. Historically the last two weeks of July include the transition of stocks from summer to fall chum salmon whereas August is dominated by fall chum salmon. Collections included two strata in July (during the transition) and two strata in August for the years 2012, 2014 and 2015 and only the two July strata in 2013. Because of the entry pattern of the run (producing extreme highs and lows within two days' time) and timing of the commercial openings, more samples were collected (n=5376) than would be analyzed. Genotyping of 3440 fish using 96 single nucleotide polymorphism markers has been completed. Three reporting groups were analyzed in this project: *Lower Summer*, *Upper U.S. Fall*, and *Canada*. The *Upper U.S. Fall* group was the largest component for nearly all strata and all years (range: 46-76%) though the *Canada* reporting group was also a large component (range: 24-52%) and dominated one stratum. The *Lower Summer* reporting group was present in low proportions in primarily the earlier strata each year (range: 0-17%).

Key words Yukon River, chum salmon *Oncorhynchus keta*, commercial harvest, genetic stock identification, single nucleotide polymorphisms, SNP

## INTRODUCTION

Fall chum salmon (*Oncorhynchus keta*) stocks of Canadian-origin have escapement objectives outlined in the Yukon River Salmon Agreement as an Annex to the Pacific Salmon Treaty, while U.S. stocks including Tanana, Chandalar and Sheenjek rivers are within the purview of Alaska Department of Fish and Game's (ADF&G) escapement goal policy. Canadian-origin stocks include both the upper Porcupine River (Fishing Branch River) and the upper Yukon River mainstem. Priority for fisheries management in the State of Alaska is first to escapement, second to subsistence uses and third to other uses such as commercial harvests. However, the occurrence of fisheries for fall chum salmon along the length of the Yukon River is typically in the opposite order, thus adding complexity to fisheries management. Fall chum salmon spawn in the most upper reaches of the drainage (river mile-RM >800), while the largest commercial harvests (>80%) are taken in the Lower Yukon Area and the largest subsistence harvests (>90%) occur in the Upper Yukon Area (Figure 1). In particular, the commercial harvests in the Lower Yukon Area are substantial; determination of stock composition in the fishery compared to the passage upriver would be useful for informing management actions to achieve escapement goals.

This project was designed to test the potential to estimate stock composition of chum salmon harvested in the fall season (beginning July 16) commercial fisheries within District 1 of Yukon River. Because the majority of the commercial fishery occurs in the lower two commercial districts, collecting and analyzing genetic harvest samples would assist in prosecution of fisheries, while ensuring that sufficient numbers of chum salmon escape the fishery to achieve other objectives within the drainage. Knowledge of the stock-specific harvest and run timing of Canadian-origin stocks can be applied to inseason run assessments in efforts to meet management objectives and allow for development of more accurate post-season run reconstructions used for assessing productivity and forecasting returns preseason. This project uses the ADF&G genetic baseline of chum salmon populations in the Yukon River to provide regional stock composition estimates. Chum salmon were allocated to the following reporting groups: *Lower Summer*, *Upper U.S. Fall*, and *Canada*.

## OBJECTIVES

The objective of this project was to test the feasibility of estimating stock composition of the commercial harvest of chum salmon at the mouth of the Yukon River drainage where a significant portion of the total commercial harvest allocation is typically harvested. This was to

be accomplished by determining the stock composition of the Yukon River District 1 fishery in up to 4 strata for each of the years 2012–2015 for the following reporting groups: *Lower Summer*, *Upper U.S. Fall*, and *Canada*.

## METHODS

### GENETIC BASELINE

The genetic baseline for Yukon River chum salmon stock composition consists of 6,535 individual chum salmon from 74 collections representing 45 populations (Table 1). For these individuals, multi-locus genotypes are available for 91 nuclear single nucleotide polymorphisms (SNPs). The majority (4,023) of these individuals were included in the baseline used for the Western Alaska Salmon Stock Identification Program (WASSIP; DeCovich et al. 2012). Notable additions include 503 individuals from the Fishing Branch River, and the addition of the Dakli River. For this project, the baseline was divided for apportioning mixture samples into three reporting groups: *Lower Summer*, *Upper U.S. Fall*, and *Canada* (all Canadian chum salmon are fall chum salmon).

Support for the accuracy and precision of these groups was evaluated with simulations using the Statistical Package for Analyzing Mixtures (SPAM version 3.7, Debevec et al. 2000). Mixture genotypes were randomly generated from the baseline allele frequencies assuming Hardy-Weinberg equilibrium. Each simulated mixture ( $N=200$ ) was composed entirely of the stock or reporting group under study. When a reporting group mixture was simulated, all stocks in the reporting group contributed equally to the mixture. Average estimates of mixture proportions and 90% confidence intervals were derived from 1,000 simulations. Reporting groups with mean correct estimates of 90% or better are considered highly identifiable in fishery applications (Seeb et al. 2000). The mean correct estimates for the three reporting groups used by this project were: *Lower Summer*, 96%; *Upper U.S. Fall*, 90%; and *Canada*, 91%.

