Inseason genetic stock identification of Chinook salmon caught in Lower Yukon River test fisheries, 2009.

Final Report to the Yukon River Panel

For project titled: "Inseason genetic stock identification of Chinook salmon harvests on the Yukon River, 2009; a pilot study to determine feasibility and application."

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by

Nicholas A. DeCovich

and

Danielle F. Evenson

Nicholas A DeCovich, Danielle F Evenson
Alaska Department of Fish and Game, Division of Commercial Fisheries, 333 Raspberry Rd. Anchorage, AK, Alaska 99701.

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Symbols and Abbreviations

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

Weights and measures (metric)	
centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

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

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

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

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

Measures (fisheries)	
fork length	FL
mideye-to-fork	MEF
mideye-to-tail-fork	METF
standard length	SL
total length	TL

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

This study evaluated the feasibility of inseason mixed stock analysis of Chinook salmon (*Oncorhynchus tshawytscha*) harvested in test fisheries of the Lower Yukon River. We utilized a 27 population, 42 single nucleotide polymorphism (SNP) baseline to analyze the stock composition of mixed fishery samples. In 2009, it was difficult to detect pulses in the Lower Yukon Test Fishery (LYTF), and 1221 fish from the LYTF and Pilot Station test fishery, representing three stratwere analyzed. The estimated proportion of Canadian-origin Chinook salmon in each stratum ranged from a high of 70% in the first stratum to a low of 43% in the third stratum. The low overall run strength combined with inseason genetic information on the Canadian-bound proportion of the run highlighted concerns regarding the run's capacity to meet the escapement goal at the Canadian border and provide for subsistence harvest opportunity. Consequently, fishery managers implemented reductions in the subsistence fishery and delayed the summer chum salmon commercial fishery.

Introduction

Management of the Yukon River salmon fishery is difficult and complex because of the inability to determine stock-specific abundance and timing, overlapping multi-species salmon runs, the gauntlet nature of Yukon River fisheries, allocation issues between lower river and upper river Alaskan fishermen, allocation and conservation issues between Alaska and Canada, and the immense size of the drainage. Salmon fisheries within the Yukon River may harvest stocks that are up to several weeks and thousands of miles from their spawning grounds. It is not possible to manage for individual stocks in most areas where commercial and subsistence fisheries occur.

A primary objective for managers is to allow a target range of Canadian-origin Chinook salmon to pass the international border, based on the Yukon River Salmon Agreement, a bilateral international treaty. Hence, successful management of mixed stock fisheries depends in large part on reliable indices of abundance and run timing, and estimates of stock composition in the run and harvest (Larkin 1981; Allendorf et al. 1987). On the Yukon River, while significant resources are expended towards estimating Chinook salmon run size inseason, managers have no inseason information on the stock composition of the Chinook salmon run or harvest. Therefore, knowing the abundance of Canadian-origin Chinook salmon in the commercial catch, or from abundance sampling programs, may inform management decisions made during the fishing season.

Since 2004, the stock composition of Chinook salmon harvests in the subsistence and commercial Chinook salmon fisheries of the Yukon River has been obtained by genetic stock identification (GSI), based on the comprehensive baseline of DNA markers (Templin et al. 2006). In 2006, stock identification of the harvest used single nucleotide polymorphism (SNP) marker baseline which had been augmented by increasing the populations represented and the number of SNP markers surveyed (Templin et al. 2008).

The SNP marker baseline has been shown to provide more complete coverage and greater resolution with the necessary levels of precision and accuracy than was previously available from scale pattern analysis. This same baseline was used for stock identification in 2007 and for this study (Table 1 or Appendix 1).

The primary application of stock-specific information has been to determine the proportion of Canadian-origin Chinook salmon in fishery harvests, or test fishery indices, in U.S. waters of the Yukon River (JTC 2008). These data have ramifications for the management of U.S and Canadian fisheries, particularly because the U.S. must meet treaty-defined goals for passage of Chinook salmon into Canada.

Objectives

Analyze Chinook salmon tissue samples from a maximum of five temporal periods in the Lower Yukon River in 2009 to estimate the stock composition of represented test fisheries inseason. As no Chinook salmon-directed commercial fishery was anticipated for 2009, all samples were to be obtained from test fisheries. Samples representing the three main pulses of Chinook salmon entering the Yukon River were to be collected from the LYTF. Samples representing the first two main pulses were to be sampled from the Pilot Station Test Fishery. The utility of these estimates was to be evaluated for the purpose of informing inseason management decisions.

Methods

Baseline Analysis

A slightly modified version of the 25 population baseline described in Templin et al. (2008) was used for this analysis. Two populations were added; the Chatanika River in the Tanana River drainage and a mainstem spawning population collected near Minto. The SNP set used was also changed slightly and included 42 loci. In the 2007 and 2008 version of the baseline, if linkage disequilibrium was significant in more than half of the collections, we produced composite haplotypes for each fish by combining the genotypes from these linked markers and treated them as a single locus in further analyses. For 2009, we instead removed one locus from each pair of putatively linked loci.

The effectiveness of this modified baseline at discriminating the reporting groups used for GSI was re-evaluated using a simulation approach. Simulations were performed 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=400) 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.

