Regional Operational Plan No. ROP.CF.4K.2024.08

Assessment of Genetic Stock of Origin of Chinook Salmon Harvested in Commercial Salmon Fisheries of the South Alaska Peninsula, 2025-2027

by

M. Birch Foster

and

Tyler H. Dann

July 2024

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

Symbols and Abbreviations

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

Weights and measures (metric)

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

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

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

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by
M. Birch Foster
Alaska Department of Fish and Game, Division of Commercial Fisheries, Kodiak
and
Tyler H. Dann
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, Anchorage

Alaska Department of Fish and Game
Division of Commercial Fisheries
333 Raspberry Road, Anchorage, AK 99518

July 2024

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M. Birch Foster,
Alaska Department of Fish and Game, Division of Commercial Fisheries,
351 Research Court
Kodiak, AK 99615

Tyler H. Dann,
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Road
Anchorage, AK 99518-1565

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Title	Name	Signature	Date
Project Leader(s)	M. Birch Foster		5/1/24
Project Leader(s)	Tyler Dann		5/1/24
Area Management Biologist	Matthew Keyse		5/1/24
Biometrician	Bobby Hsu		5/1/24
Research Coordinator	Kevin Schaberg		5/1/24
Regional Supervisor	Nick Sagalkin		5/1/24
Principal Geneticist	Sara Gilk-Baumer		5/1/24

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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 South Alaska Peninsula Management Area (southern portion of Area M) commercial salmon fisheries during the 2025 to 2027 seasons. In 2014, a limited study of Chinook salmon commercial harvest within the South Peninsula portion of Area M and Chignik was conducted and demonstrated significant proportions of Chinook salmon from British Columbia, West Coast U.S., and the Eastern Bering Sea (>20%). An updated study that accurately and precisely estimates stock-specific harvests would help identify conservation concerns and provide valuable management information regarding the area-, gear- and temporal-specific harvests of Chinook salmon in select South Peninsula salmon fisheries. This operational plan provides the Alaska Department of Fish and Game (ADF&G) with a sampling and genetic analysis plan to achieve that overall goal.

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 Alaska Peninsula (Area M) management areas. The South Alaska Peninsula (southern portion of Area M) includes waters from Kupreanof Point west to Scotch Cap on Unimak Island (Figure 1).

The South Alaska Peninsula has approximately 224 salmon streams, with sockeye salmon found in 37, pink salmon in at least 204, chum salmon in 136, and coho salmon in 81, but there are no spawning stocks of Chinook salmon documented in the South Alaska Peninsula area (Schaberg et al. 2019). However, there are 21 different streams known within the North Alaska Peninsula where Chinook salmon populations exist (Shaul and Dinnocenzo 2001). Escapement levels are primarily monitored via aerial surveys using small fixed-wing aircraft.

Three management plans guide the ADF&G's approach to managing salmon fisheries in this area annually: the South Unimak and Shumagin Islands June Salmon Management Plan (5 AAC 09.365), the Post-June Salmon Management Plan for the South Alaska Peninsula (5 AAC 09.366), and the Southeastern District Mainland Salmon Management Plan (5 AAC 09.360). Three gear types are fished in the South Alaska Peninsula fisheries: purse seine, set gillnet, and drift gillnet (Figures 2 – 4).

The South Unimak and Shumagin Islands June commercial salmon fisheries are in effect from June 6 through June 28. The South Unimak June fishery occurs in the Unimak and Southwestern Districts, a portion of the South Central District, and the Bechevin Bay Section of the Northwestern District (Figures 2 – 3). The Shumagin Islands June fishery includes the Shumagin Islands Section of the Southeastern District (Figure 2). The Post-June Salmon Management Plan for the South Alaska Peninsula covers all waters of the South Alaska Peninsula management area (except the Southeastern District Mainland) from July 1 through October 31 (Figure 4).

Historical records of the South Alaska Peninsula commercial fishery go back to 1908. From 2013 to 2022, the South Alaska Peninsula annual harvest averaged 13,799,230 salmon and was composed of 18,353 Chinook, 2,561,031 sockeye, 274,845 coho, 9,876,084 pink, and 1,068,916 chum salmon. (Table 1).

Decreased returns of Chinook salmon in the Gulf of Alaska (GOA) and Bering Sea watersheds have prompted statewide concern about the health of Chinook salmon stocks (ADF&G 2013). Within the South Alaska Peninsula Area, research on the stock of origin of Chinook salmon in the commercial salmon fisheries has been limited. In 2014, a genetic stock identification (GSI) study analyzed a combined set of Chignik and South Alaska Peninsula commercial fishery samples. Analysis demonstrated primarily British Columbia, West Coast U.S., Eastern Bering Sea, and Southeast Alaska/Northeast GOA stocks were present above the 5% level (Table 2; Shedd et al. 2016). Genetic analysis of Gulf of Alaska Chinook salmon trawl bycatch from 2014 to 2020 showed the presence of primarily British Columbia, West Coast U.S., Southeast Alaska, and Northwest GOA (Guthrie et al. 2022).

Genetic stock identification of the Chinook salmon catch in the Westward Region commercial salmon fisheries is not currently 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 stock of origin.

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 of the South Alaska Peninsula areas.

OBJECTIVES

PRIMARY OBJECTIVES

1. Collect genetic tissue (pelvic fin) from Chinook salmon caught in the major South Peninsula fisheries over the 2025–2027 fishing seasons from June through August.
2. Select subsamples of genetic tissues in proportion to catch within designated areas, gear types, and temporal strata.
3. Using genetic MSA (mixed-stock analysis) techniques, estimate stock proportions and stock-specific harvests of Chinook salmon in the South Peninsula strata.

SECONDARY OBJECTIVES

1. Estimate the age, sex, and length (ASL) composition of Chinook salmon sampled for genetic information.
2. Collect biological information (ASL) and heads from adipose-clipped (CWT) Chinook salmon observed as part of genetic sampling.

OVERVIEW

The primary objectives of this study are to sample, genotype, and estimate the stock composition and stock-specific harvests of Chinook salmon harvested in commercial salmon fisheries in marine waters of the South Alaska Peninsula (Table 3, Figure 1). Overall, the June and post-June fisheries will have different experimental designs reflecting differences in their scheduled (June) and local escapement-based management (post-June). We will estimate stock compositions of harvests by gear type (seine and drift/set gillnet) separately due to anecdotal evidence that the two gear types selectively harvest fish of different ages, maturity, and stock-of-origin. We will also analyze

harvests in two different geographic areas, Unimak and Southwestern districts, and South Central and Southeastern districts, as these two areas may harvest different stocks (Munro et al. 2012).

In general, there will be 1 temporal stratum for MSA for each month for each gear type in each area with the following exceptions: 1) Seine harvests in Southeastern and South Central districts in June and July account for the vast majority of South Alaska Peninsula harvests so each month will be represented by two strata; 2) Seine harvests in Unimak and Southwestern districts are small in July and August so those two months will be represented by a single stratum; 3) Gillnet harvests in both areas across all months are small so all gillnet harvests in both areas and all months will be represented by a single stratum (Table 3).

Collection of all Chinook salmon samples will follow the sampling procedures outlined in Appendix A. The pelvic fin clip will be removed from each fish sampled during a sampling event and preserved on Whatman Genetic Cards (WGC) specific to a singular sampling event and to be preserved via desiccation by silica beads.

FISHERY DESCRIPTION

The South Alaska Peninsula Management Area is divided into four districts: Unimak, Southwestern, South Central, and Southeastern Districts (Figure 1). The commercial salmon fishery season runs from June 1 to October 31, but a distinction is made between the June and post June fisheries. The vast majority of the harvest occurs between June and August, but fishing does often extend into September.

