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Genetic Stock Identification of Chinook Salmon Harvest on the Yukon River 2010

by

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and

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Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

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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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by
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ABSTRACT

Significant genetic variation exists among populations of Chinook salmon (*Oncorhynchus tshawytscha)* within the Yukon River drainage, and has been used to provide estimates of the composition of mixed stock fishery harvests since the early 1990s. In 2010, a single nucleotide polymorphism (SNP) baseline was used to estimate the stock composition of Chinook salmon test fishery catches and harvests in the U.S. portion of the Yukon River. Of the samples collected from test, commercial, and subsistence fisheries, 3,798 individuals were assayed for genetic variation at 42 SNPs. Mixed stock analysis of these samples was used to estimate the stock composition of the harvest at 3 hierarchical levels: country of origin (U.S. and Canada), broad scale (Lower Yukon, Middle Yukon, and Canada), and fine scale (Lower Yukon, Upper U.S. Yukon, Tanana River, Canada Border, Pelly, Carmacks and Takhini). Inseason analyses provided important and timely information for fisheries managers, while additional postseason analyses provided a more thorough perspective of the stock composition of the run and harvests. In the Pilot Station test fishery, Canadian stocks contributed between 28% and 51% of the catch over 3 strata representing the main pulses of the run. In the commercial fisheries, Canadian stocks contributed between 8% and 34% of the harvest, and in the subsistence fisheries between 20% and 90%.

Key words: Chinook salmon, *Oncorhynchus tshawytscha,* genetic stock identification, Yukon River, single nucleotide polymorphism, SNP, commercial fishery, subsistence

INTRODUCTION

Knowledge of the origin of Chinook salmon (*Oncorhynchus tshawytscha*) harvested in Yukon River fisheries is important for successful fisheries management. Under the Yukon River Salmon Agreement between the United States (U.S.) and Canada, a specified target range of Chinook salmon passing the Canadian border is an important management objective. This target range is comprised of an escapement goal and a harvest share of the total Canadian-origin run. Monitoring the proportion of Canadian-origin Chinook salmon in fishery harvests from U.S. waters of the Yukon River is critical for successfully meeting those objectives. Previous studies on stock compositions of the commercial harvest in Districts Y-1 and Y-2 (Figure 1) have shown that the proportion of Canadian-origin fish may vary significantly within a season, with a contribution ranging from 25% to 69% of the harvest (Templin et al. 2006b; DeCovich and Templin 2009). Since 2004, the stock composition of Chinook salmon harvests in test, subsistence, and commercial Chinook salmon fisheries of the Yukon River has been estimated by genetic stock identification (GSI) techniques based on a comprehensive baseline of DNA markers (Beacham and Candy 2006; Templin et al. 2006a-b; Templin et al. 2008).

Two types of genetic markers have replaced the allozyme baseline developed in the 1990s (Beacham et al. 1989; Wilmot et al. 1992; Templin et al. 2005), single nucleotide polymorphisms (SNPs) (Smith et al. 2005a; Templin et al. 2006b) and microsatellites (Flannery et al. 2006; Templin et al. 2006a,c; Beacham et al. 2008). With the exception of microsatellite use in 2005, SNPs have been the preferred GSI technique for stock composition estimates of Yukon River Chinook salmon fisheries since 2004. A SNP (single nucleotide polymorphism) is a single-base difference at a nucleotide position in a DNA sequence. The Human Genome Project and similar projects on other species have demonstrated that SNPs are ubiquitous throughout the genome. Since SNPs occur throughout the genome in many species, they are likely subject to a wider range of evolutionary rates than microsatellites, and are thus useful for addressing a broader range of questions (Brumfield et al. 2003; Morin et al. 2004). Because some SNPs are influenced by natural selection, they are particularly valuable for GSI applications where other markers cannot detect differences between geographically close populations. For example, Miller et al. (2001) found that apparent differences in selection for SNPs in the major histocompatibility complex (MHC) locus indicated strong genetic distinction between nearby populations of sockeye salmon (*O. nerka*), in contrast to observations at neutral loci. Similarly, Beacham et al. (2001) demonstrated that SNPs involved in the immune system of salmon could provide as good or better resolution for genetic stock analyses than microsatellites.

This study describes the mixed stock analysis of the Chinook salmon test fishery catches, and subsistence and commercial harvests in the U.S. portion of the Yukon River in 2010. We briefly describe the baseline used to analyze fishery samples, the simulations used to verify the accuracy and precision of estimated stock proportions, and report the results of the mixed stock analysis of fishery samples. The stock contribution estimates are provided for 3 hierarchical sets of reporting groups: 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). Country of origin stock grouping is the primary focus of this study as it is most relevant to current fishery management needs.

OBJECTIVES

The goal of this project is to provide estimates of the stock composition of Chinook salmon catches in test fisheries, and harvests in commercial and subsistence fisheries on the Yukon River in 2010. Additionally, this is a pilot study to test the feasibility and application of inseason stock composition estimates from test fisheries in Chinook salmon fisheries management. The following objectives support the goals of this study:

1) Sample Chinook salmon from each commercial and subsistence fishery in districts Y-1 through Y-5 (Figure 1) as follows:
    i. District Y-1 subsistence – 400 individuals
    ii. District Y-1 commercial (collected from chum salmon (*O. keta*)-directed fishery) – 200 individuals per period
    iii. District Y-2 commercial (collected from chum salmon-directed fishery) – 200 individuals per period
    iv. District Y-3 subsistence – 250 individuals
    v. District Y-4 subsistence – 250 individuals from each subdistrict
    vi. District Y-5 commercial – 400 individuals
    vii. District Y-5 subsistence – 400 individuals
2) Sample Chinook salmon throughout the duration of the Lower Yukon test fishery (LYTF) project – 600 individuals.
3) Sample Chinook salmon throughout the duration of the Pilot Station test fishery – 400 individuals.
4) Analyze a representative sample from each fishing district and period for genetic variation at the SNP loci in the baseline.
5) Estimate the relative contribution of stocks to the test, commercial, and subsistence fisheries of the Yukon River.
6) Analyze up to 5 groups of salmon from LYTF and Pilot Station projects inseason, representing distinct pulses of fish. Provide inseason analyses to fishery managers within 36 hours of receipt of genetic tissues for use in management decisions during the fishing season.

METHODS

BASELINE

A slightly modified version of the 25 population baseline described in Templin et al. (2008) was used for this analysis. The SNP baseline now consists of 27 populations and 52 SNPs. A subset of this baseline, consisting of all 27 populations and 42 SNPs, was used to provide the stock composition estimates reported in this study. The 42 SNPs used represent all polymorphic loci available for Yukon Chinook salmon populations. Additionally 2 populations were added to the baseline; the Chatanika River in the Tanana River drainage and a mainstem spawning population collected near Minto.

In the 2007 and 2008 version of the baseline, if linkage disequilibrium was significant in more than half of the collections, we produced composite phenotypes for each fish by combining the genotypes from these linked markers and treating them as a single locus in further analyses. Alternately, for 2009 and 2010, we removed one locus from each pair of putatively linked loci.

Simulations were conducted to evaluate the accuracy and precision of the SNP baseline to provide compositional estimates of mixtures of Chinook salmon harvested in Yukon River fisheries. These simulations were used to help assess whether the baseline of allele frequencies at the 42 SNP markers would provide sufficient information to identify individual stocks or groups of stocks (reporting groups) in mixtures. Reporting groups for genetic stock identification of Yukon River Chinook salmon were defined in previous studies based on a combination of genetic similarity, geographic features, and management applications (Flannery et al. 2006).

Reporting groups were defined hierarchically into 3 levels: 1) country of origin, 2) broad scale, and 3) fine scale. The broad scale groups (Lower Yukon, Middle Yukon, and Canada) were the same regions previously used for estimating stock composition of the harvest by scale pattern analysis (JTC 1997). Simulations performed using fine-scale reporting groups represent identifiable sets of populations useful for management and research (Table 1) (Templin et al. 2006b).

Simulations were performed using the Statistical Package for Analyzing Mixtures[1] (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 (Seeb et al. 2000).

FISHERY COLLECTIONS

For all tissue sampling, axillary processes were collected and preserved in ethanol. Chinook salmon were sampled from test, commercial, and subsistence fisheries in the U.S. portion of the river (Table 2; Figure 1). Commercial harvest samples were collected randomly during each fishing period (designated time when fishing is allowed) while sampling for age, sex, and length data from commercial processing/buying stations (DuBois and DeCovich 2008). Commercial

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[1] Product names used in this report are included for scientific completeness, but do not constitute a product endorsement.

harvest samples were collected from Districts Y-1 and Y-2. In 2010, no directed commercial harvest of Chinook salmon was allowed in U.S. waters of the Yukon River. However, the sale of Chinook salmon harvested in the directed chum fishery (<6 inch mesh size nets only) was allowed. These incidentally harvested Chinook salmon were sampled in Districts Y-1 and Y-2. Because Chinook entering the Yukon River pass through District Y-1, then District Y-2 approximately 3 days later, samples that represented the same pulse of fish passing through both districts were pooled. This was done to increase the sample size for each time strata constructed.

