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**Yukon River Chinook Salmon Genetic Baseline:
Survey of Pacific Salmon Commission Loci for U.S.
Populations**

by

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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)		General		Measures (fisheries)	
centimeter	cm	Alaska Administrative Code	AAC	fork length	FL
deciliter	dL	all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.	mid-eye-to-fork	MEF
gram	g	all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.	mid-eye-to-tail-fork	METF
hectare	ha	at	@	standard length	SL
kilogram	kg	compass directions:		total length	TL
kilometer	km	east	E		
liter	L	north	N	Mathematics, statistics	
meter	m	south	S	<i>all standard mathematical signs, symbols and abbreviations</i>	
milliliter	mL	west	W	alternate hypothesis	H _A
millimeter	mm	copyright	©	base of natural logarithm	<i>e</i>
		corporate suffixes:		catch per unit effort	CPUE
Weights and measures (English)		Company	Co.	coefficient of variation	CV
cubic feet per second	ft ³ /s	Corporation	Corp.	common test statistics	(F, t, χ^2 , etc.)
foot	ft	Incorporated	Inc.	confidence interval	CI
gallon	gal	Limited	Ltd.	correlation coefficient	
inch	in	District of Columbia	D.C.	(multiple)	R
mile	mi	et alii (and others)	et al.	correlation coefficient	(simple)
nautical mile	nmi	et cetera (and so forth)	etc.	covariance	r
ounce	oz	exempli gratia	e.g.	degree (angular)	cov
pound	lb	(for example)		degrees of freedom	°
quart	qt	Federal Information Code	FIC	expected value	df
yard	yd	id est (that is)	i.e.	greater than	<i>E</i>
		latitude or longitude	lat. or long.	greater than or equal to	>
Time and temperature		monetary symbols		harvest per unit effort	≥
day	d	(U.S.)	\$, ¢	less than	<
degrees Celsius	°C	months (tables and figures): first three letters	Jan, ..., Dec	less than or equal to	≤
degrees Fahrenheit	°F	registered trademark	®	logarithm (natural)	ln
degrees kelvin	K	trademark	™	logarithm (base 10)	log
hour	h	United States (adjective)	U.S.	logarithm (specify base)	log ₂ , etc.
minute	min	United States of America (noun)	USA	minute (angular)	'
second	s	U.S.C.	United States Code	not significant	NS
		U.S. state	use two-letter abbreviations (e.g., AK, WA)	null hypothesis	H ₀
Physics and chemistry				percent	%
all atomic symbols				probability	P
alternating current	AC			probability of a type I error (rejection of the null hypothesis when true)	α
ampere	A			probability of a type II error (acceptance of the null hypothesis when false)	β
calorie	cal			second (angular)	"
direct current	DC			standard deviation	SD
hertz	Hz			standard error	SE
horsepower	hp			variance	
hydrogen ion activity (negative log of)	pH			population	Var
parts per million	ppm			sample	var
parts per thousand	ppt, ‰				
volts	V				
watts	W				

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ABSTRACT

Significant genetic variation exists among populations of Chinook salmon from the Yukon River drainage, and use of this variation for providing estimates of stock composition of fishery harvests has been possible since 1992. Recent analyses using DNA markers confirmed the results of the earlier studies and provided the possibility for greater accuracy and precision of stock composition estimates, but one of the analyses used an unstandardized set of microsatellite markers. This report presents the results of a survey of 13 microsatellite loci (from a standardized set used by the Pacific Salmon Commission Chinook Technical Committee) in 2646 individual fish representing 11 U.S. Chinook salmon populations. Average genotyping success rate was approximately 83%, with the majority of failures in the Anvik collection (success rate ~30% in the Anvik). The number of alleles observed per locus ranged from five (*Ots9*) to forty-four (*Omm1080*), and the total across loci was 241. Estimates of per-locus F_{ST} ranged from 0.013 to 0.054, suggesting a level of divergence among collections that should be useful for management applications. Our quality control process identified no genotyping errors. A parallel project was recently completed by the Canadian Department of Fisheries and Oceans (CDFO) to survey these loci in at least the 10 Canadian populations. U.S. and Canadian data are presently being combined, and joint analyses of the resolving power of the loci will be conducted and presented to the Joint Technical Committee.

Key Words: Chinook, Yukon River, DNA marker, stock composition, alleles

INTRODUCTION

Early surveys of genetic variation among Chinook salmon populations in the Yukon River demonstrated significant genetic variation among populations (Gharrett et al. 1987; Beacham et al. 1989). While these studies discussed the potential use of this information for management of the resource, it was not until 1992 that a baseline of genetic information was completed and used for genetic stock identification (Wilmot et al. 1992; Templin et al. 2005).

In 2001, a study was initiated by laboratories from three agencies [United States Fish and Wildlife Service (USFWS), Alaska Department of Fish and Game (ADF&G), and the Canadian Department of Fisheries and Oceans (CDFO)] to survey microsatellite variation in Yukon River populations to improve information on population structure and the potential applications to genetic stock identification in the Yukon River. Each laboratory used a separate set of microsatellite loci to characterize variation, and approximately 30 loci were screened. With a few exceptions, data for 19 populations were consistently collected across all loci at each of the laboratories. However, no standardization existed among laboratories for the individual microsatellite loci. This lack of standardization meant: 1) that results were not readily repeatable among laboratories, 2) that data generated in one laboratory could not be combined easily with data generated in another to perform larger analyses with existing data, and 3) that each laboratory would individually have to bear the cost and responsibility of database development.

Concurrently, a project funded by the Chinook Technical Committee (CTC) of the Pacific Salmon Committee was developing a multi-laboratory standardized genetic baseline for the southern portion of the Chinook salmon range (Moran et al. 2005). The consortium chose 13 microsatellite loci for baseline development, based on consistency in various laboratory conditions and potential information content. To date, 110 populations (approximately 16,000 individuals) have been surveyed from Southeast Alaska to California to create an initial coastwide baseline. Use of this database is governed by a certification process by which laboratories interested in adding to the database must demonstrate the ability to accurately standardize results with other member laboratories. ADF&G and CDFO were involved in the CTC standardization process since its inception, and loci collected in those labs have already gone through the standardization process.

This report presents the results of a survey of the 13 CTC loci in 11 U.S. Chinook salmon collections (Table 1). A parallel project is currently underway at CDFO to survey the CTC loci in at least the 10 Canadian populations included in the 19-population baseline. In addition, the USFWS laboratory has received funding to complete the process of certification as a contributing laboratory to the CTC baseline. U.S. and Canadian data will be combined once both datasets are complete, and joint analyses of the resolving power of the loci will be conducted and presented to the Joint Technical Committee.

