

**Assessment of Genetic Stock of Origin of Chinook  
Salmon Harvested in Commercial Salmon Fisheries of  
the Westward Region, 2015–2016**

by

**M. Birch Foster**

and

**Tyler H. Dann**

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May 2015

Alaska Department of Fish and Game

Divisions of Sport Fish and Commercial Fisheries



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

***REGIONAL OPERATIONAL PLAN CF.4K.2015.17***

**ASSESSMENT OF GENETIC STOCK OF ORIGIN OF CHINOOK  
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THE WESTWARD REGION, 2015–2016**

by

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Alaska Department of Fish and Game  
Division of Commercial Fisheries

May 2015

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*This document should be cited as:*

*Foster, M. B., and T. H. Dann. 2015. Assessment of genetic stock of origin of Chinook salmon harvested in commercial salmon fisheries of the Westward Region, 2015–2016. Alaska Department of Fish and Game, Regional Operational Plan No. ROP.CF.4K.2015.17, Kodiak.*

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**SIGNATURE PAGE**

Project Title: Assessment of Genetic Stock of Origin of Chinook Salmon Harvested in Commercial Salmon Fisheries of the Westward Region, 2015–2016

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Division, Region and Area: Division of Commercial Fisheries, Region IV

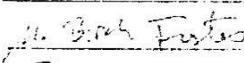
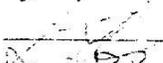
Project Nomenclature: Chinook Salmon Research Initiative

Period Covered: May 2015–April 2017

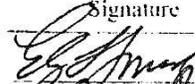
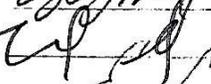
Field Dates: June 1–August 15

Plan Type: Category III

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## PURPOSE

The primary goal of this study is to estimate stock of origin, age, size, and sex composition of Chinook salmon *Oncorhynchus tshawytscha* harvested in Westward Region commercial salmon fisheries during the 2014 to 2016 seasons. Within the Westward Region, Karluk and Chignik rivers are 2 of the 12 stocks chosen by the ADF&G as indicator stocks and the lack of stock-specific commercial harvest estimates have been identified as an information gap. In addition age, sex, and size information of the harvest will allow researchers to better understand the recruitment and mortality processes of regional Chinook stocks. This operational plan provides the Alaska Department of Fish and Game (ADF&G) with a sampling plan to achieve that overall objective.

Key words: GSI, Chinook salmon, Westward Region, genetic stock composition.

## BACKGROUND

Chinook salmon *Oncorhynchus tshawytscha* are harvested incidentally to directed sockeye *O. nerka*, pink *O. gorbuscha*, coho *O. kisutch*, and chum *O. keta* salmon commercial fisheries within Alaska Department of Fish and Game (ADF&G) Westward Region's Kodiak (Area K), Chignik (Area L), and Alaska Peninsula (Area M) management areas (Figure 1).

In the Kodiak Management Area, Chinook salmon spawn in 7 known streams (Jackson and Keyse 2013). Chignik River is the only substantial Chinook salmon system in the Chignik Management Area (Anderson et al. 2013), and so far, 11 different streams within the Alaska Peninsula management areas (Witteveen and Dann 2013) have had baseline genetic information collected. Only 4 major Chinook salmon systems are monitored via salmon counting weir throughout the region (Ayakulik, Chignik, Nelson, and Karluk rivers).

The average commercial Chinook salmon harvest (1996 to 2013) is roughly 18,200 fish in Kodiak, 3,400 fish in Chignik, and 10,500 fish in Alaska Peninsula (Table 1). Since the mid 1990s harvest of Chinook salmon in the marine waters of the Westward Region has been fairly consistent (Figure 2). However, Chinook salmon escapement estimates at the major systems monitored via weir have demonstrated substantial reductions since 2005 (Figure 3), often struggling or failing to reach their respective escapement goals (Munro and Volk 2013).

Decreased returns of Chinook salmon in the region and throughout Alaska have prompted statewide concern about the health of Chinook salmon stocks (ADF&G 2013) and an increased realization that little is known about the migratory pathways and stock of origin in commercial catches. A coded-wire tag (CWT) recovery study in the Kodiak marine waters in 1994 (Swanton 1997) and from 1997 to 1999 (Clark and Nelson 2001) showed hatchery stocks from British Columbia, Alaska, and Pacific Northwest dominated in adipose fin-clipped Chinook salmon sampled. These findings are not dissimilar from observer-examined CWT Chinook salmon recovered in foreign trawl and research vessels occurring in international waters near Kodiak and the South Alaska Peninsula during the 1980s through the early 2000s (Myers et al. 2004). Genetic analysis of Bering Sea Chinook salmon trawl bycatch from 2005 to 2010 showed the presence of primarily Alaska, British Columbia, and Pacific Northwest stocks (NMFS 2009; Guyon et al. 2010a,b; Guthrie et al. 2012); however, of regional interest was the significant presence of north Alaska Peninsula Chinook salmon stocks (14%–27%).

The Western Alaska Salmon Stock Identification Program (WASSIP) was conducted from 2006 to 2009 as an objective measure of determining the stock of origin of chum and sockeye salmon caught by inshore commercial salmon fisheries of western Alaska utilizing genetic stock identification (GSI; Eggers et al. 2011). Stock compositions and stock specific harvests and harvest rates were reported in 2012 (Dann et al. 2012a; Habicht et al. 2012; Munro et al. 2012; Templin et al. 2012). However, GSI of the Chinook salmon catch in the Westward Region commercial salmon fisheries has never been conducted. Scientific knowledge of the temporal and spatial presence of both local and non-local Chinook salmon in these catches is of regional, statewide, and international importance. Currently, these harvests cannot be reliably attributed to local wild stocks, hatchery stocks, or non-local wild stocks.

In 2014, the first year of this project, sampling of Chinook salmon in the commercial salmon fisheries of the Westward Region was conducted (Table 2). Sampling took place in the ports Kodiak, Larsen Bay, Alitak, Chignik, Sand Point, King Cove, and Port Moller. A total of 2,244 fish were sampled for age, sex, and length information and genetic tissue during the early strata and a total of 2,865 fish were sampled during the late strata (Table 2).

Due to declining budgets of the department's Chinook Salmon Research Initiative (CSRI), in late 2014, CSRI cut the Alaska Peninsula- and Chignik-based portions of this project. Because fishery tender schedules result in the potential delivery of Chignik area harvested salmon to the port of Kodiak, the Chignik sampling goals were retained. The following operational plan details implementation, sampling, and reporting of a project to collect genetic tissue and age, sex, and length (ASL) data from Chinook salmon of the commercial salmon fisheries in the Kodiak and Chignik areas during the 2015 and 2016 seasons.

## **OBJECTIVES**

### **PRIMARY OBJECTIVES**

1. Collect genetic tissue (axillary process) paired with ASL data on an estimated 10% of the Chinook salmon harvest (estimated from fish tickets) within the Kodiak and Chignik area commercial salmon fisheries.
2. Estimate stock proportions of Chinook salmon in the Kodiak and Chignik area salmon harvests by general area stock groupings.

### **SECONDARY OBJECTIVES**

1. Estimate the age, sex, and length composition of Chinook salmon sampled for genetic information.
2. Collect head from adipose-clipped Chinook salmon sampled as part of genetic sampling.

## **WESTWARD REGION**

### **Overview**

The principal objective of this effort is to sample the major commercial salmon fisheries in Kodiak and Chignik areas (Figure 1) where significant catches of Chinook salmon occur. Overall, there will be two general temporal strata for GSI (early and late). The early stratum coincides with the commercial fisheries targeting early-run sockeye salmon. The late stratum coincides with the commercial fisheries targeting late-run sockeye and/or pink salmon. Exact

dates vary depending on management area (Table 3). Designated sampling areas encompass individual sections, partial districts, whole districts, or multiple districts as outlined in the explicit fishery detail below.

