Regional Operational Plan No. ROP.CF.4K.2022.02

Genetic Stock Composition of Chum Salmon Harvested in Commercial Salmon Fisheries of the South Alaska Peninsula, 2022-2026

by

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and

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May 2022

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

Symbols and Abbreviations

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Weights and measures (metric)

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

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

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

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PURPOSE

The primary goal of this study is to use mixed stock analysis to estimate the stock composition of chum salmon *Oncorhynchus keta* harvested in South Alaska Peninsula Management Area (southern portion of Area M) commercial salmon fisheries during the 2022 to 2026 seasons. Relatively large harvests of chum salmon in South Alaska Peninsula fisheries in recent years corresponding with small returns of chum salmon to Western Alaska rivers has raised concerns among some stakeholders about the stock-specific harvests in South Alaska Peninsula fisheries. Salmon tagging studies published in 1926, 1964, and 1991 and subsequent genetic stock identification projects conducted in 1993-1996 and 2007-2009 demonstrated significant numbers of non-local chum salmon in the June and early July commercial fisheries of the South Alaska Peninsula. Presently, some stakeholders believe that relative abundances among stocks in the fishery have changed since stock-specific chum harvests were last estimated in South Alaska Peninsula harvests as part of the Western Alaska Salmon Stock Identification Program (WASSIP) in 2007-2009. An updated study that accurately and precisely estimates stock-specific harvests would help resolve these concerns and provide valuable management information regarding the gear- and temporal-specific harvests of chum salmon in select South Peninsula 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

Chum salmon *Oncorhynchus keta* are harvested alongside sockeye *O. nerka*, pink *O. gorbuscha*, coho *O. kisutch*, and Chinook *O. tshawytscha* salmon in commercial fisheries within the South Alaska Peninsula Management Area (southern portion of Area M). The Alaska Department of Fish and Game's (ADF&G) South Alaska Peninsula (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 (Schaberg et al. 2019). 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 2011 to 2020, the South Alaska Peninsula annual harvest averaged 11,438,728 salmon and was

composed of 17,004 Chinook, 2,055,793 sockeye, 261,530 coho, 8,183,037 pink, and 921,364 chum salmon. From 2011 to 2020, the South Alaska Peninsula June Fishery annual harvest averaged 3,305,787 salmon and was composed of 2,344 Chinook, 1,128,033 sockeye, 2,886 coho, 1,738,756 pink, and 427,448 chum salmon (Table 1). In 2021, the South Alaska Peninsula June fishery salmon harvest was unusually high with both the sockeye (3,541,620) and chum salmon (1,168,601) the highest in the time series back to 1979 (Table 1).

Poor returns of chum salmon to Arctic-Yukon-Kuskokwim (AYK) rivers in 2021 raised concerns among some stakeholders that fish returning to AYK were harvested in large numbers during South Peninsula fisheries. While final assessments are still underway, there is considerable evidence of poor chum salmon returns throughout AYK in 2021. In Norton Sound, the commercial harvest of 6,410 chum salmon was 5% of the recent 5-year (127,216) average and just over 5% of the recent 10-year (118,336) average (Menard and Clark 2021). In the Yukon River, approximately 153,497 summer chum salmon were counted at the Pilot Station sonar (with a 90% confidence interval of 137,200 to 169,800 fish; Jallen 2021), which was well below the historical median of 1.6 million fish from years with late run timing. Season total counts of summer chum salmon at the Pilot Station sonar were the lowest since project inception (1995) and were well below the previous lowest counts of 442,546 and 448,665 in 2001 and 2000, respectively (Jallen 2021). The preliminary estimated run size of 102,000 fall chum salmon in the Yukon River in 2021 was the lowest on record for the second consecutive year (Jallen 2021). Commercial and subsistence fisheries targeting salmon, including chum salmon, remained closed in the Yukon River in 2021. In the Kuskokwim River, an estimated 26,973 chum salmon passed the sonar counter near Bethel (with a 95% confidence interval of 15,547 to 38,399 fish [1]) and commercial and subsistence fishing targeting salmon remained closed in 2021.