Table 1.—United States Yukon River collections of Chinook salmon used in the survey of the 13 standardized microsatellites.

Drainage	Location	Sample size		Year(s)
		Available	Analyzed	
Lower Yukon	Andreafsky River	236	210	2002, 2003
	Anvik River	524	96	2002, 2003, 2004
Koyukuk River	Gisasa River	228	190	2001
	Henshaw Creek	150	147	2001
	South Fork Koyukuk River	56	56	2003
Middle Yukon	Tozitna River	450	192	2002, 2003
Tanana River	Kantishna River	200	190	2005
	Chena River	200	192	2001
	Salcha River	155	150	2003, 2004
Upper Yukon	Beaver Creek	100	93	1997
	Chandalar River	117	117	2002, 2003

OBJECTIVES

The goal of this project was to analyze collections of Chinook salmon from the U.S. portion of the Yukon River for the microsatellite loci developed by CTC group. To accomplish this goal the following objectives were originally proposed:

- 1) Survey five microsatellite loci (*Omm1080*, *Ots201b*, *Ots211*, *Ots213*, *Ssa408*) in at least nine populations (Andreafsky, Anvik, Gisasa, Henshaw, Tozitna, Chena, Salcha, Beaver, and Chandalar rivers) from the U.S. portion of the Yukon River drainage, and
- 2) Survey three additional microsatellite loci (*Ots208b*, *OtsG474*, *Ots3M*) in populations where original sample sizes were small or data were incomplete.

METHODS

COLLECTIONS

Nine populations of Chinook salmon were originally selected to be surveyed in this project (Table 1; Figure 1). These populations represent the U.S. portion of the 19-population baseline developed as part of a three-lab collaboration to survey variation at microsatellites in Chinook salmon populations in the Yukon River drainage. In addition, two collections, the South Fork of the Koyukuk River (n=56) and Kantishna River (n=200) were added in an attempt to increase the

coverage of the baseline. The Canadian populations were assayed in a separate project by the CDFO laboratory at the Pacific Biological Station in Nanaimo, British Columbia. Individual samples existed in archives at the two laboratories as either tissues or extracted DNA.

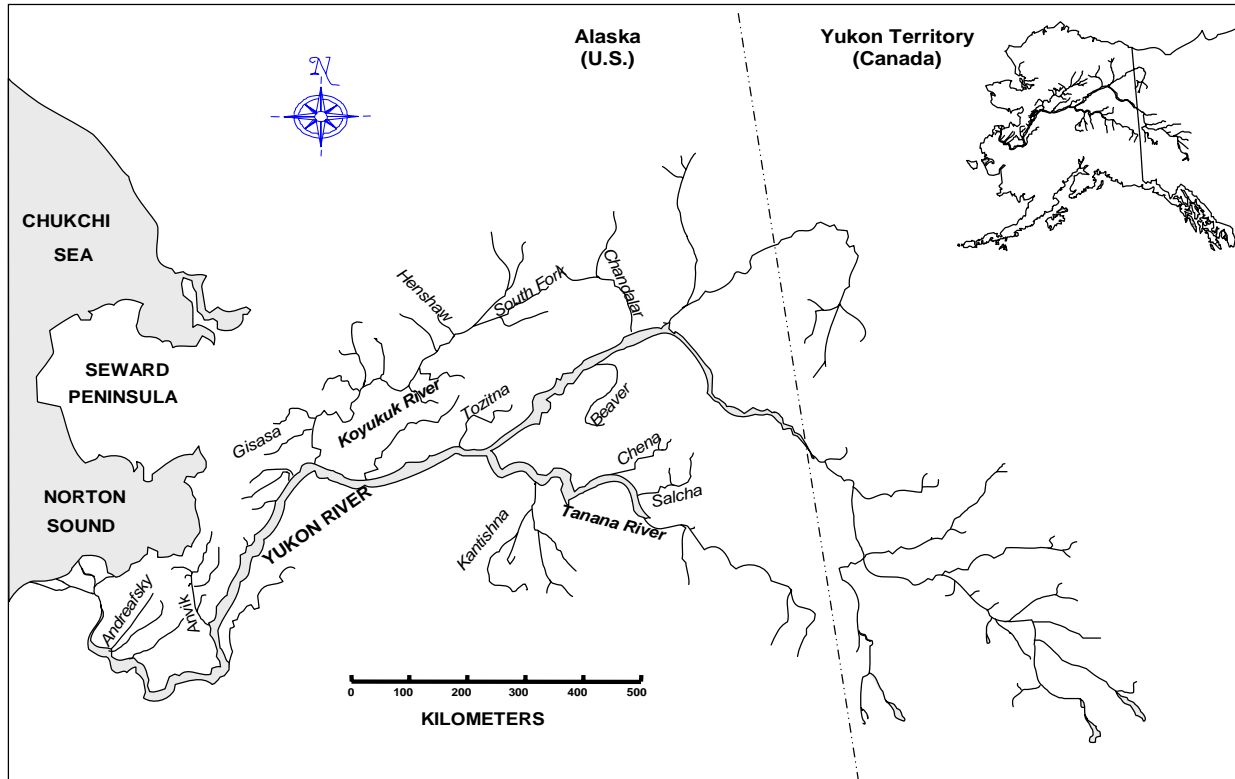


Figure 1.—Map of the locations of Chinook salmon collections in the United States portion of the Yukon River drainage.

LABORATORY METHODS

DNA was extracted from tissues using DNeasy¹ 96 Tissue Kits (QIAGEN). Polymerase chain reaction (PCR) was carried out in 384-well reaction plates in 10 μ l reaction volumes (10mM Tris-HCl, 50mM KCl, 0.2 mM each dNTP, 0.50 units *Taq* DNA polymerase (Promega) using Dual 384-Well GeneAmp Thermal Cyclers (Applied Biosystems). Primer concentrations, MgCl concentration and the corresponding annealing temperature for each locus are available upon request. PCR fragment analysis was done on an Applied Biosystems 3730 capillary DNA sequencer. 0.5 μ l PCR product was loaded into a 96-well reaction plate along with 0.5 μ l of GS500LIZ internal lane size standard and 9.0 μ l of Hi-Di (Applied Biosystems). PCR bands were visualized and separated into bin sets using AB GeneMapper software v3.7.

DATA COLLECTION

Genetic data were collected as individual multi-locus genotypes for the 13 microsatellite loci currently included in the Chinook Technical Committee (CTC) standardized database (Table 2). When more than 190 individuals were available from a population, only 190 were analyzed unless more could be added at little extra cost in time or materials.