All Chinook salmon GSI samples will be collected along with ASL data (paired sampling) as outlined in Appendix A. The axillary process will be removed from each fish sampled and placed in an individual container with ethanol. From each sampled fish biological information will also be collected (age, sex, and length). During sampling, all Chinook will be monitored for the presence of clipped adipose fins. Fish missing an adipose fin will be sampled using the procedures outlined in Appendix B.

### **Kodiak Management Area Fishery (Area K)**

Sampling areas and strata for the Kodiak fishery were identified based on historical patterns of catch and general fishing schedules. Four distinct sampling areas were designated based on geographic location, harvest magnitude, and management nature of fishery. The Mainland District is exclusively a purse seine area encompassing all Alaska Peninsula waters within the Kodiak Management Area. The NW Kodiak/Afognak districts area, where both purse seine and set gillnet gear can be used, represents historically the largest source of Chinook harvest in the Kodiak area. The SW Kodiak/Alitak districts area also allows the use of both purse seine and set gillnet gear (gillnets are restricted to the inner areas of Alitak Bay); this area contains the two largest Chinook salmon systems in Kodiak, the Karluk and Ayakulik rivers (Figure 1). Harvest methods in the Eastside Kodiak/Afognak districts area consist of purse seine gear only. For all sampling areas, two temporal strata are defined. The first stratum runs from June 1 to July 5 and coincides with targeted early-run sockeye fisheries (Jackson and Keyse 2013). The second stratum runs from July 6 to August 5 and coincides with targeted fisheries for pink and/or mid-late sockeye salmon (Table 3).

For the entirety of Kodiak Management Area non-retention of Chinook salmon (>28 inches) in the purse seine harvest applies during the first stratum. This of course is a major sampling caveat since the magnitude of fish not retained is unknown. During the second stratum the non-retention is relaxed but still in effect for SW Kodiak District and that portion of NW Kodiak District south of Cape Kuliuk. For purposes of GSI, a representative sample of 400 tissues stratified roughly proportional to catch is targeted for each area and temporal stratum. Samples from all locations in Kodiak will be collected primarily at three ports where technicians will be stationed: Kodiak, Larsen Bay, and Alitak (Figure 1). Sampling in Kodiak will typically be conducted at Ocean Beauty, Alaska Pacific, and Island Seafoods. Larsen Bay has only one processing facility (Icicle) as does Alitak (Ocean Beauty) where sampling will be conducted.

### **Chignik Management Area Fishery (Area L)**

Sampling areas and strata for the Chignik fishery were identified based on historical patterns of catch and general fishing schedules. Two distinct sampling areas were designated based on geographic location and harvest magnitude. Purse seine gear is the only allowable commercial harvest method in Area L. The Chignik Bay District is a fishery that is terminal to Chignik River which has the only significant Chinook salmon run in the area. The outside area (Eastern, Central, Western, and Perryville districts) consists of the remainder of Area L. Due to a lack of historical Chinook salmon harvest in what would be the early stratum, sampling will only be conducted after June. For both sampling areas, one temporal stratum is defined as July 1 to August 5 and generally coincides with the early/late overlap and late-run sockeye fishery

(Anderson et al. 2013; Table 3). For the 2015 and 2016 season only the outside districts in the Chignik Management Area will be targeted. For purposes of GSI, a representative sample of 400 tissues stratified roughly proportional to catch is targeted for the area. Samples will be collected, if available, at Trident Seafoods and International Seafoods in Kodiak.

## **STUDY DESIGN**

In 2015 and 2016, collection and analysis of data to determine population age structure and genetic stock of origin will be conducted through temporally stratified sampling of Chinook salmon commercial harvest throughout Kodiak and Chignik management areas of Westward Region. Due to relatively low harvest levels and the protracted nature of the fishery (June–August) strata will be limited and many district areas grouped to increase the samples sizes to levels that promote scientifically defensible estimates of stock of origin following the general broad scale reporting areas described for Chinook salmon in Templin et al. (2011) and Larson et al. (2013). Strata chosen for this study are based on historical peaks of Chinook harvest in defined geographic areas and do not necessarily coincide with run timing of local Chinook salmon stocks.

Catch samplers will sample commercial harvests at processing facilities located at the major regional fish processing ports; Kodiak, Larsen Bay, and Alitak, at specific timeframes during the season. Sampling will, at times, be conducted in conjunction with existing sockeye salmon age sampling currently performed by field staff. Daily catch reports will be monitored by project biologists as daily sampling objectives will be tied directly to harvest magnitude. The catch from each area stratum will be sampled at a level sufficient to construct the GSI sample for the time and area strata (Table 3). Since the potential exists for only having mixed loads from multiple catch areas available, the directive will be to sample these loads when available or when discrete samples from targeted areas are not likely to be obtained.

The GSI tissue samples for laboratory analysis will be selected from the available harvest samples post-season by stratified sampling of samples within strata proportional to the catch in the respective strata. A random sample proportional to the catch from fishing periods within a GSI stratum will be constructed for each area and time stratum ( $n = 400$ ; Table 3). This ensures that the stock compositions estimated from the GSI analysis are representative of the catch in the strata. Sampling proportional to catch does come with caveats since it entails not only tracking daily harvest but projecting harvest throughout the stratum. In post-season sample selection, some samples will be randomly eliminated from analysis to create the desired proportionality. The end result is that the actual number of fish sampled in the stratum will be a number greater than the desired analysis sample size of 400.

### **Sample size**

A pilot study in 1994 (Swanton 1997) showed that approximately 9%–10% of Chinook harvested in the Kodiak area could be realistically sampled, but was quite variable depending on area and timing. In general, the stratum sample size roughly equates to approximately 10% of the expected harvest in a sampling area. However, Chinook salmon harvests, like all species of salmon, show considerable year to year variation and thus inseason sample size adjustments will undoubtedly occur specific to the actual harvest. The stratum sample size (400 fish) will enable all stock proportions (regardless of number of stocks) to be simultaneously estimated within 0.05 of the true proportions with 90% confidence assuming finite population correction (Bromaghin

1993, Thompson 1987). Additional uncertainty will originate from mixed stock analysis and will be estimated via baseline evaluation tests.

## **TISSUE AND DATA COLLECTION**

The Chinook salmon samplers will obtain fish ticket information before collecting samples to determine if the fish were exclusively harvested from the area and timeframe designated to be sampled. If fish ticket data are not available, the processing facility dock foreman or tender operator will be interviewed. Once fish ticket information becomes available, the origin of the catch will be confirmed. Tenders or fishing vessels selected for sampling will have all Chinook salmon onboard sampled. Often the large Chinook will be separated in the hold on a stringer because of an inability to pump the fish in a manner typical of sockeye, chum, pink and smaller Chinook salmon. It is important to sample not only the large Chinook salmon but the smaller individuals that enter the processor pump and are sorted into totes off of the belts. While many processing facilities sort small Chinook salmon by size (<21 inches and/or < 10 lbs depending on processing facility) and often assign a separate species code (of no commercial value) for these fish, it is important that samplers attempt to attain the sample in the absence of size selective sorting if possible.

Tissue samples and ASL samples will be collected from all fish selected for sampling (Appendix A). The axillary process will be collected from the left side of the fish and placed in an individually labeled cryovial containing ethanol following the procedures outlined in Appendices A1 and A2. All sample and biological information will be recorded on the Chinook Genetics Sampling Form (Appendix A3). Length (mideye to tail fork; METF) will be measured to the nearest millimeter and sex determined (Appendix A4).

Scales, when possible, will be collected from the preferred area of each fish following the methods described by International North Pacific Fish Commission (1963). Three scales per fish will be collected and mounted on scale “gum” cards and impressions made on acetate/diacetate cards (Clutter and Whitesel 1956; Appendices A5–A7). Fish ages will be assigned by examining scale impressions for annual growth increments using a microfiche reader fitted with a 48X lens following designation criteria established by Mosher (1968). The most common method of age determination in Pacific salmon is the analysis of the concentric rings (circuli) on the scale and is the method to be used by this project. Age validation will be accomplished via comparison of known age CWT sampled Chinook with assigned ages from scales. A test of symmetry matrix will be calculated and qualified according to visual methods developed by Bowker (1948) and described in Hoenig et al. (1994) to assess bias and precision.