### FISHERY SAMPLING

Genetic sampling of chum salmon occurred in the fall season commercial fisheries in District 1 of the Yukon River in 2012 through 2015 seasons by ADF&G and Yukon Delta Fisheries Development Association (YDFDA) crewmembers at the local buying stations. Two methods of collecting genetic samples were most often used: 1) each tissue sample was stored in an individual numbered vial allowing association with other data such as age, sex and length (ASL); and 2) tissue samples from multiple fish were pooled or mixed together in a larger container as one bulk collection, in this case based in a time frame (commercial period). In bulk collections individual tissue samples could not be matched with data like ASL. For all tissue sampling, axillary processes were collected and preserved in ethanol.

Sampling occurred during commercial periods when harvest was expected to be larger than 5,000 fall chum salmon between July 16 and August 30. Harvest sampling occurred during four to twelve commercial periods per season. More commercial fishing periods were sampled than were analyzed. Postseason the harvest of each commercial period relative to the abundance was evaluated and a total of four time strata were selected for analysis (220 samples times 4 strata;  $N=880$ ). Priority for analyzing samples was given to the commercial periods during the expected transition of summer to fall chum salmon in July. Second priority was to analyze the largest commercial harvests sampled during the August fishing periods.



The test fish crew operating out of the Middle/North mouth camp (Figure 3) assisted with collecting samples directly from that portion of the Yukon River Delta. During commercial openings at least one of their two daily drifts were cancelled (usually the evening drift); therefore instead of sampling the test fish catch they were assigned to sample the commercial harvest. The remote crew had access to potentially three different fishing areas including Middle Mouth proper (334-15), North Mouth proper (334-16) and the area upstream where the two mouths converge (334-17; Figure 3). If samples were collected from more than one of these areas they were collected in separate bulk bottles.

The South Mouth (Statistical Areas 334-12, 334-13 and 334-14) samples were collected in bulk at the buyer's station in Emmonak as the fish were delivered to the dock along with ASL sampling efforts. The harvest and sampling regimes were evaluated post season based on groupings of statistical areas covering each distributary.

## **LABORATORY ANALYSIS**

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 96 SNPs (Table 2). Genomic DNA was extracted using a DNeasy® 96 Tissue Kit by QIAGEN®, (Valencia, CA). All SNPs were detected using a TaqMAN SNP Genotyping Assay (Life Technologies). SNP assays were generally performed using the BioMark 96.96 Dynamic Array (Fluidigm). Re-analyses of failed assays was performed on the Applied Biosystems Prism 7900HT Sequence Detection System. Genotype data are stored in an *Oracle* database (*LOKI*) on a network drive maintained by ADF&G computer services. Quality control measures included reanalysis of 8% of each collection beginning at DNA extraction for all markers to ensure that genotypes are reproducible and in order to identify laboratory errors and measure rates of inconsistencies during repeated analyses.

## **MIXTURE ANALYSIS**

Genotypes were retrieved from *LOKI* and imported into *R* (R Development Core Team 2010). All subsequent analyses were performed in *R* unless otherwise noted. Prior to MSA, two statistical QC analyses were conducted. First, individuals missing genotypes for 20% or more of loci were excluded, because these individuals likely have poor-quality DNA that could lead to genotyping errors and reduce accuracy and precision of MSA. Second, individuals with duplicate genotypes at 95% or more of markers screened were identified and removed from further analyses.

The stock composition of fishery mixtures was estimated using the program BAYES (Pella and Masuda 2001). For each fishery mixture, five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations were run. A flat prior was used (prior stock contributions were calculated as  $1/N$ ). Each chain had different starting values and the first 20,000 iterations were discarded to remove the influence of the initial start values. In order to assess the among-chain convergence, Gelman-Rubin shrink factors were computed for all stock groups in BAYES (Gelman and Rubin 1992). If a shrink factor for any stock group in a mixture was greater than 1.2, the mixture was reanalyzed with 80,000 iterations. The last 20,000 iterations of the five chains were combined to form the posterior distribution and means, 90% credibility intervals, and standard deviations were derived from a total of 100,000 iterations. Misallocations to reporting groups either absent or at low proportions within mixtures can occur in MSA when the

discriminant methods do not produce perfect identifiability (Pella and Milner 1987; Xu et al. 1994; Pella and Masuda 2001).

## **RESULTS AND DISCUSSION**

### **FISHERY SAMPLING**

Sampling of tissues in 2012 was conducted prior to development of this project. Sampling was included in the routine ASL sampling, which consisted of 160 chum salmon per commercial period. In total, chum salmon were collected from 11 of 13 commercial periods (Table 3). Generally, the first fish to arrive at the buying station located in Emmonak were from local fishermen operating in the South Mouth area.

As the project was developed the samples sizes were increased from 160 to 220 chum salmon per commercial period. Tissue sampling goals in 2013 consisted of 110 chum salmon from each of two locations (South Mouth and Middle/North mouth) for a total of 220 fish per commercial period (Table 4). Sample collections were concentrated on the July 16-31 portion of the run during the expected transition from summer to fall chum salmon stocks (four commercial periods). Effort was made in 2013 to collect half the samples from the Middle/North mouth harvests by waiting for boats and tenders to arrive in Emmonak. Contacting the buyer and tenders to get accurate arrival times of tenders was difficult.