¹ Product names used in this report are included for scientific completeness but do not constitute product endorsement

Table 2.—Background information, range of allele sizes in both the Chinook Technical Committee (CTC) and Yukon datasets, number of alleles (A), observed heterozygosity (H_o), expected heterozygosity (H_e), and F_{ST} among United States Yukon River Chinook salmon stocks for 13 standardized microsatellite loci.

Locus Name	Citation	Size Range (base pairs)	A		H_o	H_e	F_{ST}
			CTC ^a	Yukon			
<i>Ogo2</i>	Olsen et al. 1998	200-258	27	13	0.656	0.692	0.026
<i>Ogo4</i>	Olsen et al. 1998	130-170	20	14	0.689	0.677	0.040
<i>Oki100</i>	Beacham unpublished	160-365	53	29	0.899	0.931	0.018
<i>Omm1080</i>	Rexroad et al. 2001	160-460	74	44	0.913	0.931	0.016
<i>Ots201b</i>	Banks unpublished	130-345	52	27	0.899	0.893	0.017
<i>Ots208b</i>	Greig et al. 2003	140-380	58	30	0.946	0.946	0.013
<i>Ots211</i>	Greig et al. 2003	195-350	47	25	0.910	0.918	0.019
<i>Ots212</i>	Greig et al. 2003	120-265	37	22	0.704	0.698	0.018
<i>Ots213</i>	Greig et al. 2003	175-410	55	28	0.900	0.915	0.013
<i>Ots3M</i>	Banks et al. 1999	120-170	19	8	0.521	0.554	0.038
<i>Ots9</i>	Banks et al. 1999	97-115	10	5	0.471	0.468	0.054
<i>OtsG474</i>	Williamson et al. 2002	140-220	19	6	0.091	0.093	0.017
<i>Ssa408</i>	Cairney et al. 2000	180-320	39	18	0.834	0.839	0.018

^a Based on the CTC baseline updated February, 2006.

According to the convention implemented by the CTC, at each locus, a standardized allele is one that has a recognized holotype specimen from which the standardized allele can be reproduced using commonly applied fragment analysis techniques. The determination of whether or not an allele is standardized is made by the curator of the locus from which the allele is derived. The curator of a locus is responsible for distributing a document which lists each allele for a particular locus and a corresponding holotype specimen from which a unique allele can be reproduced. By the process of sizing the alleles from the holotype specimens, any individual laboratory should be able to convert allele sizes obtained in the laboratory to standardized allele names.

Genotype data were stored as GeneMapper (*.fsa) files on a network drive that was backed up nightly. Long term storage of the data was in the Gene Conservation Laboratory's Oracle database, LOKI.

QUALITY CONTROL METHODS

Several measures were implemented to insure the quality of data produced.

- 1) Each sample that arrived in our laboratory was assigned a unique accession identifier (SILLY code). At the time DNA was extracted or analyzed from each sample, a sample sheet was created that linked each individual sample's SILLY code to a specific well number in a uniquely numbered 96-well plate. This sample sheet then followed the sample through all phases of a project, minimizing the risk of misidentification of samples through human-induced errors.
- 2) Genotypes were assigned to individuals using a double-scoring system. Two observers independently produced allele scores for an entire project before the two data sets were compared. Discrepancies between the two sets of scores were then resolved with one of three possible outcomes: 1) one score was accepted and the other rejected, 2) both scores were rejected and the score was blanked, or 3) the sample was rerun.

- 3) Approximately 8% of the individuals, eight samples from each 96-well DNA extraction plate, were reanalyzed for all loci. This insured that the data are reproducible and any errors created from the processing of individual plates were corrected.
- 4) The final data were checked for duplicated multi-locus genotypes for 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 to insure that any given individual does not appear more than once in the baseline.

STATISTICAL ANALYSIS

Individual genotype data were summarized as allele frequencies for each microsatellite locus in each population. Estimates of the population frequency of individual alleles for each locus were calculated from the observed frequency of the allele in the representative sample. The numbers of alleles at each locus were calculated for each population. Observed and expected heterozygosity was calculated using *FSTAT* (Goudet 1995), and conformation of genotype frequencies to Hardy-Weinberg equilibrium (HWE) expected ratios was assessed using the exact test in *GENEPOP* (Raymond and Rousset 1995). The significance of departures from HWE for each locus in each population was determined using $\alpha=0.05$ adjusted for the number of loci ($n=13$) assayed in each population using the Bonferroni adjusted significance levels ($\alpha'=\alpha/n=0.0038$). Two measures of population subdivision were calculated from allele frequency differences: Cavalli-Sforza and Edwards' chord distances (Cavalli-Sforza and Edwards 1967) and F_{ST} (Weir and Cockerham 1984). *FSTAT* was used to calculate F_{ST} values. Population structure was visualized as a tree (unweighted pair-group method, Sneath and Sokal 1973) to view genetic similarities between populations reflected in the interpopulation chord distances.

RESULTS

A total of 2,646 individuals from 13 collections representing 11 populations were available for analysis (Table 1). From these, genotypes were assayed from 1,633 individuals (summarized in Table 3, allele frequencies available in Appendix 1). The overall failure rate for successfully assaying genotypes at the 13 CTC microsatellites was 17.1%. Most failures occurred in the samples from Anvik (success rate approximately 30%) and were due to poor tissue quality. The quality control checks employed demonstrated an error rate of 0.0%. The quality control checks also revealed pairs of individuals in some populations that had identical multi-locus genotypes. The following populations had individuals with duplicate genotypes: Anvik River (2 pairs), Gisasa River (2 pairs), Tozitna River (2 pairs), Henshaw Creek (1 pair), Chena River (3 pairs), Salcha River (15 pairs), and Chandalar River (4 pairs). In most cases, duplicates appear to have been the result of sampling the same fish into two consecutive vials. The genotype matches in the Salcha River collection were caused by the fact that the collection contained multiple tissue types (muscle, heart, and liver) from the same individuals for use in a parasite study.

In an attempt to increase the sample size for Anvik River, DNA was extracted from the scales of 190 individual carcasses sampled in 2004 as part of the carcass surveys. Despite two scales being used for each individual, initial analyses revealed that the yield and quality of the DNA obtained from these samples was too poor to warrant analysis of the full set of microsatellite markers. Analysis of these individuals for genotypes at the 13 microsatellites was not continued.

Table 3.—Locus sample sizes for 13 microsatellite loci assayed in Chinook salmon from United States populations of the Yukon River.