Ages will be recorded using European notation (Koo 1962), with a decimal separating the number of winters spent in fresh water (after emergence) from the number of winters spent in salt water. All age data will be recorded directly into the database via the Kodiak intranet salmon aging utility using a programmable keyboard (X-keys).

Presence of adipose fin clip will be recorded on the sampling form (Appendix B1). Any Chinook salmon sampled as part of the genetics tissue sampling and displaying an adipose clip will be set aside and sampled additionally for CWT information. A uniquely numbered cinch strap will be attached to the head (Appendix B2) and recorded in the Chinook Genetics Sampling Form (Appendix A3) comments field. The head will be removed carefully with a serrated utility knife. Each head, with the numbered cinch strap visible, will be placed in an individual plastic bag. After tissue sampling is complete, a CWT sampling form will be completed for each processor

delivery (tender) if any adipose-clipped fish were present. All data recorded on the CWT sampling form will be able to be transposed from the Chinook Genetics Sampling Form (Appendix A3). It is important to differentiate the Chinook (410) from the “jack” Chinook (code 411 <660 METF) on the “*Sampling Information*” portion of the CWT form in the lower left area. All Chinook salmon heads collected will be frozen and returned to the Westward Regional office in Kodiak when logistics allow. Head collections will be shipped to the ADF&G Mark, Tag, and Age Laboratory (MTA) in Juneau.

## **DATA REDUCTION**

It is the responsibility of the technician to insure that all data are recorded on a daily basis. Data forms will be kept up to date at all times. Inspection for errors will include, but is not limited to: incorrect dates, transposed nonsensical lengths (e.g., 371 mm when the fish was actually 731 mm), incorrect statistical areas, incorrect genetics vial numbers, and blank spaces. Scale cards will be checked to ensure that scales are clean and mounted correctly, and that the cards are correctly and completely labeled and *paired* with the corresponding ASL data form.

At the end of every sampling day, the Chinook genetics sampling form(s) will be double checked for accuracy and digitally reproduced using an HTML5-based offline data entry application proprietary to the Westward Region. The resultant digital file of daily information will be emailed to the Kodiak office for upload to the ASL database, so near-real time progress of sampling can be ascertained. See *Wattum in prep* for data entry methods.

The MTA is the clearinghouse for all information on CWTs. All CWT data (sampled fish, decoded tags, location, data type, samplers, etc.) are archived and accessible on a permanent ADF&G statewide database and once per year are provided to the permanent coastwide database at the Pacific States Marine Fisheries Commission. Completed CWT tagging summary and release information will be sent to the MTA, after first being given to the project leader and error checked using computer software.

## **DATA ANALYSIS**

### **Genetic Analysis**

GSI will be conducted by the ADF&G Gene Conservation Laboratory (GCL) following standardized procedures similar to those described by Dann et al. (2012a). Genomic DNA will be extracted from tissue samples using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA). DNA will be screened for 96 SNP (single-nucleotide polymorphism) markers using a Fluidigm® platform. If necessary, SNPs may be rescreened on an Applied Biosystems® platform as a backup method for assaying genotypes. Approximately 8% of individuals analyzed for this project will be re-extracted and genotyped as a quality control measure to identify laboratory errors and to measure the background discrepancy rate of the genotyping process. Genotypes will be imported and archived in the GCL Oracle database, LOKI.

Estimates of stock composition will be based on the most current genetic baseline representing spawning Chinook salmon from known origins throughout the Pacific Rim. At this time, the baseline is composed of 172 populations of spawning Chinook salmon ranging from the Russia to California genotyped for 45 SNPs (Templin et al. 2011). Additional baseline collections have been collected and will be incorporated into the baseline used for this project. Baseline development will follow procedures similar to Dann et al. (2012b). Collections that do not

conform to Hardy-Weinberg Equilibrium will be removed from the baseline and will not be used for mixed stock analysis (MSA). Collections will be pooled when appropriate to obtain better estimates of allele frequencies. Each pair of nuclear SNPs in each population in the baseline will be tested for linkage disequilibrium and adjusted to ensure that analyses will be based on independent markers. If significant linkage disequilibrium is identified, either one of the linked SNPs will be removed or the pair will be combined into a composite, haploid marker, depending on the relative value of information the single or combined marker provide for MSA (e.g.,  $f_{ORCA}$ ; Rosenberg 2005).

The utility of the baseline for GSI will be determined by assessing the identifiability of reporting groups using baseline evaluation tests. Templin et al. (2011) described the existing baseline's ability to identify 11 broad and 44 fine-scale reporting groups based upon genetic data from 45 SNPs. A majority of fine-scale groups, and all broad-scale groups, exhibited correct allocations greater than 90%, a standard bar of success for GSI (Seeb et al. 2000). However, interest in greater resolution among Western Alaska populations of Chinook salmon precipitated further marker development. This marker development work has resulted in thousands of new SNPs, and a panel of 96 SNPs is anticipated for use that will allow for accurate and precise estimates of stock composition for Chinook salmon reporting groups of interest in the region fisheries. The baseline will be evaluated with "100% proof tests", where individuals are sampled without replacement from each reporting group and analyzed as a mixture against the reduced baseline.

Only individuals with high quality data will be included in MSA. Data quality control will include identifying and removing individuals missing >20% genotypic data, duplicate individuals, and non-Chinook salmon. Stock composition of the mixtures will be estimated using the program BAYES (Pella and Masuda 2001). A series of independent Markov Chain Monte Carlo chains with different starting values for each population will be combined to form the posterior distribution. Summary statistics from these distributions will be tabulated to describe stock compositions, and apply stock proportions to the harvest each area time stratum represents to provide estimates of stock-specific harvests.

From previous genetic differentiation studies (Templin et al. 2011; Larson et al. 2013) the following reporting groups can be identified with acceptable certainty and will serve as the basis of reporting for this study.

1. Russia
2. Coastal West Alaska/Yukon
3. Cook Inlet
4. Copper
5. SE Alaska/NE Gulf of Alaska
6. British Columbia
7. West Coast U.S.
8. Alaska Peninsula
9. Chignik
10. Kodiak

Recognizing the error caused by miss-assignment among genetically similar reporting groups and the potentially small sample sizes available, these reporting groups may be combined. Alternatively, while the Chinook salmon baseline for the Westward Region is currently in the process of being developed, every attempt will be made to genetically differentiate individual

Westward Region stocks including separate hatchery components in Kodiak of Karluk brood source.

Sample selection and DNA extraction at the GCL will be completed by March 1, following each field data collection season. Samples collected from the 2014 and 2015 seasons will be analyzed in the laboratory during the winter of 2015/2016. This allows time for the baseline to be updated and reduces the number of samples to be analyzed the winter prior to final reporting. Samples collected from the 2016 season will be analyzed in the laboratory during the winter of 2016/2017.

### **Age and Sex Composition of Harvest**

Within a stratum the proportion of sampled Chinook salmon by age and sex is defined by the calculation:

$$\hat{p}_{ij} = \frac{n_{ij}}{n_i}, \quad (1)$$

where  $n_i$  = the number in the stratum sample of sex  $i$  and  $n_{ij}$  = the number in the sample of age  $j$  of sex class  $i$  within  $n_i$ . The estimated variance of the estimated proportion is calculated as:

$$\text{var}(\hat{p}_{ij}) = \frac{\hat{p}_{ij}(1-\hat{p}_{ij})}{n_i} \quad (2)$$

Numbers of fish by age within a stratum will be estimated as the sum of the products of estimated age composition and estimated abundance within a sex category:

$$\hat{N}_j = \sum_i (\hat{p}_{ij} \hat{N}_i), \quad (3)$$

where  $\hat{N}_i$  is the product of the estimated total Chinook salmon harvest and estimated sex proportion within the stratum.

Standard sample summary statistics will be used to calculate estimates of mean length at age and its variance (Cochran 1977).