While the stock composition of 2021 South Peninsula fisheries is not known, there is a long history of studies to determine chum salmon stock of origin in the area. In general, studies have demonstrated a high abundance of non-local chum in June and early July. Various chum salmon tagging experiments have been conducted in the South Peninsula area over the last century. In 1923 the U.S. Bureau of Fisheries tagged chum salmon in July in the vicinity of Unga Island and Ikatan and Morzhovoi bays (Gilbert and Rich 1925). In June 1939 the bureau again tagged chum salmon in the vicinity of both South Unimak and Shumagin Islands (Shaul 2005). Tagging studies were conducted by the International North Pacific Fisheries Commission between 1956 and 1966 and one area of chum salmon releases was the offshore area of South Unimak Island in May and June (Brannian 1984). Chum salmon were tagged by the U.S. Fish and Wildlife service between June 15 and July 14, 1961 in the South Unimak and Ikatan Bay area (Thorsteinson and Merrell 1964). Other smaller chum tagging projects were conducted in the 1960s but unpublished (Shaul 2005). A large chum tagging project was conducted by ADF&G in June and early July 1987 around South Unimak and Shumagin Islands (Eggers et al. 1991).

[1] Escapement Monitoring Inseason and Historical Data. 2022. Alaska Department of Fish and Game, Division of Commercial Fisheries, Juneau, AK. https://www.adfg.alaska.gov/index.cfm?adfg=commercialbyareakuskokwim.emihd (accessed February 17, 2022).

Other methods of determining stock or origin have been used in the modern era. An unpublished scale pattern analysis project was conducted in 1983 on June harvests of chum salmon in South Unimak and Shumagin Islands. From 1993 to 1996 genetic mixed stock analysis (MSA) techniques were used to determine stock of origin of chum salmon harvested in the South Alaska Peninsula commercial fishery in June (Seeb et al. 1997) and in July 1996 and 1997 (Crane and Seeb 2000).

The most current and scientifically rigorous study, the Western Alaska Salmon Stock Identification Program (WASSIP), sampled catches from 2006 to 2009 as an objective measure of the stock of origin of chum and sockeye salmon caught by inshore commercial salmon fisheries of western Alaska utilizing genetic MSA (Eggers et al. 2011). Chum salmon sampled in 2007 to 2009 were subsequently analyzed for MSA. These data can be used to guide a framework of the current study. Stock compositions and stock-specific harvests and harvest rates were reported in 2012 (Dann et al. 2012a; Habicht et al. 2012a; Munro et al. 2012; Templin et al. 2012). Summarizing across 2007–2009, the Coastal Western Alaska (CWAK) reporting group comprised a majority of the chum salmon harvests in the June fishery (57%; Table 2), followed by Asia (25%) and East of Kodiak (8%). South Peninsula dominated the post-June fishery average (70%; Table 3), followed by Chignik/Kodiak (11%) and Asia (9%). Important aspects to understand when interpreting WASSIP estimates of stock-specific chum salmon harvests in South Peninsula fisheries are that the WASSIP experimental design 1) grouped harvests and samples among gear types, 2) included 5 temporal strata in the June fishery for most areas, 3) included 3 temporal strata in the post-June fishery for the Shumagin Islands, and 4) did not analyze harvests in the post-June fishery for the Unimak District. While averages of 2007–2009 harvests may not be representative of recent harvests due to changes in relative abundance among reporting groups, prosecution of the fisheries, or migratory behavior due to ocean conditions, these estimates provide the most recent information regarding stock-specific harvests in South Peninsula fisheries.

The following operational plan details implementation, sampling, and reporting of a project to collect genetic tissues from chum salmon of the commercial salmon fisheries of the South Peninsula.

OBJECTIVES

PRIMARY OBJECTIVES

1. Collect genetic tissue (pelvic fin) from chum salmon caught in the major South Peninsula fisheries over the 2022–2026 fishing seasons from June to August.
2. Select subsamples of genetic tissues in proportion to catch within designated areas and temporal strata.
3. Using genetic MSA techniques, estimate stock proportions of chum salmon in the South Peninsula strata using reporting groups defined herein.

SECONDARY OBJECTIVES

1. Estimate the age, sex, and length (ASL) composition of chum salmon sampled for genetic information.

OVERVIEW

The primary objectives of this study are to sample, genotype, and estimate the stock composition of the major chum salmon commercial fisheries in marine waters of the South Peninsula where significant catches of salmon occur (Table 4, 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 the different geographic areas, Unimak and Southwestern Districts, and South Central and Southeastern Districts, fisheries separately as these two areas may harvest different stocks (Munro et al. 2012).