Sample collection

Alaska Department of Fish and Game (ADF&G) field crews collected tissue (axillary process) during normal age, sex, and length (ASL) sampling of the LYTF and Pilot Station Test Fishery. LYTF samples were collected over the course of the Chinook salmon run (approximately June 1 to July 15, 2009) from all three mouths of the Yukon River using set gillnets with 8.5-inch mesh. Pilot Station samples were collected from approximately June 9 through July 19, 2009, using a broad array of mesh size drift gillnets, ranging from 2.75-inch to 8.5-inch stretch mesh. An attempt was made to sample distinct pulses of Chinook salmon passing through the test fisheries. Pulses are identified by increases in catch per unit effort (CPUE) for a sustained period of 3-5 days followed by a substantial decrease in CPUE. Tissues were clipped from each salmon, placed in an individually labeled plastic tube, and preserved in denatured ethanol. Samples were flown back to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage and analyzed with results reported within 36 hours of receipt at the GCL.

Laboratory analyses

All Chinook salmon samples collected were genotyped by the GCL for 48 SNP loci using a BioMark 48.48 Dynamic Array (Fluidigm http://www.fluidigm.com/biomark_genotyping.htm). The BioMark 48.48 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 48 inlets to accept the sample DNA from each individual fish, and on the other are 48 inlets to accept the assays for each of the SNP markers. Once in the wells, the components are pressurized into the chip using the NanoFlex 4-IFC Controller. The 48 samples and 42 assays (only 42 assays were used for this analysis) are then systematically combined into 2,304 parallel reactions. Each reaction was conducted in a 6.75 nL volume consisting of 1xTaqMan Universal Buffer (Applied Biosystems), 1.5 U AmpliTaq Gold DNA Polymerase (Applied Biosystems), 9 mM of each polymerase chain reaction (PCR) primer, 2 mM of each probe, 1xDA Assay Loading Buffer (Fluidigm), 12.5xROX (Invitrogen), and 0.01% Tween-20. Thermal cycling were performed on a BioMark IFC Cycler as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92° for 15 s and 60° for 1 min. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using BioMark Genotyping Analysis software (Fluidigm).

Genotypes collected were entered into the Gene Conservation Laboratory Oracle database, LOKI. Quality control measures were performed post-season and included reanalysis of 8% of each collection for all markers to ensure that genotypes were reproducible and to identify laboratory errors.

Mixture Analysis

Stock composition estimates for the stock groups of management interest were generated using BAYES (Pella and Masuda 2001). Individual population estimates were first calculated, and then summed into reporting regions (stocks). The 90% confidence interval for all group contribution estimates was computed from the posterior distribution of stock composition estimates generated during the estimation procedure.

Stock composition estimates were reported for three hierarchical levels when sample sizes were > 200 as follows: 1) country of origin (U.S and Canada), 2) broad scale (Lower Yukon, Middle Yukon, and Canada), and 3) fine scale (Lower Yukon, Tanana, Upper U.S. Yukon, Canada Border, Pelly, Carmacks and Takhini). When sample sizes were < 200, only the first two levels of the hierarchy were reported. Increasing the resolution to three reporting groups in the U.S. (Lower River, Tanana, and Upper Koyukuk/Upper U.S. Yukon) has been supported by simulation studies of the baseline.

Results

Baseline Analysis

The 27 population baseline was evaluated using 42 SNP loci (Table 2). All fine-scale reporting regions had mean correct allocations of >90% for the 100% simulation tests. The reader is referred to Templin et al. (2008) for a comprehensive discussion of the baseline analysis results.

Mixture Analysis

Difficult fishing conditions in the LYTF made it impossible to detect specific pulses of Chinook salmon. Therefore, the decision was made to shift some of the inseason analysis efforts to the Pilot Station test fishery for the purpose of characterizing the stock composition of the run.

A total of 1040 Chinook salmon were sampled from the LYTF in 2009. Of these, 511 were from the Big Eddy site and 529 were from Middle Mouth and North Mouth (henceforth referred to as Middle Mouth) sites combined. A subsample of 500 Chinook salmon, 300 and 200 from Big Eddy and Middle Mouth respectively (representing two strata) were analyzed for this study. A total of 868 samples were collected from the Pilot Station test fishery, and 721 of these fish (representing three strata) were analyzed inseason. All remaining samples from this fishery were subsequently analyzed post-season (Table 1) (Fig. 1). Each sample was analyzed for 42 SNP loci (Table 2). Quality control analysis indicated an overall genotyping success rate of 96.61% and an overall discrepancy rate between the initial and re-analyzed genotypes of 0.02%. The success rate represents the number of samples that amplified successfully during PCR, averaged over all loci. The discrepancy rate is based on the re-analysis of 8% of the total number of samples.

An attempt was made to identify the first pulse of Chinook salmon entering the LYTF, and samples collected through June 17 (Big Eddy) and June 18 (Middle Mouth) were flown to the GCL and analyzed (Figure 2). The conclusion of the first pulse was identified by a decline in the daily catch from a high of 54 on June 16, and 296 samples caught through June 18 were flown back to Anchorage and analyzed. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF from June 3 through June 18 was 63% for Big Eddy (Table 3) and 53% for Middle Mouth (Table 4).

The conclusion of a second pulse through the LYTF was detected by a decline in the daily catch from a high of 70 on June 18 and 204 samples caught between June 18 and June 22 were flown to the GCL and analyzed (Figure 2). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF for this time period was 63% for Big Eddy (Table 3) and 45% for Middle Mouth (Table 4).