## **SCHEDULE AND DELIVERABLES**

Sampling efforts will begin approximately June 1 and end approximately August 5 for the 2015 and 2016 field seasons. Raw field data will be entered and final error checked by November 1 after each sampling season. Age and size composition of the samples will be reported on an annual basis in the respective management area catch and escapement sampling results published in Fisheries Data Series reports the winter proceeding sampling.

The CWT lab will annually process all samples and report CWT information to the data repository within a week of receiving the shipment. Annual CWT data will be reported within the aforementioned catch and escapement sampling results by management area.

All samples will be statistically analyzed during the winter and spring of 2016–2017. An ADF&G Fishery Manuscript will be published documenting all project information (stock of origin, age, size, and CWT information) and finalized in the fall of 2017.

## **RESPONSIBILITIES**

M. Birch Foster, Fishery Biologist III (sampling project leader)

Duties: This position is responsible for supervising all aspects of the overall project, including planning, budget, sample design, permits, and final reporting.

Tyler Dann, Fisheries Geneticist II, (genetics project leader)

Duties: This position is responsible for supervising all aspects of the genetic analysis, including planning, budget, personnel, training, and final reporting.

David Barnard, Biometrician III

Duties: Provides input to and approves the sampling design. Reviews and provides biometric support for operational plan, data analysis, and final report.

Kevin Schaberg, Salmon Research Coordinator

Duties: This position is the Salmon Research Coordinator for Westward Region and provides program and budget planning oversight. Also reviews the operational plan, data analysis, and final report.

Michelle Moore, Fishery Biologist II (supervise Kodiak sampling)

Duties: This position supervises field activities in Kodiak from June 1 through the end of the project. Responsible for training and deploying staff. Responsible for arranging logistics with field crew, adjusting personnel hours and schedules as appropriate to achieve objectives. In her absence, Mark Witteveen will cover her duties.

Molly McFarland, Fishery Biologist I (Field Crew leader)

Duties: Participate and lead crew field sampling in Kodiak, Larsen Bay, and Alitak.

Michelle Canete, Fish and Wildlife Technician III: Larsen Bay

Duties: This position will conduct sampling at the Icicle Seafoods plant in Larsen Bay June 1 to August 5.

Rose Wallin, Fish and Wildlife Technician III: Alitak

Duties: This position will conduct sampling at the Ocean Beauty plant in Alitak June 1 to August 5.

Laura Griffing, Fish and Wildlife Technician III: Kodiak

Duties: This position will conduct sampling at the Ocean Beauty plant in Kodiak June 1 to August 5.

Chloe Ivanoff, Fish and Wildlife Technician II: Kodiak.

Duties: This position will conduct sampling at the port of Kodiak processing plants from June 1 to August 5.

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## **TABLES**

Table 1.—Westward Region Chinook salmon commercial harvest, 1996–2014.

Year	Kodiak (Area K)			Chignik (Area L)			Alaska Peninsula (Area M)		
	Number	Pounds	Avg Wt (lbs)	Number	Pounds	Avg Wt (lbs)	Number	Pounds	Avg Wt (lbs)
1996	13,071	178,538	13.66	3,105	62,603	20.16	10,012	171,017	17.08
1997	18,728	186,869	9.98	3,025	47,075	15.56	17,515	283,992	16.21
1998	17,341	249,285	14.38	4,374	66,080	15.11	10,724	163,726	15.27
1999	18,299	232,505	12.71	3,296	56,706	17.20	9,701	146,230	15.07
2000	12,293	183,423	14.92	2,592	34,757	13.41	9,009	138,935	15.42
2001	23,827	330,896	13.89	2,845	39,252	13.80	6,714	95,046	14.16
2002	19,263	192,096	9.97	1,441	13,725	9.52	10,251	137,175	13.38
2003	18,531	189,436	10.22	2,757	39,716	14.41	7,257	97,489	13.43
2004	28,899	328,129	11.35	2,337	43,652	18.68	17,452	278,757	15.97
2005	14,411	168,336	11.68	3,136	55,615	17.73	13,685	185,145	13.53
2006	20,283	209,359	10.32	2,187	38,015	17.38	13,045	180,573	13.84
2007	17,222	163,518	9.49	1,746	29,745	17.04	12,921	166,121	12.86
2008	17,176	138,103	8.04	955	14,463	15.14	6,166	102,446	16.61
2009	7,219	66,207	9.17	3,244	30,791	9.49	9,036	144,085	15.95
2010	14,550	116,085	7.98	10,262	102,684	10.01	10,622	147,055	13.84
2011	18,454	173,049	9.38	6,440	72,305	11.23	9,577	126,812	13.24
2012	14,785	108,955	7.37	3,636	48,850	13.44	8,697	138,717	15.95
2013	34,028	255,031	7.49	2,983	36,364	12.19	7,224	85,609	11.88
2014	7,224	52,446	7.26	8,602	73,977	8.60	7,661	80,644	10.53
Average									
1996–2013	18,243	192,768	10.67	3,353	46,244	14.53	10,534	154,941	14.65

Note: 2014 harvest numbers are preliminary as of fish tickets entered by 10/2/14

Table 2.–Westward Region Chinook salmon genetic sampling results, 2014.

Area	District(s)	Statistical Areas	Sampling Site	Gear Type	strata					
					(1) early		(2) late		post sampling	
					Harvest	Samples	Harvest	Samples	Harvest	Samples
Kodiak	Mainland	262	Kodiak	Seine	-	-	335	462	-	*
	NW Kodiak/Afognak	251, 253, 254	Larsen Bay	Seine/Gillnet	975	667	846	481	839	*
	SW Kodiak/Alitak	255, 256, 257	Alitak	Seine	270	268	1,252	416	712	*
	NE Kodiak/Eastside Kodiak	252, 258, 259	Kodiak	Seine	377	294	2,533	465	56	*
Chignik	Chignik Bay	271	Chignik	Seine	-	*	239	84	116	*
	Eastern/Central/Western/Perryville	272, 273, 275	Chignik	Seine	-	*	5,742	503	2,860	*
S. Peninsula	Southeastern/South Central	282, 283	Sand Point	Seine/Gillnet	941	342	3,745	384	1	*
	Unimak/Southwestern	284, 285	King Cove	Seine/Gillnet	1,179	405	601	*	0	*
N. Peninsula	Northern District <sup>a</sup>	314, 315, 316, 317	Port Moller	Gillnet	167	52	237	73	3	*
	Nelson Lagoon	313-30	Port Moller	Gillnet	434	182	19	*	0	*
Total					4,343	2,210	15,459	2,868	4,554	

\* Not in sampling plan (- in harvest column indicated zero harvest)

<sup>a</sup> Northern District comprised only sampling from Harbor Point to Outer Port Heiden Sections

Table 3.–Westward Region Chinook salmon genetic sampling schedule, 2015–2016.

Area	Sampling Area	District(s)	Primary Sampling Site	Gear Type(s)	Strata		Number Analyzed	
					Early	Late	Per Strata	Total
Kodiak								
	Mainland	262	Kodiak	Seine	June 1–July 5	July 6–August 5	400	800
	NW Kodiak/Afognak	251, 253, 254	Larsen Bay	Seine/Gillnet	June 1–July 5	July 6–August 5	400	800
	SW Kodiak/Alitak	255, 256, 257	Alitak	Seine	June 1–July 5	July 6–August 5	400	800
	NE Kodiak/Eastside Kodiak	252, 258, 259	Alitak	Seine	June 1–July 5	July 6–August 5	400	800
Chignik								
	East./Central/West./Perryville	272, 273, 275	Kodiak	Seine		July 1–August 5	400	400
Total								3,600