Subsistence harvests were sampled in Districts Y-1, Y-3, Y-4, and Y-5 (Table 2). The subsistence samples from District Y-4 were collected from subdistricts Y-4A (Kaltag and Nulato), Y-4B (Bishop Rock and Galena), and Y-4C (Ruby). The subsistence samples from District Y-5 were collected from subdistricts Y-5B (Tanana), and Y-5C (Rapids and Fort Yukon). In District Y-1, subsistence sampling was conducted by Alaska Department of Fish and Game (ADF&G) staff opportunistically when fishermen would allow their catch to be sampled. In all other districts, subsistence sampling was conducted by trained subsistence fishermen from each community, who sampled their entire subsistence harvest. The number of subsistence fishermen and duration of harvest sampling was variable among communities.

Test fishery sample collection occurred in the Coastal District (Dall Point), District Y-1 (LYTF) and District Y-2 (Mountain Village and Pilot Station), and DistrictY-5 (Eagle sonar test fishery located near the U.S. /Canada border) (Table 2). All fish caught in each test fishery were sampled. For inseason analyses an attempt was made to sample distinct pulses of Chinook salmon passing through the LYTF and Pilot Station test fisheries, and analyzed promptly to support management objectives. LYTF samples were collected between June 11 and July 15, 2010 from all 3 mouths of the Yukon River, using set gillnets with 8.5 inch mesh. Pilot Station samples were collected from approximately June 12 through July 25, 2010, using a broad array of mesh size drift gillnets, ranging from 2.75 inch to 8.5 inch stretch mesh. Pulses were identified by increases in catch per unit effort (CPUE) for a sustained period of 3 to 5 days followed by a substantial decrease in CPUE. Samples were flown to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage, analyzed and reported on within 36 hours of receipt at the GCL. Additional samples for inseason analysis were collected from the Mountain Village test fishery from June 14 through July 17.

Commercial and subsistence fishery samples were analyzed postseason. Samples from the Pilot Station test fishery and subdistrict Y-5C subsistence fishery at Rapids were also stratified temporally postseason. Sample sets were defined to be representative of catch proportion estimates while maintaining minimum sample size requirements.

LABORATORY METHODS

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 42 SNPs (Table 3). The SNP data collected were individual diploid genotypes for each locus. More SNPs were assayed in this study than in 2008 (26 SNPs) because recent advancements in laboratory technology reduced the cost per genotype, and it is no longer cost effective for the GCL to run only 26 SNPs. Even though it would be most cost effective to assay 48 or 96 SNPs, only 42 SNPs have been found to be polymorphic in Yukon River Chinook salmon, and hence only 42 were used.

Genomic DNA was extracted using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA). Chinook salmon samples were genotyped using a BioMark 48.48 Dynamic Array (Fluidigm http://www.fluidigm.com/products/biomark-genotype-profiling.html), which systematically combines 48 samples and 48 assays 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 was performed on a BioMark IFC Cycler. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using BioMark Genotyping Analysis software (Fluidigm).

QUALITY CONTROL METHODS

The following measures were implemented to ensure the quality and consistency of data produced by laboratory procedures:

1) Each individual was assigned a unique accession identifier. When DNA was extracted and analyzed from each individual, a sample sheet was created that linked each individual's code to a specific well in a uniquely numbered 96-well plate. This sample sheet accompanied the individual through all phases of a project, minimizing the risk of misidentification of samples.

2) Genotypes were assigned to individuals using a double-scoring system. Two researchers designated allele scores for each individual.

3) Approximately 8% of individuals, 8 samples from each 96-well DNA extraction plate, were reanalyzed for all markers by staff not involved with the original analysis. Assuming that the inconsistencies among analyses were due equally to errors in original genotyping and errors during the quality control, error rates in the original genotyping can be estimated as half the rate of inconsistencies.

4) Failure rates were calculated, representing the number of samples that did not amplify during PCR, averaged over all loci.

5) A threshold of 80% scorable markers per individual was established and all individuals that did not meet this threshold were excluded from mixed stock analysis (MSA). This threshold was set to exclude individuals with poor quality DNA. Poor quality DNA leads to lower reproducibility and therefore adds error to the multi-locus genotype.

6) The final data were checked for duplicated multi-locus genotypes, an indication of errors caused prior to extraction of the DNA. When duplicate genotypes were found, the genotype was attributed to the first individual, and subsequent individuals with the same genotype were removed from the analysis.

7) The data have been permanently stored in an Oracle database, *LOKI,* administered by ADF&G.

MIXED STOCK 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 estimation was run using a single chain, without thinning, and a Markov Chain Monte Carlo sample size of 10,000. Three chains were run beginning with different starting conditions. The Dirichlet prior distribution parameters for stock proportions were equal (1/N). Inference was founded on the posterior distribution based on a combined set of the last 5,000 steps of each chain. The mean of the posterior distribution is reported as the best estimate, and the central 90% of the distribution was reported as the 90% credibility interval.

Stock composition estimates were reported for 3 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 2 levels of the hierarchy were reported. Increasing the resolution to 3 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 (Templin et al. 2006a). Primarily this study focuses on the country of origin reporting group, as this is most crucial for current fishery management objectives. The broad scale and fine scale estimates are given in the tables when sample sizes are sufficient.

RESULTS

COLLECTIONS

During 2010, 6,361 Chinook salmon were sampled as part of 18 collections from test, commercial, and subsistence fisheries in the U.S. portion of the Yukon River drainage (Table 2; Figure 1). Samples from Eagle sonar test fishery (Y-5) were shipped to the Canadian Department of Fisheries and Oceans (CDFO) genetics lab in Nanaimo B.C. for processing, but are included in Table 2 for completeness.

In 2010, all Yukon River commercial fishing targeted chum salmon, and only incidentally harvested Chinook salmon were sampled. Unlike 2009, the sale of these incidentally harvested fish was allowed in 2010, and enough samples were available to analyze. Mesh sizes in this fishery were restricted to 6 inches or less for the purpose of targeting chum salmon. Samples from the Dall Point test fishery were too small to warrant analyses.

There were several cases where sample sizes were just below the minimum threshold for fine-scale estimation. Because of this, the sample threshold was lowered post season to 190 fish. It should be noted that this may increase the variance of estimates, and examining the credibility intervals of the estimates is strongly encouraged.

LABORATORY / QUALITY CONTROL ANALYSIS

Of the fishery samples, a total of 3,798 individuals were analyzed for allelic variation (Table 2). The quality control analysis demonstrated an overall discrepancy rate of 1.21%. The overall genotyping failure rate was 0.89%, and ranged from a low of 0.06% for samples collected at Kaltag to a high of 5.461% for samples collected at Fort Yukon. Duplicated genotype pairs were discovered in the samples from the District Y-1 and Y-2 commercial harvest (one in each), and 70 duplicate pairs were detected in the sample of the District Y-4 subsistence harvest from Nulato. The second individual of each pair was removed before using the sample for MSA.

BASELINE ANALYSIS

Linkage disequilibrium within each collection yielded significant results in >90% of collections at 2 marker pairs: *Ots_FGF6A* and *Ots_FGF6B*; and *Ots_HSP90B-100* and *Ots_HSP90B-385*.

The second marker in each pair, *Ots_FGF6B* and *Ots_HSP90B-385,* was removed from subsequent analyses.

Simulations

All fine scale reporting regions had mean correct allocations of >90% for the 100% simulation tests. Only 3 reporting regions, Upper U.S., Stewart, and Carmacks had lower 90% confidence interval bounds of less than 90% (0.856, 0.868, and 0.885, respectively) (Table 4).

MIXED STOCK ANALYSIS

Test Fishery

The first pulse of Chinook salmon was identified by the LYTF and 228 samples collected from June 11 through June 19 were flown to the GCL and analyzed. Samples from the South, Middle, and North mouths were pooled, and subsampling of each location was stratified based on relative CPUE by day and by month. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the first pulse (stratum 1) at LYTF was 54% for the pooled sample (Table 5). The largest proportion of the Canadian component (29%) was from the Pelly region, and the largest proportion of the U.S. catch was from the Lower Yukon region (22%) (Table 5).

A second inseason analysis was done on 219 samples caught between June 20 and June 25. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF for this time period (stratum 2) was 49%. The largest proportion of the Canadian component shifted to the Carmacks region (27%), and the largest proportion of the U.S. catch (29%) shifted to the Tanana region (Table 5).