The June fishery of the South Alaska Peninsula occurs in the Shumagin Islands Section of the Southeastern District, the East and West Pavlof Bay Sections of the South Central District, the Southwestern District, the Unimak District, and the Bechevin Bay Section of the Northwestern District (Figures 1 – 2). Set gillnet gear is allowed in all areas (Figure 2), drift gillnet gear is allowed in the Bechevin Bay Section of the Northwestern District, the Unimak District, and portions of the Southwestern District (Figure 3), and purse seine gear is allowed in the Shumagin Islands Section, portions of the Southwestern District, the Unimak District, and the Bechevin Bay Section of the Northwestern District during the June fishery (Figure 2).

The post-June fishery of the South Alaska Peninsula can occur in all areas with the exception of Southeastern District Mainland (SEDM), which has allocative restrictions with Chignik Management Area, and Dolgoi Island Area, which has harvest limits through July 25. Purse seine and set gillnet gear is allowed throughout the area during the post-June fishery with the exception of the SEDM and Dolgoi Island areas regulations. Drift gillnet gear is allowed in the Unimak District and the Ikatan Bay Section of the Southwestern District. For detailed description on this complex fishery, refer to the Area Management Report authored by Fox et al. (2021).

STUDY DESIGN

Tissues to determine stock of origin will be collected through temporally stratified sampling of the commercial harvest of Chinook salmon throughout South Alaska Peninsula fisheries from 2025 to 2027. Due to the varied nature of the June and post-June fisheries, temporal strata will be defined separately for the two time periods. The June fishery has a predetermined schedule including an initial opening for set gillnet gear only, followed by 4 openings for set gillnet, drift gillnet, and seine gear. The post-June fishery has a combination of predetermined schedules and openings based upon local pink and chum salmon escapement. A majority of the Chinook salmon harvest occurs in two districts, the Southeastern and South Central Districts, by the seine fleet. Temporal

strata will be defined as described above: two temporal strata each for the seine fleet in the months of June and July in the Southeastern and South Central districts; a single stratum for the seine fleet in June in the Unimak and Southwestern districts; a single stratum for the seine fleet in the months of July and August in the Unimak and Southwestern districts; a single stratum for the seine fleet in August in the Southeastern and South Central districts; and a single stratum for the gillnet fleet representing both areas through the months of June, July and August. Catch samplers will sample commercial harvests at processing facilities located at the three major South Alaska Peninsula fish processing ports: False Pass, King Cove, and Sand Point (Figure 1) but the processing facility in King Cove is unlikely to operate in 2025. 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 MSA sample for the time and area strata, which will be double that of the analysis sample sizes listed in Table 3 (380 individuals/stratum). The areas and dates that fish were caught, and an estimate of other relative proportions will be documented.

Post-season, MSA tissue samples for laboratory analysis will be selected from the available harvest samples by subsampling within strata proportional to the daily catches of the respective strata. A random sample proportional to the catch from fishing periods within a MSA stratum will be constructed for each area, gear, and time stratum (Table 3). This will ensure that the stock compositions estimated from the MSA analysis are representative of the catch in the stratum. Sampling proportional to catch does come with caveats since it entails not only tracking daily harvest but projecting harvest throughout the stratum and oversampling to facilitate post-season subsampling. In post-season sample selection, some samples will be excluded from analysis to approximate the daily catch proportions of a stratum's harvest.

TISSUE AND DATA COLLECTION

Samplers will obtain fish ticket information before collecting samples to determine if the fish were exclusively harvested from the area, gear, 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. It is important to sample without regard to size so fish will be randomly selected.

Tissue samples will be collected from all fish selected for sampling (Appendix A). The pelvic fin will be collected from the left side of the fish and placed onto a numbered grid on a numbered Whatman genetic card (WGC) following the procedures outlined in Appendix A1. Each WGC will hold up to 10 samples that will match the layout on the Genetics Sampling Form (Appendix A2). All sample information will be recorded on the Chinook Genetics Sampling Form which will pair tissue WGC card and grid numbers with paired age, sex, and length (ASL). Each WGC will hold samples from a single sampling event and multiple WGCs may be required to hold all the samples from a single sampling event. Length (mideye to tail fork) will be measured to the nearest millimeter and sex determined if possible (Appendix A4). A guide to Chinook salmon identification using external metrics and comparison with the other salmon species is listed in Appendix A3.

Scales, when possible, will be collected from the preferred area of each fish following the methods described by International North Pacific Fish Commission (1963). Four scales per fish will be collected and mounted on scale "gum" cards and impressions made on acetate/diacetate cards (Clutter and Whitesel 1956). 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.

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 Westward Region intranet salmon aging utility using a programmable keyboard (X-keys).

Presence of adipose fin clip will be recorded on the sampling form. 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 (Appendix B1). 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 (Appendix B1) 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 MEF) on the "*Sampling Information*" portion of the CWT form in the lower left hand 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 forms will be kept up to date at all times. Inspection for errors will include, but are not limited to: incorrect dates, transposed lengths (i.e., 371 mm when the fish was actually 731 mm), incorrect statistical areas, incorrect Whatman card 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 a web browser-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.

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

Statistical MSA will be accomplished by the ADF&G Gene Conservation Laboratory following standardized procedures similar to those described by Dann et al. (2023) but based upon genotypic data collected with different chemistry. Chemistry used for data collection will be accomplished by the ADF&G Gene Conservation Laboratory following standardized laboratory procedures similar to those described by Barclay et al (2019). Genomic DNA will be extracted from tissue samples using a NucleoSpin 96 Tissue Kit by Macherey-Nagel® (Düren, Germany). DNA will be screened for a panel of 299 amplicons common to the IDF&G_299 panel described by Janowitz-Koch et al. (2019) using a chemistry called Genotyping in Thousands by Sequencing (GT-Seq; Campbell et al. 2015). An updated coastwide genetic baseline based upon the IDF&G_299 panel is currently in development. We expect greater accuracy and precision of stock composition estimates for finer-scale reporting groups than have been previously available given the large increase in number of genetic markers characterizing allele frequency differences among reporting groups (48 → 299 SNPs).

Mixed Stock Analysis

Estimates of stock composition will be based on the most current genetic baseline representing spawning Chinook salmon from known origins throughout the Pacific Rim. ADF&G developed a comprehensive, coastwide genetic baseline for MSA based on Templin et al. (2011) with additional collections from Barclay and Habicht (2015) and Witteveen and Shedd (2016) to estimate the stock compositions of Chinook salmon harvests in the Westward Region commercial salmon fisheries (Foster and Dann 2014, 2015) and Kodiak sport marine fisheries (Tracy and Dann 2014; Tracy and Shedd 2015) from 2014 to 2016. That coastwide baseline is being currently updated to incorporate more genetic markers; laboratory analyses are complete and statistical analysis is ongoing.

Defining reporting groups

Stocks, in the context of MSA, may be grouped together into "reporting groups". Reporting groups are made up of one or more identifiable units that are geographically and/or temporally grouped (Habicht et al. 2012b). Management needs are used to establish initial reporting groups. These initial reporting groups are then subjected to guidelines that incorporate genetic distinctiveness, representation in the baseline, and expectations for the fishery mixture to come up with reporting groups appropriate for specific fishery mixtures (Habicht et al. 2012b). These guidelines include:

1. *Adequate MSA performance*. Performance of the proposed reporting groups will be tested using evaluation simulations as outlined in Barclay et al. (2019) and described below.
2. *Adequate numerical representation in the baseline*. Numbers of individuals available within reporting groups will be set at a minimum of 400 fish.
3. *Adequate representation of within-reporting group genetic variation in the baseline*. Variation within reporting groups will be visualized using trees or multidimensional scaling (MDS) as outlined in Dann et al. (2012). Verification that adequate representation is present in the baseline will be obtained from (1) people who have local knowledge that the abundant spawning aggregates are represented in the baseline, (2) the clustering of

spawning aggregates on trees and MDS, and (3) the provision of acceptable results from baseline evaluation tests.