In general, there will be 1 temporal strata for MSA for each of the scheduled openings in the June fishery for each gear type with the following exceptions: 1) Because the first opening is for the set gillnet fleet only, seine and drift gillnet harvests will be represented by each of the last 4 scheduled openings. 2) Drift gillnet harvests in South Unimak are larger than set gillnet harvests in the Shumagin Islands fishery and will be represented by 4 strata (1/opening) while 3) Shumagin Islands set gillnet harvests will be represented by a single stratum representing all 5 openings for a total of 13 strata for the June fishery (Table 4).

Post-June harvests will be represented by 5 temporal strata for seine and 4 temporal strata for gillnet for each geographic area, Unimak and Southwestern Districts, and South Central and Southeastern Districts, for a total of 18 area and temporal strata (Table 4). We will group harvests of each geographic area into temporal strata that represent roughly equal harvests or temporal periods that represent distinct management time periods. Designated sampling areas encompass districts or partial districts as outlined in the fishery description below and are based on geographic location, harvest magnitude, and management discreteness, with consideration given to port delivery location.

Collection of all chum salmon samples will follow the sampling procedures outlined in Appendix A. The pelvic fin 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 silicone 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 general 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 chum salmon throughout South Alaska Peninsula fisheries from 2022 to 2026. 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 is opened based upon local pink and chum salmon escapement. A majority of the chum salmon harvest occurs in two geographic areas, the Southeastern and South Central Districts and the Southwestern and Unimak Districts. Temporal strata will be defined by the five scheduled openings in June and by 3 time periods of harvest in July that represent roughly equal harvest. Additionally, there will be 2 temporal strata in 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). 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 4 (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 4). 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 40 samples that will match the layout on the Genetics Sampling Form (Appendix A2). All sample information will be recorded on the chum 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 chum 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). One scale 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).

DATA ANALYSIS

Genetic Analysis

MSA will be accomplished by the ADF&G Gene Conservation Laboratory following standardized procedures similar to those of WASSIP described by Templin et al. (2012) with some minor differences. Genomic DNA will be extracted from tissue samples using a NucleoSpin 96 Tissue Kit by Macherey-Nagel® (Düren, Germany). DNA will be screened for the same 96 single nucleotide polymorphism (SNP) markers used in Templin et al. (2012; Table 5) 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 Gene Conservation Laboratory Oracle database, LOKI. The differences in methods from Templin et al. (2012) include the genetic baseline and software to be used for MSA (see below).

Mixed Stock Analysis

Estimates of stock composition will be based on the most current genetic baseline representing spawning chum salmon from known origins throughout the Pacific Rim. An updated baseline is currently in development following procedures similar to DeCovich et al. (2012) but will include new collections genotyped for the same 96 SNPs used in the WASSIP baseline. These new collections are either populations throughout Alaska sampled since WASSIP by ADF&G staff or collaborators or were included in studies that improve representation of chum salmon production

from the Alaska Peninsula (Petrou et al. 2014) and British Columbia and Washington state (Small et al. 2015). Collections and SNPs that do not conform to Hardy-Weinberg Equilibrium (HWE) will be removed from the baseline and will not be used for MSA. Collections will be pooled into populations 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, one of the linked SNPs will be removed based on the relative value of information each marker provides for MSA.

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. The starting point for reporting groups for this study will be those used in the WASSIP study except that we will evaluate the potential to identify smaller groups of populations that were combined in WASSIP (DeCovich et al. 2012; Table 6):

1. Japan
2. Korea/Southern Russia
3. Northern Russia
4. Kotzebue Sound
5. Coastal Western Alaska (CWAK)
6. Upper Yukon River Canada
7. Upper Yukon River USA
8. Upper Kuskokwim

9. Northern District
10. Northwestern District
11. South Peninsula
12. Chignik
13. Kodiak/Afognak
14. Sturgeon River Stock
15. Kodiak Mainland
16. Cook Inlet
17. Prince William Sound
18. Northern Southeast Alaska
19. Southern Southeast Alaska
20. Haida Gwaii
21. Northern BC Mainland
22. East Vancouver Island/Fraser River
23. West Vancouver Island
24. Washington State

It is likely that many of these reporting groups will not meet our criteria and will be combined into larger reporting groups. The following reporting groups were used based on similar criteria for defining reporting groups and a similar baseline for WASSIP:

1. Asia
2. Kotzebue Sound
3. Coastal Western Alaska (CWAK)
4. Upper Yukon River
5. Northern District
6. Northwestern District
7. South Peninsula
8. Chignik/Kodiak
9. East of Kodiak

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%. However, deviation from this guideline will be permitted if there is a willingness to accept higher levels of MSA uncertainty for specific reporting groups to support improved information to meet a management need. 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 describe 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, duplicate individuals, and non-chum salmon. 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 Chum Salmon in the South Peninsula

Estimates of the stock-specific harvest of sockeye 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 2022 and 2023 seasons will be analyzed in the laboratory during the winter of 2023–2024. 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 a complete three years of sampling have 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 the 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.

Chris Habicht, 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.

REFERENCES CITED

Clutter, R. and L. Whitesel. 1956. Collection and interpretation of sockeye salmon scales. International Pacific Salmon Fisheries Commission, Bulletin 9, New Westminster, British Columbia, Canada.

Brannian, L. K. 1984. Recovery distribution of chum salmon (Oncorhynchus keta) tagged in the North Pacific offshore of the Alaska Peninsula and Eastern Aleutian Island chain. Alaska Department of Fish and Game, Division of Commercial Fisheries, Informational Leaflet No. 237, Juneau.

Crane, P. A., and L. W. Seeb. 2000. Genetic analysis of chum salmon harvested in the South Peninsula post June fishery, 1996–1997. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J00-05, Juneau.

Dann, T. H., C. Habicht, S. D. R. Olive, H. L. Liller, E. K. C. Fox, J. R. Jasper, A. R. Munro, M. J. Witteveen, T. T. Baker, K. G. Howard, E. C. Volk, and W. D. Templin. 2012. Stock composition of sockeye salmon harvests in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2006-2008. Alaska Department of Fish and Game, Special Publication No. 12-22, Anchorage.

DeCovich, N. A., T. H. Dann, S. D. Rogers Olive, H. L. Liller, E. K. C. Fox, J. R. Jasper, E. L. Chenoweth, C. Habicht, and W. D. Templin. 2012. Chum salmon baseline for the Western Alaska Salmon Stock Identification Program. Alaska Department of Fish and Game, Special Publication No. 12-26, Anchorage.

Eggers, D. M., K. A. Rowell, and B. M. Barrett. 1991. Stock composition of sockeye and chum salmon catches in Southern Alaska Peninsula fisheries in June. Alaska Department of Fish and Game, Division of Commercial Fisheries, Fishery Research Bulletin 91-01, Juneau.

Eggers, D. M., M. J. Witteveen, T. T. Baker, D. F. Evenson, J. M. Berger, H. A. Hoyt, H. L. Hildebrand, W. D. Templin, C. Habicht, and E. C. Volk. 2011. Results from sampling the 2006–2009 commercial and subsistence fisheries in the Western Alaska Salmon Stock Identification Project. Alaska Department of Fish and Game, Special Publication No. 11-10, Anchorage

Fox, E. K. C., T. D. Lawson, and R. L. Renick. 2021. South Alaska Peninsula salmon management strategy, 2021. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report No. 4K21-05, Anchorage.

Gilbert, C. H., and W. H. Rich. 1925. Second experiment in tagging salmon in the Alaska Peninsula Fisheries Reservation summer of 1923. Bulletin of the Bureau of Commercial Fisheries, Volume 62, Document 991.

Habicht, C., A. R. Munro, T. H. Dann, D. M. Eggers, W. D. Templin, M. J. Witteveen, T. T. Baker, K. G. Howard, J. R. Jasper, S. D. R. Olive, H. L. Liller, E. L. Chenoweth and E. C. Volk. 2012a. Harvest and harvest rates of sockeye salmon stocks in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2006–2008. Alaska Department of Fish and Game, Special Publication No. 12-24, Anchorage.

Habicht, C., J. R. Jasper, T. H. Dann, N. DeCovich, and W. D. Templin. 2012b. Western Alaska salmon stock identification program technical document 11: defining reporting groups. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-16, Anchorage.

International North Pacific Fisheries Commission. 1963. Annual Report 1961, Vancouver, British Columbia.

