Report to Yukon River Panel: Project No. URE-05-16

Genetic mixed stock analysis of chum salmon in subsistence harvest from the Tanana Area, Yukon River, 2014–2016

by

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April 2017Alaska Department of Fish and Game **Divisions of Commercial Fisheries**

Symbols and Abbreviations

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General

Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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ABSTRACT

Chum salmon (*Oncorhynchus keta*) genetics samples were collected from the community of Tanana subsistence fishery. Sample collections were made in Subdistrict 5-B (right bank) of the Yukon River below the confluence of the Tanana River and the portion of the upper Yukon River immediately upstream of the confluence. Collection strata were based upon a historical run timing curve and included one period in August and two periods in September for all years (2014–2016). Genotyping of 2,449 fish using 96 single nucleotide polymorphism markers has been completed. Estimates are provided in a hierarchical manner with harvest apportioned to the following groups in each level: a) *U.S.* and *Canada*, and b) *Lower Summer*, *U.S. Fall*, and *Canada*. The *Canada* group was the dominant component for the first two periods in 2014 and 2015 (range: 56–68%) while the *U.S.* group dominated all periods in 2016 (range: 54–74%). This project provides additional information necessary to test the ability to produce stock composition estimates in fisheries that will help refine management tools for Yukon River fall chum salmon.

Key words: Yukon River, Tanana River, chum salmon *Oncorhynchus keta*, subsistence harvest, genetic stock identification, single nucleotide polymorphisms, SNP.

INTRODUCTION

Chum salmon (*Oncorhynchus keta*) returns to the Yukon River are made up of two genetically distinct runs: summer run and fall run chum salmon. Summer chum salmon are characterized by earlier run timing (entering the river from early June to mid-July), rapid maturation in freshwater, and smaller body size. Summer chum salmon spawn primarily in run-off streams in the lower 700 miles of the drainage and in the Tanana River drainage. Fall chum salmon are characterized by a later run timing (entering the river from mid-July to early September), slower maturation, and larger body size. Fall chum salmon spawn primarily spring-fed streams in the upper portion of the drainage.

Fall chum salmon 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, Sheenjek, and Black 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 within Canada (Figure 1). 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. This prioritization is difficult to manage for because fall chum salmon migrate through the lowest-priority fishery (commercial) first and then the highest use priority fishery (subsistence) before escapement. Information on stock composition is important both to enumerate stock-specific harvest through time of Canadian-origin components in the subsistence fishery, and to provide a better understanding of fish passage necessary to achieve specified escapement goals.

The purpose of this project was to estimate the proportions of Canadian- and U.S.-origin chum salmon caught in the Tanana subsistence fishery throughout the fall season. Households in U.S. Yukon River District 5 are estimated to harvest on average 60% of the fall chum salmon taken for subsistence in the Yukon River in Alaska, and the community of Tanana is estimated to harvest between 40% and 50% of the total District 5 harvest (on average 20,000 fall chum salmon; Figure 2; Jallen et al. 2015). The other large harvesting communities in District 5 include Fort Yukon and Eagle, both of which are located upstream of the Porcupine River and would consist of primarily Canadian-origin fish. In this study, genetic tissue samples were collected and analyzed for stock composition from fish caught in the Yukon River near the community of Tanana on the right bank upstream to the Rampart-Rapids area. Typically, chum

salmon migrating along this bank have been bound for the upper Yukon River, while fish migrating along the left bank have been primarily bound for the Tanana River (Buklis 1981; Spearman and Miller 1997). For 2014–2016, genetic mixed stock analysis (MSA) was used for each of 3 time strata between August 15 and September 30 to allocate fish to the following hierarchical reporting groups: a) *U.S.* and *Canada*, and b) *Lower Summer*, *Upper U.S. Fall*, and *Canada*. Knowing the stock composition of Canadian-origin fall chum salmon in this large and concentrated fishery in Tanana will inform future management practices and improved ability to meet treaty objectives.

OBJECTIVES

The objective of this project was to estimate the proportion of Canadian- and U.S.-origin fall chum salmon caught in the Tanana subsistence fishery throughout the fall season over a 3-year period. This was accomplished by determining the stock composition of chum salmon caught in the Yukon River near the community of Tanana on the right bank upstream to the Rampart-Rapids area (Subdistrict 5-B) in 3 time strata in 2014–2016 for the following hierarchical reporting groups: a) *U.S* and *Canada*, and b) *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 96 nuclear single nucleotide polymorphisms (SNPs; Table 2). 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 fine-scale reporting groups: *Lower Summer*, *Upper U.S. Fall*, and *Canada* (all Canadian chum salmon are fall chum salmon). The baseline was also divided into two broad-scale reporting groups: *U.S.* and *Canada*.