4. *Adequate expected number of fish from reporting groups in the mixture*. The minimum number of fish from a reporting group expected to occur within the mixture is 5%, or 19 fish.

Adequate MSA performance will be determined by assessing the identifiability of reporting groups using baseline evaluation simulations described below. We expect the 10 reporting groups used by Shedd et al. (2016) will form a beginning basis of reporting groups for this study: 1) Russia, 2) Eastern Bering Sea, 3) North Alaska Peninsula, 4) Chignik, 5) Kodiak, 6) Cook Inlet, 7) Copper, 8) Southeast Alaska/Northeast Gulf of Alaska, 9) British Columbia, and 10) West Coast US (Table 2.

Baseline Evaluation Tests

Baseline evaluation tests will assess the identifiability of reporting groups in simulated mixtures of fish. Test mixtures of up to 380 individuals will be constructed by randomly sampling from the baseline without replacement in predetermined mixture compositions. These mixtures will be analyzed against the reduced baseline (full baseline minus the individuals removed for the test mixture). To explore a range of stock compositions, up to 100 test mixtures will be constructed for each reporting group with compositions varying from 1% to 100% of that group, and the composition randomly split among the remaining groups. Because the removal of individuals from the baseline can reduce the accuracy of population allele frequency estimates and, consequently, the identifiability of reporting groups for MSA, test mixture compositions will be limited to remove no more than half of the total number of fish in a reporting group. Therefore, the range of test mixture compositions will be reduced for reporting groups represented by fewer than 760 fish. For example, if a reporting group is represented by 300 fish, the largest stock composition tested for that reporting group will be 39% (150 fish). For reporting groups containing fewer than 450 fish and populations with fewer than 50 fish, random samples will be selected in proportion to the number of fish in each population to avoid random sample sizes exceeding the total number of fish in a population.

The stock composition of the test mixtures will be estimated using the R (R Core Team, 2021) package *rubias* (Moran and Anderson 2019). The *rubias* package is a Bayesian approach to the conditional genetic stock identification model based upon computationally efficient C code implemented in R. It uses cross-validation and simulation to quantify and correct for biases in reporting group estimates. Each mixture will be analyzed for 1 Markov Chain Monte Carlo (MCMC) chain with 25,000 iterations and the first 5,000 iterations will be discarded to remove the influence of starting values. The prior parameters for each reporting group will be defined to be equal (i.e., a flat prior). Within each reporting group, the population prior parameters will be divided equally among the populations within that reporting group. Stock proportion estimates and the 90% credibility intervals for each test mixture will be calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the single chain output. After the MCMC analysis, 100 parametric bootstrap simulations will be performed to correct for biases in the stock proportion estimates.

The performance of each reporting group will be assessed by calculating the proportion of tests with correct allocations within 10% of the true test mixture proportion and overall bias among tests. As a guideline, we will consider a reporting group's performance to be adequate for MSA if at least 90% of tests are within 10% of the true test mixture proportion and overall bias does not exceed ±5%. These tests will provide an indication of the power of the baseline for MSA when all populations from a reporting group are assumed to be represented in the baseline.

Misallocation Assessment

To understand the direction of bias among reporting groups when estimating stock proportions, additional mixtures will be created by randomly sampling without replacement up to 380 fish from a single reporting group in the baseline and then rebuilding the baseline without the sampled fish. Stock compositions for these mixtures will be estimated following the *rubias* protocol described above. This will be repeated 10 times for each reporting group using different mixtures and baselines to account for variation among populations within reporting groups. Mean allocations will be summarized for each reporting group by averaging allocations across the 10 sample repeats.

Mixed Stock Analysis

Only catch samples with high-quality data will be included in MSA. Data quality control will include identifying and removing individuals missing >20% genotypic data and duplicate individuals. We will use the R package *rubias* (Moran and Anderson 2019) following the protocols described above to estimate fishery stock compositions.

Estimating Stock-Specific Harvest of Chinook Salmon in the South Peninsula

Estimates of the stock-specific harvest of Chinook salmon will be estimated following Munro et al. (2012) by applying the stock specific composition proportions ($p_{f,y}$) to the stratum harvest C_f.

$$C_{f,y} = p_{f,y} C_f$$

The estimate ($\hat{C}_{f,y}$) and distribution of stock specific harvest for each reporting group (y) and component fishery (f) will be obtained by Monte Carlo simulation. Here, K = 100,000 independent realizations of the reporting group-specific harvest ($C_{f,y}^{(i)}$) drawn randomly from the joint distribution of the harvest ($C_f^{(i)}$) and stock composition ($p_{f,y}^{(i)}$) for each stratum

$$C_{f,y}^{(i)} = p_{f,y}^{(i)} C_f^{(i)}$$

$$\hat{C}_{f,y} = median\ of\ the\ K\ observations\ of\ C_{f,y}^{(i)}.$$

Note that the 90% credibility interval (CI) will be determined by 5th and 95th quantiles of the K observations of $C_{f,y}^{(i)}$. The median, 90% CI, mean, SD and CV (coefficient of variation) of the stock specific harvests will be estimated directly from K observations of $C_{f,y}^{(i)}$.

Generation of stock-specific catch distributions requires an estimate of the distribution of each component. The distributions of the stock compositions ($p_{f,y}^{(i)}$) will be the Bayesian posterior

distributions of stock proportions from the mixed stock analysis described above. The lognormal probability distribution for the harvest ($C_f^{(i)}$) from each stratum will be based upon fish ticket data.

SCHEDULE AND DELIVERABLES

Sampling efforts will begin approximately June 1 and end approximately August 29 in each field season. Raw field data will be entered and final error checked by October 1. Sampling results will be reported on an annual basis in the South Alaska Peninsula catch and escapement sampling results published in Fisheries Data Series reports the winter following seasonal sampling.

It is anticipated that samples collected from the 2025 and 2026 seasons will be analyzed in the laboratory during the winter of 2026–2027. 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 subsequent seasons will be analyzed in the laboratory during the winter following each season. No results will be reported until three years of sampling has been achieved.

RESPONSIBILITIES

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

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

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

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

Andy Barclay, Fisheries Biologist III, (genetics baseline development)

Duties: This position is responsible for coordinating genetic laboratory analysis, conducting statistical analyses of the baseline and mixture samples, and final reporting of an updated genetic baseline that will be used to conduct genetic MSA and MSA estimates for the South Alaska Peninsula fisheries.

Bobby Hsu, 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 Supervisor

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

Sara Gilk-Baumer, Principal Geneticist

Duties: This position is the Principal Geneticist and provides program and budget planning oversight. Also reviews the operational plan, data analysis, and final report.

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TABLES

Table 1.–South Alaska Peninsula commercial salmon harvest by species and year, 1980–2023.