## **FIGURES**

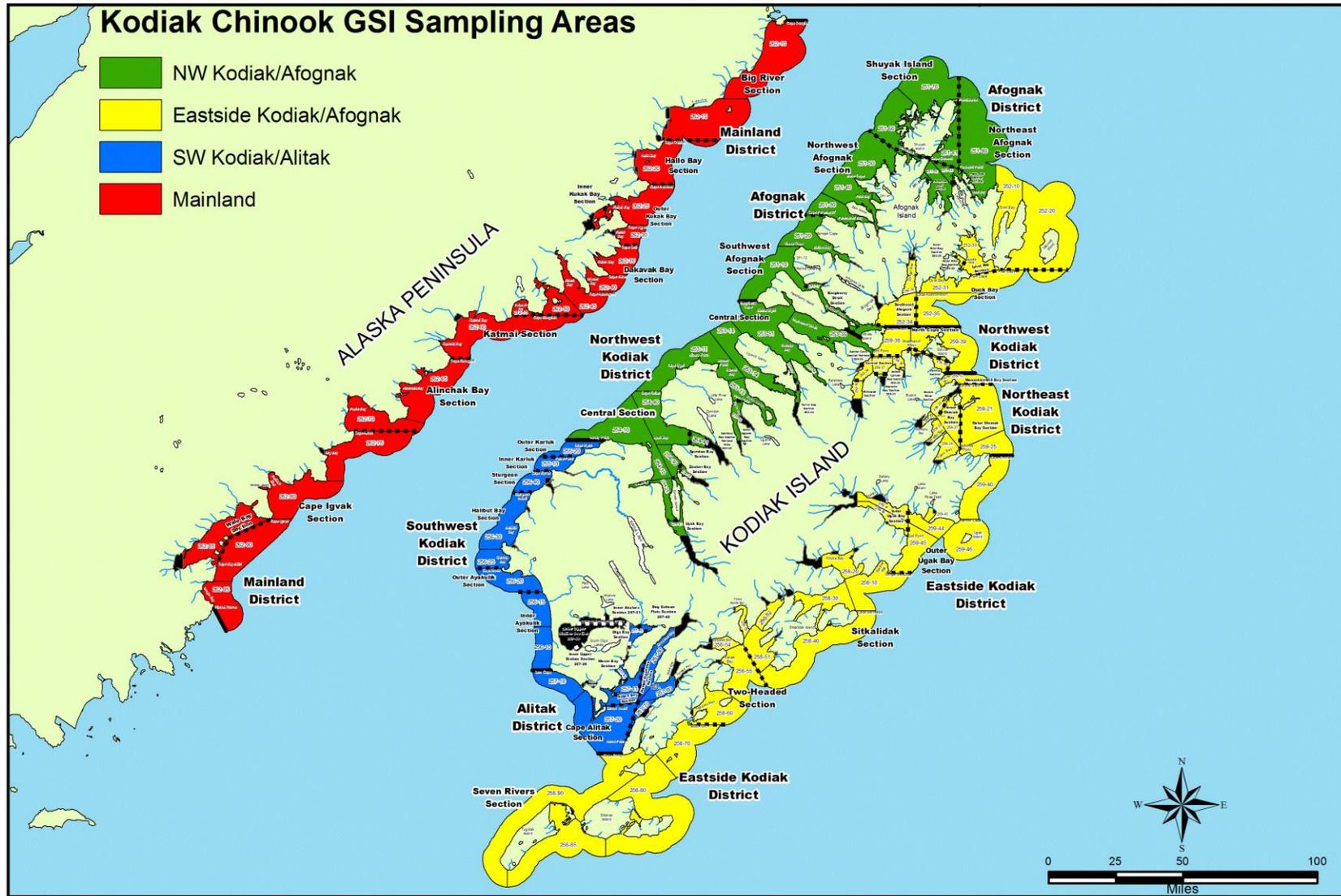


Figure 1.–Map depicting the Kodiak Management Area commercial salmon fishery districts and the Chinook GSI sampling areas.

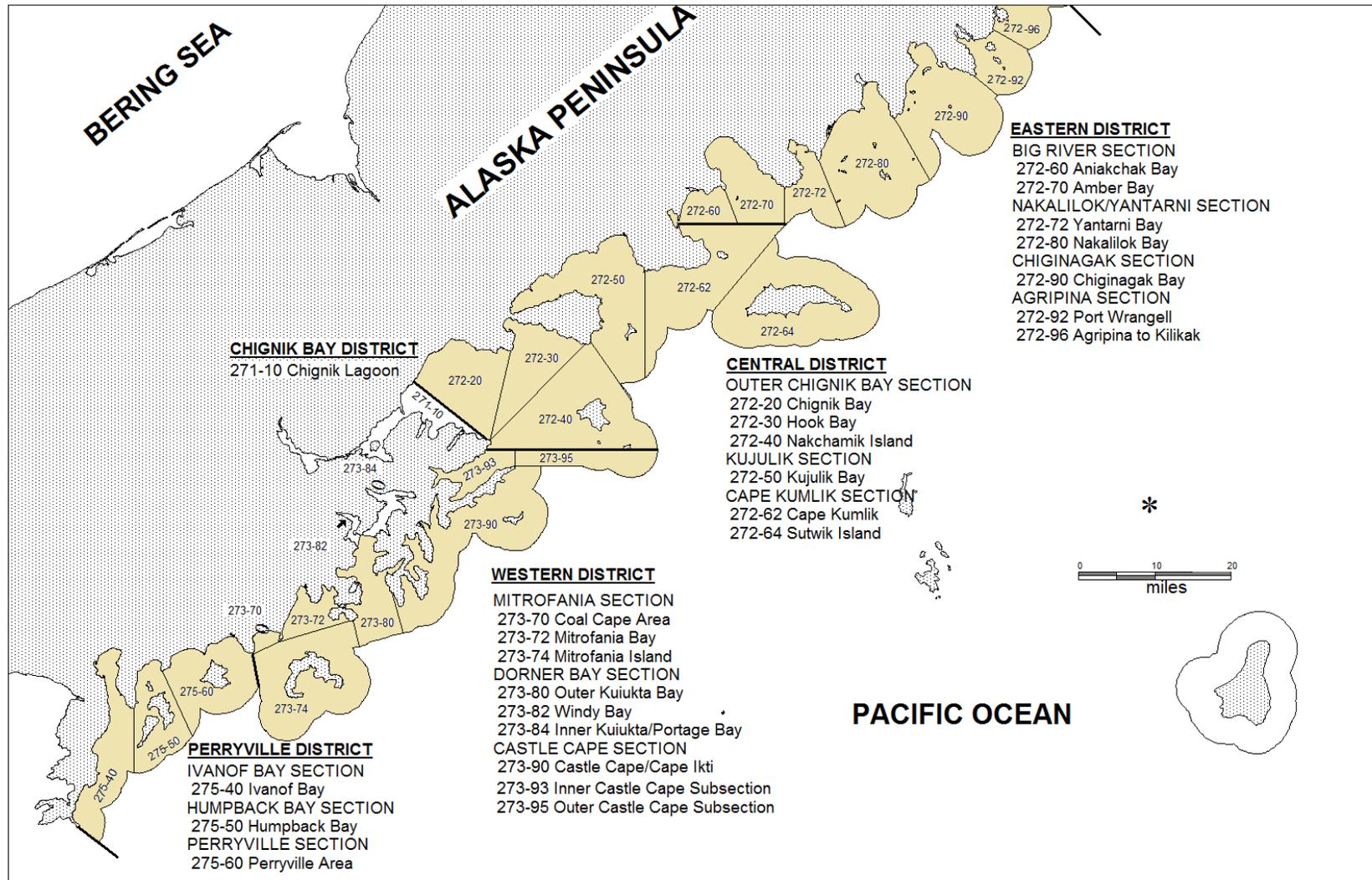


Figure 2.—Map depicting the Chignik Management Area commercial salmon fishery districts and the Chinook GSI sampling area.