Locus	S. Fork										
	Andreafsky	Anvik	Gisasa	Henshaw	Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
<i>Ogo2</i>	196	31	154	144	40	93	189	148	74	92	103
<i>Ogo4</i>	184	20	166	142	26	176	189	148	81	85	97
<i>Oki100</i>	181	31	170	142	29	182	185	166	75	90	96
<i>Omm1080</i>	203	40	168	142	41	187	189	114	69	86	93
<i>Ots201b</i>	184	35	141	144	45	183	184	161	80	89	100
<i>Ots208b</i>	177	26	147	142	36	122	185	144	69	89	98
<i>Ots211</i>	202	39	161	144	30	170	188	157	72	89	94
<i>Ots212</i>	189	22	162	142	31	166	188	152	76	86	92
<i>Ots213</i>	173	20	171	142	32	186	189	98	73	84	94
<i>Ots3M</i>	201	55	178	142	39	188	189	150	86	91	101
<i>Ots9</i>	206	59	177	142	48	184	189	149	72	88	103
<i>OtsG474</i>	206	52	168	145	40	175	189	164	88	91	109
<i>Ssa408</i>	168	20	139	143	43	179	183	151	56	89	98

An average of 50% of the alleles (range: 27-70%) observed by the CTC in the survey of southern Chinook salmon populations were observed in the 11 populations in the U.S. portion of the Yukon River (Table 2). Survey of the U.S. populations revealed three alleles not included in the list of standardized CTC allele designations. These alleles were pooled with standardized alleles following procedures established by the CTC. The new allele *Ogo4**131 (ADF&G designation) was observed in the Salcha River (one observation) and was pooled with CTC allele *132. The new allele *Ots201b**169 (ADF&G designation) was observed in the Salcha River (one observation), Tozitna River (one observation) and the Gisasa River (two observations) and was pooled with CTC allele *169. The new allele *Ots212**158 (ADF&G designation) was observed in the Anvik River (one observation) and was pooled with CTC allele *159.

After correcting for multiple tests, significant departures from HWE were found in four populations: 1) Andreafsky River – *Oki100*, 2) Anvik River – *Omm1080* and *Ots3M*, 3) Chandalar River – *Ssa408*, and 4) Salcha River – *Ogo4*. Each significant departure from HWE was due to heterozygote excess; eliminating the Wahlund effect (an excess of homozygotes resulting from pooling of populations; Hartl and Clark 1989) as a potential cause. No pattern was found in departures from HWE across either loci or populations.

Genetic differences between populations were measured using CSE distances calculated from allele frequencies at the 13 CTC microsatellites showed two major clusters of populations (Figure 2). Two populations from the middle of the drainage (Gisasa and Tozitna rivers; Figure 1) grouped with populations from the lower portion of the drainage (Andreafsky and Anvik rivers). Within the second cluster, populations from the upper portion of the U.S. Yukon River drainage (Chandalar River and Beaver Creek) clustered together, while populations from the upper Koyukuk River were closely associated with populations from the Tanana River.

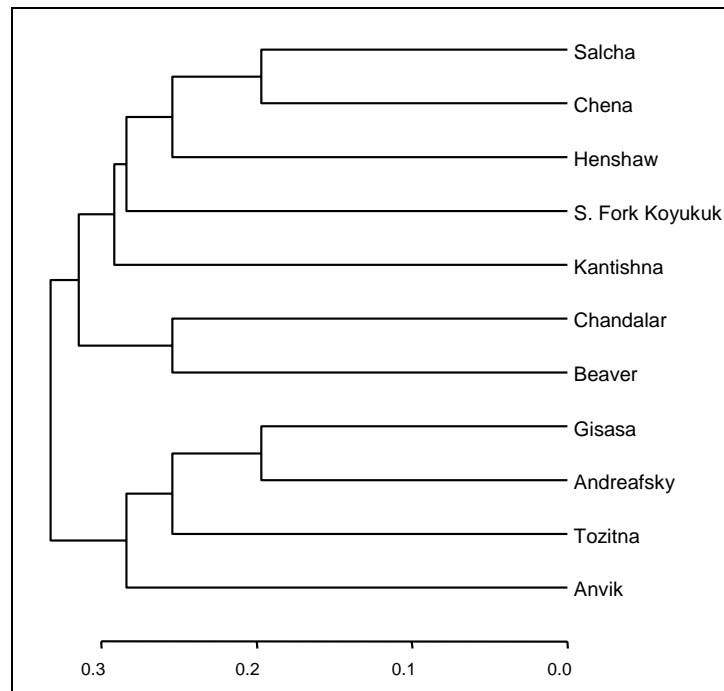


Figure 2.—Unweighted paired group-mean clustering tree based on genetic distances between pairs of Chinook salmon populations in the United States portion of the Yukon River drainage.

DISCUSSION

The objectives of this project stipulate that a minimum of five microsatellite loci would be analyzed for all the U.S. populations and three others would be analyzed for a few of the populations. At the ADF&G laboratory, the 13 CTC microsatellite loci are assayed in three multiplex panels (sets of loci analyzed in a single process). Due to the multiplex nature of the laboratory analysis, it is inefficient to assay variation at microsatellite loci without analyzing the entire set, and the additional cost to analyze all loci in a panel is minimal. All 13 CTC microsatellites were analyzed for each of the populations. No comparison has been made between these data and the unstandardized data from the eight microsatellites which were included in the 30 loci surveyed under the previous three-laboratory collaboration.

All nine of the original U.S. populations in the baseline were surveyed, and data from two additional populations (South Fork Koyukuk and Kantishna rivers) were added. In general, the success rate for determining genotypes was adequate to meet the requirements for inclusion in the baseline, with the exception of the Anvik River. The tissue collections from the Anvik River were in poor condition, and the usefulness of the 2003 collection is uncertain due to contamination of the collected tissues. Inclusion of the population in the baseline is probably still warranted, but additional individuals from this population should be added in the near future.

Population structure in the U.S. populations is similar to that described previously Templin et al. (2005) using allozyme markers, by Smith et al. (2005) using single nucleotide polymorphisms, and by a collaboration of three laboratories using microsatellite markers. The two new populations surveyed here (South Fork Koyukuk and Kantishna rivers) remain grouped with their geographically neighboring populations, forming a more comprehensive representation of Chinook salmon populations of the Koyukuk and Tanana rivers.