In both 2014 and 2015, sampling was directed at pulses of chum salmon. In these years, there were twelve commercial periods of which six were sampled each year. In both years, the chum run consisted of six pulses: two in July, one August 1 and three others approximately a week apart throughout August. In 2014, five of the commercial sampling periods coincided with pulses of chum salmon and one period (collection 3) occurred between pulses 4 and 5 (Table 5). For 2014, collection 3 was not analyzed because the harvest was extremely low (approximately 1,000 chum salmon) and collection 6 was not analyzed because it occurred during the same pulse of fish as collection 5 with an equivalent harvest. In 2015, five of the six sampling periods coincided with pulses of fish; the first pulse was missed and collection 1 was not analyzed, collections 2 and 3 sampled the same pulse and were combined and weighted by harvest (Table 6). Collections 4–6 each coincided with respective large pulses. Because of the difficulty collecting samples from Middle Mouth, sample goals were only met during four periods (commercial periods 2 and 8 in 2014 and periods 2 and 5 in 2015).

This project was a feasibility study, and results indicate that tissue sampling can successfully be conducted in the Yukon River District 1 commercial fishery. However, most of the samples tend to come from the South Mouth area. There were difficulties sampling other areas due to: limited sampling resources, difficulties tracking tenders, and uncertainty in the statistical area of the delivered harvest. On average, 39% of the harvest occurs in the statistical areas 334-12, 334-13 and 334-14, 14% of the harvest occurs within 334-15 Middle Mouth proper, and 14% of the harvest occurs within 334-16 North Mouth proper. Harvests registered within 334-17 (26% on average) can be from either mouth as the distributaries begin merging in this area and determining where a tender may be or might be passing through this area does not help separate harvest by mouth. Harvests from statistical area 334-18 only represent on average 7% of the catch but this area is located the farthest from the processing facility and is within the area of completely mixed harvest. Harvests in statistical area 334-11 are 1% on average and therefore negligible.

## **LABORATORY ANALYSIS**

The number of individual tissue samples analyzed was as follows: 2012, 800 fish representing 4 strata; 2013, 440 fish representing 2 strata; 2014, 952 fish representing 4 strata; and 2015, 1234 fish representing 4 strata. Of the 3,440 fish that were genotyped, 301 were re-genotyped (8.75% of the project). The average failure rate (representing the fish that could not be genotyped for a locus) was 2.4%. The overall discrepancy rate (fish that had a different genotype in the QC versus the original run) was 0.3%.

## **MIXTURE ANALYSIS**

Mixtures of fish representing catches by strata were analyzed for each year 2012-2015. Stock composition estimates can be found in Figures 3-6. Although the samples collected in 2012 were opportunistic and not part of a formal study plan, the results generated from them show similar trends to years 2013-15 and their inclusion is warranted.

The prominent stock group present in all fishery strata was the *Upper U.S. Fall* group, followed by *Canada* then *Lower Summer* reporting groups. The *Lower Summer* groups was never present in any strata at greater than 17%, and in every year the largest proportion of this stock was observed in the first temporal strata and declined throughout the year. These results corroborate what was known about chum salmon in the Yukon River: that summer chum salmon migrate through the Lower Yukon River earlier than fall chum salmon, although the run timing distributions overlap. The ratio of *Upper U.S. Fall* to *Canada* groups remained relatively constant through the season for each year. However, in 2015, the stock proportions were more similar for each stock compared to the previous 3 years, where the *Upper U.S. Fall* stock was predominant.

## **PROJECT PRODUCTS**

A comprehensive ADF&G Fishery Data Series report detailing the results for 2012 through 2015 is expected spring of 2017. Results from this project will be presented at various fisheries and stakeholders meetings as needed.

## **ACKNOWLEDGEMENTS**

This investigation was financed by the Yukon River Restoration and Enhancement Fund and the Department of Fish and Game under Project URE-01-14N and URE-01-15. The authors would like to thank all the individuals that collected samples out of Emmonk including: Yukon Delta Fisheries Development Association employees Evan Charles, Isaiah Charles, Alexander Peterson and Henry Uisok alongside Alaska Department of Fish and Game employees Keegan Birchfield, Amy Bower, Jeff Estensen, Tara Harrington, Joel Hunt and Mick Leach.

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## **TABLES AND FIGURES**

Table 1.–Reporting group, location, collection year, and sample size of baseline collections used in this study.