Samples from the Pilot Station test fishery caught through June 15 were also flown to Anchorage and analyzed concurrently with the samples from the first pulse at the LYTF. Early season conditions made sampling the first part of the run difficult at the LYTF and Pilot Station, and early arriving fish were likely missed at both locations. In general, sampling at Pilot Station was done in proportion to the passage estimate determined by the sonar project (Figure 3). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in Pilot Station test fishery for this time period was 70% (Table 5; Figure 4).

An additional two inseason analyses were done on samples from Pilot Station. Pulses were difficult to detect in this fishery, and samples were flown back to Anchorage based on the availability of a U.S. Fish and Wildlife Service aircraft making scheduled flights between Pilot Station and Anchorage. The strata used for these inseason analyses are shown in Figure 3 and represent the samples caught between June 16-24 (stratum 2) and June 26-29 (stratum 3). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the Pilot Station Test Fishery for these two time periods (strata 2 and 3) was 47% and 43%, respectively (Table 5; Figure 4).

The estimates for each of the four separate inseason analyses were available within 36 hours of receipt of samples at the GCL.

Upon completion of the ADF&G Pilot Station sonar project, data on daily passage estimates were available for the entire season, and more samples were available from Chinook salmon representing the fourth quarter of the run. After reviewing this information, new strata were constructed (Figure 5). Once the additional samples were assayed, stock composition estimates were re-calculated for the new strata. The Canadian-origin Chinook salmon present in the Pilot Station test fishery ranged from a high of 68% in stratum 1 to a low of 17% in stratum 4 (Table 6; Figure 6).

Discussion

The 2009 Yukon River Chinook salmon run was below average. The preseason outlook predicted a below average to poor Chinook salmon run, and it was clear that projected Chinook salmon run abundance would not support normal subsistence harvests in Alaska (approximately 50,000 Chinook salmon), meet escapement goals in Alaska, and meet the interim management escapement goal (IMEG) of >45,000 fish in Canada agreed to and adopted by the Yukon River Panel. Despite low overall run strength estimated at Pilot Station sonar early in the run, inseason GSI information on the Canada-bound proportion of the run identified a stronger presence of these stocks than had been documented during 2007 and 2008.

The preseason management plan called for no Chinook salmon-directed commercial fishery, a closure of subsistence fishing activity on the first pulse of mainstem Chinook salmon, and reduced subsistence fishing activity thereafter. Although difficult for Alaskan fishermen, these restrictions ensured most escapement goals were met, including border passage of Canadian-origin Chinook salmon above the minimum required by treaty agreement.

The proposed objective of sampling the three pulses of Chinook salmon passing through the LYTF was not achieved. The performance of the LYTF was affected by high water and heavy debris. Ice dams moving down the river caused substantial flooding along the entire U.S. portion of the Yukon River. This flooding coincided with the start of the Chinook salmon run. Once it was determined that pulses would be undetectable in the LYTF, efforts were shifted to analyzing catches from the Pilot Station Test Fishery. Post-season examination of daily fish passage at Pilot Station revealed that the initial inseason strata could be modified to create four new strata with the fourth strata represented by all available samples through the end of the season. These strata were intended to represent the four quartiles of the run passing through the Pilot Station test fishery. The major difference between the inseason and post-season estimates is the dramatic increase in Lower Yukon Stocks in the fourth strata. This result was expected based on previous years' GSI studies showing the bulk of the Canadian-origin component of the run to pass through the lower river by the mid-point of the run (Templin et al. 2006, Templin et al. 2008, DeCovich and Templin 2009).

This pilot study showed that rapid production of stock composition estimates is possible for lower Yukon River Chinook salmon fisheries. Frequent flight service from Emmonak and the availability of a U.S Fish and Wildlife service aircraft servicing Pilot Station enabled timely delivery of samples, and all estimates were provided within 36 hours of receipt at the GCL.

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References

Allendorf, F.W., and N. Ryman. 1987. Genetic management of hatchery stocks. In: Population Genetics and Fisheries Management, edited by N. Ryman and F.M. Utter. University of Washington Press, pp. 141-159.

Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (Version 3.2): Statistics program for analyzing mixtures. Journal of Heredity 91:509-511.

DeCovich, N. A., and W. D. Templin. 2009. Genetic stock identification of Chinook salmon harvest on the Yukon River 2007. Alaska Department of Fish and Game, Fishery Data Series No. 09-39, Anchorage.

JTC (Joint Technical Committee of the Yukon River US/Canada Panel). 2008. Summary and 2008 season outlook. Alaska Department of Fish and Fisheries, Regional Information Report No. 3A08-01, Anchorage.

Larkin, P.A. 1981. A perspective on stock genetics and salmon management. Canadian Journal of Fisheries and Aquatic Sciences 38:1469-1475.

Pella, J. and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fisheries Bulletin 99(1):151-167.

Smith, C.T., C.M. Elfstrom, J.E. Seeb, L.W. Seeb. 2005a. Use of sequence data from rainbow trout and Atlantic salmon for SNP detection in Pacific salmon. Molecular Ecology 14:4193-4203.

Smith C.T., J.E. Seeb, P. Schwenke, L.W. Seeb. 2005b. Use of the 5’-nuclease reaction for SNP genotyping in Chinook salmon. Transactions of the American Fisheries Society 134:207-217.