An analysis of the resolving power of these markers for Yukon River Chinook is presently underway as a collaborative effort between ADF&G and CDFO. The results of that analysis will be presented to the JTC and will be submitted for publication in a peer-reviewed management journal. In addition, these 13 CTC microsatellite loci are currently being surveyed in populations of Chinook salmon from Cook Inlet, Kodiak Island, the Kuskokwim Management Area, and the Copper River. Completion of the remaining areas of the range of Chinook salmon is anticipated in the near future. These standardized data can be integrated with the CTC baseline to allow genetic stock identification applications across the range of Chinook salmon in both freshwater and marine areas.

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APPENDIX.

Appendix A.—Allele frequencies for 13 microsatellite loci surveyed in Chinook salmon populations from the United States portion of the Yukon River drainage.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
Locus: <i>Ogo2</i>											
n	196	31	154	144	40	93	189	148	74	92	103
200	0.005	0.000	0.003	0.000	0.000	0.000	0.016	0.000	0.000	0.000	0.000
212	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
214	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
216	0.148	0.161	0.172	0.236	0.225	0.140	0.212	0.385	0.378	0.342	0.243
218	0.041	0.065	0.036	0.010	0.000	0.032	0.000	0.000	0.007	0.000	0.000
220	0.337	0.274	0.334	0.483	0.538	0.360	0.384	0.402	0.405	0.462	0.485
222	0.041	0.032	0.052	0.069	0.000	0.075	0.034	0.014	0.000	0.000	0.000
224	0.043	0.000	0.049	0.035	0.025	0.027	0.019	0.051	0.034	0.033	0.000
226	0.344	0.435	0.289	0.156	0.213	0.349	0.296	0.149	0.169	0.136	0.257
228	0.010	0.016	0.013	0.000	0.000	0.011	0.000	0.000	0.007	0.000	0.000
230	0.003	0.016	0.010	0.000	0.000	0.005	0.000	0.000	0.000	0.005	0.010
232	0.005	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.005
234	0.023	0.000	0.019	0.010	0.000	0.000	0.040	0.000	0.000	0.016	0.000
Locus: <i>Ogo4</i>											
n	184	20	166	142	26	176	189	148	81	85	97
132	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000
136	0.310	0.475	0.310	0.563	0.519	0.401	0.381	0.503	0.568	0.529	0.356
140	0.016	0.000	0.003	0.000	0.000	0.000	0.013	0.000	0.000	0.029	0.000
144	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000
148	0.003	0.050	0.003	0.000	0.000	0.037	0.000	0.007	0.000	0.000	0.000
152	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000
154	0.022	0.050	0.021	0.004	0.000	0.011	0.005	0.000	0.000	0.012	0.005
156	0.063	0.000	0.015	0.063	0.154	0.028	0.095	0.115	0.117	0.024	0.088
158	0.065	0.050	0.048	0.113	0.115	0.043	0.016	0.054	0.093	0.182	0.160
160	0.408	0.325	0.476	0.180	0.173	0.338	0.434	0.277	0.142	0.182	0.273
162	0.071	0.025	0.063	0.000	0.000	0.043	0.011	0.000	0.025	0.041	0.113
164	0.043	0.025	0.057	0.067	0.038	0.099	0.045	0.044	0.019	0.000	0.005
166	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000
168	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000

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Appendix A.–Page 2 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
Locus: <i>Oki100</i>											
n	181	31	170	142	29	182	185	166	75	90	96
208	0.000	0.000	0.000	0.000	0.000	0.041	0.035	0.042	0.027	0.028	0.021
212	0.003	0.000	0.000	0.053	0.069	0.003	0.003	0.012	0.060	0.000	0.026
216	0.011	0.016	0.021	0.004	0.000	0.019	0.000	0.042	0.033	0.011	0.031
220	0.011	0.016	0.026	0.000	0.000	0.016	0.000	0.063	0.020	0.039	0.078
224	0.017	0.000	0.038	0.011	0.000	0.022	0.035	0.015	0.007	0.000	0.047
228	0.110	0.113	0.121	0.130	0.086	0.060	0.049	0.048	0.033	0.033	0.036
232	0.050	0.016	0.065	0.000	0.052	0.011	0.041	0.027	0.033	0.056	0.016
236	0.028	0.032	0.044	0.028	0.017	0.060	0.019	0.024	0.007	0.011	0.026
240	0.047	0.016	0.015	0.000	0.000	0.019	0.027	0.006	0.007	0.000	0.000
244	0.036	0.016	0.009	0.021	0.034	0.066	0.081	0.039	0.067	0.133	0.073
248	0.052	0.048	0.079	0.000	0.000	0.041	0.014	0.033	0.007	0.022	0.094
252	0.069	0.081	0.115	0.039	0.052	0.055	0.014	0.006	0.013	0.061	0.021
256	0.072	0.161	0.062	0.053	0.086	0.088	0.065	0.033	0.033	0.006	0.021
260	0.072	0.032	0.047	0.060	0.069	0.014	0.065	0.036	0.113	0.011	0.031
264	0.064	0.048	0.056	0.088	0.155	0.047	0.014	0.060	0.060	0.106	0.078
268	0.055	0.065	0.079	0.134	0.069	0.060	0.027	0.108	0.080	0.078	0.021
272	0.072	0.016	0.041	0.011	0.017	0.096	0.049	0.024	0.033	0.039	0.010
275	0.047	0.000	0.047	0.116	0.086	0.038	0.059	0.063	0.080	0.006	0.031
279	0.011	0.081	0.021	0.099	0.034	0.025	0.057	0.054	0.053	0.056	0.135
283	0.039	0.065	0.026	0.081	0.052	0.162	0.211	0.151	0.147	0.178	0.073
287	0.039	0.097	0.035	0.053	0.000	0.027	0.089	0.024	0.007	0.094	0.068
290	0.039	0.048	0.000	0.018	0.034	0.000	0.019	0.051	0.067	0.000	0.021
294	0.017	0.000	0.012	0.004	0.086	0.008	0.030	0.021	0.013	0.000	0.010
298	0.011	0.016	0.026	0.000	0.000	0.005	0.000	0.015	0.000	0.006	0.000
302	0.017	0.016	0.006	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.005
305	0.011	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
309	0.003	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.005
317	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
321	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.022	0.010