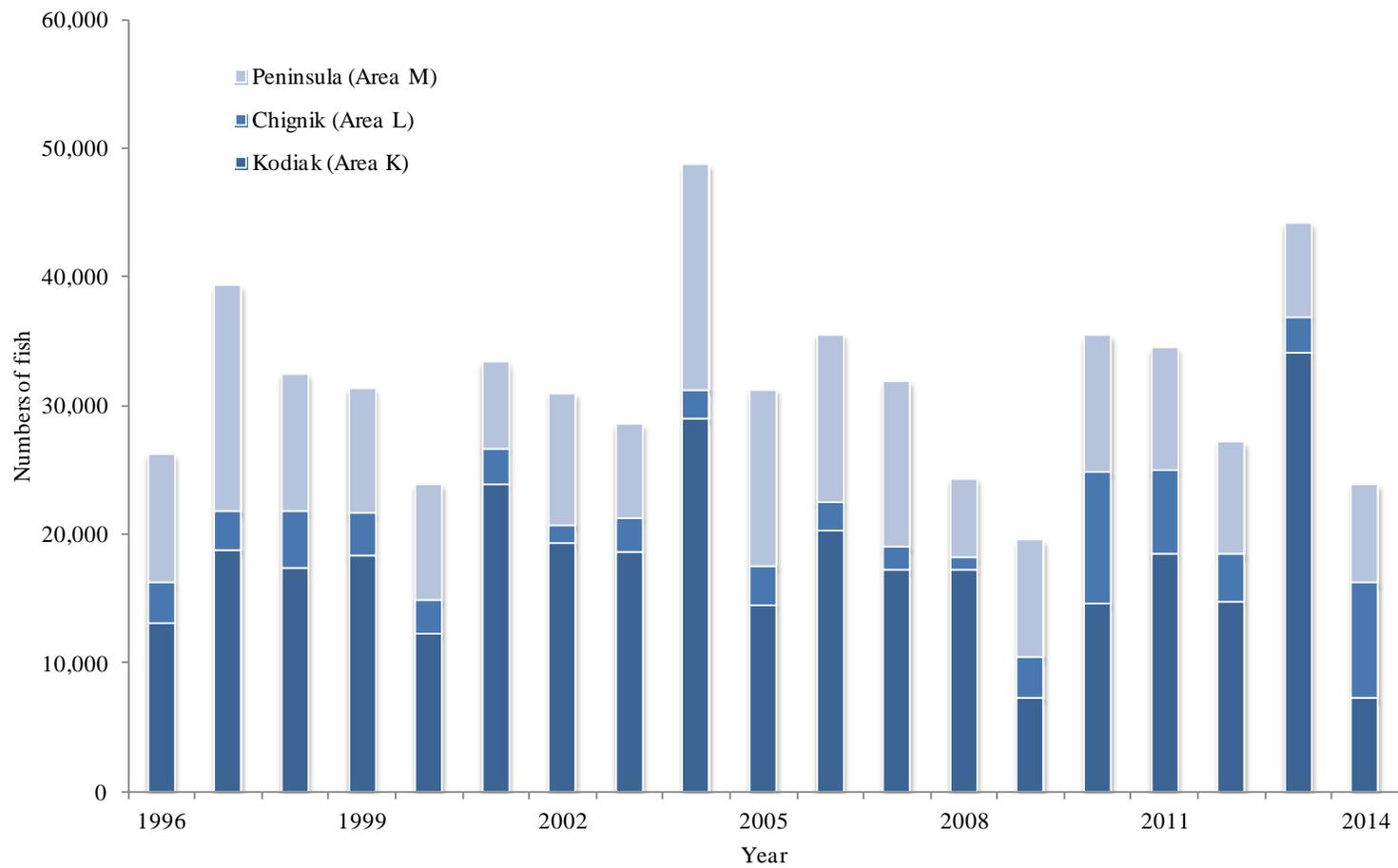


Figure 3.—Westward Region Chinook salmon harvest in commercial salmon fisheries by Kodiak, Chignik, and Alaska Peninsula management areas by year, 1996–2014.

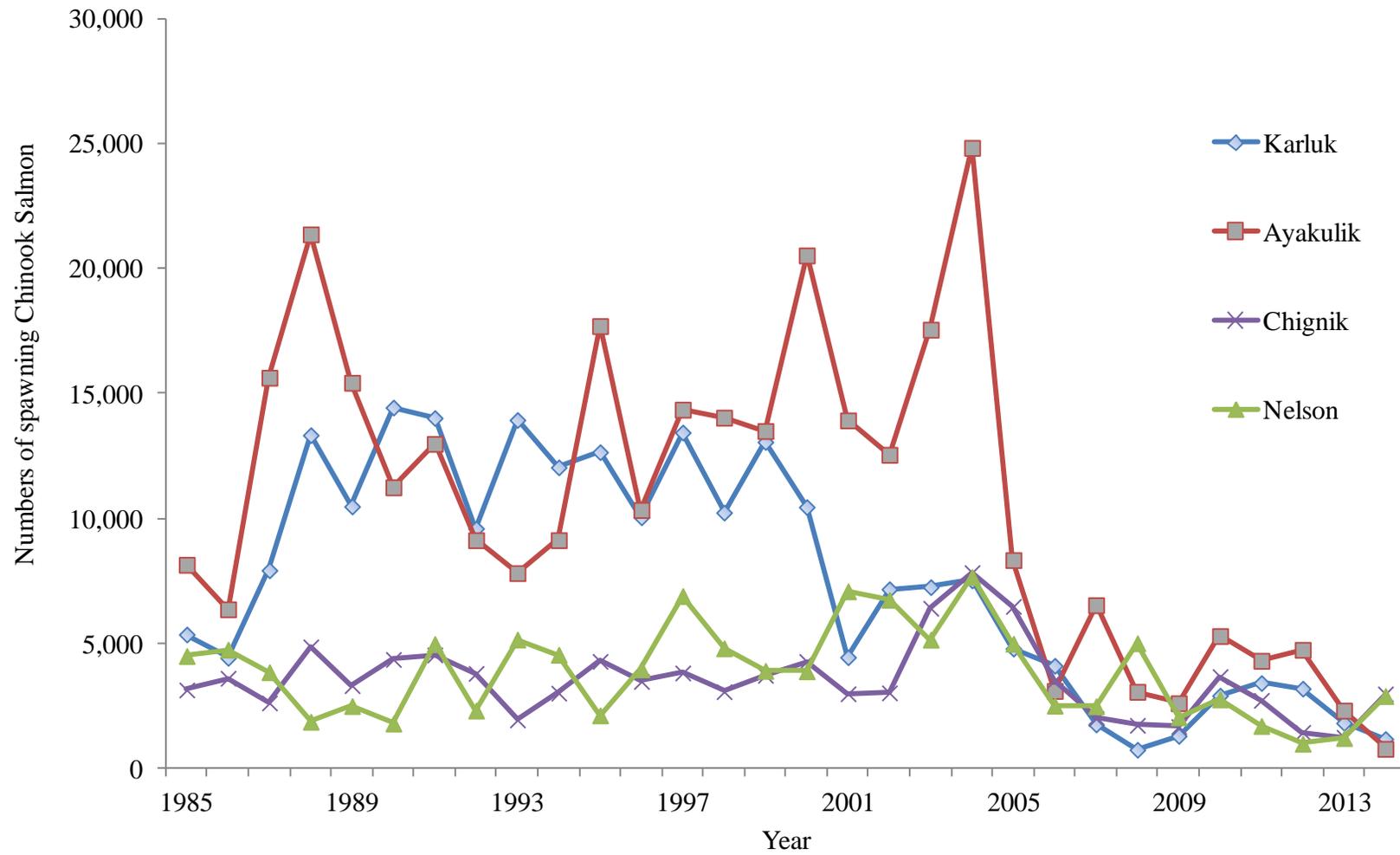


Figure 4.— Westward Region Chinook salmon escapement estimates at the major systems monitored via weir, 1985–2014.



## **APPENDIX A. CHINOOK SALMON GENETICS SAMPLING**

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Appendix A1.–Procedure for collecting genetic and biological information from Chinook salmon.

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I. General Information

Axillary process tissue samples are collected from individual fish to determine the genetic characteristics. When sampling the commercial harvest, tissues need to be as “fresh” and as cold as possible; do not sample from fungal fins. The sample preservative is ethanol (ETOH) which preserves tissues for later DNA extraction without having to store frozen tissues. Avoid extended contact with skin.