Reporting Group	Location	Year(s) Collected	Sample Size
Lower Summer	Black River	2006	95
	Atchuelinguk River	1989	51
	Andrafsky River	1993, 2004	190
	Chulinak River	1989	93
	Innoko River	1993	85
	California Creek	1997	95
	Tolstoi Creek	1997	95
	Anvik River	1992, 1993	380
	Rodo River	1989	75
	Kaltag River	1992	93
	Nulato River	1994, 2003	190
	Gisasa River	2004	95
	Huslia River	1993	95
	<sup>1</sup> Dakli River	2012	56
	Clear Creek	2002	95
	Henshaw Creek Early	2004	95
	South Fork KoyukukRiver - Early	1996	93
	Melozitna River	1004, 2004, 2012	273
	Tozitna River	2003	95
	Upper U.S. Fall	Henshaw Creek Late	1995
South Fork KoyukukRiver - Late		1996	95
Middle Fork Koyukuk River		2011, 2012, 2013	183
Jim River		2002, 2010, 2012, 2013	254
Kantishna River		2001	95
Toklat River		1994	190
17 Mile Slough		2010	97
Tanana River Mainstem		1993	95
Chena River		1994, 2013	271
Salcha River		2001, 2013	279
Clearwater Creek		1990	80
Delta River		1994	150
Bluff Cabin		1992	100
Big Salt River		2001	71
Chandalar River		2001, 2011	158
Black River		1995	95
Sheenjek River		1992, 2011	269
Canada	Porcupine River at Old Crow	2007	95
	<sup>2</sup> Fishing Branch	1987, 1989, 1992, 1994, 1997, 2007	598
	Donjek River	1994	69
	Kluane River	2007, 2012, 2013	209
	Pelly River	1993	84
	Big Creek	1995	100
	Minto Slough	1989, 2013	198
	Tatchun Creek	1992, 2013	205
Teslin River	1992, 2013	94	

<sup>1</sup> This collection is new to this study and was not included in the referenced WASSIP baseline.

<sup>2</sup> Fishing Branch collections from 1987, 1989, 1992, 1994, and 1997 are new to this study and were not included in the referenced WASSIP baseline.

Table 2.–Assay name and source of the 96 SNP markers used in this study.

Assay	Source	Assay	Source	Assay	Source
<i>Oke_ACOT-100</i>	A	<i>Oke_LAMP2-186</i>	A	<i>Oke_U1022-139</i>	A
<i>Oke_AhR1-78</i>	B	<i>Oke_mgll-49</i>	A	<i>Oke_U1023-147</i>	A
<i>Oke_arf-319</i>	C	<i>Oke_MLRN-63</i>	A	<i>Oke_U1024-113</i>	A
<i>Oke_ATP5L-105</i>	A	<i>Oke_Moesin-160</i>	C	<i>Oke_U1025-135</i>	A
<i>Oke_azin1-90</i>	A	<i>Oke_nc2b-148</i>	A	<i>Oke_u200-385</i>	C
<i>Oke_brd2-118</i>	A	<i>Oke_ND3-69</i>	A	<i>Oke_U2006-109</i>	A
<i>Oke_brp16-65</i>	A	<i>Oke_NUPR1-70</i>	A	<i>Oke_U2007-190</i>	A
<i>Oke_CATB-60</i>	A	<i>Oke_pgap-111</i>	A	<i>Oke_U2011-107</i>	A
<i>Oke_ccd16-77</i>	A	<i>Oke_pgap-92</i>	A	<i>Oke_U2015-151</i>	A
<i>Oke_CD81-108</i>	A	<i>Oke_PPA2-635</i>	B	<i>Oke_U2025-86</i>	A
<i>Oke_CD81-173</i>	A	<i>Oke_psm9-57</i>	A	<i>Oke_U2029-79</i>	A
<i>Oke_CKS1-94</i>	A	<i>Oke_rab5a-117</i>	A	<i>Oke_U2031-37</i>	A
<i>Oke_CKS-389</i>	D	<i>Oke_ras1-249</i>	B	<i>Oke_U2032-74</i>	A
<i>Oke_Cr30</i>	A	<i>Oke_RFC2-618</i>	C	<i>Oke_U2034-55</i>	A
<i>Oke_Cr386</i>	A	<i>Oke_RH1op-245</i>	C	<i>Oke_U2035-54</i>	A
<i>Oke_ctgf-105</i>	B	<i>Oke_RS27-81</i>	A	<i>Oke_U2037-76</i>	A
<i>Oke_DCXR-87</i>	A	<i>Oke_RSPRY1-106</i>	A	<i>Oke_U2041-84</i>	A
<i>Oke_e2ig5-50</i>	A	<i>Oke_serpin-140</i>	C	<i>Oke_U2043-51</i>	A
<i>Oke_eif4g1-43</i>	A	<i>Oke_slc1a3a-86</i>	A	<i>Oke_U2048-91</i>	A
<i>Oke_f5-71</i>	A	<i>Oke_sylc-90</i>	A	<i>Oke_U2050-101</i>	A
<i>Oke_FANK1-166</i>	A	<i>Oke_TCP1-78</i>	B	<i>Oke_U2053-60</i>	A
<i>Oke_FBXL5-61</i>	A	<i>Oke_Tf-278</i>	B	<i>Oke_U2054-58</i>	A
<i>Oke_gdh1-191</i>	A	<i>Oke_thic-84</i>	A	<i>Oke_U2056-90</i>	A
<i>Oke_gdh1-62</i>	A	<i>Oke_U1002-262</i>	A	<i>Oke_U2057-80</i>	A
<i>Oke_GHII-3129</i>	B	<i>Oke_U1008-83</i>	A	<i>Oke_U212-87</i>	C
<i>Oke_glrx1-78</i>	A	<i>Oke_U1010-251</i>	A	<i>Oke_u217-172</i>	C
<i>Oke_GPDH-191</i>	C	<i>Oke_U1012-241</i>	A	<i>Oke_U302-195</i>	B
<i>Oke_GPH-105</i>	B	<i>Oke_U1015-255</i>	A	<i>Oke_U502-241</i>	B
<i>Oke_HP-182</i>	B	<i>Oke_U1016-154</i>	A	<i>Oke_U504-228</i>	B
<i>Oke_il-1racp-67</i>	C	<i>Oke_U1017-52</i>	A	<i>Oke_U506-110</i>	B
<i>Oke_IL8r2-406</i>	A	<i>Oke_U1018-50</i>	A	<i>Oke_U507-286</i>	B
<i>Oke_KPNA2-87</i>	B	<i>Oke_U1021-102</i>	A	<i>Oke_U509-219</i>	B