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Appendix A.–Page 3 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
Locus: <i>Omm1080</i>											
n	203	40	168	142	41	187	189	114	69	86	93
166	0.034	0.038	0.027	0.000	0.000	0.013	0.032	0.039	0.051	0.000	0.011
186	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
190	0.017	0.013	0.006	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
194	0.027	0.025	0.036	0.000	0.012	0.024	0.021	0.000	0.000	0.000	0.005
198	0.032	0.025	0.006	0.011	0.000	0.000	0.021	0.009	0.007	0.000	0.005
202	0.032	0.050	0.065	0.007	0.012	0.056	0.019	0.004	0.000	0.006	0.011
206	0.067	0.063	0.006	0.070	0.012	0.056	0.019	0.026	0.043	0.017	0.032
210	0.062	0.050	0.104	0.025	0.037	0.067	0.103	0.018	0.022	0.023	0.011
214	0.071	0.025	0.065	0.099	0.098	0.144	0.138	0.140	0.109	0.029	0.070
218	0.010	0.000	0.000	0.011	0.073	0.021	0.032	0.009	0.007	0.035	0.038
222	0.034	0.025	0.006	0.032	0.122	0.029	0.021	0.004	0.014	0.041	0.048
226	0.010	0.000	0.006	0.000	0.000	0.032	0.056	0.000	0.000	0.052	0.011
230	0.015	0.063	0.018	0.000	0.000	0.032	0.003	0.004	0.000	0.006	0.011
234	0.025	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000
238	0.012	0.038	0.054	0.000	0.000	0.027	0.034	0.000	0.014	0.012	0.011
242	0.012	0.075	0.027	0.000	0.000	0.016	0.005	0.013	0.014	0.052	0.005
246	0.017	0.038	0.009	0.011	0.000	0.019	0.000	0.004	0.007	0.006	0.000
250	0.057	0.100	0.060	0.116	0.049	0.019	0.005	0.018	0.014	0.000	0.005
254	0.047	0.050	0.048	0.025	0.037	0.019	0.021	0.044	0.058	0.070	0.118
258	0.037	0.025	0.039	0.053	0.085	0.059	0.050	0.092	0.058	0.215	0.054
262	0.039	0.025	0.036	0.137	0.159	0.064	0.053	0.105	0.130	0.122	0.129
266	0.039	0.050	0.098	0.049	0.037	0.013	0.058	0.096	0.094	0.064	0.081
270	0.030	0.050	0.057	0.158	0.110	0.144	0.143	0.123	0.159	0.140	0.118
274	0.054	0.013	0.068	0.074	0.049	0.032	0.058	0.083	0.036	0.012	0.070
278	0.027	0.025	0.045	0.025	0.049	0.051	0.061	0.070	0.051	0.012	0.016
282	0.076	0.063	0.042	0.021	0.012	0.008	0.016	0.026	0.029	0.023	0.011
286	0.015	0.013	0.021	0.011	0.000	0.000	0.005	0.048	0.029	0.041	0.011
290	0.010	0.000	0.000	0.021	0.000	0.008	0.003	0.000	0.007	0.006	0.059
294	0.007	0.038	0.000	0.032	0.000	0.008	0.000	0.009	0.014	0.006	0.011
298	0.007	0.013	0.009	0.000	0.000	0.003	0.013	0.000	0.000	0.006	0.038

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Appendix A.–Page 4 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
302	0.002	0.000	0.000	0.014	0.000	0.005	0.000	0.004	0.000	0.000	0.005
306	0.000	0.013	0.003	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000
310	0.007	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000
314	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000
318	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000
322	0.015	0.000	0.006	0.000	0.000	0.013	0.000	0.000	0.007	0.000	0.000
326	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
330	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
334	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
342	0.000	0.000	0.003	0.000	0.000	0.000	0.011	0.000	0.007	0.000	0.005
346	0.012	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000
350	0.012	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
354	0.010	0.000	0.006	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000
358	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000
Locus: <i>Ots201b</i>											
n	184	35	141	144	45	183	184	161	80	89	100
161	0.008	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
165	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
169	0.008	0.029	0.092	0.003	0.022	0.036	0.041	0.040	0.038	0.000	0.005
173	0.196	0.171	0.160	0.104	0.044	0.213	0.043	0.093	0.088	0.242	0.210
178	0.019	0.043	0.000	0.031	0.033	0.014	0.041	0.065	0.050	0.056	0.075
182	0.063	0.029	0.057	0.045	0.044	0.033	0.073	0.028	0.025	0.028	0.005
186	0.052	0.043	0.043	0.031	0.067	0.052	0.073	0.062	0.013	0.051	0.030
190	0.008	0.029	0.011	0.014	0.056	0.008	0.022	0.053	0.069	0.006	0.005
194	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
198	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
202	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
206	0.014	0.000	0.011	0.000	0.000	0.046	0.000	0.000	0.000	0.000	0.000
210	0.005	0.000	0.018	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000
214	0.065	0.014	0.018	0.035	0.000	0.022	0.024	0.003	0.006	0.011	0.015
218	0.068	0.071	0.085	0.038	0.133	0.112	0.014	0.016	0.050	0.011	0.045

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Appendix A.—Page 5 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
222	0.082	0.057	0.103	0.156	0.044	0.115	0.125	0.096	0.100	0.180	0.205
226	0.182	0.157	0.160	0.128	0.156	0.123	0.231	0.224	0.206	0.157	0.185
230	0.090	0.214	0.110	0.038	0.122	0.101	0.092	0.025	0.088	0.112	0.080
234	0.065	0.029	0.043	0.156	0.133	0.036	0.098	0.118	0.063	0.039	0.030
238	0.038	0.043	0.028	0.104	0.033	0.027	0.024	0.047	0.075	0.022	0.065
242	0.014	0.014	0.039	0.028	0.000	0.030	0.022	0.025	0.013	0.034	0.020
246	0.005	0.057	0.018	0.066	0.044	0.011	0.005	0.022	0.025	0.022	0.005
250	0.000	0.000	0.000	0.021	0.056	0.019	0.063	0.081	0.094	0.028	0.020
254	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000
258	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
262	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000
266	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Locus: <i>Ots208b</i>											
n	177	26	147	142	36	122	185	144	69	89	98
154	0.000	0.019	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.005
158	0.006	0.000	0.017	0.004	0.014	0.016	0.003	0.010	0.029	0.017	0.082
162	0.025	0.058	0.034	0.004	0.000	0.057	0.000	0.000	0.000	0.039	0.041
166	0.082	0.096	0.054	0.007	0.056	0.033	0.005	0.035	0.036	0.067	0.026
170	0.048	0.038	0.031	0.011	0.014	0.033	0.084	0.076	0.029	0.039	0.051
174	0.051	0.058	0.027	0.056	0.028	0.115	0.016	0.017	0.043	0.028	0.020
178	0.054	0.019	0.017	0.025	0.000	0.061	0.122	0.069	0.043	0.022	0.000
182	0.071	0.058	0.065	0.014	0.014	0.053	0.019	0.021	0.036	0.045	0.066
186	0.023	0.019	0.034	0.067	0.111	0.012	0.032	0.038	0.051	0.022	0.026
190	0.065	0.058	0.061	0.039	0.056	0.033	0.008	0.035	0.043	0.022	0.031
194	0.006	0.000	0.000	0.046	0.014	0.004	0.000	0.028	0.058	0.011	0.000
198	0.003	0.019	0.017	0.000	0.014	0.012	0.016	0.003	0.007	0.006	0.000
202	0.020	0.019	0.034	0.000	0.000	0.004	0.008	0.003	0.000	0.039	0.020
206	0.023	0.038	0.017	0.000	0.000	0.025	0.005	0.010	0.000	0.022	0.026
210	0.028	0.058	0.027	0.081	0.056	0.041	0.046	0.073	0.072	0.011	0.056
214	0.051	0.038	0.099	0.070	0.056	0.049	0.149	0.090	0.087	0.129	0.026
218	0.073	0.038	0.051	0.081	0.083	0.041	0.011	0.076	0.036	0.124	0.117
222	0.048	0.058	0.051	0.060	0.014	0.008	0.024	0.035	0.036	0.073	0.066