Smith C.T., A. Antonovich, W.D. Templin, C.M. Elfstom, S.R. Narum, and L.W. Seeb. 2007. Impacts of marker class bias relative to locus-specific variability on population inferences in Chinook salmon; a comparison of SNPs to STRs and allozymes. Transactions of the American Fisheries Society. 136:1647-1687.

Templin, W. D., J. M. Berger, N. A. DeCovich, and L. W. Seeb. 2006. Genetic stock identification of Chinook salmon harvest on the Yukon River in 2004. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report No. 3A06-06, Anchorage.

Templin, W. D., N. A. DeCovich, and L. W. Seeb. 2008. Genetic stock identification of Chinook salmon harvest on the Yukon River, 2006. Alaska Department of Fish and Game, Division of Commercial Fisheries, Fishery Data Series No. 08-15, Anchorage.

Table 1. Chinook salmon fishing districts, gear types, target sample sizes, sample sizes, and number analyzed inseason from Yukon River test fisheries, 2009.

District	Test Fishery	Gear Type	Target	Sample size	Number Analyzed
Y-1	LYTF-Big Eddy	Set gillnet	600	511	300
Y-1	LYTF-Middle Mouth	Set gillnet	600	529	200
	Total LYTF		1200	1040	500
Y-2	Pilot Station	Drift gillnet	600	868	721/ 868[1]
	Total		**1800**	**1908**	**1221/ 1368**[1]

[1]Represents the number of samples analyzed post-season.

Table 2. Single nucleotide polymorphism loci and their source used in this study.

Locus	**Source**
GTH2B-550	GAPs locus
NOD1	GAPs locus
Ots_E2-275	Smith et al. 2005a
Ots_arf-188	Smith et al. 2005a
Ots_AsnRS-60	Smith et al. 2005a
E9BAC	GAPs locus
Ots_ETIF1A	GAPs locus
Ots_FARSLA-220	Smith et al. 2007
Ots_FGF6A	Unpublished
Ots_GH2	Smith et al. 2005b
Ots_GPDH-338	Smith et al. 2005a
Ots_GPH-318	Smith et al. 2007
Ots_GST-207	Smith et al. 2007
Ots_hnRNPL-533	Smith et al. 2007
Ots_HSP90B-100	Smith et al. 2007
Ots_IGF-I.1-76	Smith et al. 2005a
Ots_Ikaros-250	Smith et al. 2005a
Ots_il-1racp-166	Smith et al. 2005a
Ots_LEI-292	Smith et al. 2007
Ots_MHC1	Smith et al. 2005b
Ots_MHC2	Smith et al. 2005b
Ots_ZNF330-181	Smith et al. 2005a
Ots_LWSop-638	Smith et al. 2005a
Ots_SWS1op-182	Smith et al. 2005a
Ots_P450	Smith et al. 2005b
Ots_P53	Smith et al. 2005b
Ots_Prl2	Smith et al. 2005b
Ots_ins-115	Smith et al. 2005a
Ots_SClkF2R2-135	Smith et al. 2005a
Ots_SERPC1-209	Smith et al. 2007
Ots_SL	Smith et al. 2005b
Ots_TAPBP	GAPs locus
Ots_Tnsf	Smith et al. 2005b
Ots_u202-161	Smith et al. 2005a
Ots_u211-85	Smith et al. 2005a
Ots_U212-158	Smith et al. 2005a
Ots_u4-92	Smith et al. 2005a
Ots_u6-75	Smith et al. 2005a
Ots_Zp3b-215	Smith et al. 2005a
RAG3	GAPs locus
S7-1	GAPs locus
unkn526	GAPs locus

Table 3. Estimated proportional contributions (Est), standard deviations (S.D.), and 90% credibility intervals by reporting group of Chinook salmon caught in the Lower Yukon Test Fishery, Big Eddy site, from stratum 1 and 2 in 2009. The estimated reporting group proportions are given for each of three hierarchical levels. Samples sizes (N) allowed for country-of-origin and broad-scale estimates only.

	Stratum 1			Stratum 2		
	June 5-17			June 18-22		
	N =	196		N =	104	
Reporting Group	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**
Country						
United States	0.375	0.048	(0.298-0.455)	0.368	0.070	(0.255-0.487)
Canada	0.625	0.048	(0.545-0.702)	0.632	0.070	(0.513-0.745)
Broad-scale						
Lower Yukon	0.074	0.024	(0.037-0.117)	0.104	0.037	(0.051-0.170)
Middle Yukon	0.301	0.047	(0.225-0.380)	0.265	0.068	(0.157-0.381)
Canada	0.625	0.048	(0.545-0.702)	0.632	0.070	(0.513-0.745)

Table 4. Estimated proportional contributions (Est), standard deviations (S.D.), and 90% credibility intervals by reporting group of Chinook salmon caught in the Lower Yukon Test Fishery, Middle Mouth site, from stratum 1 and 2 in 2009. The estimated reporting group proportions are given for each of three hierarchical levels. Samples sizes (N) allowed for country-of-origin estimates only.

	Stratum 1			Stratum 2		
	June 5-18			June 18-22		
	N =	100		N =	100	
Reporting Group	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**
Country						
United States	0.474	0.069	(0.362-0.589)	0.549	0.062	(0.447-0.650)
Canada	0.526	0.069	(0.411-0.638)	0.451	0.062	(0.350-0.553)

Table 5. Estimated proportional contributions (Est), standard deviations (S.D.), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station Test fishery, as analyzed inseason, from stratum 1, 2, and 3 in 2009. The estimated reporting group proportions are given for each of three hierarchical levels. The estimated group proportions are given for each of three hierarchical levels.