Sources: A) International Program for Salmon Ecological Genetics at the University of Washington; B) Elfstrom et al. 2007; C) Smith et al. 2005a; and D) Smith et al. 2005b.

Table 3.–Summary of the 2012 genetic collections for chum salmon in the fall season commercial fishery in South Mouth of District 1 of the Yukon River.

Commercial Period / Collection Number	Start Time	Start Date/ Sample Date	Hours Fished	Harvest Amount	Pulse Number	Number of Samples
2/1	10:00 AM	19-Jul	9	23,784	1	160*
3/2	1:00 PM	23-Jul	6	2,831		160
4/3	1:00 PM	26-Jul	6	29,116	2	160*
5/4	1:00 PM	30-Jul	6	20,158	3	160*
6/5	1:00 PM	2-Aug	9	5,296		160
7/6	10:00 AM	5-Aug	5	11,500	4	160*
8/7	10:00 AM	9-Aug	9	4,327		160
9/8	10:00 AM	18-Aug	9	17,294	5	160*
10/9	12:00 PM	20-Aug	9	8,309		160
11/10	9:00 AM	23-Aug	9	4,571		160
12/11	9:00 AM	27-Aug	9	5,711		160
13/0	9:00 AM	30-Aug	9	3,034		NA
Total			104	139,236		1,760
Total Analyzed						800

Note: Duplicate pulse numbers appear when pulses were present for more than one commercial period. Sample sizes by mouth noted with an asterisk (\*) were included for genotyping in this analysis.

Table 4.–Summary of 2013 genetic collections for chum salmon in the fall season commercial fishery in District 1 (focus was on the transition period from summer to fall chum salmon) of the Yukon River.

Commercial Period / Collection Number	Start Time	Start Date/ Sample Date	Hours Fished	Harvest Amount	Pulse Number	Number of Samples		
						South Mouth	Middle & North Mouths	Total per Strata
1/1	12:00 PM	18-Jul	9	3,824		110	110	220
2/2	3:00 PM	22-Jul	6	15,935	1	110*	110*	220
3/3	3:00 PM	25-Jul	6	5,789		110	110	220
4/4	6:00 PM	29-Jul	6	16,992	2	110*	110*	220
5/0	6:00 PM	1-Aug	6	539		NA	NA	
6/0	3:00 PM	5-Aug	6	10,526	3	NA	NA	
7/0	5:00 PM	17-Aug	6	22,676	4	NA	NA	
8/0	9:00 PM	19-Aug	6	19,675	5	NA	NA	
9/0	12:00 PM	22-Aug	6	5,082		NA	NA	
10/0	4:00 PM	26-Aug	6	2,557		NA	NA	
11/0	5:00 PM	29-Aug	6	2,993		NA	NA	
Total			69	106,588		440	440	880
Total Analyzed						220	220	440

Note: Sample sizes by mouth noted with an asterisk (\*) were included for genotyping in this analysis.



Table 5.–Summary of 2014 genetic collections for chum salmon in the fall season commercial fishery in District 1of the Yukon River.

Commercial Period / Collection Number	Start Time	Start Date/ Sample Date	Hours Fished	Harvest Amount	Pulse Number	Number of Samples		
						South Mouth	Middle & North Mouths	Total per Strata
1/1	4:00 PM	17-Jul	6	12,524	1	112*	15*	127
2/2	6:00 PM	21-Jul	6	8,520	2	228*	187*	415
3/0	4:00 PM	25-Jul	6	3,746		NA	NA	
4/0	4:00 PM	28-Jul	6	1,694		NA	NA	
5/3	4:00 PM	15-Aug	6	1,048	4	220		220
6/4	5:00 PM	19-Aug	6	10,011	5	168*	27*	195
7/5	12:00 PM	25-Aug	9	3,994	6	215*		215
8/6	5:00 PM	26-Aug	4	4,342	6	NA	110	110
9/0	12:00 PM	28-Aug	9	3,564		NA	NA	
10/0	12:00 PM	1-Sep	9	1,529		NA	NA	
11/0	9:00 AM	3-Sep	9	478		NA	NA	
12/0	11:00 AM	5-Sep	9	373		NA	NA	
Total			85	51,823		943	339	1,282
Total Analyzed						723	229	952

Note: Pulse 3 entered on 1-2 August but commercial periods did not occur at that time. Duplicate pulse numbers appear when pulses were present for more than one commercial period. Sample sizes by mouth noted with an asterisk (\*) were included for genotyping in this analysis.