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Appendix A.–Page 6 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
226	0.062	0.077	0.061	0.035	0.069	0.049	0.049	0.073	0.051	0.017	0.036
230	0.048	0.115	0.122	0.092	0.056	0.078	0.016	0.024	0.029	0.056	0.107
234	0.048	0.000	0.024	0.021	0.042	0.041	0.068	0.000	0.022	0.000	0.020
238	0.034	0.019	0.027	0.039	0.014	0.057	0.103	0.031	0.065	0.056	0.026
242	0.025	0.038	0.014	0.042	0.028	0.049	0.089	0.069	0.051	0.017	0.051
246	0.031	0.000	0.014	0.025	0.069	0.020	0.019	0.052	0.043	0.062	0.026
250	0.025	0.038	0.031	0.014	0.097	0.025	0.049	0.045	0.065	0.039	0.026
254	0.006	0.019	0.041	0.046	0.028	0.025	0.019	0.035	0.036	0.011	0.005
258	0.011	0.000	0.014	0.123	0.069	0.020	0.027	0.049	0.014	0.011	0.020
262	0.017	0.000	0.010	0.000	0.000	0.008	0.000	0.000	0.014	0.011	0.020
266	0.008	0.000	0.003	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.005
270	0.008	0.000	0.003	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000
Locus: <i>Ots211</i>											
n	202	39	161	144	30	170	188	157	72	89	94
216	0.005	0.000	0.006	0.000	0.000	0.003	0.000	0.000	0.007	0.000	0.000
220	0.005	0.013	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.005
224	0.030	0.000	0.047	0.038	0.067	0.029	0.011	0.035	0.056	0.140	0.133
228	0.054	0.141	0.096	0.073	0.083	0.206	0.152	0.134	0.118	0.073	0.048
232	0.119	0.128	0.127	0.240	0.233	0.053	0.157	0.131	0.188	0.112	0.053
236	0.054	0.090	0.053	0.028	0.050	0.059	0.138	0.108	0.090	0.017	0.096
240	0.035	0.090	0.056	0.108	0.050	0.044	0.048	0.057	0.049	0.112	0.170
244	0.035	0.038	0.009	0.042	0.017	0.006	0.056	0.054	0.021	0.034	0.048
248	0.047	0.051	0.071	0.017	0.050	0.076	0.019	0.070	0.021	0.051	0.064
252	0.072	0.026	0.040	0.000	0.000	0.044	0.000	0.003	0.000	0.017	0.011
256	0.042	0.077	0.059	0.035	0.050	0.006	0.005	0.022	0.007	0.028	0.005
260	0.114	0.103	0.087	0.014	0.067	0.103	0.037	0.022	0.035	0.000	0.064
264	0.114	0.090	0.040	0.021	0.017	0.038	0.104	0.003	0.000	0.056	0.016
268	0.062	0.051	0.059	0.028	0.000	0.062	0.027	0.013	0.035	0.000	0.090
270	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.030	0.000	0.019	0.000	0.000	0.012	0.008	0.000	0.000	0.062	0.059
276	0.054	0.013	0.034	0.101	0.100	0.079	0.082	0.086	0.104	0.084	0.032
280	0.020	0.013	0.009	0.104	0.083	0.038	0.016	0.061	0.049	0.022	0.027

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Appendix A.–Page 7 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
284	0.030	0.000	0.084	0.045	0.000	0.068	0.032	0.032	0.090	0.056	0.027
288	0.032	0.064	0.053	0.014	0.000	0.024	0.000	0.010	0.014	0.028	0.005
292	0.032	0.000	0.028	0.076	0.050	0.021	0.024	0.076	0.049	0.011	0.021
296	0.012	0.000	0.009	0.014	0.000	0.009	0.056	0.019	0.035	0.028	0.021
300	0.000	0.013	0.012	0.000	0.067	0.021	0.021	0.022	0.028	0.006	0.000
304	0.002	0.000	0.000	0.000	0.000	0.000	0.008	0.041	0.007	0.056	0.000
308	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.005
Locus: <i>Ots212</i>											
n	189	22	162	142	31	166	188	152	76	86	92
123	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
127	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
131	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
135	0.032	0.000	0.015	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.011
139	0.058	0.091	0.170	0.088	0.097	0.036	0.213	0.122	0.132	0.058	0.125
143	0.529	0.682	0.410	0.408	0.371	0.512	0.465	0.480	0.461	0.564	0.549
147	0.087	0.068	0.077	0.183	0.258	0.072	0.040	0.105	0.151	0.122	0.114
151	0.056	0.023	0.083	0.162	0.129	0.226	0.152	0.102	0.125	0.128	0.087
155	0.071	0.045	0.102	0.018	0.032	0.084	0.029	0.079	0.072	0.064	0.049
159	0.040	0.023	0.049	0.088	0.000	0.024	0.080	0.039	0.026	0.006	0.038
163	0.042	0.023	0.028	0.021	0.032	0.027	0.021	0.030	0.020	0.000	0.011
167	0.034	0.045	0.034	0.025	0.081	0.000	0.000	0.043	0.013	0.058	0.016
171	0.011	0.000	0.006	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
175	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
183	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
187	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
191	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
195	0.003	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
207	0.000	0.000	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
211	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
219	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
223	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