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

During 2014–2016, chum salmon tissue samples were collected from subsistence harvests in Subdistrict 5-B, on the right (north) bank including that section upstream of the confluence of the Tanana River to Rampart-Rapids (Figure 2). This was done to concentrate the samples on upper Yukon River stocks. Area fishers were paid on a per fish sampled basis. Spearfish Research

distributed sampling supplies and gave instruction on sampling technique. Tissue samples were collected in 3 time strata between August 15 and September 30 in each year based on a historical harvest timing curve (Figure 3). The three periods were 1) August 15 – 31, 2) September 1 – 15, and 3) September 16 – 30. For all tissue sampling, axillary processes were collected and preserved in ethanol in individually labeled vials. At the end of sampling each year, samples were shipped to the ADF&G Gene Conservation Lab in Anchorage for analysis.

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 (QC) 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. Prior parameters for the first time stratum of 2014 were defined to be equal (i.e., a *flat* prior). Prior parameters for the first time stratum of subsequent years were defined as the posterior means (i.e., the stock composition estimates) of the first statum of the previous year. For subsequent time strata within the same year, the priors were the posterior means of the previous time strata. For all mixtures, the prior for a reporting group was divided equally to populations within that reporting group for population prior parameters. 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; Pella and Masuda 2001).

RESULTS AND DISCUSSION

FISHERY SAMPLING

Subsistence fishers were contacted in June and July of each year to see if they wanted to participate in the project. Three families agreed to sample in 2014–2015, and two families agreed to sample in 2016. Two samplers fished with fish wheels on the right bank of the Yukon River near Tanana and the third sampler had a fish wheel in the Rampart-Rapids area upstream from Tanana. In 2016, both samplers fished with fish wheels on the right bank near Tanana. A Spearfish Research representative travelled to Tanana in the middle of August each year to provide the samplers with sampling kits and a training session on sampling protocols. All fin clips were stored in individual vials and a calendar was provided to record the vial numbers used. Participants were told to sample each day that they were allowed to fish and to sample a certain number of fish. This number changed based on how many days subsistence fishing was open and also tried to mirror the harvest pattern, with more samples collected during the height of the harvest and less at the beginning and end of the subsistence activity.

The participants sampled from August 15 to September 30. Subsistence fishing was open 7 days a week throughout the duration of the project. Paige Drobny of Spearfish Research returned to Tanana after the first 2 weeks of sampling to pick up samples and to do a quality control check. At the conclusion of sampling, the target of 600 samples was exceeded in each year (Table 3).

LABORATORY ANALYSIS

A total of 2,449 tissue samples were genotyped from fish sampled in 2014–2016 (Table 3). Genotype data were collected from fishery samples as individual multi-locus genotypes for 96 SNPs (Table 2). Genotypes produced were imported and archived in the Gene Conservation Laboratory Oracle database, LOKI.

For QC analysis, 215 fish were re-analyzed beginning with the DNA extraction step (8.8% of the project). The average failure rate (representing the fish that could not be genotyped for a locus) was 2.7%. The overall discrepancy rate (fish that had a different genotype in the QC versus the original run) was 0.3%. Discrepancies did not appear to be related to a catastrophic laboratory error. Assuming that the discrepancies among analyses were due equally to errors during the original genotyping and to errors during QC, the project error rate is estimated to be 0.15%. Fourty-seven fish were missing genotypes for greater than 20% of markers, and 55 fish were determined to be duplicates (i.e. sampled more than once); these individuals were dropped from further analysis and were not included for mixture analysis.

MIXTURE ANALYSIS

Mixtures of fish representing catches by strata were analyzed for each year 2014–2016 (Table 4). Estimates were made for two sets of reporting groups: a) *U.S.* and *Canada*, (Figure 4) and b) *Lower Summer, Upper U.S. Fall*, and *Canada* (Figure 5).