Table 6.–Summary of 2015 genetic collections for chum salmon in the fall season commercial fishery in District 1of the Yukon River.

Commercial Period / Collection Number	Start Time	Start Date/ Sample Date	Hours Fished	Harvest Amount	Pulse Number	Number of Samples		
						South Mouth	Middle & North Mouths	Total per Strata
1/0	4:00 PM	20-Jul	6	3,698		NA	NA	
2/1	6:00 PM	23-Jul	6	4,078		110	110	220
3/2	7:00 PM	28-Jul	6	8,165	2	220*	NA	220
4/3	1:00 PM	30-Jul	7	5,859	2	220*	24*	244
5/4	10:00 AM	2-Aug	9	15,625	3	220*	110*	330
6/0	2:00 PM	6-Aug	6	4,779		NA	NA	
7/5	10:00 AM	10-Aug	6	20,006	4	220*	NA	220
8/0	12:00 AM	13-Aug	6	12,925	4	NA	NA	
9/6	6:00 PM	19-Aug	4	12,687	5	220*	NA	220
10/0	4:00 PM	23-Aug	6	3,374		NA	NA	
11/0	12:00 PM	27-Aug	9	7,599	6	NA	NA	
12/0	12:00 PM	30-Aug	6	1,000		NA	NA	
Total			77	99,822		1,210	244	1,454
Total Analyzed						1,100	134	1,234

Note: Pulse 1 entered on 16-17 July but commercial periods did not occur at that time. Duplicate pulse numbers appear when pulses were present for more than one commercial period. Sample sizes by mouth noted with an asterisk (\*) were included for genotyping in this analysis.