II. Sample procedure:

1. Tissue type: Axillary process; clip one axillary process from each fish (Appendix A2).
2. Prior to sampling, fill the tubes half way with ETOH from the squirt bottle. Fill only the tubes that you will use for a particular sampling period.
3. To avoid any excess water or fish slime in the vial, wipe the axillary process dry prior to sampling. Using the dog toe nail clipper or scissors, clip off axillary process (1/2–1” max) to fit into the cryovial.
4. Place axillary process into ETOH. The ethanol/tissue ratio should be slightly less than 3:1 to thoroughly soak the tissue in the buffer.
5. Top off tubes with ETOH and screw cap on securely. Invert tube twice to mix ETOH and tissue. After each sample, wipe the dog toe nail clippers or scissor blade so not to cross contaminate samples.
6. Record vial number to paired data information (Appendix A3).
7. Measure fish length in millimeters from mideye to tail fork (METF) and record on the paired data form. Measure to the nearest mm (Appendix A4).
8. Determine the sex of the fish and record on paired data form (Appendix A4).
9. Remove three (3) scales from the preferred area (on the left side of fish) by grasping the scale’s exposed posterior edge with forceps and pulling free (Appendix A5). Wipe slime, grit, and skin from the scale (neoprene wristers work well for this). Select scales within the preferred area on the other side of the fish. If no scales are present in the preferred area on either side of the fish, sample a scale as close to the preferred area as possible. Do not select a scale located on the lateral line.
10. Place three (3) scales vertically on gum card (Appendices A6 and A7). It is important to take care that scales adhere to the gum card, rough side up. Therefore, without turning the forceps over, clean, moisten, and mount the scale on the gum card with your thumb or forefinger. Exert just enough pressure to spread and smooth the scales directly over the number as shown in Appendix A5. The ridges on the sculptured side can be felt with a fingernail or forceps. Mount the scale with the anterior end oriented toward top of gum card. All scales should be correctly oriented on the card in the same direction (Appendix A7).
11. Check for presence or absence of adipose fin (if absent see Appendix B).
12. Salmon species identification guide is depicted in Appendix 8.
13. Repeat steps 1 through 11 for up to 10 fish on each card.

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-continued-

III. Supplies included with sampling kit:

1. Clippers – used for cutting the axillary process.
2. Cryovial – a small (2.0 ml) plastic vial, pre-labeled.
3. Caps – to prevent evaporation of ETOH.
4. Cryovial box – box for holding cryovials while sampling.
5. ETOH – in bulk Nalgene bottle.
6. Squirt bottle – to fill or “top off” each cryovial with ETOH. Squirt bottle not for ethanol storage.
7. Forceps (tweezers) – to grasp and collect scales.
8. Gum Cards – to accommodate scale collection.
9. Acetate cards – separates and protects gum cards.
10. Measuring board – to measure fish (mm) mideye to tail fork.
11. Aluminum clipboard – holding sampling forms, pencils, and gum cards.
12. Uniquely number CWT cinch strap – locked through mouth of adiposed clipped fish head.
13. Plastic bags – for holding CWT heads to be frozen.

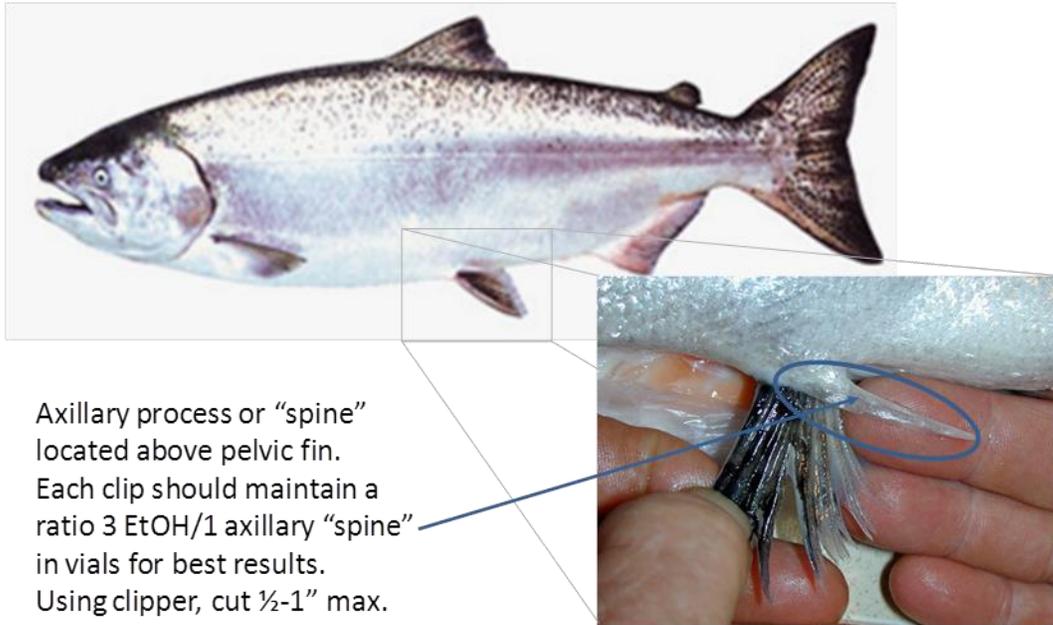
IV. What to do after sampling:

1. Double check the sample forms with gum cards, cryovials and with the log book to ensure accuracy.
2. Store cryovials containing tissues at cool or room temperature, away from heat in the white sample boxes provided. In the field: keep samples out of direct sun, rain and store capped vials in a cool, dry location. Do not Freeze.
3. Let gum cards dry in a warm area, stack with other gum cards placing acetate cards between each. Rubber band together and retain in plastic storage file case with sampling forms (IMPORTANT).
4. Carefully copy data from sampling forms to HTML5-based offline data entry form with personal computing device. Email resultant file daily to [michelle.wattum@alaska.gov](mailto:michelle.wattum@alaska.gov) if samples were collected that day.
5. If adipose-clipped fish was sampled, make sure that CWT paperwork is filled out and matches up with cinch strap numbers on collected heads.



Appendix A2.–Procedure for clipping axillary process from Chinook salmon.

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Appendix A3.–Chinook Genetics Sampling Form example.

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**Harvest Date:**      **Month:** \_\_\_\_\_ **Day:** \_\_\_\_\_ **Year:** \_\_\_\_\_      **Species:** \_\_\_\_\_

**Sampling Area:** \_\_\_\_\_

**Statistical Areas:** \_\_\_\_\_

**Sampler:** \_\_\_\_\_      **Sampling Port:** \_\_\_\_\_

**Gear:** \_\_\_\_\_      **Tender or F/V:** \_\_\_\_\_

**Gum Card No:** \_\_\_\_\_      Port Gum card prefixes: Kod-1; LB-2; ALZ-3; Chig-4; SP-5; KC-6; PM-7.

Fish Number	Sex	Length (mm)	Adipose Fin	Axillary Tissue	No. Scales	Comments/CWT #
	(M or F)	METF	√    ∅	Vial Number	per Fish	

1						
2						
3						
4						
5						
6						
7						
8						
9						
10						



Adult salmon length is measured from mideye to tail fork because the shape of the salmon's snout changes as it approaches sexual maturity. The procedure for measuring by this method is as follows.

1. Place the salmon flat on its right side (on the measuring board) with its head to your left and the dorsal fin away from you.
2. Slide the fish in place so that the middle of the eye is in line with the edge of the meter stick and hold the head in place with your left hand.
3. Flatten and spread the tail against the board with your right hand.
4. Read and record the mideye to tail fork length to the nearest millimeter.

Sexual characteristics on maturing Chinook salmon can be difficult to determine:

A) Male: Large Head, *concave forehead*, large adipose fin, no vent protrusion.

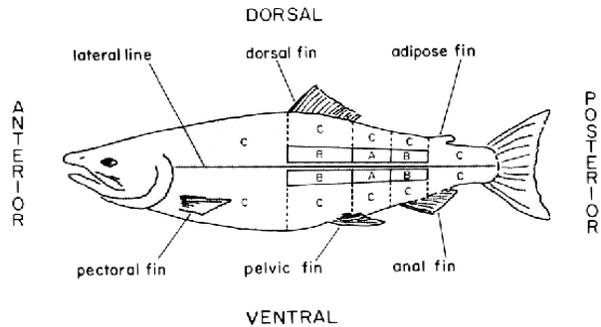


B) Female: Smaller head, *convex forehead*, smaller adipose fin, slight vent protrusion.