There were some interannual differences in the fall stock compositions over the study period. In 2014 and 2015, trends were similar in that the *Canada* group was predominant in the first two strata (range: 56–68%), while the *Upper U.S. Fall* group dominated the third stratum (range: 52–58%). In contrast to 2014 and 2015, the *Upper U.S. Fall* group dominated all strata in 2016 (range: 54–74%), with lower proportions of the *Canada* group in all strata (range: 26–46%).

There were very few fish from the *Lower Summer* group in any stratum over all three years. This was expected since the majority of summer chum salmon spawning occurs downstream of the study area.

Currently all analysis of run size for Yukon River fall chum salmon is lacking information on stock composition of the harvest that is required to thoroughly evaluate stock productivities, spawning escapement goals, and management strategies. Assumptions have had to be made that all stock components have similar run timing through mixed-stock fisheries, similar exploitation rates, and that the catch for a particular stock is proportional to escapement abundance. This project provides additional information necessary to test the ability to produce stock composition estimates in fisheries that will help refine management tools for Yukon River fall chum salmon.

PROJECT PRODUCTS

A comprehensive ADF&G Fishery Data Series report detailing the results for 2014 through 2016 is expected in the spring of 2018. Results from this project will be presented at various fisheries and stakeholders meetings as needed.

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TABLES AND FIGURES

Table 1.–Reporting group, location, collection year, and sample size of baseline collections used in this study. Baseline populations are organized hierarchically into reporting groups for mixed stock analysis

Reporting Groups				
Broad-Scale	Fine-Scale	Location	Year(s) Collected	Sample Size
U.S.	Lower Summer	Black River	2006	95
		Atchuelinguk River	1989	51
		Andreafsky 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
		[1]Dakli River	2012	56
		Clear Creek	2002	95
		Henshaw Creek Early	2004	95
		S Fork Koyukuk River - Early	1996	93
		Melozitna River	1004, 2004, 2012	273
		Tozitna River	2003	95
	Upper U.S. Fall	Henshaw Creek Late	1995	62
		S Fork Koyukuk River - 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	Canada	Porcupine River at Old Crow	2007	95
		[2]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

[1] This collection is new to this study and was not included in the referenced WASSIP baseline.

[2] 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
Oke_ACOT-100	A	*Oke_LAMP2-186*	A	*Oke_U1022-139*	A
Oke_AhR1-78	B	*Oke_mgll-49*	A	*Oke_U1023-147*	A
Oke_arf-319	C	*Oke_MLRN-63*	A	*Oke_U1024-113*	A
Oke_ATP5L-105	A	*Oke_Moesin-160*	C	*Oke_U1025-135*	A
Oke_azin1-90	A	*Oke_nc2b-148*	A	*Oke_u200-385*	C
Oke_brd2-118	A	*Oke_ND3-69*	A	*Oke_U2006-109*	A
Oke_brp16-65	A	*Oke_NUPR1-70*	A	*Oke_U2007-190*	A
Oke_CATB-60	A	*Oke_pgap-111*	A	*Oke_U2011-107*	A
Oke_ccd16-77	A	Oke_pgap-92	A	*Oke_U2015-151*	A
Oke_CD81-108	A	*Oke_PPA2-635*	B	*Oke_U2025-86*	A
Oke_CD81-173	A	*Oke_psmd9-57*	A	*Oke_U2029-79*	A
Oke_CKS1-94	A	*Oke_rab5a-117*	A	*Oke_U2031-37*	A
Oke_CKS-389	D	*Oke_ras1-249*	B	*Oke_U2032-74*	A
Oke_Cr30	A	*Oke_RFC2-618*	C	*Oke_U2034-55*	A
Oke_Cr386	A	*Oke_RH1op-245*	C	*Oke_U2035-54*	A
Oke_ctgf-105	B	*Oke_RS27-81*	A	*Oke_U2037-76*	A
Oke_DCXR-87	A	*Oke_RSPRY1-106*	A	*Oke_U2041-84*	A
Oke_e2ig5-50	A	*Oke_serpin-140*	C	*Oke_U2043-51*	A
Oke_eif4g1-43	A	*Oke_slc1a3a-86*	A	*Oke_U2048-91*	A
Oke_f5-71	A	*Oke_sylc-90*	A	*Oke_U2050-101*	A
Oke_FANK1-166	A	*Oke_TCP1-78*	B	*Oke_U2053-60*	A
Oke_FBXL5-61	A	*Oke_Tf-278*	B	*Oke_U2054-58*	A
Oke_gdh1-191	A	*Oke_thic-84*	A	*Oke_U2056-90*	A
Oke_gdh1-62	A	*Oke_U1002-262*	A	*Oke_U2057-80*	A
Oke_GHII-3129	B	*Oke_U1008-83*	A	*Oke_U212-87*	C
Oke_glrx1-78	A	*Oke_U1010-251*	A	*Oke_u217-172*	C
Oke_GPDH-191	C	*Oke_U1012-241*	A	*Oke_U302-195*	B
Oke_GPH-105	B	*Oke_U1015-255*	A	*Oke_U502-241*	B
Oke_HP-182	B	*Oke_U1016-154*	A	*Oke_U504-228*	B
Oke_il-1racp-67	C	*Oke_U1017-52*	A	*Oke_U506-110*	B
Oke_IL8r2-406	A	*Oke_U1018-50*	A	*Oke_U507-286*	B
Oke_KPNA2-87	B	*Oke_U1021-102*	A	*Oke_U509-219*	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.– Stratum and number of fish sampled by each of 2–3 fishers participating in sampling the Tanana area subsistence chum salmon fishery in 2014–2016.