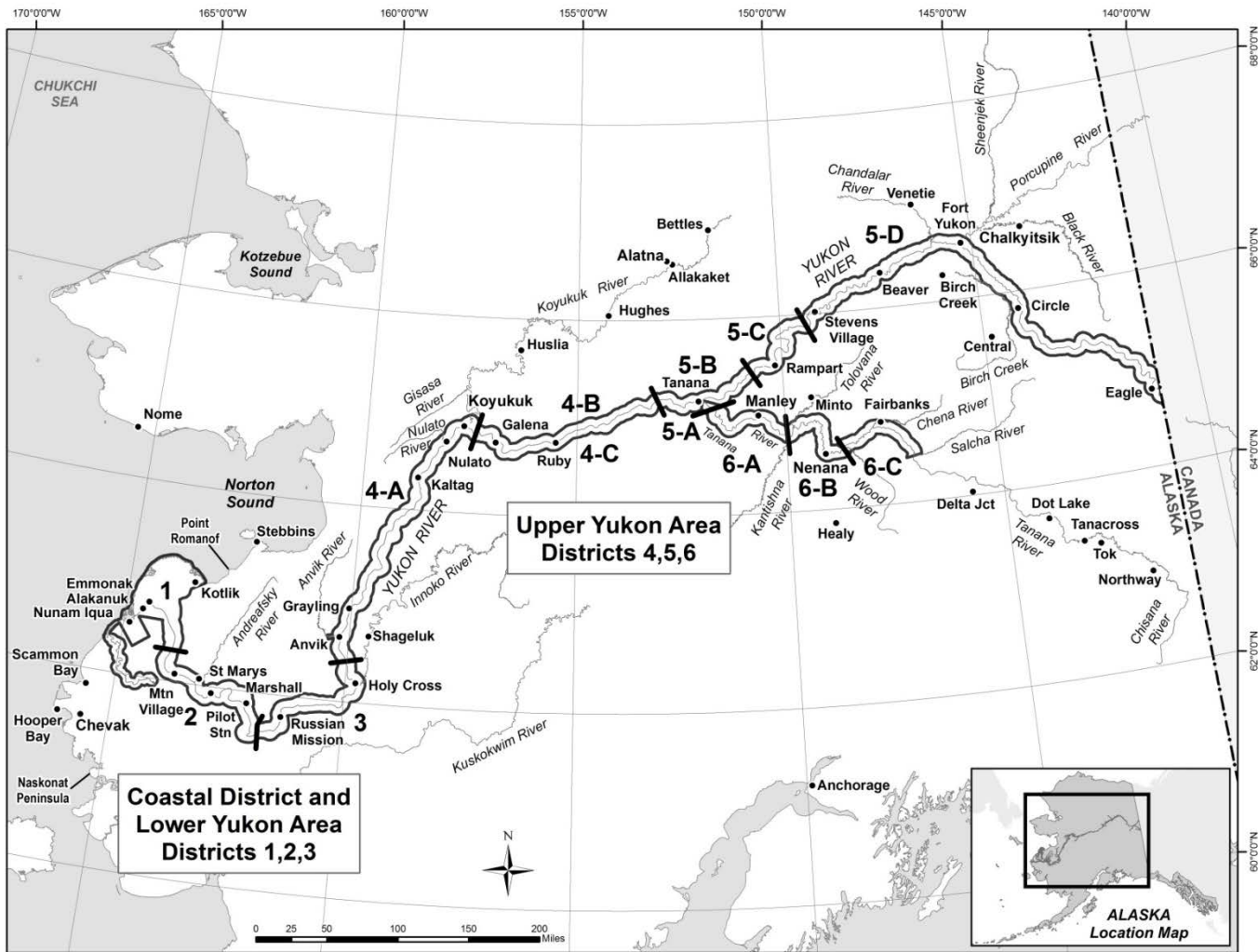


Figure 1.—Location of the fishing districts used for management of salmon fisheries in the United States portion of the Yukon River drainage.

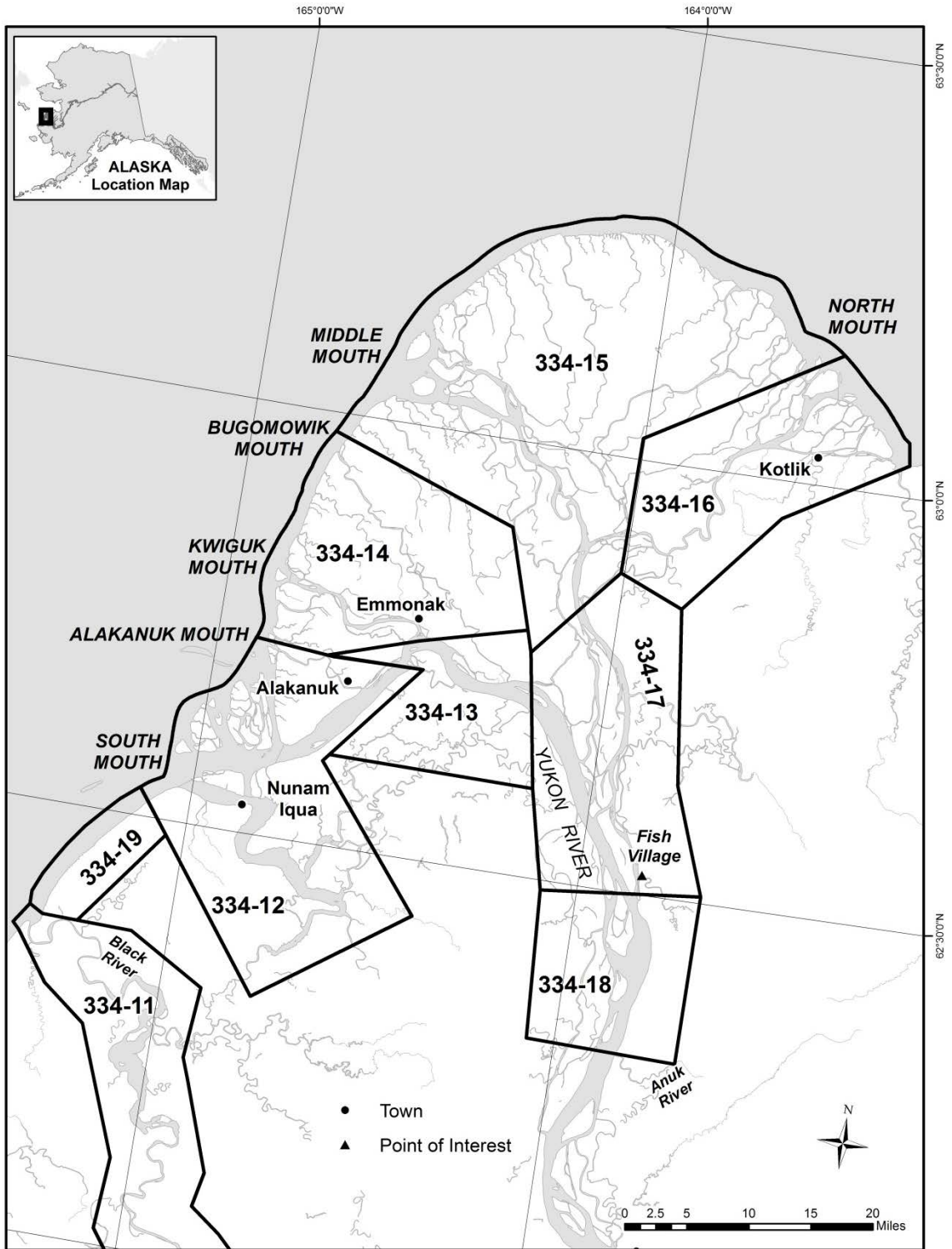


Figure 2.—District Y-1 of the Lower Yukon Area showing commercial statistical areas, Yukon River.