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	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
Locus: <i>Ots213</i>											
n	173	20	171	142	32	186	189	98	73	84	94
218	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.032
222	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.020	0.014	0.048	0.085
226	0.003	0.000	0.003	0.000	0.000	0.013	0.021	0.005	0.000	0.006	0.005
230	0.023	0.000	0.038	0.032	0.016	0.040	0.074	0.056	0.062	0.036	0.016
234	0.029	0.075	0.012	0.000	0.000	0.011	0.008	0.005	0.000	0.012	0.021
238	0.095	0.025	0.114	0.141	0.063	0.016	0.029	0.071	0.082	0.018	0.064
242	0.130	0.075	0.108	0.155	0.219	0.258	0.132	0.066	0.116	0.220	0.191
246	0.055	0.100	0.076	0.049	0.063	0.065	0.063	0.112	0.048	0.107	0.090
250	0.003	0.025	0.026	0.018	0.016	0.008	0.011	0.000	0.007	0.030	0.059
254	0.009	0.000	0.000	0.028	0.000	0.005	0.000	0.000	0.000	0.000	0.000
258	0.014	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
262	0.029	0.000	0.029	0.000	0.016	0.000	0.003	0.005	0.000	0.006	0.000
266	0.003	0.050	0.000	0.000	0.000	0.011	0.024	0.000	0.000	0.012	0.000
270	0.026	0.025	0.009	0.000	0.000	0.000	0.013	0.010	0.007	0.000	0.000
274	0.012	0.025	0.041	0.025	0.078	0.035	0.008	0.010	0.021	0.000	0.011
278	0.032	0.050	0.041	0.063	0.078	0.013	0.053	0.036	0.062	0.036	0.032
282	0.052	0.025	0.041	0.000	0.016	0.000	0.026	0.005	0.000	0.024	0.011
286	0.055	0.025	0.079	0.127	0.063	0.048	0.175	0.061	0.062	0.131	0.048
290	0.061	0.050	0.064	0.077	0.047	0.065	0.106	0.061	0.041	0.060	0.064
294	0.110	0.125	0.061	0.106	0.078	0.070	0.077	0.158	0.137	0.060	0.064
298	0.069	0.150	0.061	0.067	0.094	0.126	0.098	0.163	0.137	0.060	0.138
302	0.058	0.025	0.073	0.074	0.078	0.083	0.040	0.102	0.123	0.054	0.032
306	0.046	0.100	0.064	0.018	0.031	0.067	0.021	0.046	0.041	0.083	0.027
310	0.026	0.025	0.029	0.021	0.031	0.048	0.019	0.000	0.034	0.000	0.005
314	0.052	0.025	0.015	0.000	0.000	0.016	0.000	0.005	0.000	0.000	0.000
318	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
322	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
334	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.005

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Appendix A.—Page 9 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
Locus: <i>Ots3M</i>											
n	201	55	178	142	39	188	189	150	86	91	101
138	0.132	0.209	0.183	0.053	0.090	0.120	0.275	0.060	0.110	0.077	0.104
140	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.003	0.012	0.000	0.005
142	0.020	0.018	0.028	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000
144	0.060	0.100	0.028	0.011	0.013	0.016	0.000	0.000	0.006	0.005	0.005
146	0.450	0.482	0.483	0.687	0.577	0.543	0.611	0.760	0.698	0.599	0.688
148	0.326	0.191	0.272	0.236	0.308	0.298	0.114	0.147	0.163	0.319	0.198
150	0.002	0.000	0.006	0.014	0.000	0.013	0.000	0.030	0.012	0.000	0.000
152	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Locus: <i>Ots9</i>											
n	206	59	177	142	48	184	189	149	72	88	103
103	0.005	0.008	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
105	0.439	0.449	0.528	0.820	0.813	0.546	0.685	0.698	0.736	0.665	0.597
107	0.451	0.458	0.418	0.169	0.156	0.413	0.278	0.238	0.236	0.324	0.364
109	0.104	0.085	0.048	0.011	0.031	0.041	0.037	0.064	0.028	0.000	0.005
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.034
Locus: <i>OtsG474</i>											
n	206	52	168	145	40	175	189	164	88	91	109
156	0.973	0.971	0.967	0.938	0.863	0.934	0.910	0.960	0.977	0.973	0.986
160	0.002	0.000	0.000	0.000	0.013	0.000	0.000	0.003	0.006	0.000	0.000
164	0.019	0.019	0.009	0.062	0.125	0.054	0.090	0.037	0.017	0.027	0.014
176	0.002	0.000	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
180	0.002	0.010	0.006	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000
184	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Locus: <i>Ssa408</i>											
n	168	20	139	143	43	179	183	151	56	89	98
188	0.012	0.000	0.007	0.028	0.000	0.003	0.014	0.000	0.000	0.000	0.005
192	0.006	0.025	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000
196	0.042	0.000	0.094	0.003	0.023	0.014	0.005	0.003	0.000	0.000	0.000

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Appendix A.– Page 10 of 10.

	Andreafsky	Anvik	Gisasa	Henshaw	S. Fork Koyukuk	Tozitna	Kantishna	Chena	Salcha	Beaver	Chandalar
200	0.015	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.005
204	0.000	0.025	0.004	0.017	0.058	0.000	0.003	0.020	0.027	0.000	0.000
208	0.024	0.050	0.036	0.000	0.012	0.022	0.005	0.007	0.000	0.000	0.005
212	0.006	0.000	0.018	0.000	0.000	0.025	0.000	0.000	0.009	0.000	0.000
216	0.021	0.025	0.025	0.021	0.000	0.028	0.033	0.026	0.027	0.011	0.036
220	0.071	0.025	0.072	0.171	0.093	0.039	0.221	0.129	0.161	0.073	0.015
224	0.101	0.175	0.129	0.084	0.058	0.106	0.041	0.129	0.143	0.163	0.179
228	0.179	0.125	0.173	0.108	0.256	0.212	0.268	0.189	0.250	0.157	0.209
230	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
232	0.167	0.125	0.176	0.262	0.314	0.179	0.216	0.199	0.179	0.354	0.276
236	0.238	0.350	0.090	0.115	0.047	0.179	0.093	0.172	0.143	0.174	0.122
240	0.063	0.075	0.115	0.122	0.081	0.115	0.071	0.096	0.063	0.062	0.128
244	0.048	0.000	0.061	0.031	0.058	0.020	0.027	0.007	0.000	0.006	0.000
248	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.005
252	0.000	0.000	0.000	0.035	0.000	0.056	0.000	0.017	0.000	0.000	0.005