			Number of fish sampled				
Year	Stratum	Date range	Fisher 1	Fisher 2	Fisher 3	Total	Genotyped
2014	1	Aug. 15–31	76	95	24		
	2	Sept. 1–15	163	174	26		
	3	Sept. 16–30	161	36	0		
		Total	400	305	50	755	748
2015	1	Aug. 15–31	0	120	0		
	2	Sept. 1–15	168	105	34		
	3	Sept. 16–30	224	175	0		
		Total	387	400	34	821	798
2016	1	Aug. 15–31	129	136	0		
	2	Sept. 1–15	248	134	0		
	3	Sept. 16–30	122	134	0		
		Total	499	405	0	904	903

Table 4.– Stock composition estimates of U.S. and Canadian chum salmon harvested in the Tanana area subsistence fishery, 2014–2016. Estimates are given for two hierarchical reporting group levels, and include standard deviation (SD) and 90% lower and upper credibility interval bounds.

				Broad-Scale Reporting Groups		Fine-Scale Reporting Groups		
Year	Stratum (Dates)	Sample Size	Estimate	U.S.	Canada	Lower Summer	Upper U.S. Fall	Canada
2014	1	178	**Mean**	**0.323**	**0.677**	**0.003**	**0.321**	**0.677**
	(Aug 15–31)		SD	0.068	0.068	0.005	0.068	0.068
			Lower	0.211	0.564	0.000	0.209	0.564
			Upper	0.436	0.789	0.012	0.434	0.789
	2	340	**Mean**	**0.359**	**0.641**	**0.000**	**0.359**	**0.641**
	(Sept 1–15)		SD	0.057	0.057	0.001	0.057	0.057
			Lower	0.263	0.548	0.000	0.263	0.548
			Upper	0.452	0.737	0.000	0.452	0.737
	3	185	**Mean**	**0.583**	**0.417**	**0.000**	**0.583**	**0.417**
	(Sept 16–30)		SD	0.081	0.081	0.001	0.081	0.081
			Lower	0.447	0.288	0.000	0.447	0.288
			Upper	0.712	0.553	0.000	0.712	0.553
2015	1	117	**Mean**	**0.438**	**0.562**	**0.001**	**0.436**	**0.562**
	(Aug 15–31)		SD	0.120	0.120	0.007	0.120	0.120
			Lower	0.244	0.358	0.000	0.242	0.358
			Upper	0.642	0.756	0.002	0.642	0.756
	2	283	**Mean**	**0.394**	**0.606**	**0.000**	**0.394**	**0.606**
	(Sept 1–15)		SD	0.068	0.068	0.001	0.068	0.068
			Lower	0.282	0.493	0.000	0.282	0.493
			Upper	0.507	0.718	0.000	0.507	0.718
	3	373	**Mean**	**0.517**	**0.483**	**0.000**	**0.517**	**0.483**
	(Sept 16–30)		SD	0.056	0.056	0.001	0.056	0.056
			Lower	0.424	0.392	0.000	0.424	0.392
			Upper	0.608	0.576	0.000	0.608	0.576
2016	1	254	**Mean**	**0.540**	**0.460**	**0.000**	**0.539**	**0.460**
	(Aug 15–31)		SD	0.065	0.065	0.002	0.065	0.065
			Lower	0.435	0.352	0.000	0.435	0.352
			Upper	0.648	0.565	0.000	0.648	0.565
	2	374	**Mean**	**0.737**	**0.263**	**0.000**	**0.737**	**0.263**
	(Sept 1–15)		SD	0.063	0.063	0.001	0.063	0.063
			Lower	0.631	0.161	0.000	0.631	0.161
			Upper	0.839	0.369	0.000	0.839	0.369
	3	243	**Mean**	**0.609**	**0.391**	**0.000**	**0.609**	**0.391**
	(Sept 16–30)		SD	0.077	0.077	0.001	0.077	0.077
			Lower	0.477	0.270	0.000	0.477	0.270
			Upper	0.730	0.523	0.000	0.730	0.523