	Stratum 1			Stratum 2			Stratum 3		
	June 9-15			June 16-24			June 26-29		
	N =	121		N =	441		N =	159	
Reporting Group	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**
Country									
United States	0.297	0.051	(0.217-0.384)	0.530	0.036	(0.470-0.590)	0.570	0.050	(0.488-0.651)
Canada	0.703	0.051	(0.616-0.783)	0.470	0.036	(0.410-0.530)	0.430	0.050	(0.349-0.512)
Broad-scale									
Lower Yukon	0.047	0.032	(0.000-0.106)	0.165	0.024	(0.127-0.207)	0.366	0.049	(0.286-0.448)
Middle Yukon	0.250	0.054	(0.165-0.342)	0.364	0.038	(0.302-0.427)	0.204	0.048	(0.129-0.286)
Canada	0.703	0.051	(0.616-0.783)	0.470	0.036	(0.410-0.530)	0.430	0.050	(0.349-0.512)
Fine-scale									
Lower Yukon				0.165	0.024	(0.127-0.207)			
Upper U.S. Yukon				0.163	0.054	(0.082-0.256)			
Tanana				0.202	0.045	(0.123-0.273)			
Canada Border				0.046	0.027	(0.000-0.092)			
Pelly				0.168	0.048	(0.093-0.250)			
Carmacks				0.245	0.041	(0.178-0.312)			
Takhini				0.012	0.014	(0.000-0.039)			

Table 6. Estimated proportional contributions (Est), standard deviations (S.D.), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station Test fishery, as analyzed post-season, from stratum 1, 2, 3, and 4 in 2009. The estimated reporting group proportions are given for each of three hierarchical levels.

	Stratum 1			Stratum 2			Stratum 3			Stratum 4		
	June 9-16			June 17-22			June 23-29			June 30 - July 19		
	N = 133			N = 309			N = 280			N = 145		
Reporting Group	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**	**Est**	**S.D.**	**90%CI**
Country												
United States	0.321	0.051	(0.241-0.408)	0.473	0.040	(0.408-0.539)	0.589	0.042	(0.519-0.658)	0.828	0.036	(0.767-0.883)
Canada	0.679	0.051	(0.592-0.759)	0.527	0.040	(0.461-0.592)	0.411	0.042	(0.342-0.481)	0.172	0.036	(0.117-0.233)
Broad-scale												
Lower Yukon	0.038	0.027	(0.000-0.088)	0.153	0.027	(0.111-0.200)	0.288	0.036	(0.229-0.348)	0.691	0.043	(0.620-0.759)
Middle Yukon	0.283	0.053	(0.199-0.374)	0.320	0.040	(0.255-0.388)	0.301	0.043	(0.231-0.373)	0.137	0.035	(0.082-0.199)
Canada	0.679	0.051	(0.592-0.759)	0.527	0.040	(0.461-0.592)	0.411	0.042	(0.342-0.481)	0.172	0.036	(0.117-0.233)
Fine-scale												
Lower Yukon				0.153	0.027	(0.111-0.200)	0.288	0.036	(0.229-0.348)			
Upper U.S. Yukon				0.094	0.048	(0.015-0.177)	0.144	0.052	(0.065-0.234)			
Tanana				0.226	0.045	(0.152-0.299)	0.157	0.046	(0.084-0.233)			
Canada Border				0.074	0.031	(0.027-0.127)	0.025	0.020	(0.000-0.062)			
Pelly				0.232	0.056	(0.140-0.326)	0.105	0.059	(0.003-0.204)			
Carmacks				0.213	0.045	(0.144-0.291)	0.258	0.049	(0.179-0.340)			
Takhini				0.008	0.012	(0.000-0.033)	0.023	0.021	(0.000-0.062)			