A sample was collected at the District Y-2 test fishery at Mountain Village (*N*=151) between June 14 and 22 and analyzed concurrently with samples from the LYTF. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in this fishery for this time period was 58%, and the largest proportion of the U.S. catch (29%) was from the Middle Yukon broad-scale region (Table 5).

First pulse samples from the Pilot Station test fishery caught through June 21 were also flown to the GCL and analyzed inseason. In general, sampling at Pilot Station was conducted in proportion to the passage estimate determined by the sonar project. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in Pilot Station test fishery for this time period (stratum 1) was 49%, with the majority of U.S.-bound fish originating in the Middle Yukon (Table 6).

A second inseason analysis was completed for the Pilot Station test fishery. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the Pilot Station test fishery for this time period (stratum 2) was also 49%, and Middle Yukon region proportion declined to 38% (Table 6).

Postseason, after reviewing the complete daily sonar passage estimates and receiving all available genetic samples, new strata were constructed for Pilot Station test fishery samples (Figure 2). Once all available samples were assayed, stock composition estimates were calculated for 3 strata, as opposed to 2 strata analyzed inseason. The Canadian-origin Chinook salmon present in the Pilot Station test fishery ranged from a high of 50% in stratum 2 to a low of 28% in stratum 3, and there was a distinct shift towards lower river stocks during the progression of the run (Table 7; Figure 3).

Commercial

Samples from the District Y-1 and Y-2 commercial harvest were pooled to increase sample sizes for the 4 strata constructed. An attempt was made to pool samples representing the same pulses of fish passing through both fisheries. Subsampling was also required to reduce the total number of samples assayed due to funding constraints. The subsampling scheme attempted to provide sufficient sample sizes for providing fine-scale estimates while maintaining a constant proportion of samples analyzed to harvest within each strata. This was challenging because sampling of the fisheries was not kept in proportion to harvest during all fishing periods; in fact, two periods in District Y-2 were substantially underrepresented in the sample. For these periods (stratum 2 and 3), additional samples were added from the corresponding strata in District Y-1 to reach sample size requirements (Table 8). Target subsample sizes were set at 200, the minimum required to provide fine-scale estimates, and a total sample size of 800–900 was allocated for analysis of commercial harvests. A proportion of 0.09 (sample/ harvest number) both within each district and across districts (pooled) was determined to meet these requirements. Under this scheme 4 strata were constructed using pooled subsamples. The Canadian-origin Chinook salmon present in the commercial harvest ranged from a high of 34% in stratum 2 to a low of 8% in stratum 4, and there was a distinct shift towards lower river stocks during the progression of the run (Table 9; Figure 4).

Subsistence

In the District Y-1 subsistence fishery, 58% of the harvest samples were comprised of Canadian populations (Table 10). Only 79 samples were taken in this fishery, below the 100 sample threshold set for this study for reporting country of origin; therefore caution should be used when considering this estimate. The harvest from the Y-3 subsistence fishery showed a lower proportion of Canadian populations (48%), with the largest contribution of this component being from the Carmacks region (30%). The greatest proportion of the U.S. component was the Tanana region 31% (Table 10).

The estimated contribution of Canadian populations to the subsistence harvest in District Y-4 varied from a high of 51% in Kaltag (subdistrict Y-4A) to a low of 20% in Ruby (subdistrict Y-4C) (Tables 11–13; Figure 5). The Carmacks region comprised the greatest portion of the Canadian estimate in subdistricts Y-4A and Y-4B, and the point estimate for the Carmacks region was slightly lower than the estimate for the Pelly region in Y-5C (Ruby), 7% and 9%, respectively. The Tanana region was the largest contributor of U.S. stocks for all samples from District Y-4, with the Ruby sample having the greatest proportion of Tanana populations, 71%. Bishop Mountain (Y-4B), had an insufficient sample size for fine-scale estimates.

Samples were collected at Tanana in District Y-5B, and Canadian populations contributed 77% to this sample, and the Carmacks region contributed the largest proportion to this component, 47% (Table 13).

Samples were collected at Rapids throughout the run. Out of 705 samples collected, 200 samples representing two strata were analyzed. The Canadian contribution to the subsistence harvest in this fishery was 80% for both strata. The estimated contribution of Canadian populations for the sample from Y-5C, Fort Yukon, was 90%, and the Carmacks region contributed the largest proportion to this component, 37% (Table 14).

DISCUSSION

The 2010 Yukon River Chinook salmon run abundance was below average, and projections indicated that Chinook salmon 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 42,500–55,000 Canadian-origin fish. Because of the particular concern for Canadian-origin stocks in recent years, GSI information was an important indicator for inseason management. 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.

Management actions implemented for subsistence fisheries were not as severe as in 2009, and included voluntary restrictions and reduced extended sharing throughout the drainage. However, fishermen in middle and upper river districts experienced difficulties fishing due to high water conditions later in the season. Further, there was no commercial fishery for Chinook salmon, but nearly 10,000 fish were taken incidentally in the chum directed fishery. Of these incidentally caught Chinook, only about 21% were of Canadian-origin.

Fishing conditions in the LYTF made it difficult 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. Postseason examination of daily fish passage at Pilot Station sonar revealed that the initial inseason strata could be modified to create 3 strata with the third stratum represented by all available samples through the end of the season. These strata were intended to represent the 3 pulses of the run passing through the Pilot Station test fishery. The major difference between the inseason and postseason estimates was the dramatic increase in Lower Yukon stocks in the third stratum. 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 midpoint of the run (Templin et al. 2006b; Templin et al. 2008; DeCovich and Templin 2009).

While the country of origin reporting group has been the focus of this study, the patterns seen in fine scale reporting group estimates are generally similar to past years. For example, in the Pilot Station test fishery, the Pelly region makes up the highest proportion of the Canadian component in the early time strata, and the Carmacks region predominates in later time strata. This is a pattern seen in previous years in both Pilot Station samples (DeCovich et Al. 2010), and in Lower Yukon River fishery harvests (Templin et al. 2008). Lower Yukon River stocks are generally present in low proportions in earlier time strata, and dominate the stock composition in later time strata. This pattern in seen in test fishery catches, and in harvests from commercial and subsistence fisheries (DeCovich et Al. 2010; Templin et al. 2008).

Improvements to the baseline could improve overall estimates, particularly for fine scale reporting groups. The baseline used for this analysis has been proven, through simulation studies, to provide accurate and precise stock composition estimates at each level of the hierarchy. However, not all spawning populations are present in the baseline. Gaps in baseline population coverage are present in the Koyukuk, Tanana, and Porcupine drainages. Also, several spawning populations from rivers in U.S. waters near the U.S./Canada border are absent from the baseline. The ADF&G Anadromous Waters Catalog lists the Kandik, Nation, and Tatonduk rivers as having spawning populations of Chinook salmon (Johnson and Blanche 2010). The absence of these populations in the baseline could bias the results of mixed-stock analysis if individuals from these populations are present in mixture samples. For example, if these populations are genetically more similar to those in Canadian waters, individuals from these populations would be allocated to the Canadian component under our current model. This bias will be small if these border rivers support relatively small populations of Chinook salmon. However, further study is warranted to assess the size of these populations, characterize their genetic stock structure, and evaluate any implications to mixed-stock analysis models.

To appropriately characterize the harvest, it must be representatively sampled, which can be particularly challenging in subsistence harvest collections. Subsistence fishermen utilize a variety of fishing gear, fish in different sites and at different times, and maintain different harvest levels. While sample size goals were met for many subsistence community samples, these samples are sometimes heavily weighted by one or two harvesters and may not be fully representative of the harvest for the overall community. As such, stock composition of subsistence harvests should be interpreted with some caution, particularly at the fine scale stock grouping level. Overall stock compositions of the harvest at the country of origin level appear to be consistent with previous estimates from those communities and more robust to these potential biases (DeCovich and Howard 2010; DeCovich et al. 2009).

Postseason analyses could also be enhanced with more strategic subsistence sampling efforts, to identify and then better capture particular harvest patterns in some communities. For instance, the community of Ruby appears to have harvest patterns that are not representative of the rest of its district. In 2010, the Canadian proportion was 20% in the sample from Ruby, and the Middle Yukon component was 71%. This is similar to the results of the 2009 analysis, where the Tanana component dominated the Ruby sample. It is hypothesized that since the bulk of the fish sampled at Ruby come from the south bank, Chinook salmon caught at this location are following the plume of water generated by the Tanana River. Contrary to 2009, Ruby sample sizes in 2010 were large enough to determine fine-scale stock groupings and most of those Canadian-origin fish harvested were from Pelly stocks.

As has been seen in previous years, GSI analyses demonstrate a pattern of generally increasing harvest of Canadian-origin Chinook salmon in upper fishing districts. As the farthest upstream fishing subdistrict, Y-5C subsistence fishery samples were predominately Canadian-origin fish. Within Y-5C, the lowest Canadian component (70%) was estimated from the mainstem sample near Hess Creek. This seems reasonable since the sample site is the farthest downstream among those in the Y-5C subdistrict, thus increasing the potential that U.S. populations could be present in the harvest.