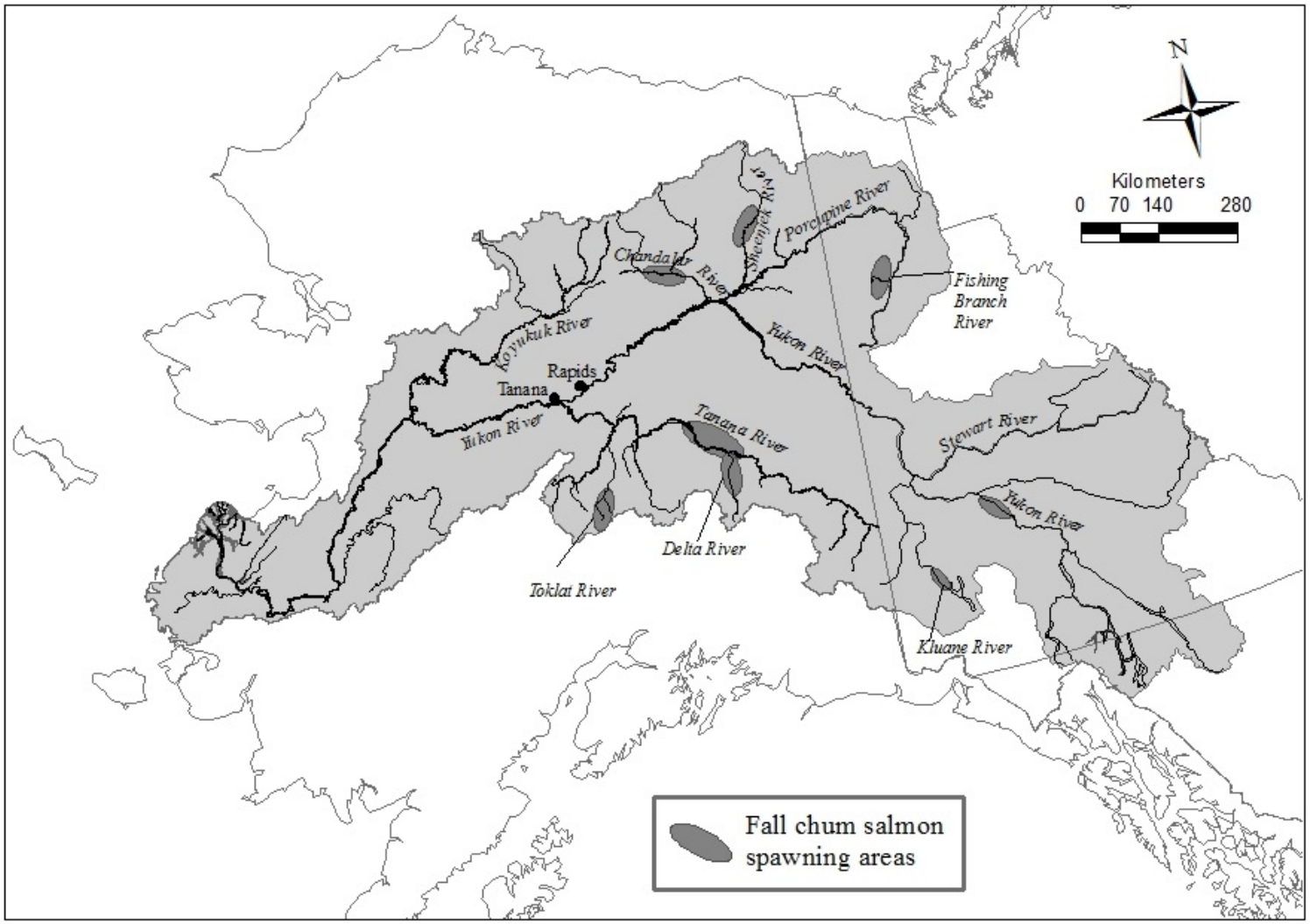

Figure 1.–Map of fall chum salmon spawning areas within the Yukon drainage.