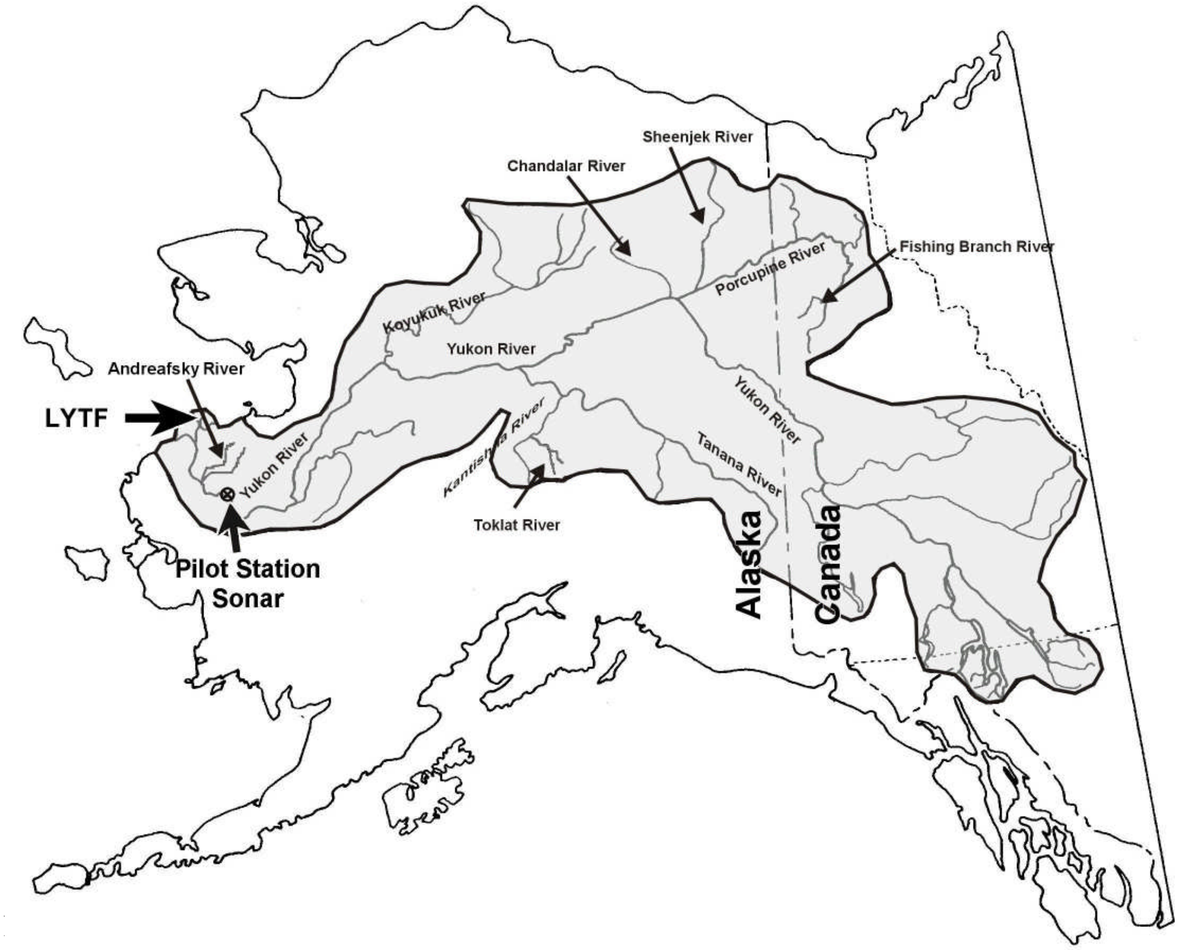

Figure 1. The LYTF and Pilot Station site location for the Yukon River drainage

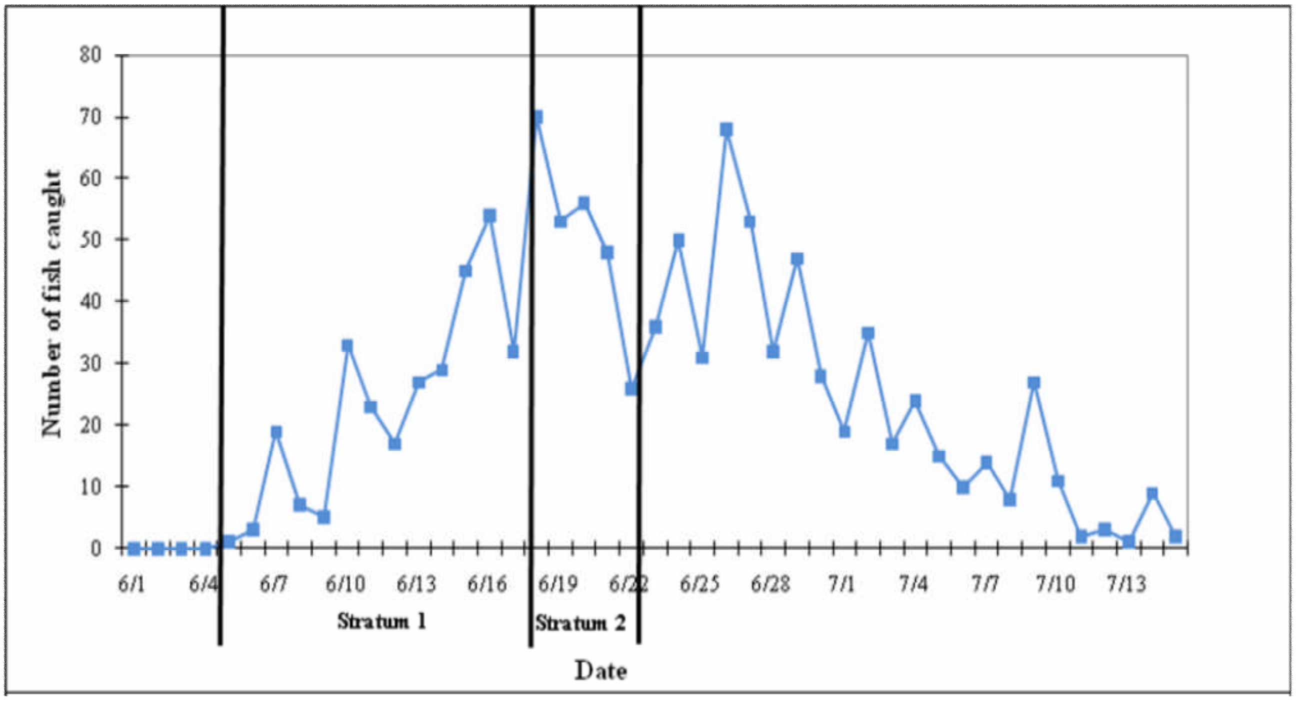

Figure 2. Daily catch of Chinook salmon in the LYTF, 2009. Vertical lines denote the temporal separation of collections for creating strata for GSI estimates.