Despite the tremendous challenges of sampling and providing timely information inseason, GSI analyses provided important insight for fisheries managers to make timely decisions during the 2010 fishing season. Yukon River managers will continue to use this information, in conjunction with run abundance indices, to make stock-specific management decisions. Because each season presents a unique set of challenges, the utility of inseason analyses will continue to be evaluated in subsequent seasons. Postseason analyses have been useful to managers to understand harvest patterns among various regions of the Yukon River and to better understand potential impacts of different management actions. In light of the recent volatility of Canadian-origin stocks, GSI analysis has proven necessary, and improvements to the genetic baseline and sampling strategies will only improve the power of this technique for fisheries management on the Yukon River.

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REFERENCES CITED

Beacham, T. D., C. B. Murray, and R. E. Withler. 1989. Age, morphology, and biochemical genetic variation of Yukon River Chinook salmon. Transactions of the American Fisheries Society 118:46–63.

Beacham, T. D., J. R. Candy, K. J. Supernault, T. Ming, B. Deagle, A. Schulze, D. Tuck, K. H. Kaukinen, J. R. Irvine, K. M. Miller, and R. E. Withler. 2001. Evaluation and application of microsatellite and major histocompatibility complex variation for stock identification of coho salmon in British Columbia. Transactions of the American Fisheries Society 130:1116-1149.

Beacham, T. D., and J. R. Candy. 2006. Stock identification of Yukon River Chinook and chum salmon using microsatellite DNA loci. Final report to Yukon River Panel Restoration and Enhancement Fund Project CRE 79-05.

Beacham, T. D., M. Wetklo, C. Wallace, J. B. Olsen, B. G. Flannery, J. K. Wenburg, W. D. Templin, A. Antonovich, and L. W. Seeb. 2008. The application of microsatellites for stock identification of Yukon River Chinook salmon. North American Journal of Fisheries Management 28:283-295.

Brumfield, R. T., P. Beerli, D. A. Nickerson, and S. V. Edwards. 2003. The utility of single nucleotide polymorphisms in inferences of population history. Trends in Ecology and Evolution 18:249-256.

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 K.G. Howard. 2010. Genetic stock identification of Chinook salmon harvest on the Yukon River 2009. Alaska Department of Fish and Game, Fishery Data Series No. 10-58, Anchorage.

DeCovich, N. A., W. D. Templin, and D. F. Evenson. 2010. Genetic stock identification of Chinook salmon harvest on the Yukon River 2008. Alaska Department of Fish and Game, Fishery Data Series No. 10-20, Anchorage.

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.

DuBois, L., and N. A. DeCovich. 2008. Origins of Chinook salmon in the Yukon River fisheries, 2005. Alaska Department of Fish and Game, Fishery Data Series No. 08-02, Anchorage.

Flannery B., T. Beacham, M. Wetklo, C. Smith, W. D. Templin, A. Antonovich, L. Seeb, S. Miller , O. Schlei, J. K. Wenburg. 2006. Run timing, migratory patterns, and harvest information of Chinook salmon stocks within the Yukon River. Alaska Fisheries Technical Report 92, U.S. Fish and Wildlife Service, Anchorage.

REFERENCES CITED (Continued)

Johnson, J., and P. Blanche. 2010. Catalog of waters important for spawning, rearing, or migration of anadromous fishes – Interior Region, Effective June 1, 2010. Alaska Department of Fish and Game, Special Publication No. 10-05, Anchorage.

JTC (Joint Technical Committee). 1997. Review of stock identification studies on the Yukon River. The United States and Canada Yukon River Joint Technical Committee, Whitehorse, Yukon Territory.

Miller, K. M., K. H. Kaukinen, T. D. Beacham, and R. E. Withler. 2001. Geographic heterogeneity in natural selection on an MHC locus in sockeye salmon. Genetica 111: 237-257.

Morin, P. A., G. Luikart, and R. K. Wayne. 2004. SNPs in ecology, evolution and conservation. Trends in Ecology and Evolution 19: 208-216.

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

Seeb, L. W., C. Habicht, W. D. Templin, K. E. Tarbox, R. Z. Davis, L. K. Brannian, and J. E. Seeb. 2000. Genetic diversity of sockeye salmon of Cook Inlet, Alaska, and its application to management of populations affected by the Exxon Valdez oil spill. Transactions of the American Fisheries Society 129(6):1223-1249.

Smith, C. T., W. D. Templin, J. E. Seeb, and L.W. Seeb. 2005a. Single nucleotide polymorphisms (SNPs) provide rapid and accurate estimates of the proportions of U.S. and Canadian Chinook salmon caught in Yukon River fisheries. North American Journal of Fisheries Management 25:944-953.

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., R. L. Wilmot, C. M. Guthrie III, and L. W. Seeb. 2005. United States and Canadian Chinook salmon populations in the Yukon River can be segregated based on genetic characteristics. Alaska Fishery Research Bulletin 11(1):44-60.

Templin, W. D., N. A. DeCovich, and L. W. Seeb. 2006a. Yukon River Chinook salmon genetic baseline: Survey of Pacific Salmon Commission loci for U.S. populations. Alaska Department of Fish and Game, Fishery Data Series No. 06-46, Anchorage.

Templin, W. D., J. M. Berger, N. A. DeCovich, and L. W. Seeb. 2006b. 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 3A06-06, Anchorage.

Templin, W. D., N. A. DeCovich, and L. W. Seeb. 2006c. Genetic stock identification of Chinook salmon harvest on the Yukon River, 2005. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 3A06-05, 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, Fishery Data Series No. 08-15, Anchorage.

Wilmot, R. L., R. J. Everett, W. J. Spearman, and R. Baccus. 1992. Genetic stock identification of Yukon River chum and Chinook salmon – 1987-1990. Progress Report U.S. Fish and Wildlife Service, Anchorage.

TABLES AND FIGURES

Table 1.–Chinook salmon collections from the Yukon River drainage organized hierarchically into reporting groups for mixed stock analysis using genetic stock identification.

Country	Broad scale	Fine scale	Population	Year(s)	Sample size
United States					
	Lower Yukon				
		Lower Yukon			
			Andreafsky River	2003	208
			Anvik River	2002	99
			Tozitna River	2002, 2003	450
			Gisasa River	2001	228
	Middle Yukon				
		Upper U.S. Yukon			
			Sheenjek River	2002, 2004, 2006	51
			Beaver Creek	1997	100
			Chandalar River	2002, 2003, 2004	178
			Henshaw Creek	2001	150
			S. Fork Koyukuk River	2003	56
		Tanana River			
			Kantishna River	2005	200
			Chatanika River	2001, 2007	50
			Chena River	2001	200
			Salcha River	2005	200
Canada					
	Canada				
		Border			
			Chandindu River	2001	158
			Klondike River	2001, 2003	80
		Pelly			
			Mayo River	1997, 2003	62
			Stewart River	1997	99
			Blind Creek	1997, 2003	139
			Pelly River	1996, 1997	150
		Carmacks			
			Little Salmon	1987, 1997	100
			Big Salmon	1987, 1997	119
			Mainstem at Minto	2007	105
			Tatchun Creek	1987, 1997, 2002, 2003	169
			Nordenskiold River	2003	56
			Nisutlin River	1987, 1997	56
		Takhini			
			Takhini River	1997, 2003	101
			Whitehorse Hatchery	1985, 1987, 1997	242
				Total	3,651

Table 2.–Chinook salmon collections from test fishery catches, and commercial and subsistence fishery harvests in the Yukon River drainage, 2010.

District	Gear Type	Location	Target	Sample size	Number analyzed
Test Fishery					
Y-1	DGN	Dall Point	600	19	0
Y-1	SGN	LYTF-Big Eddy	600	827	198
	SGN	LYTF-Middle Mouth	600	800	251
		Total LYTF	1,200	1,627	449
Y-2	SGN	Mountain Village	800	476	151
Y-2	DGN	Pilot Station	600	376	376
Y-5	DGN	Eagle Sonar	500	468	0
		Total Test Fishery	2,900	2,490	976
Commercial					
Y-1	≤6 Restricted	Emmonak	1,000	846	608
Y-2	≤6 Restricted	Saint Marys	800	469	276
		Total Commercial	1,800	1,315	884
Subsistence					
Y-1	SGN	Emmonak	400	79	79
Y-3	SGN	Holy Cross	250	365	200
Y-4A	DGN	Kaltag	250	240	240
Y-4A	SGN	Nulato	250	277	268
Y-4B	SGN	Bishop Rock	250	113	113
Y-4B	SGN/ DGN	Galena	250	427	200
Y-4C	SGN/ FW	Ruby	250	235	235
		Total Y-4 Subsistence	1,250	1,292	1,056
Y-5B	FW	Tanana-north bank	300	350	200
Y-5C	FW	Rapids	900	705	200
Y-5C	SGN/FW	Fort Yukon	250	209	203
		Total Y-5 Subsistence	1,450	1,264	603
		Total Subsistence	2,700	2,556	1,938
		Grand Total	7,400	6,361	3,798

Note: Gear types used were set gillnet (SGN), drift gillnet (DGN), and fish wheels (FW). Commercial fisheries in Districts Y-1 and Y-2 used drift gillnets with ≤6 inch restricted mesh sizes.