Year	Permits	Landings	Number of salmon[a]					
			Chinook	Sockeye	Coho	Pink	Chum	Total
1980	288	5,107	4,794	3,613,025	274,181	7,861,470	1,353,112	13,106,582
1981	304	5,617	11,182	2,241,513	162,223	5,033,028	1,768,475	9,216,421
1982	305	6,286	9,845	2,345,981	256,046	6,734,905	2,272,495	11,619,272
1983	324	5,241	26,571	2,556,557	127,657	2,827,622	1,704,072	7,242,479
1984	334	6,378	9,198	2,318,028	310,950	11,589,258	1,654,622	15,882,056
1985	336	5,325	6,642	2,144,416	172,514	4,431,016	1,348,726	8,103,314
1986	335	5,137	5,589	1,223,565	235,854	4,031,487	1,749,811	7,246,306
1987	327	5,256	9,174	1,449,747	225,117	1,208,556	1,376,040	4,268,634
1988	330	6,476	11,075	1,473,611	505,531	7,044,824	1,908,507	10,943,548
1989	341	5,597	7,065	2,661,217	443,843	7,292,658	994,231	11,399,014
1990	352	6,410	16,522	2,386,917	307,218	2,865,864	1,237,945	6,814,466
1991	354	6,440	7,975	2,319,957	317,129	10,616,756	1,588,791	14,850,608
1992	341	6,512	8,026	3,445,914	418,232	9,770,386	1,316,709	14,959,267
1993	352	6,204	14,413	3,689,074	220,148	9,928,107	1,048,257	14,899,999
1994	343	6,750	10,002	2,107,233	255,905	9,179,853	2,192,079	13,745,072
1995	352	8,193	17,453	3,016,211	264,346	16,311,942	1,728,321	21,338,273
1996	331	5,875	5,520	1,543,134	293,374	2,207,503	794,642	4,844,173
1997	307	5,803	7,780	2,281,566	116,136	2,321,371	627,996	5,354,849
1998	311	8,014	4,919	2,183,776	154,194	8,047,998	721,068	11,111,955
1999	310	7,021	5,074	2,991,819	192,503	8,456,449	840,030	12,485,875
2000	311	7,110	5,445	2,006,487	257,245	3,562,866	1,066,653	6,898,696
2001	242	3,277	2,620	614,080	214,252	4,021,381	933,014	5,785,347
2002	199	3,883	6,428	1,036,722	202,728	2,170,809	820,257	4,236,944
2003	195	3,909	2,874	1,055,218	132,374	4,262,920	639,772	6,093,158
2004	204	4,670	7,123	2,206,683	236,144	6,681,447	794,660	9,926,057
2005	209	4,948	4,554	2,338,294	145,754	9,423,314	741,600	12,653,516
2006	204	4,921	5,433	1,851,240	170,060	4,264,078	1,185,661	7,476,472
2007	205	5,301	5,324	2,450,061	151,736	7,306,366	681,087	10,594,574
2008	231	5,551	4,378	2,249,144	227,550	12,723,983	814,123	16,019,178
2009	239	5,823	5,875	1,725,616	248,941	7,921,119	1,684,944	11,586,495
2010	247	4,266	7,863	1,284,882	164,824	837,985	792,369	3,087,923
2011	250	5,614	7,214	1,919,235	153,482	5,004,314	979,187	8,063,432
2012	249	5,330	7,697	2,017,684	91,934	491,281	623,967	3,232,563
2013	249	6,845	6,705	2,242,305	294,867	7,800,873	952,160	11,296,910
2014	242	4,402	7,353	1,429,333	297,776	722,186	505,197	2,961,845
2015	245	6,097	53,236	3,208,991	271,570	16,711,506	680,167	20,925,470
2016	236	4,496	15,275	2,491,351	190,896	2,894,412	429,703	6,021,637
2017	241	5,931	11,278	3,222,952	350,447	21,864,700	1,960,576	27,409,953
2018	249	3,173	17,027	1,330,913	259,633	762,817	998,585	3,368,975
2019	258	5,095	22,755	1,625,532	521,559	20,526,804	1,168,952	23,865,602
2020	245	3,135	21,501	1,069,943	183,139	5,051,480	915,147	7,241,210
2021	247	4,132	13,898	4,601,985	331,944	16,561,273	2,256,363	23,765,463
2022	245	3,792	14,505	4,387,007	46,619	5,864,792	822,314	11,135,237
2023	239	3,366	11,368	1,756,569	200,277	17,177,929	1,135,428	20,281,571
Average 2013-2022	246	4,710	18,353	2,561,031	274,845	9,876,084	1,068,916	13,799,230

[a] Does not include test fish harvests or personal use.

Table 2.–Summary of estimates of stock composition (%) and stock-specific harvest of Chinook salmon for the South Peninsula and Chignik Management Areas, Alaska 2014 (June 1-August 5; Harvest = 12,209; n=376). Estimates include median, 90% credibility interval (CI), the probability that the group estimate is equal to zero (P=0), mean, and standard deviation (SD).

	Stock Composition						Stock-specific Harvest				
		90% CI						90% CI			
Reporting Group	Median	5%	95%	P=0	Mean	SD	Median	5%	95%	Mean	SD
Russia	2.1	1.1	3.6	0.00	2.2	0.8	257	134	436	268	93
Eastern Bering Sea	20.5	16.9	24.3	0.00	20.5	2.2	2,498	2,064	2,962	2,503	273
North Alaska Peninsula	0.0	0.0	0.3	0.42	0.0	0.2	0	0	35	6	19
Chignik	2.3	1.1	4.0	0.00	2.4	0.9	281	136	487	292	108
Kodiak	0.6	0.0	1.8	0.01	0.7	0.6	72	6	224	88	70
Cook Inlet	1.7	0.5	3.8	0.00	1.9	1.0	209	58	460	227	125
Copper	0.0	0.0	0.2	0.43	0.0	0.1	0	0	28	5	16
Southeast Alaska / Northeast Gulf of Alaska	7.8	5.0	11.0	0.00	7.9	1.8	954	612	1,345	963	224
British Columbia	42.3	37.6	47.1	0.00	42.4	2.9	5,169	4,596	5,756	5,172	352
West Coast US	21.9	18.3	25.9	0.00	22.0	2.3	2,678	2,235	3,160	2,685	282
									Total	12,209	

Note: Stock composition estimates may not sum to 100% and stock-specific harvest estimates may not sum to the total harvest due to rounding error.

Table 3.–Summary of recent 10-year harvest averages for the June and post-June (July and August) fisheries for the South Alaska Peninsula, divided into Unimak and Southwestern Districts and Southeastern and South Central Districts, experimental design to be used to estimate the stock composition of South Peninsula Chinook salmon harvests, 2025-2027.

Harvest (10-yr avg)[a]

Fishery (Districts)	Seine			Gillnet			Total
	June	July	August	June	July	August	
Unimak and Southwestern	1,431	783	39	521	60	6	2,840
Southeastern and South Central	6,255	7,487	1,124	129	93	5	15,093

Design (#Temporal Strata x Sample Size)

Fishery (Districts)	Seine			Gillnet			Total
	June	July	August	June	July	August	
Unimak and Southwestern [b]	1 x 380	1 x 380		1x 380			
Southeastern and South Central [c]	2 x 380	2 x 380	1 x 380				3,040

[a] Average harvest over ten years (2013 to 2022) if the area received effort and harvest by the gear type during that respective timeframe.

[b] Unimak and Southwestern Districts harvest is primarily from drift gillnet gear type.

[c] Southeastern and South Central District harvest is primarily from set gillnet gear type.