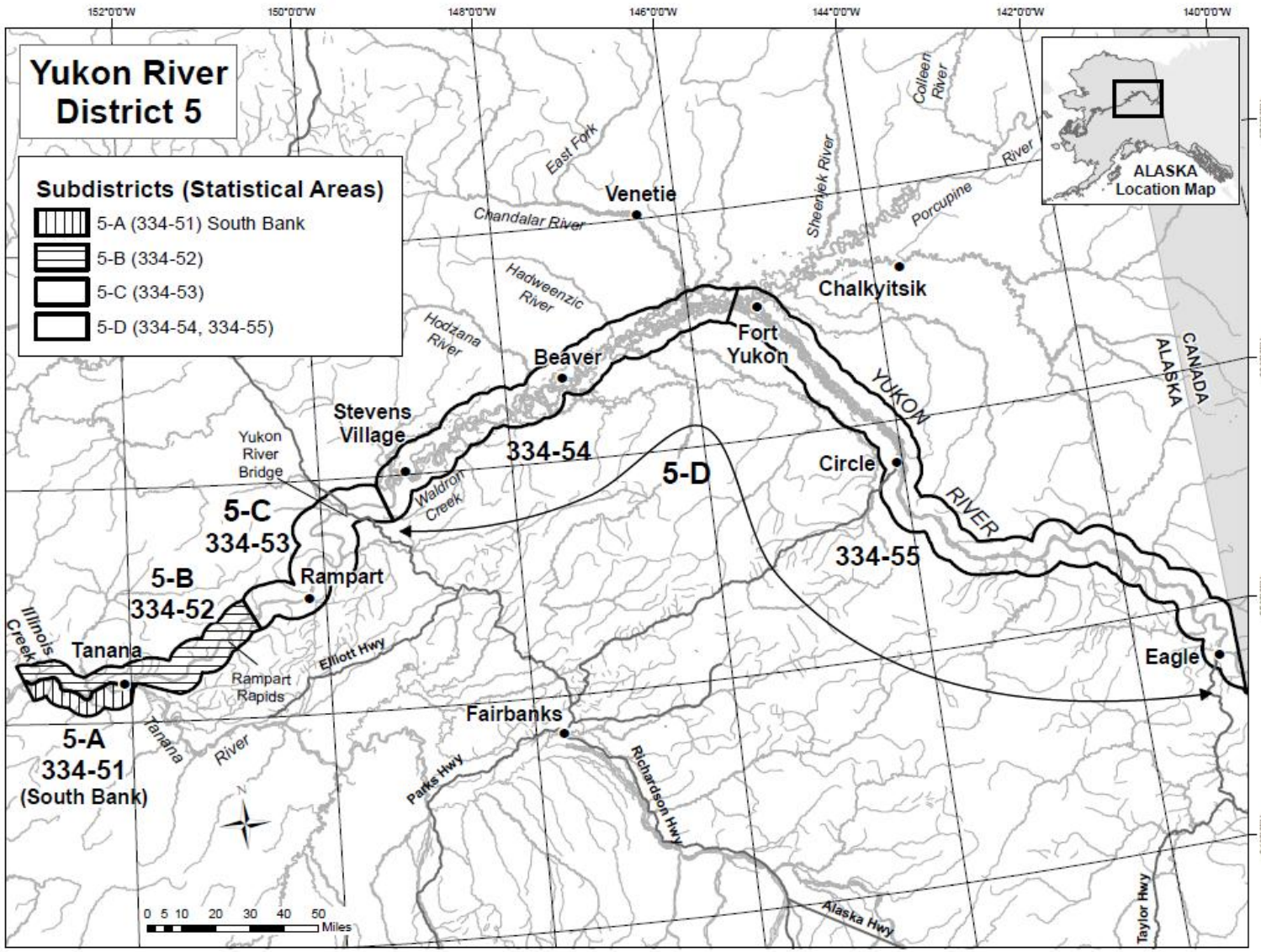

Figure 2.–Map of District 5 Yukon Management Area showing subdistricts and commercial statistical areas. (Area of interest for this study is Subdistrict 5-B.)