Table 3.–Single nucleotide polymorphisms assayed in individual Chinook salmon sampled in the U.S. portion of the Yukon River drainage, 2010.

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 4.–Mean reporting group allocations of simulated mixtures of Yukon River Chinook salmon from the baseline of 26 SNPs.

Reporting Region		Est	90% CI
Country			
	United States	0.983	(0.962-0.999)
	Canada	0.987	(0.965-1.000)
Broad-scale			
	Lower Yukon	0.990	(0.975-1.000)
	Middle Yukon	0.971	(0.941-0.994)
	Canada	0.987	(0.965-1.000)
Fine-scale			
	Lower Yukon	0.988	(0.969-0.999)
	Upper US	0.921	(0.856-0.973)
	Tanana	0.951	(0.905-0.991)
	Canada Border	0.973	(0.946-0.995)
	Stewart	0.929	(0.868-0.988)
	Carmacks	0.943	(0.885-0.987)
	Takhini	0.973	(0.936-0.997)

Table 5.–Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the District Y-1 Lower Yukon test fishery, from stratum 1 and 2, and from the District Y-2 test fishery at Mountain Village, analyzed inseason, in 2010.

	District Y-1 LYTF						District Y-2 Mountain Village		
	Stratum 1			Stratum 2					
	June 11-19			June 20-25			June 14-22		
	N = 228			N = 219			N = 151		
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country									
United States	0.463	0.042	(0.393-0.533)	0.512	0.042	(0.443-0.581)	0.419	0.050	(0.337-0.501)
Canada	0.537	0.042	(0.467-0.607)	0.488	0.042	(0.419-0.557)	0.581	0.050	(0.499-0.663)
Broad-scale									
Lower Yukon	0.223	0.033	(0.171-0.279)	0.175	0.030	(0.127-0.228)	0.131	0.035	(0.078-0.192)
Middle Yukon	0.240	0.040	(0.176-0.307)	0.337	0.042	(0.269-0.407)	0.288	0.052	(0.204-0.377)
Canada	0.537	0.042	(0.467-0.607)	0.488	0.042	(0.419-0.557)	0.581	0.050	(0.499-0.663)
Fine-scale									
Lower Yukon	0.223	0.033	(0.171-0.279)	0.175	0.030	(0.127-0.228)			
Upper U.S. Yukon	0.092	0.052	(0.002-0.179)	0.049	0.040	(0.000-0.123)			
Tanana	0.148	0.048	(0.072-0.231)	0.288	0.044	(0.216-0.360)			
Canada Border	0.127	0.031	(0.079-0.181)	0.051	0.023	(0.017-0.092)			
Pelly	0.294	0.058	(0.199-0.392)	0.130	0.046	(0.059-0.210)			
Carmacks	0.115	0.045	(0.042-0.191)	0.271	0.048	(0.195-0.352)			
Takhini	0.003	0.006	(0.000-0.016)	0.036	0.020	(0.007-0.073)			

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 6.–Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station test fishery, as analyzed inseason, from stratum 1 and 2 in 2010.

	Stratum 1			Stratum 2		
	June 12-21			June 22-28		
	N =	99		N =	152	
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.511	0.065	(0.405-0.620)	0.513	0.055	(0.422-0.605)
Canada	0.489	0.065	(0.380-0.595)	0.487	0.055	(0.395-0.578)
Broad-scale						
Lower Yukon	0.081	0.036	(0.030-0.148)	0.137	0.038	(0.081-0.205)
Middle Yukon	0.431	0.068	(0.319-0.544)	0.376	0.058	(0.283-0.473)
Canada	0.489	0.065	(0.380-0.595)	0.487	0.055	(0.395-0.578)

Note: Samples sizes (*N*) allowed for country of origin and broad-scale estimates only.

Table 7.–Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station test fishery, as analyzed postseason, from stratum 1, 2, and 3 in 2010.

	Stratum 1			Stratum 2			Stratum 3		
	June 12-21			June 22-27			June 28-July 17		
	N =	99		N =	132		N =	139	
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country									
United States	0.511	0.065	(0.405-0.620)	0.495	0.060	(0.398-0.593)	0.719	0.045	(0.642-0.791)
Canada	0.489	0.065	(0.380-0.595)	0.505	0.060	(0.407-0.602)	0.281	0.045	(0.209-0.358)
Broad-scale									
Lower Yukon	0.081	0.036	(0.030-0.148)	0.163	0.048	(0.093-0.250)	0.478	0.054	(0.389-0.567)
Middle Yukon	0.431	0.068	(0.319-0.544)	0.333	0.063	(0.231-0.438)	0.242	0.050	(0.164-0.329)
Canada	0.489	0.065	(0.380-0.595)	0.505	0.060	(0.407-0.602)	0.281	0.045	(0.209-0.358)

Note: Samples sizes (*N*) allowed for country of origin and broad-scale estimates only.

Table 8.–Commercial fishery stratum, total harvest, number sampled, number subsampled (*N*), and proportion of harvest subsampled for District Y-1 and Y-2 commercial fisheries in 2010.

Stratum (dates)	Total harvest	Number sampled	Number subsampled (*N*)	Proportion of harvest subsampled
District Y-1				
Stratum 1 (June 28)	2,122	200	191	0.09
Stratum 2 (July 2)	863	200	143	0.17
Stratum 3 (July 3, 6)	1,553	321	165	0.11
Stratum 4 (July 9,11,13,15)	1,206	179	109	0.09
Total Y-1				
District Y-2				
Stratum 1 (July 1)	1,215	200	109	0.09
Stratum 2 (July 4)	865	13	13	0.02
Stratum 3 (July 7)	823	35	35	0.04
Stratum 4 (July 10,12,14,16)	1,321	251	119	0.09
Total Y-2				
Districts Pooled				
Stratum 1 (June 28, July 1)	3,337	400	300	0.09
Stratum 2 (July 2, 4)	1,728	213	156	0.09
Stratum 3 (July 3, 6, 7)	2,376	356	200	0.08
Stratum 4 (July 9-16)	2,527	430	227	0.09
Grand Total	9,968	1,399	884	

Table 9.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-1 and District Y-2 commercial fishery, 2010.

	Stratum 1			Stratum 2			Stratum 3			Stratum 4		
	June 28 - July 1			July 2 - 4			July 3 - 7			July 9 - 16		
	N =	297		N =	153		N =	200		N =	228	
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	0.754331	0.029116	(0.706-0.801)	0.658658	0.042627	(0.587-0.728)	0.787136	0.03358	(0.730-0.840)	0.918894	0.021447	(0.881-0.952)
Canada	0.245669	0.029116	(0.199-0.294)	0.341342	0.042627	(0.272-0.413)	0.212864	0.03358	(0.160-0.270)	0.081106	0.021447	(0.048-0.119)
Broad-scale												
Lower Yukon	0.649448	0.03137	(0.597-0.701)	0.449442	0.045171	(0.375-0.524)	0.656017	0.038143	(0.592-0.717)	0.77937	0.031632	(0.726-0.830)
Middle Yukon	0.104883	0.025019	(0.067-0.149)	0.209216	0.038703	(0.148-0.275)	0.131119	0.031507	(0.083-0.186)	0.139524	0.028181	(0.096-0.188)
Canada	0.245669	0.029116	(0.199-0.294)	0.341342	0.042627	(0.272-0.413)	0.212864	0.03358	(0.160-0.270)	0.081106	0.021447	(0.048-0.119)
Fine-scale												
Lower Yukon	0.649448	0.03137	(0.597-0.701)	0.449442	0.045171	(0.375-0.524)	0.656017	0.038143	(0.592-0.717)	0.77937	0.031632	(0.726-0.830)
Upper U.S. Yukon	0.013112	0.016597	(0.000-0.048)	0.054492	0.031727	(0.009-0.112)	0.023833	0.026414	(0.000-0.079)	0.020943	0.022883	(0.000-0.067)
Tanana	0.091772	0.022634	(0.058-0.131)	0.154724	0.036163	(0.098-0.217)	0.107286	0.032008	(0.057-0.161)	0.118581	0.030547	(0.070-0.170)
Canada Border	0.002786	0.007003	(0.000-0.017)	0.001368	0.004856	(0.000-0.008)	0.002903	0.006934	(0.000-0.018)	0.000544	0.001909	(0.000-0.003)
Pelly	0.060125	0.037425	(0.000-0.123)	0.059178	0.044252	(0.000-0.138)	0.005849	0.011997	(0.000-0.031)	0.007335	0.011931	(0.000-0.034)
Carmacks	0.181631	0.03671	(0.123-0.244)	0.210407	0.062748	(0.109-0.315)	0.201281	0.033968	(0.147-0.258)	0.071329	0.021446	(0.038-0.108)
Takhini	0.001128	0.00343	(0.000-0.007)	0.07039	0.035105	(0.016-0.132)	0.002831	0.007203	(0.000-0.018)	0.001898	0.004833	(0.000-0.012)

Note: The estimated group proportions are given for each of 3 hierarchical levels.