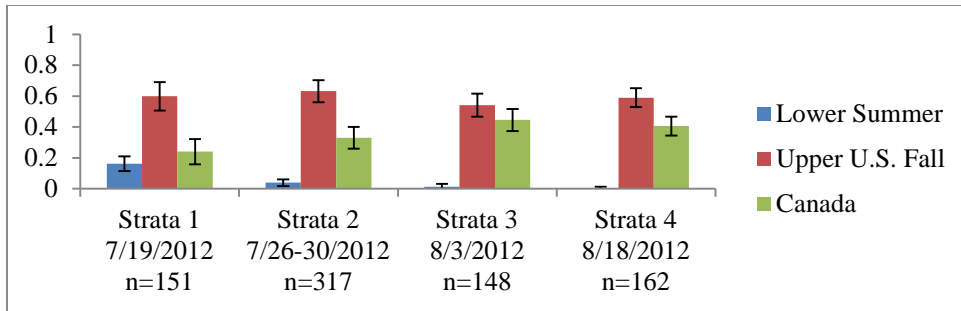


Figure 3.–Stock composition estimates of chum salmon caught in the Yukon River District 1 commercial fishery in 2012. Sample size is noted (n). Sample size are lower than those noted in table three because individuals missing genotypes for > 80% of loci were removed.

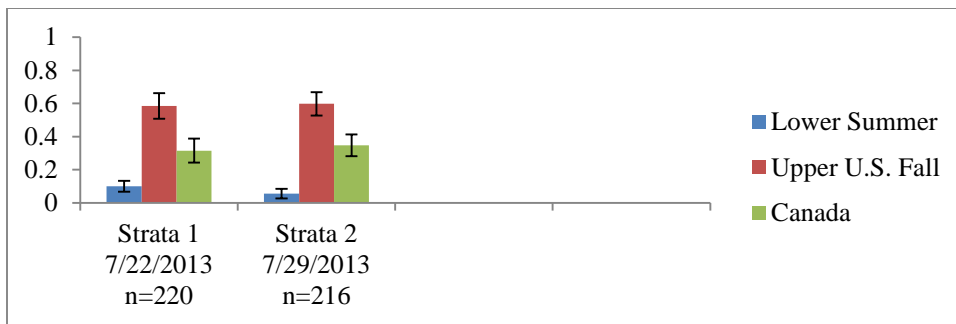


Figure 4.–Stock composition estimates of chum salmon caught in the Yukon River District 1 commercial fishery in 2013. Sample size is noted (n). Sample size are lower than those noted in table four because individuals missing genotypes for > 80% of loci were removed.

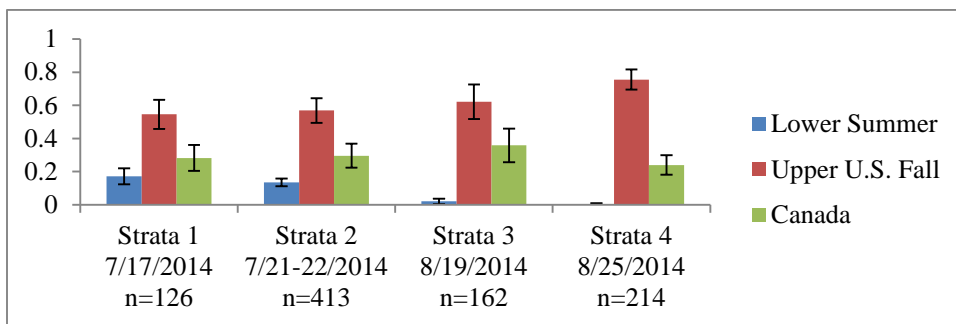


Figure 5.–Stock composition estimates of chum salmon caught in the Yukon River District 1 commercial fishery in 2014. Sample size is noted (n). Sample size are lower than those noted in table five because individuals missing genotypes for > 80% of loci were removed.

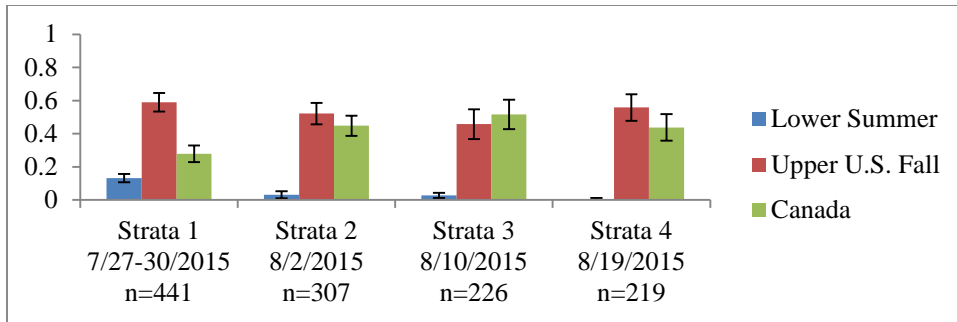


Figure 6.—Stock composition estimates of chum salmon caught in the Yukon River District 1 commercial fishery in 2015. Sample size is noted (n). Sample size are lower than those noted in table six because individuals missing genotypes for > 80% of loci were removed.