FIGURES

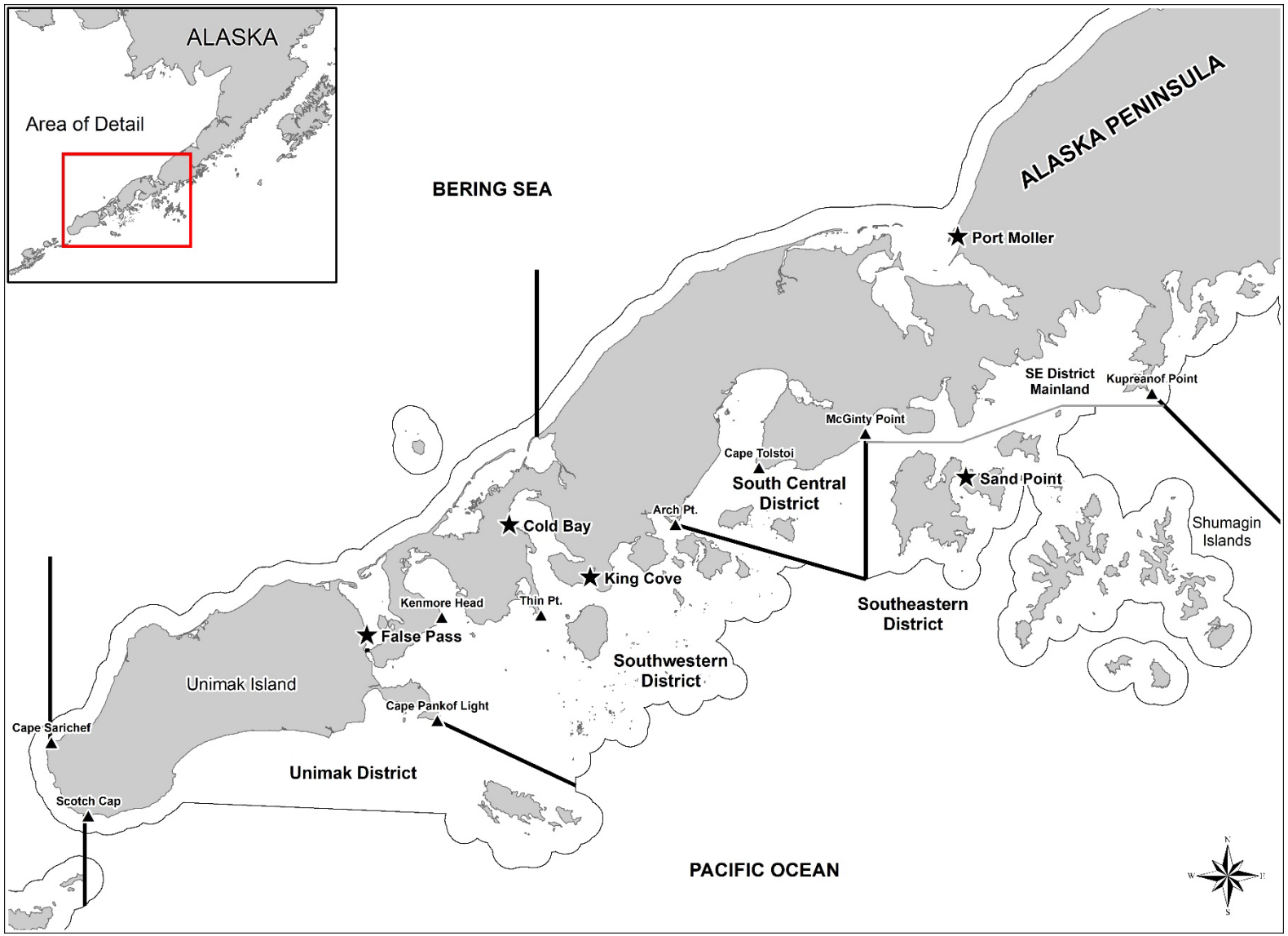


Figure 1.–Map of Alaska Peninsula Management Area from Kupreanof Point to Scotch Cap with South Peninsula salmon fishing districts defined.

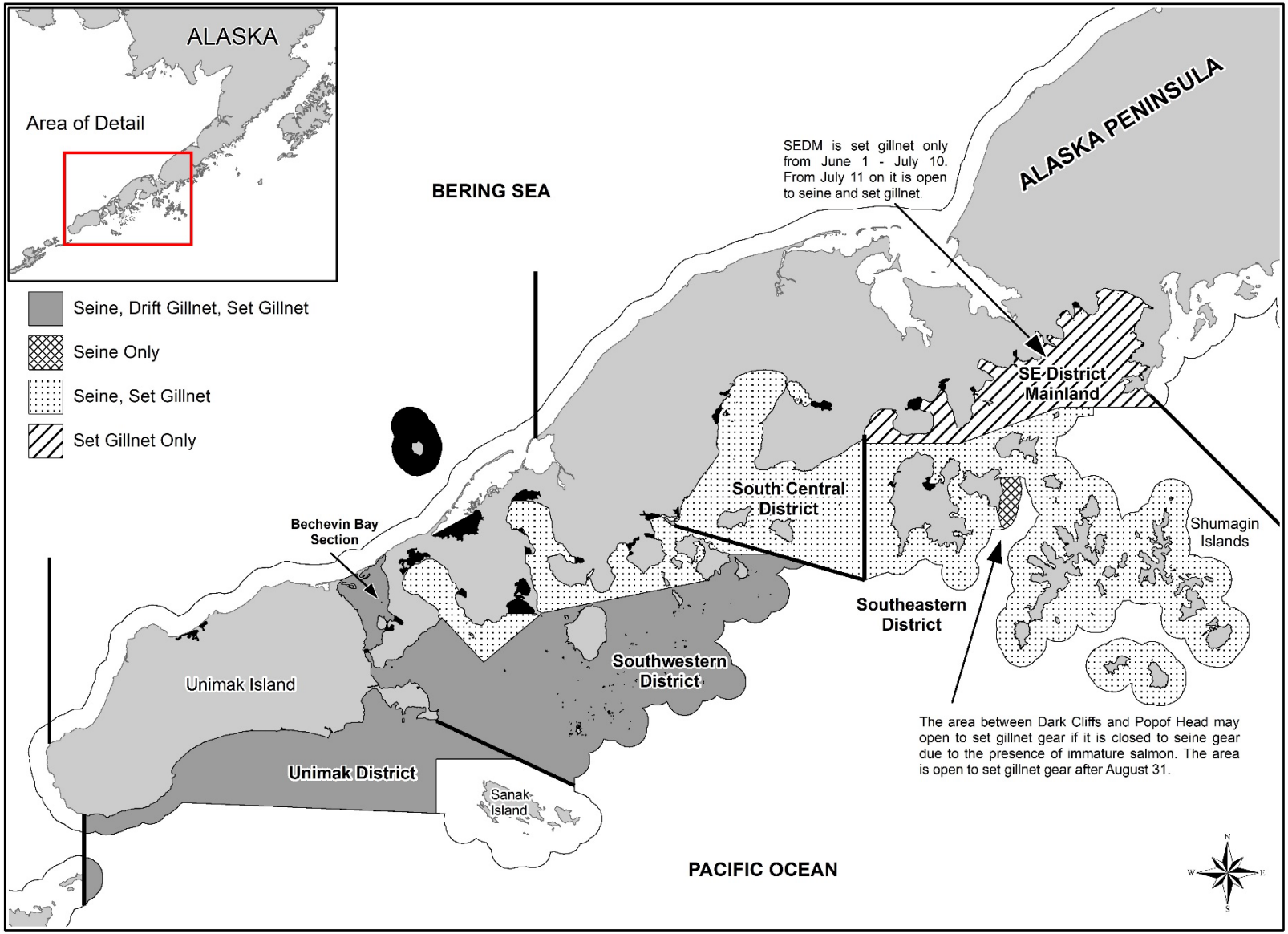


Figure 2.–Map depicting the locations of June South Alaska Peninsula fisheries for all gear types listed.