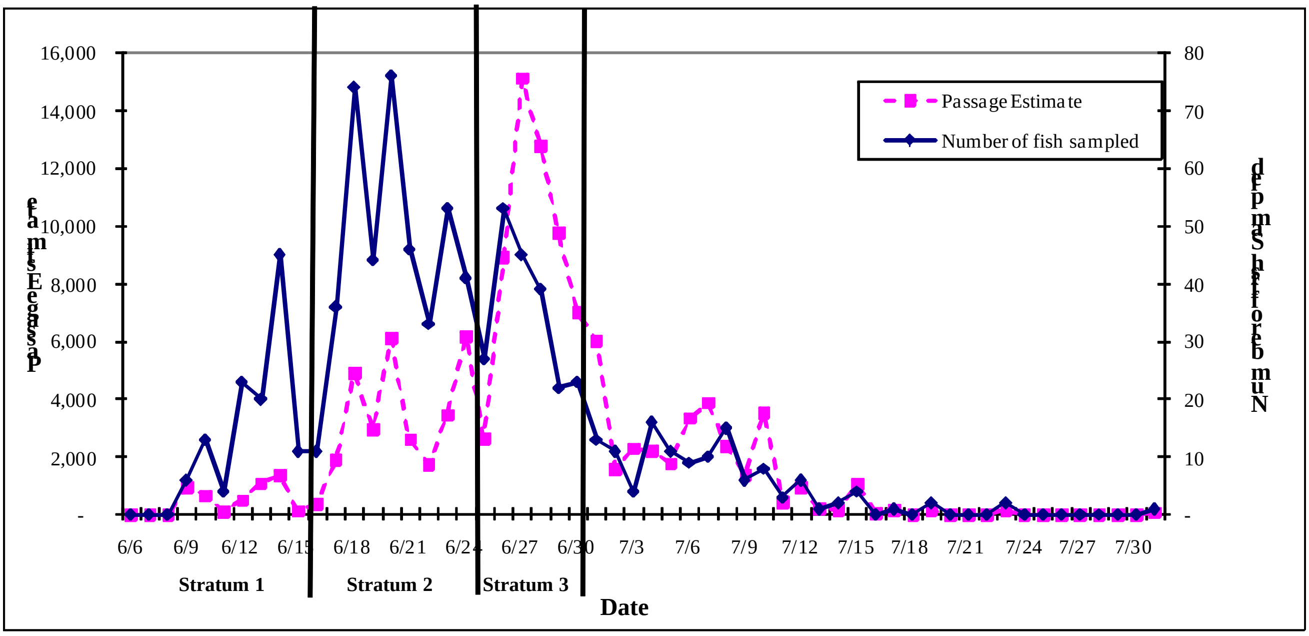

Figure 3. Daily catch of Chinook salmon in the Pilot Station Test Fishery (right-hand scale) and daily passage estimates (left-hand scale), 2009. Vertical lines denote the temporal separation of collections for creating inseason strata for GSI estimates.

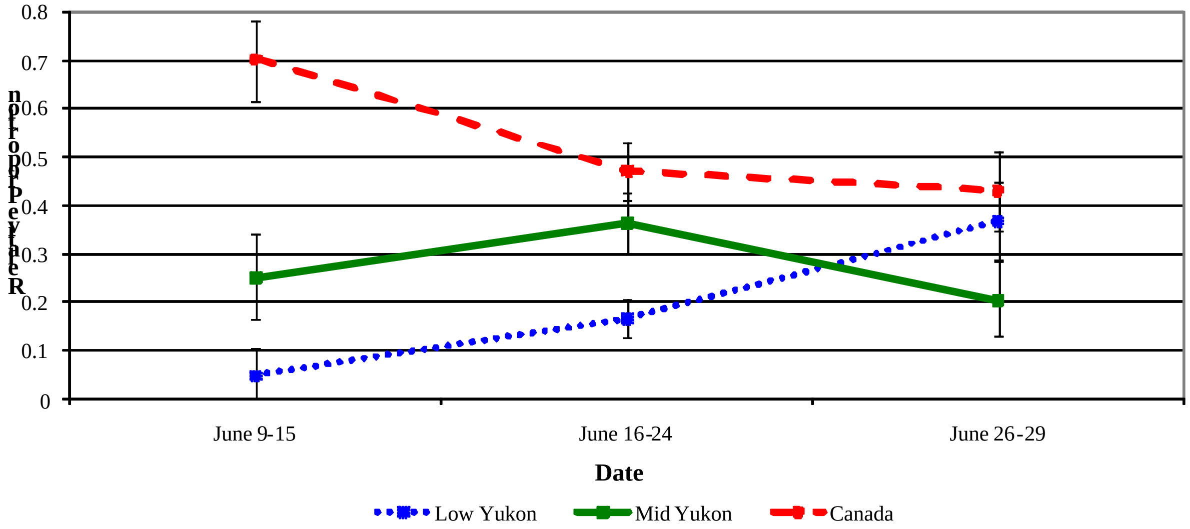

Figure 4. Relative stock composition of three broad-scale reporting groups in the Chinook salmon caught in the Pilot Station Test Fishery, as analyzed inseason, 2009. Error bars denote the bounds of the 90% bootstrap credibility interval.