Table 10.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-1 and Y-3 subsistence fisheries, 2010.

	Y-1			Y-3 Holy Cross		
	N =	79		N =	197	
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.420	0.074	(0.300-0.544)	0.525	0.050	(0.443-0.608)
Canada	0.580	0.074	(0.456-0.700)	0.475	0.050	(0.392-0.557)
Broad-scale						
Lower Yukon				0.099	0.030	(0.055-0.152)
Middle Yukon				0.426	0.052	(0.342-0.513)
Canada				0.475	0.050	(0.392-0.557)
Fine-scale						
Lower Yukon				0.099	0.030	(0.055-0.152)
Upper U.S. Yukon				0.107	0.067	(0.003-0.225)
Tanana				0.318	0.058	(0.223-0.412)
Canada Border				0.049	0.035	(0.000-0.110)
Pelly				0.113	0.065	(0.001-0.223)
Carmacks				0.303	0.059	(0.205-0.401)
Takhini				0.010	0.013	(0.000-0.035)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 11.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4A subsistence fisheries, 2010.

	Y-4A Kaltag			Y-4A Nulato		
	N = 240			N = 194		
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.490	0.040	(0.424-0.555)	0.497	0.052	(0.412-0.582)
Canada	0.510	0.040	(0.445-0.576)	0.503	0.052	(0.418-0.588)
Broad-scale						
Lower Yukon	0.065	0.030	(0.019-0.118)	0.037	0.024	(0.002-0.081)
Middle Yukon	0.424	0.048	(0.345-0.502)	0.460	0.054	(0.371-0.550)
Canada	0.510	0.040	(0.445-0.576)	0.503	0.052	(0.418-0.588)
Fine-scale						
Lower Yukon	0.065	0.030	(0.019-0.118)	0.037	0.024	(0.002-0.081)
Upper U.S. Yukon	0.064	0.043	(0.000-0.142)	0.088	0.060	(0.000-0.190)
Tanana	0.360	0.048	(0.280-0.440)	0.373	0.056	(0.280-0.466)
Canada Border	0.077	0.027	(0.036-0.124)	0.101	0.038	(0.043-0.167)
Pelly	0.071	0.051	(0.000-0.160)	0.161	0.067	(0.046-0.267)
Carmacks	0.360	0.053	(0.272-0.446)	0.233	0.059	(0.142-0.335)
Takhini	0.003	0.008	(0.000-0.020)	0.008	0.014	(0.000-0.039)

Note: The estimated group proportions are given for each of 3 hierarchical levels.

Table 12.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4B subsistence fisheries, 2010.

	Y-4B Bishop Mountain			Y-4B Galena		
	N =	113		N =	198	
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.500	0.063	(0.398-0.608)	0.697	0.045	(0.621-0.770)
Canada	0.500	0.063	(0.392-0.602)	0.303	0.045	(0.230-0.379)
Broad-scale						
Lower Yukon	0.146	0.051	(0.069-0.237)	0.068	0.025	(0.031-0.112)
Middle Yukon	0.354	0.067	(0.249-0.469)	0.629	0.049	(0.549-0.709)
Canada	0.500	0.063	(0.392-0.602)	0.303	0.045	(0.230-0.379)
Fine-scale						
Lower Yukon	*Insufficient Samples*			0.068	0.025	(0.031-0.112)
Upper U.S. Yukon				0.135	0.053	(0.052-0.226)
Tanana				0.494	0.052	(0.408-0.579)
Canada Border				0.051	0.033	(0.000-0.107)
Pelly				0.102	0.054	(0.004-0.192)
Carmacks				0.142	0.043	(0.074-0.216)
Takhini				0.007	0.012	(0.000-0.035)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 13.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4C and District Y-5B subsistence fishery, 2010.

	Y-4C Ruby			Y-5B Tanana		
	N = 226			N = 200		
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.801	0.034	(0.744-0.854)	0.228	0.042	(0.160-0.299)
Canada	0.199	0.034	(0.146-0.256)	0.772	0.042	(0.701-0.840)
Broad-scale						
Lower Yukon	0.075	0.033	(0.028-0.134)	0.012	0.011	(0.000-0.034)
Middle Yukon	0.725	0.042	(0.653-0.793)	0.216	0.042	(0.148-0.288)
Canada	0.199	0.034	(0.146-0.256)	0.772	0.042	(0.701-0.840)
Fine-scale						
Lower Yukon	0.075	0.033	(0.028-0.134)	0.012	0.011	(0.000-0.034)
Upper U.S. Yukon	0.019	0.032	(0.000-0.090)	0.203	0.044	(0.133-0.275)
Tanana	0.706	0.050	(0.619-0.780)	0.013	0.017	(0.000-0.049)
Canada Border	0.005	0.011	(0.000-0.029)	0.104	0.037	(0.047-0.169)
Pelly	0.094	0.041	(0.031-0.165)	0.193	0.064	(0.090-0.302)
Carmacks	0.072	0.035	(0.018-0.133)	0.470	0.065	(0.360-0.575)
Takhini	0.028	0.018	(0.000-0.060)	0.005	0.012	(0.000-0.031)

Note: The estimated group proportions are given for each of 3 hierarchical levels.

Table 14.–Estimated proportional contributions (Est), standard deviations (SD), 90% credibility (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-5C subsistence fisheries, 2010.

	Y-5C Rapids						Y-5C Fort Yukon		
	Stratum 1			Stratum 2					
	July 5 - 12			July 13 - 17					
	N =	100		N =	100		N =	192	
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country									
United States	0.202	0.067	(0.096-0.316)	0.205	0.062	(0.109-0.311)	0.096	0.036	(0.041-0.159)
Canada	0.798	0.067	(0.684-0.904)	0.795	0.062	(0.689-0.891)	0.904	0.036	(0.841-0.959)
Broad-scale									
Lower Yukon							0.011	0.010	(0.000-0.031)
Middle Yukon							0.086	0.035	(0.032-0.147)
Canada							0.904	0.036	(0.841-0.959)
Fine-scale									
Lower Yukon							0.011	0.010	(0.000-0.031)
Upper U.S. Yukon	*Insufficient samples*			*Insufficient samples*			0.083	0.035	(0.029-0.145)
Tanana							0.002	0.005	(0.000-0.013)
Canada Border							0.172	0.041	(0.107-0.241)
Pelly							0.284	0.063	(0.183-0.389)
Carmacks							0.365	0.061	(0.265-0.465)
Takhini							0.083	0.026	(0.043-0.130)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