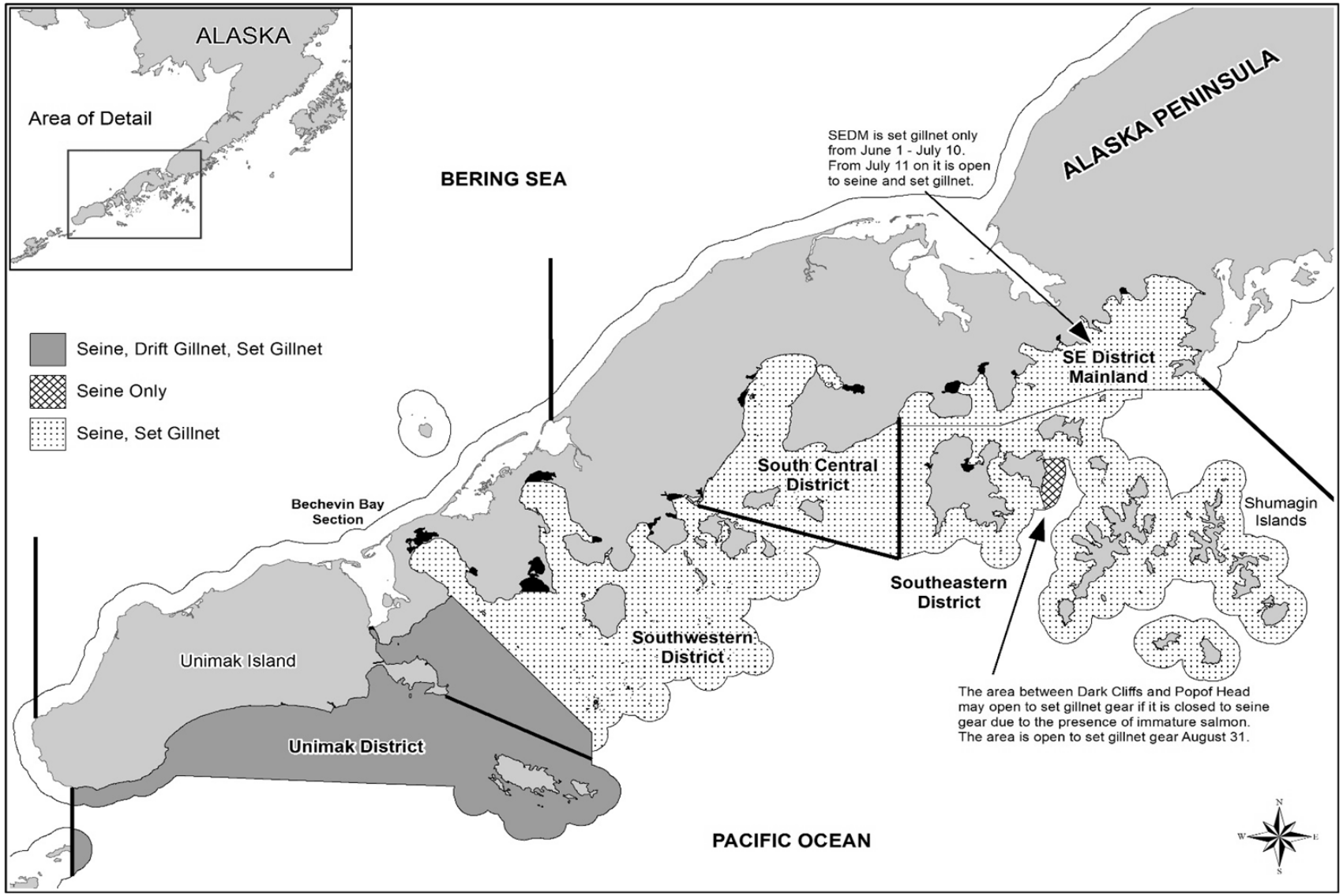


Figure 3.–Map depicting the locations of post-June South Alaska Peninsula fisheries and permitted gear types.

APPENDIX A. CHINOOK SALMON GENETICS SAMPLING

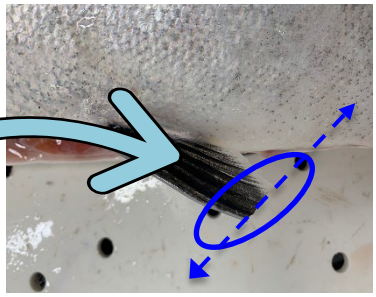
Adult Finfish Tissue Sampling for DNA Analysis

ADF&G Gene Conservation Lab, Anchorage

I. GENERAL INFORMATION We use fin tissues as a source of DNA to genotype fish. Genotyped fish are used to determine the genetic characteristics of fish stocks or to determine stock compositions of fishery mixtures. The most important thing to remember in collecting samples is that **only quality tissue samples give quality results**. If sampling from carcasses: tissues need to be as "fresh" and as cold as possible.

Preservative used: Silica desiccant bead packet dries and preserves tissues for later DNA extraction. Quality DNA preservation requires **Dry storage** in Pelican box with desiccant packs.

II. SAMPLING METHOD



At tip edge, cut small clip of pelvic fin ½-1" max (dotted line) and place on WGC card. One fish only per numbered grid.

III. SAMPLING INSTRUCTIONS

1. **Prior to sampling**: Set up workspace, fill out required collection information (upper left-hand corner only), fold back landscape cloth and place Whatman genetics card (40WGC) on clipboard, secure with clip; ready to sample.
2. **Sampling:**
   (A) Wipe fin prior to sampling.
   (B) Briefly wipe or rinse scissors between samples reducing cross contamination.
   (C) Using scissors, cut one fin clip per fish.
   (D) Place one clipped fin tissue onto # 1 grid space. Follow numerical sampling order (#'s 1-40) printed on card - **do not deviate**. If large tissue sample, center tissue diagonally on grid space.
   (E) **Only one fin clip per fish into each numbered grid space**.
   (F) **Staple** each sample to 40WGC (see photo).
   (G) Sampling complete, fold the landscape cloth "rain fly" over samples to the papers **edge** protecting tissue samples for storage and transport.

-continued-

1. **Loading the Pelican Case:**
    1. First card: Remove blotter papers and desiccant packs (remove vacuum pack plastic) from Pelican Case. Place first card in Pelican Case with tissues facing up. Next, place blotter paper directly over card and place 2 desiccant packs on top. Close and secure lid so drying begins.
    2. Up to 4 cards can be added per case. Add them so the tissue samples always face the desiccant pack through blotter paper: 2nd card facing down between desiccant packs; 3rd card facing up between desiccant packs; and 4th card facing down on top of second desiccant pack. Close and secure Pelican Case after inserting each card.
    3. All Whatman cards **remain in Pelican 1150 case** to dry cards flat.
        1. **Post-sampling storage:** All cards with tissue samples will remain inside of Pelican case or file box with desiccant packs at room temperature for duration of sampling and for return shipment to Anchorage genetics lab. Two desiccant packs are allocated for Pelican case. Be sure to **remove plastic vac wrap** before using desiccant packs for best drying results.
2. **Shipping at end of the season:** Pack and seal Pelican case and place inside priority mailer box to accommodate Pelican box and supplies. Tape box shut, fix a return address on box and drop in mail.