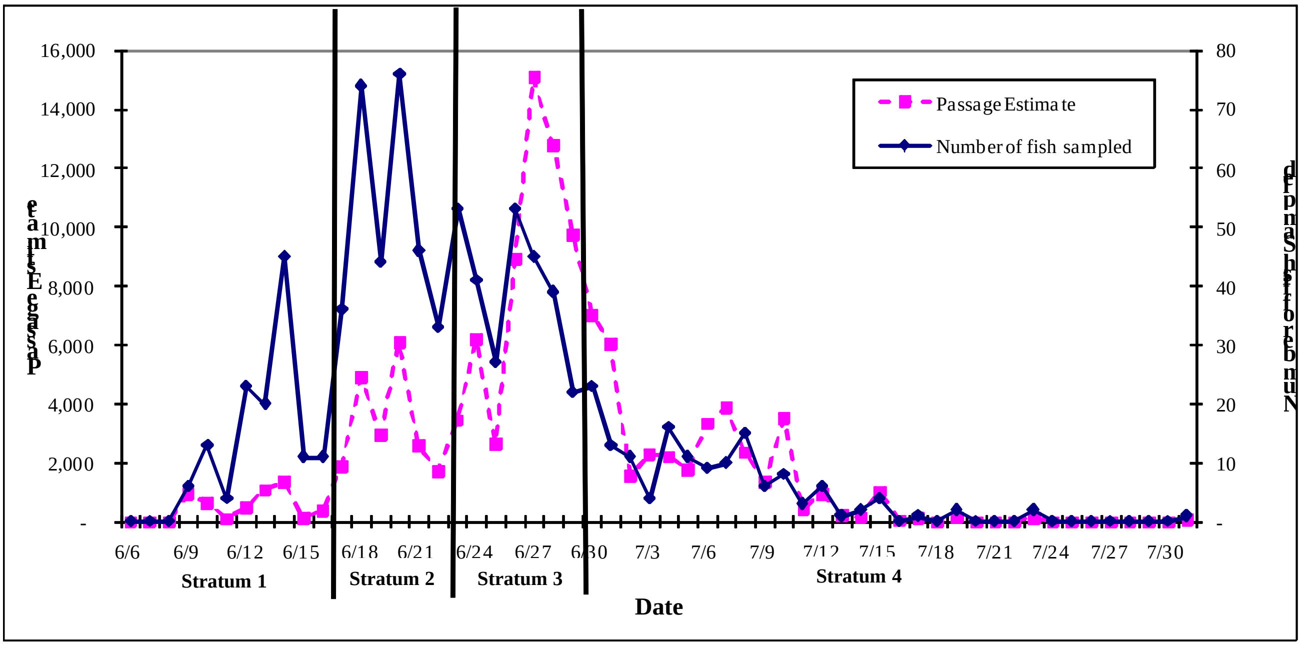

Figure 5. Daily catch of Chinook salmon in the Pilot Station Test Fishery (right-hand scale) and daily passage estimates (left-hand scale), 2009. Vertical lines denote the temporal separation of collections for creating post-season strata.

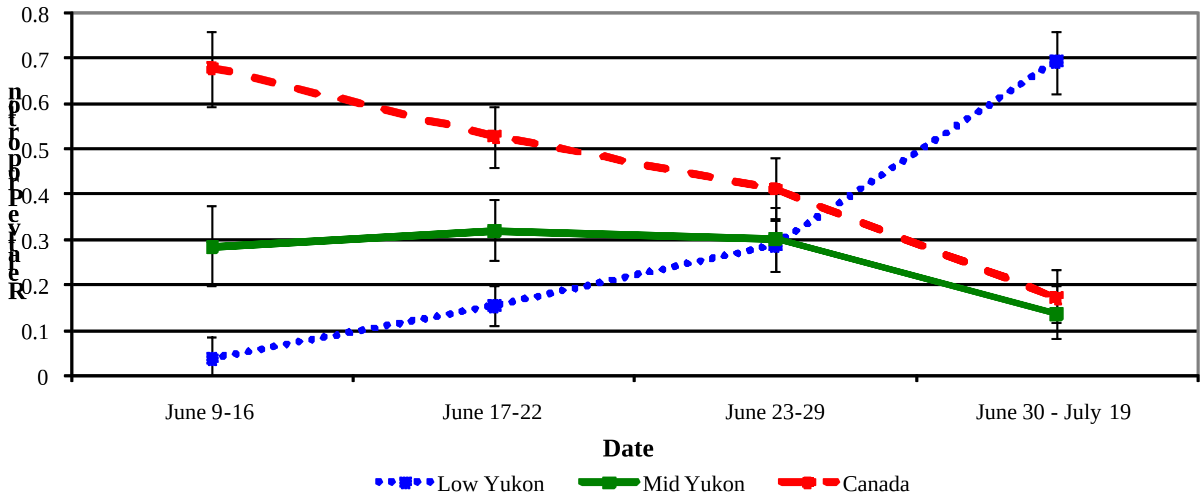

Figure 6. Relative stock composition of three broad-scale reporting groups in the Chinook salmon caught in the Pilot Station Test Fishery, as analyzed post-season, 2009. Error bars denote the bounds of the 90% bootstrap credibility interval.