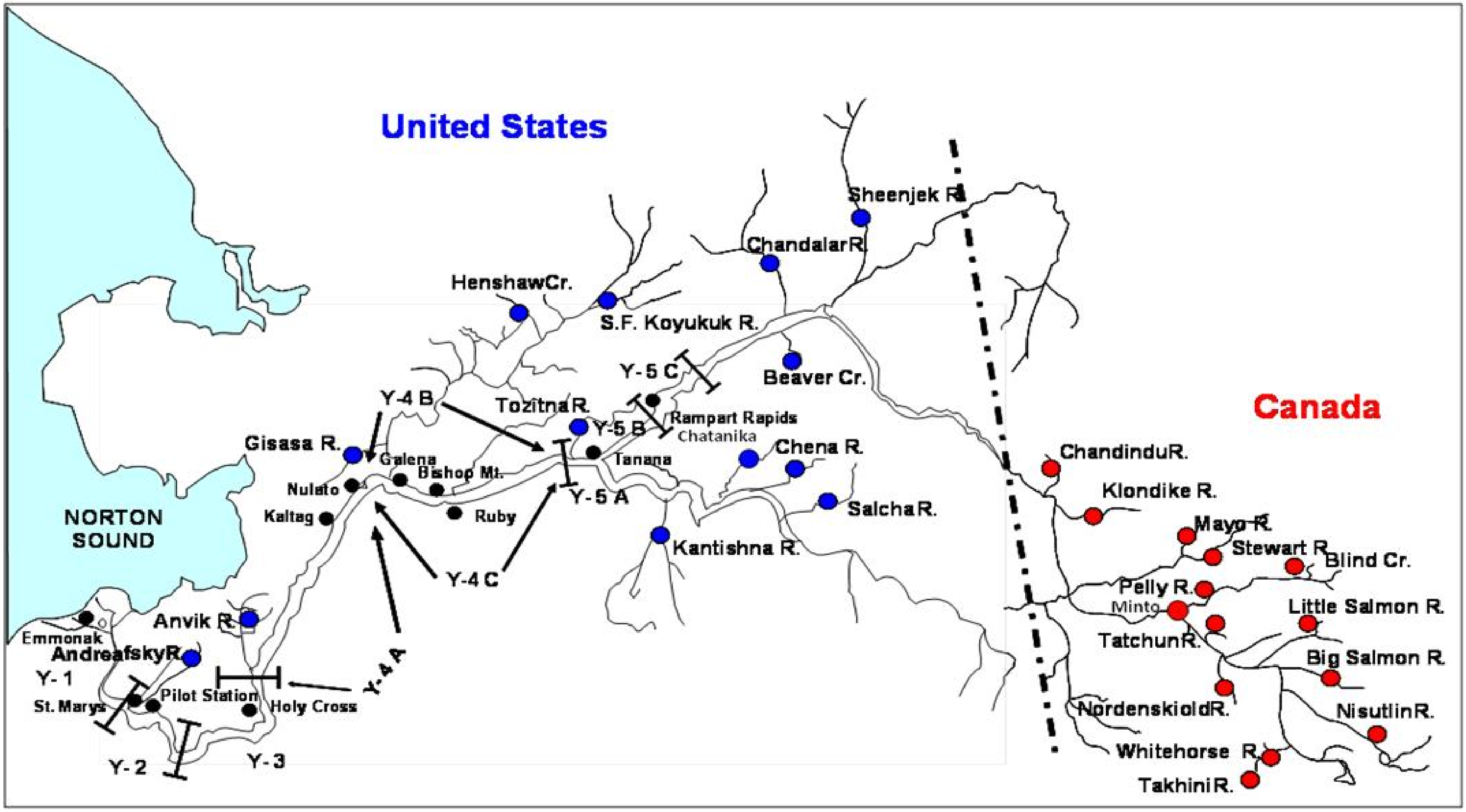
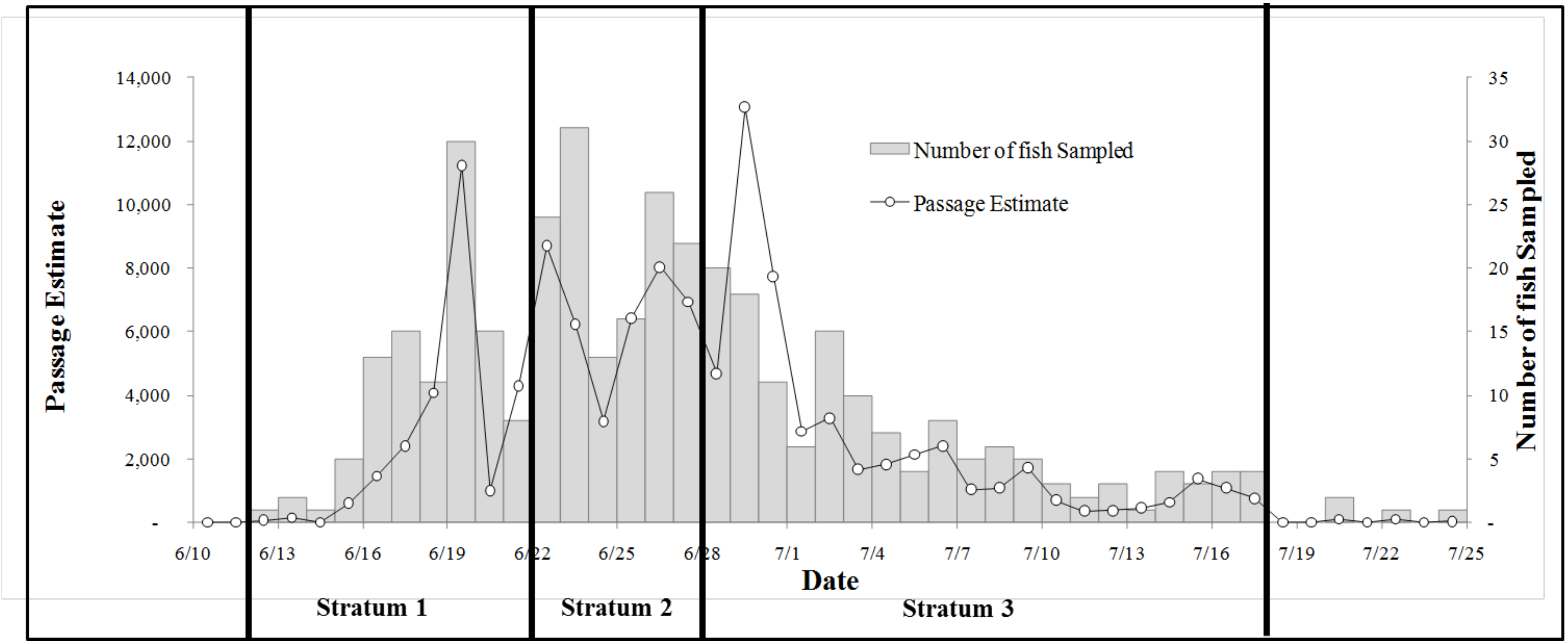
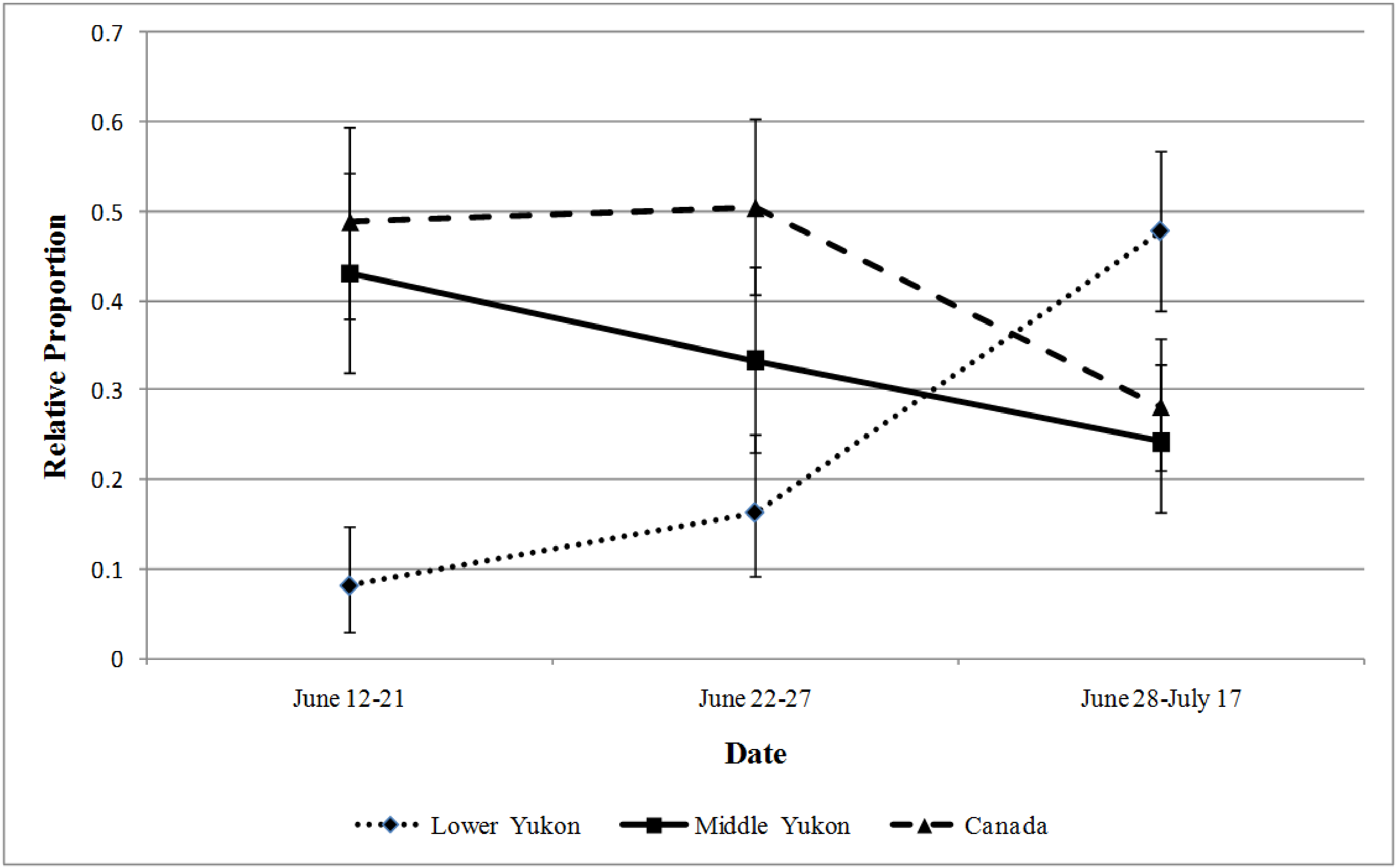


Figure 1.–Baseline collection locations, and fishing districts (and mainstem subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.