IV. SUPPLIES INCLUDED IN SAMPLING KIT:

1. Scissors - for cutting a portion of selected fin.
2. Whatman genetics card – holds 40 fish/card.
3. Bostitch stapler – staple secures fin clip to card.
4. Pelican Case - 1st stage of drying/holding card with samples.
5. File box – long term dry storage with desiccant packs for all cards.
6. Desiccant packs – removes moisture from samples.
7. Pre-cut blotter paper – covers full sample card for drying.
8. Shipping box – put sealed Pelican case inside a box.
9. Clipboard – holds Whatman genetics card while sampling.
10. Zip ties – to secure the Pelican case for return shipment.
11. Laminated “return address” labels.
12. Sampling instructions.
13. Pencil

V. Shipping: Address the sealed mailer box for return shipment to ADF&G Genetics lab.

RETURN TO ADF&G ANCHORAGE LAB:

ADF&G – Genetics
333 Raspberry Road
Anchorage, Alaska 99518

Lab staff: 907-267-2247
Heather Hoyt: 907-267-2175
Freight code: _____

Appendix A2.–Chinook Genetics Sampling Form example.

Harvest Date(s): **Month: _____ Day: _____** **Year: _____** **Species: Chinook**

Sampling Area: **Unimak or Southwestern** **Southeastern and South Central**

Statistical Areas: _____ _____ _____ _____

Sampler: _____ **Sampling Port: SP KC FP**

Gear: **Seine Drift Set GN** **Vessel/Tender** _____

Gum (Scale) Card No: _____ **Port Gum card prefixes: SP: Seine 1,000-1,499 ; GN: 1,500 - 1,999 FP: Seine 3,000 - 3,499 ; GN 3,500 - 3,999**

Whatman # _____

Fish Number	Sex (M or F)	Length (mm) METF	Adipose Fin √ ∅	Axillary Tissue CWT #	No. Scales per Fish	Comments
1	M F					
2	M F					
3	M F					
4	M F					
5	M F					
6	M F					
7	M F					
8	M F					
9	M F					
10	M F					

Appendix A3.–Marine-phase salmon identification.

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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Source: Washington State Department of Fish and Wildlife.

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.

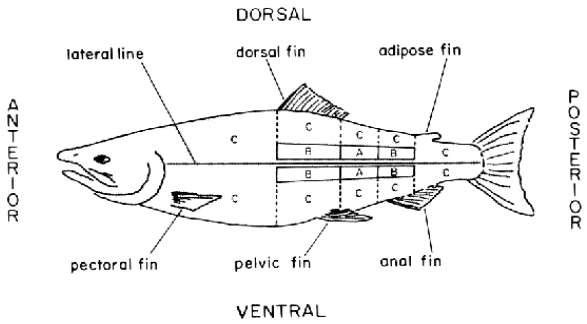
Sexual characteristics on maturing Chinook salmon can be difficult to determine:

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

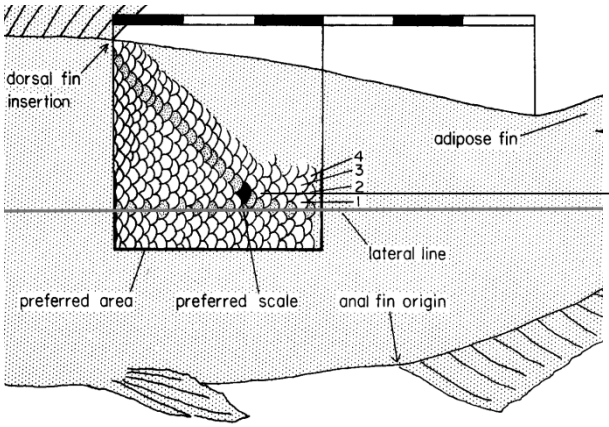
B) Female: Smaller head, *convex forehead*, smaller adipose fin, slight vent protrusion.

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.

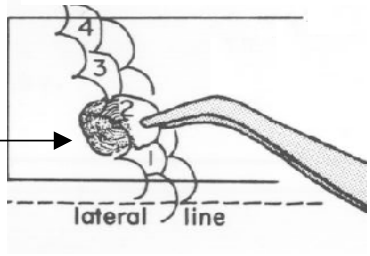
-continued-

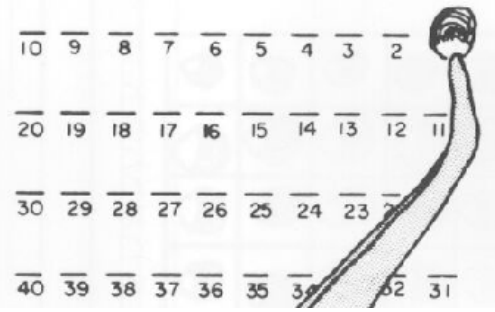


Area A is the preferred area. If scales on the left side are missing, try the right side. Area B is the second choice if there are no scales in Area A on either side of the fish. Area C designates non-preferred areas.



Do not turn scale over.





The preferred scale in the 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.

Figure 1.–Removal and placement of the preferred salmon scale onto the scale card.