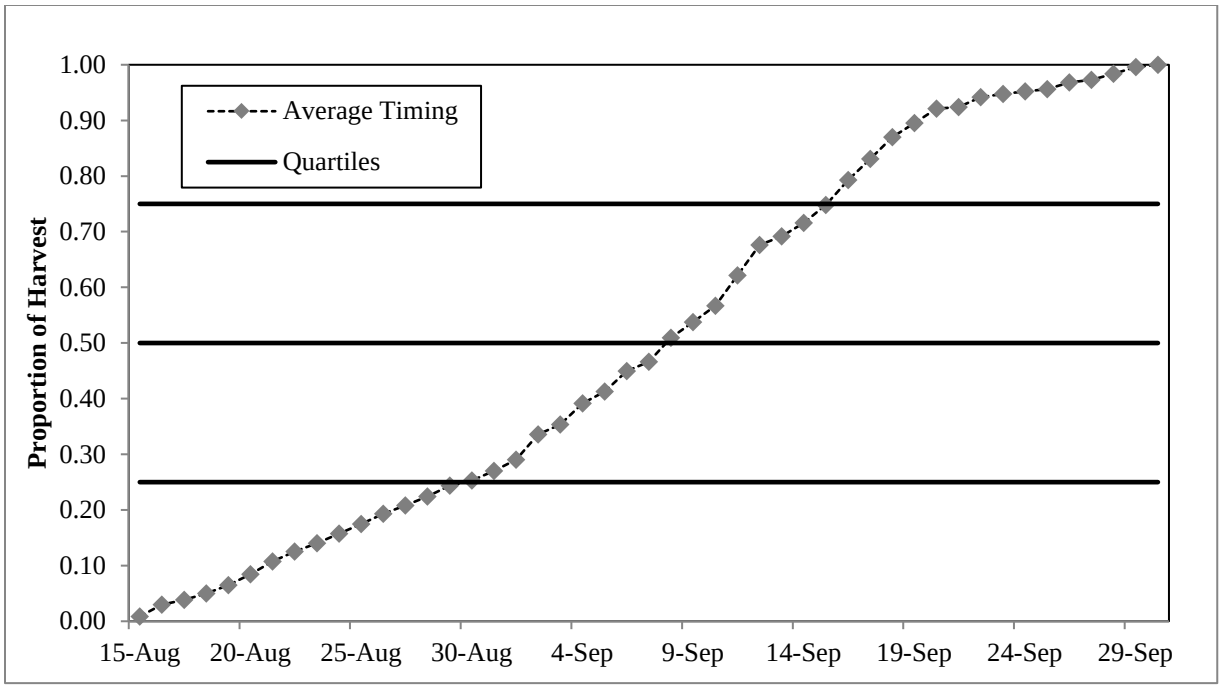

Figure 3.–Timing of fall chum salmon harvest in the community of Tanana, based on the average proportion by day, 2003–2012.