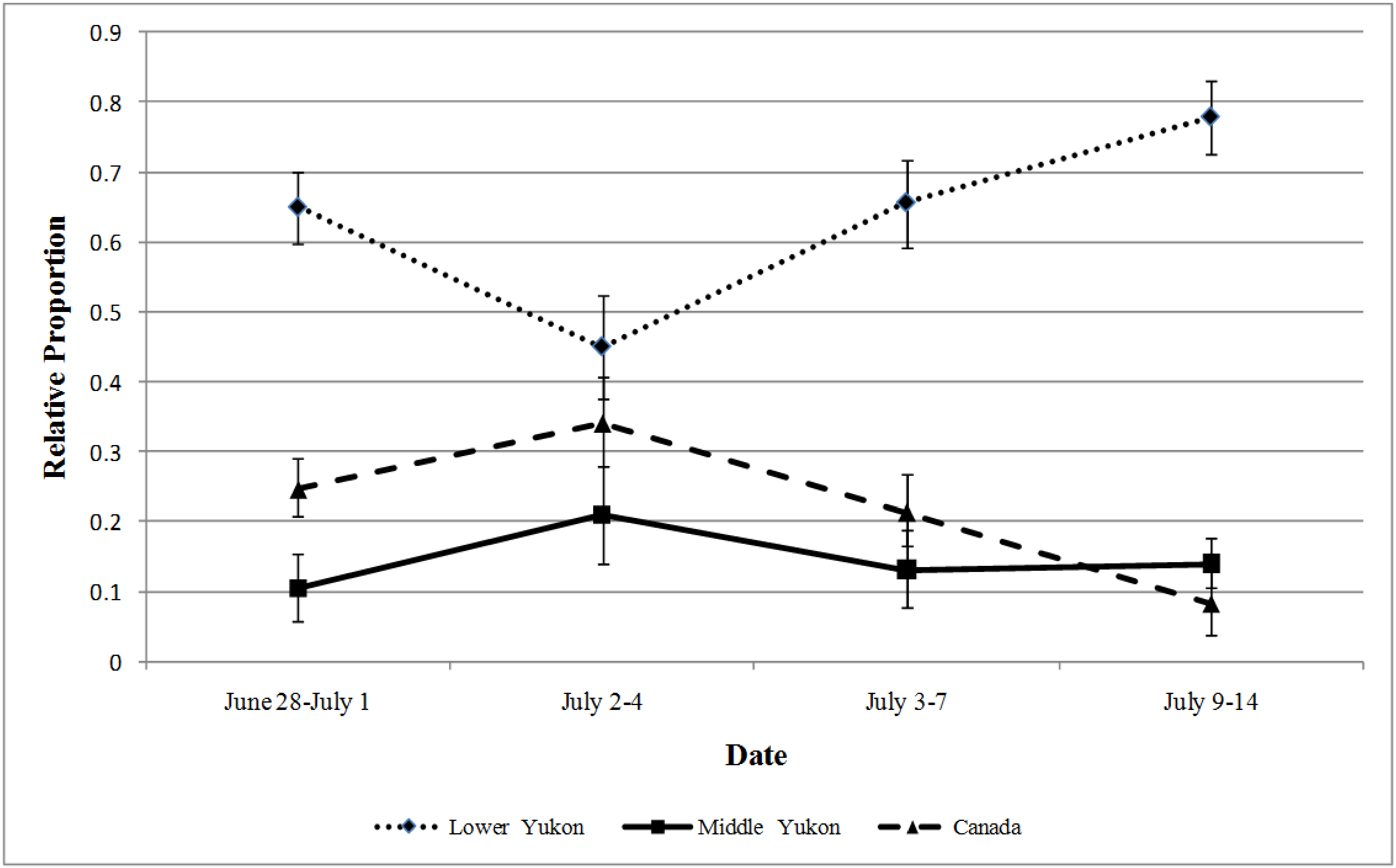
Note: Vertical lines denote the temporal separation of collections for creating postseason strata.

Figure 2.– Daily sample size of Chinook salmon from the Pilot Station test fishery and daily passage estimates, 2010.



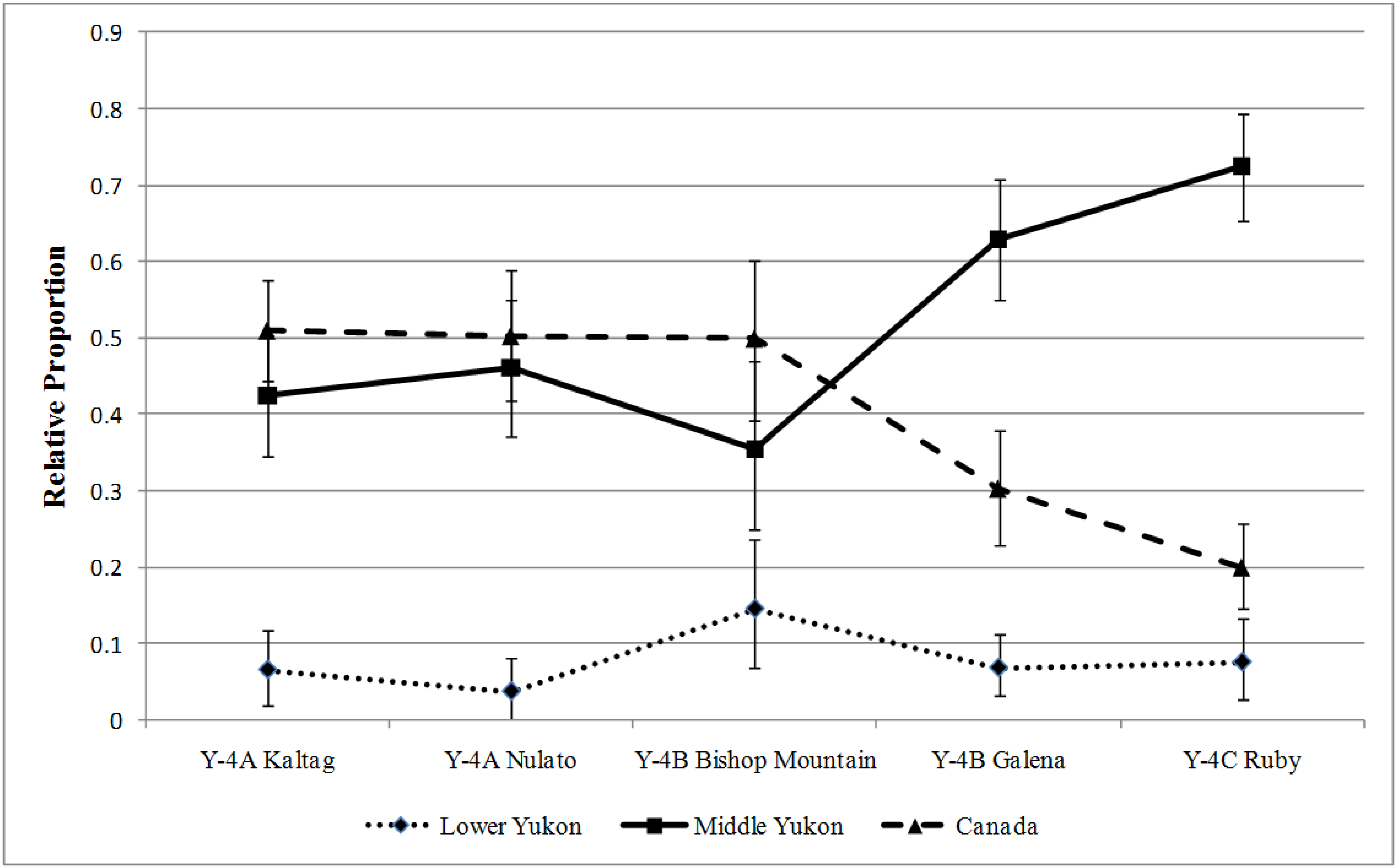
Note: Error bars denote the bounds of the 90% credibility interval.

Figure 3.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Pilot Station test fishery, as analyzed postseason, 2010.



Note: Error bars denote the bounds of the 90% credibility interval.

Figure 4.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the District Y-1 and Y-2 Commercial fishery, 2010.



Note: Error bars denote the bounds of the 90% credibility interval.

Figure 5.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in District Y-4 subsistence fisheries, 2010.