-continued-

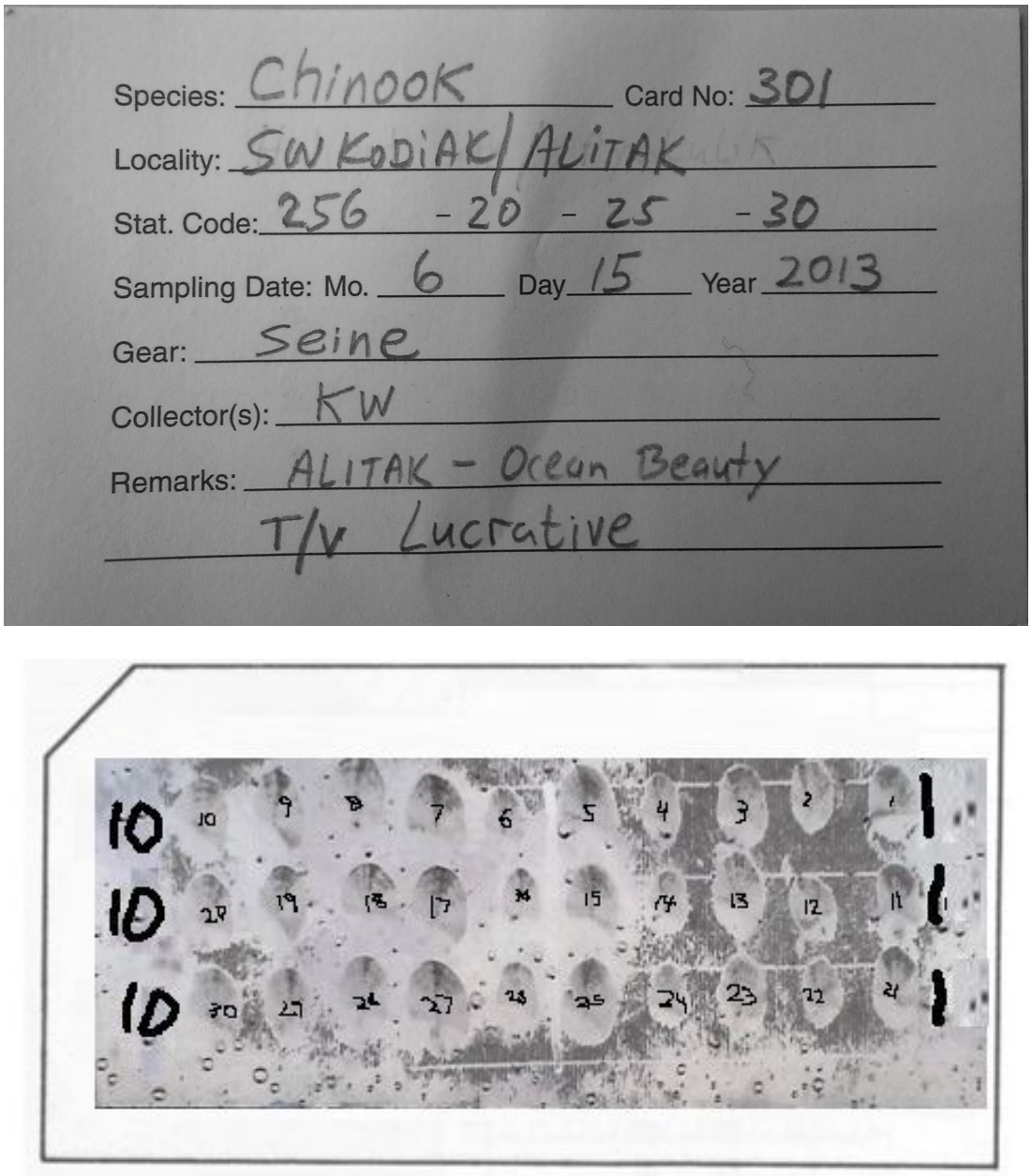
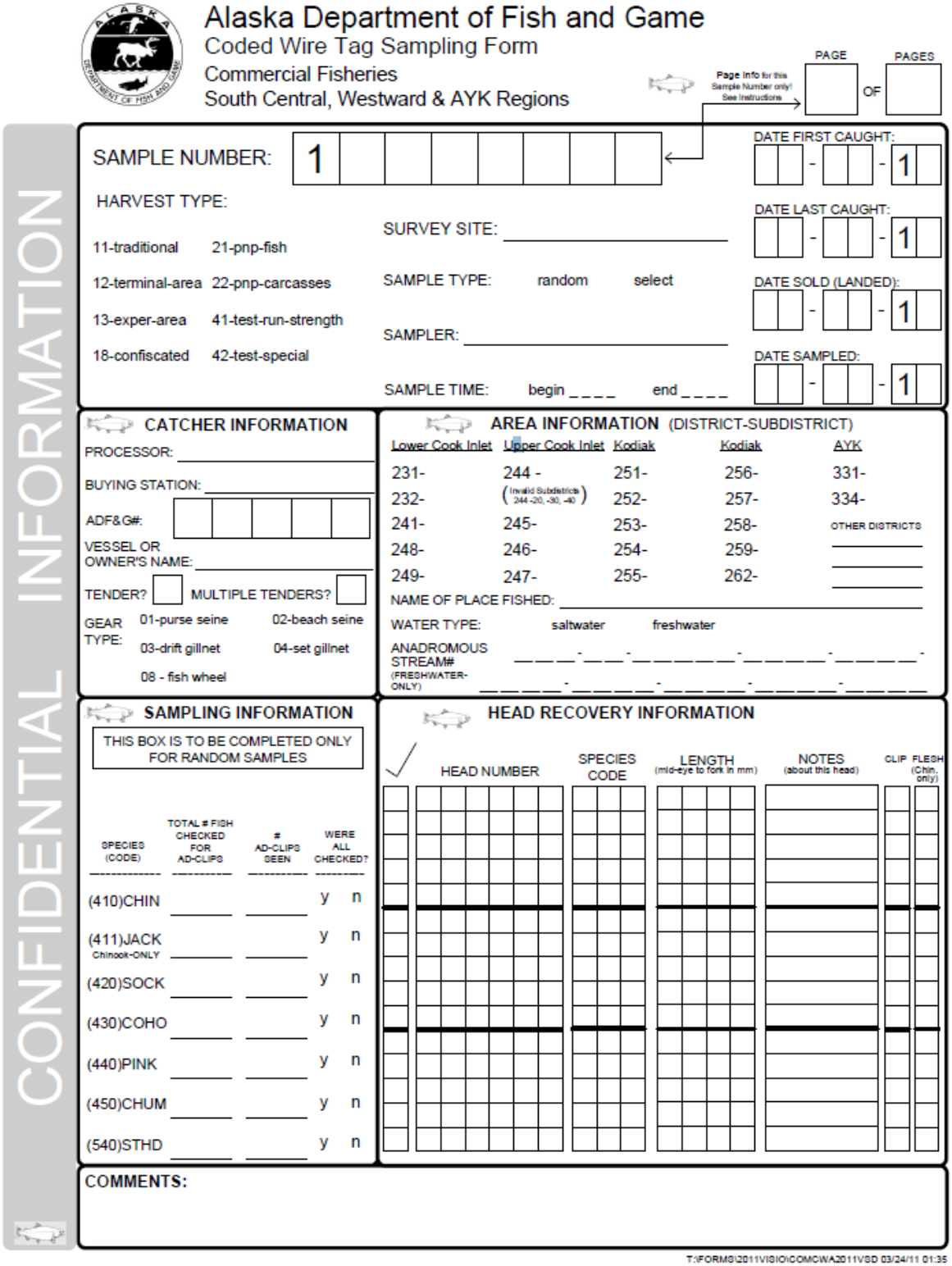


Figure 2.–Scale "gum" card labeling and scale orientation.

APPENDIX B. CHINOOK CWT SAMPLING

Appendix B5.–Coded Wire Tag Sampling Form.



Alaska Department of Fish and Game
Coded Wire Tag Sampling Form
Commercial Fisheries
South Central, Westward & AYK Regions

PAGE ____ OF ____ PAGES

Page info for this Sample Number only! See instructions

CONFIDENTIAL INFORMATION

SAMPLE NUMBER: 1

DATE FIRST CAUGHT: __ - __ - 1

DATE LAST CAUGHT: __ - __ - 1

DATE SOLD (LANDED): __ - __ - 1

DATE SAMPLED: __ - __ - 1

HARVEST TYPE:

11-traditional 21-pnp-fish
12-terminal-area 22-pnp-carcasses
13-exper-area 41-test-run-strength
18-confiscated 42-test-special

SURVEY SITE: _____

SAMPLE TYPE: random select

SAMPLER: _____

SAMPLE TIME: begin ____ end ____

CATCHER INFORMATION

PROCESSOR: _____

BUYING STATION: _____

ADF&G#: _____

VESSEL OR OWNER'S NAME: _____

TENDER? ☐ MULTIPLE TENDERS? ☐

GEAR TYPE: 01-purse seine 02-beach seine 03-drift gillnet 04-set gillnet 08 - fish wheel

AREA INFORMATION (DISTRICT-SUBDISTRICT)

Lower Cook Inlet	Upper Cook Inlet	Kodiak	Kodiak	AYK
231-	244 - (Invalid Subdistricts 244-20, -30, -40)	251-	256-	331-
232-		252-	257-	334-
241-	245-	253-	258-	OTHER DISTRICTS
248-	246-	254-	259-	_____
249-	247-	255-	262-	_____
				_____

NAME OF PLACE FISHED: _____

WATER TYPE: saltwater freshwater

ANADROMOUS STREAM# (FRESHWATER-ONLY) ___-___-___-___-___-___-___

SAMPLING INFORMATION

THIS BOX IS TO BE COMPLETED ONLY FOR RANDOM SAMPLES

SPECIES (CODE)	TOTAL # FISH CHECKED FOR AD-CLIPS	# AD-CLIPS SEEN	WERE ALL CHECKED?
(410)CHIN			y n
(411)JACK Chinook-ONLY			y n
(420)SOCK			y n
(430)COHO			y n
(440)PINK			y n
(450)CHUM			y n
(540)STHD			y n

HEAD RECOVERY INFORMATION

✓	HEAD NUMBER	SPECIES CODE	LENGTH (mid-eye to fork in mm)	NOTES (about this head)	CLIP	FLESH (Chin. only)

COMMENTS:

T:\FORMS\2011VISIO\COMC\WA2011VSD 03/24/11 01:35

Appendix B6.–Sampling CWT Chinook salmon and attaching cinch strap to the head of an adipose-clipped fish.

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).