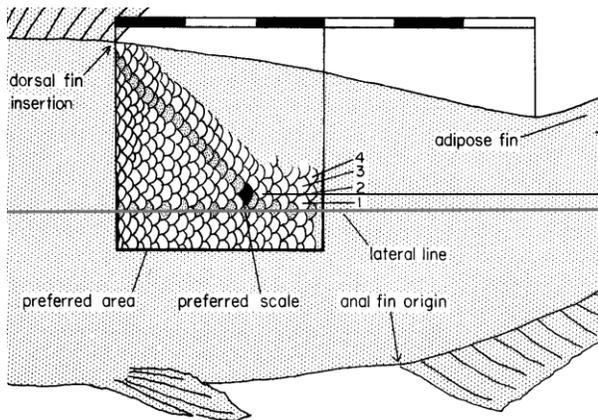


If acceptable with the processor, sampler can make a small slit in belly with serrated utility knife for sex determination via visual inspections of gonads.

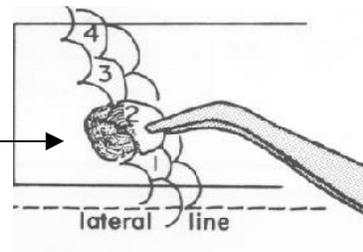
Appendix A5.—Removal and mounting of the preferred salmon scales.



INPFC rated areas for scale removal. Area A is the preferred area. If scales on the left side are missing, try the right side. Area B is the second choice if there are no scales in Area A on either side of the fish. Area C designates non-preferred areas.



Do not turn scale over.



The preferred 3 scales would be 2, 3, 4 in the picture above.

The preferred scale in this diagram is solid black. It is located 2 rows up from the lateral line, on a diagonal from the insertion (posterior) of the dorsal fin “back” toward the origin of the anal fin.

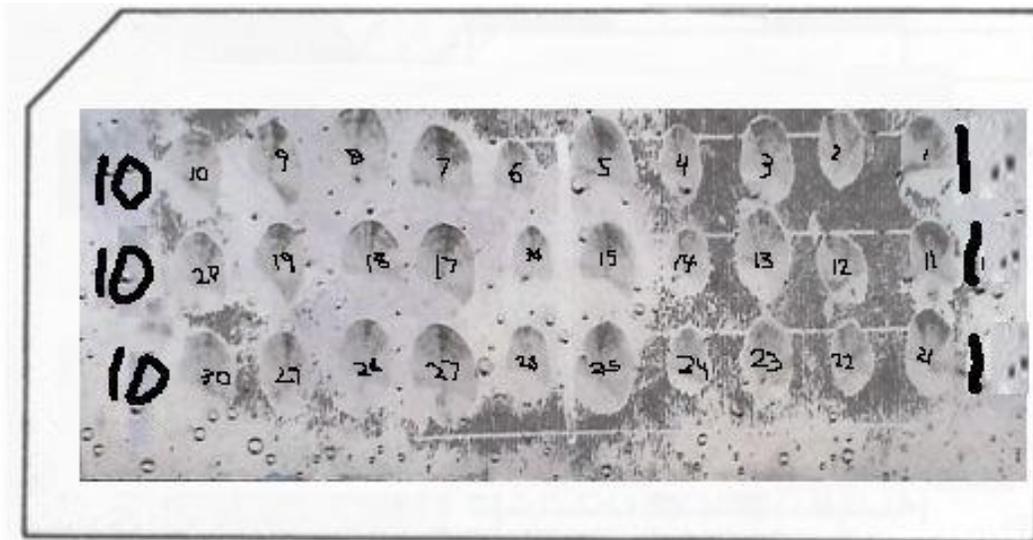
Appendix A6.—Completed Scale (gum) Cards.

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Species: Chinook Card No: 301  
Locality: SW KODIAK/ALITAK  
Stat. Code: 256 - 20 - 25 - 30  
Sampling Date: Mo. 6 Day 15 Year 2013  
Gear: Seine  
Collector(s): KW  
Remarks: ALITAK - Ocean Beauty  
T/v Lucrative

Appendix A7.—Chinook sampling scale orientation (3 scales per fish) 10 fish per card going right to left.

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Appendix A8.—Marine phase salmon identification (courtesy of Washington Department of Fish and Wildlife).

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**Chinook (king)**

- Mouth is dark with a black gum line
- Large, sharp teeth
- Spots on both lobes of tail
- Large spots on back



**Coho (silver)**

- Mouth is light with a white gum line
- Medium size, sharp teeth
- Spots only on upper lobe of tail
- Spots on back
- Wide caudal peduncle



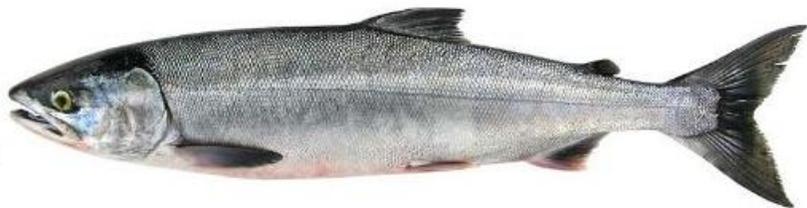
**Pink (humpy)**

- Mouth is white with a black gum line.
- In marine areas, almost no teeth
- Large oval spots on both lobes of tail
- Large black spots on back
- Pointed lower jaw
- No silver on tail
- Very small scales



**Chum (dog)**

- Mouth is white with a white gum line
- Well developed teeth
- No spots on tail or back
- Calico markings (vertical bars) – faint on bright fish
- Narrow caudal peduncle
- White tip on anal fin



**Sockeye (red)**

- Mouth is white with a white gum line
- Almost toothless
- No spots on tail or back
- Large, bright gold, glassy eye



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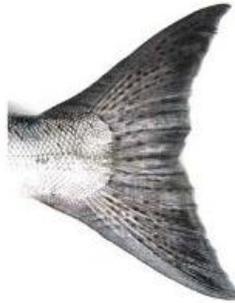
-continued-



**Chinook**

Jaw – The chinook has a dark mouth and black gums at the base of its teeth. Immature chinook are known as a “blackmouth”

Tail – Both the upper and lower lobes of the tail are covered with spots and silver is prominent.



**Coho**

Jaw – The mouth is white and the gum line is almost white, but the tongue may be black. The teeth are sharp and strong.

Tail – The coho tail has just a few scattered spots, usually on the upper lobe, with silver streaks. It has a wide caudal peduncle.



**Pink**

Jaw – The mouth of a pink is white, but the gums and tongue are black, as they are in a chinook. It does not have “teeth” on its tongue.

Tail – The pink salmon tail is covered with large oval spots. It does not have silver on the tail. The scales are very small compared to other salmon of the same size.



**Chum**

Jaw – The mouth is white and the gum line is white, but the tongue may be black. The lips are fleshy with well developed teeth in both jaws, but there are no teeth on the base of the tongue.

Tail – The tail has no spots, but does have silver streaks covering about half of the fin. The caudal peduncle is narrow.



**Sockeye**

Jaw – The mouth is white and the gum line is white. The lips are fleshy. The teeth are small and well developed in both jaws. There are no teeth on the base of the tongue.

Tail – There are no spots on the tail.



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**APPENDIX B. CHINOOK SALMON CODED WIRE TAG  
SAMPLING**



Appendix B2.–Sampling CWT Chinook salmon and attaching cinch strap to the head of an adipose-clipped fish.

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II. Sample procedure:

1. Attach uniquely numbered cinch strap to head of Chinook.
2. Record cinch strap number on Chinook Genetics Sampling Form (Appendix A3).
3. Using a serrated utility knife, carefully cut head off of Chinook salmon.
4. Place head in plastic bag to be frozen at the end of sampling.
5. When genetics sampling is done, enter all biological information from CWT, only Chinook from same offload on one form (Appendix B1).