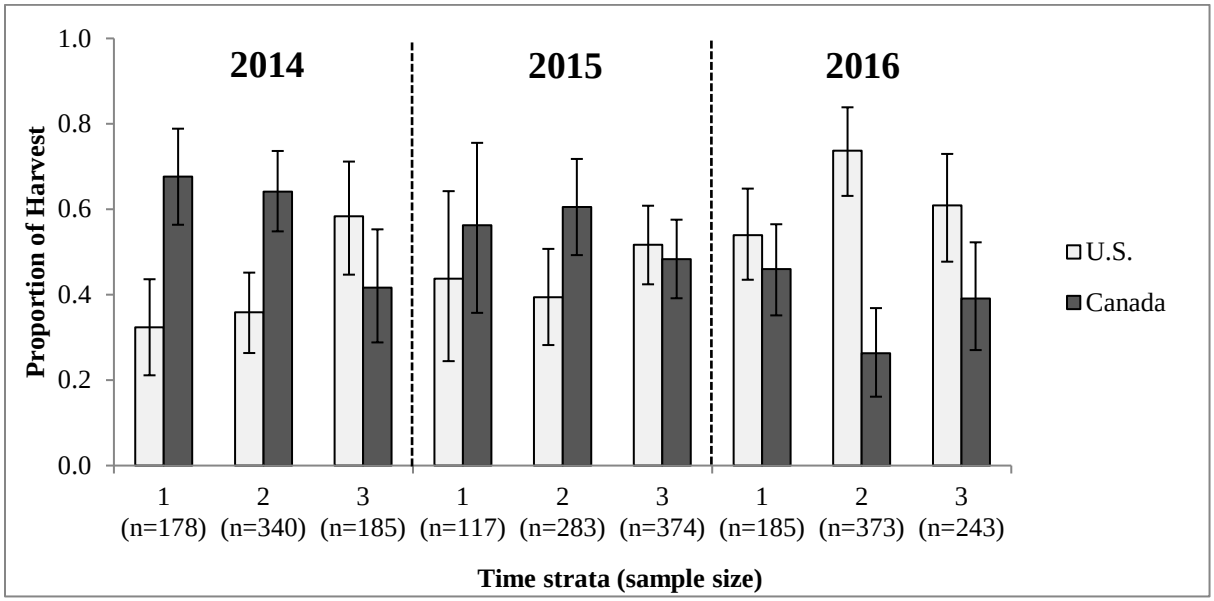

Figure 4.–Stock composition estimates of *U.S.* and *Canada* chum salmon harvested in the Tanana area subsistence fishery in 2014–2016 for each of three time strata: Stratum 1 (Aug 15–31), Stratum 2 (Sept 1–15), and Stratum 3 (Sept 15–30). Sample size is noted (n).

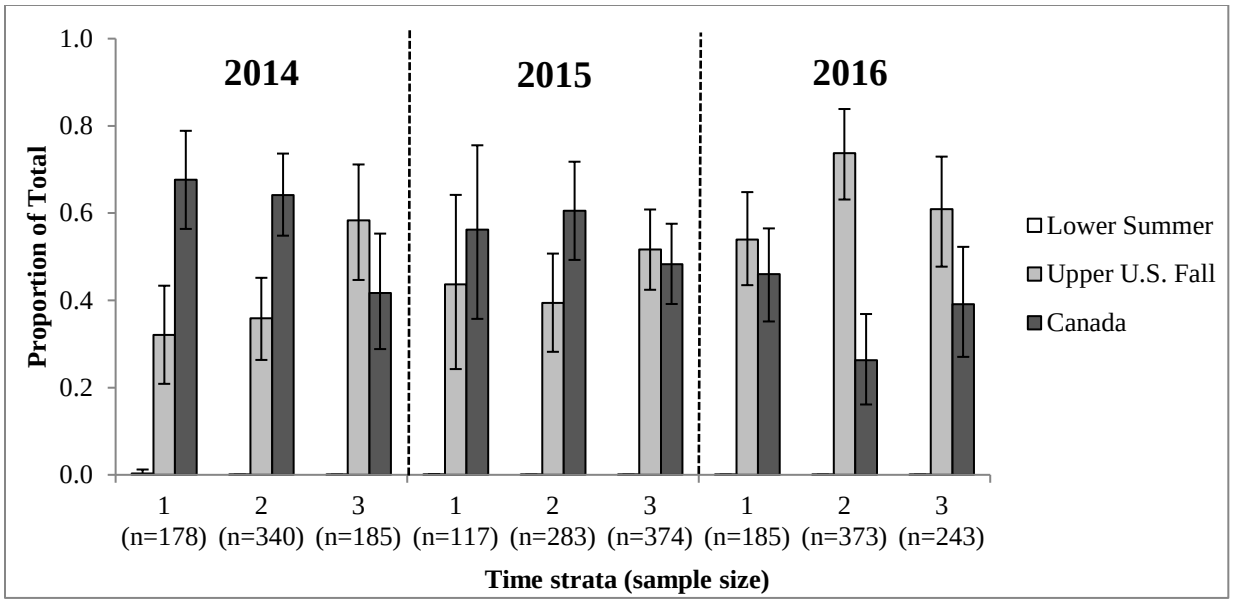

Figure 5.– Stock composition estimates of *Lower Summer*, *Upper U.S. Fall*, and *Canada* chum salmon harvested in the Tanana area subsistence fishery in 2014–2016 for each of three time strata: Stratum 1 (Aug 15–31), Stratum 2 (Sept 1–15), and Stratum 3 (Sept 15–30). Sample size is noted (n).