Jallen, D. 2021. 2021 Yukon River Summer Season Summary. Alaska Department of Fish and Game, Division of Commercial Fisheries, Advisory Announcement, Anchorage, AK. Issued October 26, 2021. http://www.adfg.alaska.gov/static/applications/dcfnewsrelease/1344517999.pdf (accessed February 17, 2022).

Koo, T. 1962. Age designation in salmon. Pages 37–48. [*In*] T.S.Y. Koo, editor. Studies of Alaska red salmon. University of Washington Publications in Fisheries, New Series, Volume I, Seattle.

Menard, J., and K. Clark. 2021. 2021 Norton Sound Salmon Season Summary [Revised]. Alaska Department of Fish and Game, Division of Commercial Fisheries, Advisory Announcement, Anchorage, AK. Issued November 29, 2021. http://www.adfg.alaska.gov/static/applications/dcfnewsrelease/1347621568.pdf (accessed February 17, 2022).

Moran, B. M., and E. C. Anderson. 2019. Bayesian inference from the conditional genetic stock identification model. Canadian Journal of Fisheries and Aquatic Sciences 76(4):551–560.

REFERNCES CITED (Continued)

Mosher, K. 1968. Photographic atlas of sockeye salmon scales. Bureau of the U.S. Fish and Wildlife Service. Fishery Bulletin 67(2):243–280.

Munro, A. R., C. Habicht, T. H. Dann, D. M. Eggers, W. D. Templin, M. J. Witteveen, T. T. Baker, K. G. Howard, J. R. Jasper, S. D. Rogers Olive, H. L. Liller, E. L. Chenoweth, and E. C. Volk. 2012. Harvest and harvest rates of chum salmon stocks in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2007–2009. Alaska Department of Fish and Game, Special Publication No. 12-25, Anchorage.

Petrou, E. L., J. E. Seeb, L. Hauser, M. J. Witteveen, W. D. Templin, L. W. Seeb. 2014. Fine-scale sampling reveals distinct isolation by distance patterns in chum salmon (Oncorhynchus keta) populations occupying a glacially dynamic environment. Conservation Genetics 15(1): 229-243.

R Core Team (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Seeb, L. W., P. A. Crane and E. M. Debevec. 1997. Genetic analysis of chum salmon harvested in the South Unimak and Shumigan Islands June fisheries, 1993–1996. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J97-17, Juneau.

Shaul, A. R. 2005. Summary of a previously unexamined 1939 Alaska Peninsula salmon tagging study. Alaska Department of Fish and Game, Special Publication No. 05-11, Anchorage.

Small, M. P., S. D. Rogers Olive, L. W. Seeb, J. E. Seeb, C. E. Pascal, K. I. Warheit, and W. D. Templin. 2015. Chum salmon genetic diversity in the north-eastern Pacific Ocean assessed with single nucleotide polymorphisms (SNPs): applications to fishery management. North American Journal of Fisheries Management 35(5):974-987. doi: 10.1080/02755947.2015.1055014

Templin, W. D., N. A. DeCovich, S. D. Rogers Olive, H. L. Liller, E. K. C. Fox, J. R. Jasper, T. T. Baker, K. G. Howard, A. R. Munro, E. C. Volk, and C. Habicht. 2012. Stock composition of chum salmon harvests in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2007-2009. Alaska Department of Fish and Game, Special Publication No. 12-23, Anchorage.

Thorsteinson, F. V. and T. R. Merrill, Jr. 1964. Salmon tagging experiments along the south shore of Unimak and the southwestern shore of the Alaska Peninsula. U.S. Fish and Wildlife Service Special Scientific; Report Fisheries No. 486, Washington, D.C.

TABLES

Table 1.– South Unimak and Shumagin Islands June commercial salmon harvest by species and year, 1979–2021

			Number of salmon[a]					
Year	Permits	Landings	Chinook	Sockeye	Coho	Pink	Chum	Total
1979	196	1,695	1,050	851,351	290	154,813	104,103	1,111,607
1980	225	2,044	3,193	3,206,275	853	1,526,306	508,865	5,245,492
1981	243	2,400	5,672	1,820,965	320	451,250	563,947	2,842,154
1982	251	2,612	7,131	2,118,701	1,241	1,718,825	1,095,044	4,940,942
1983	281	1,721	13,456	1,961,569	4	55,875	785,631	2,816,535
1984	280	1,117	3,854	1,388,203	14	919,876	337,120	2,649,067
1985	305	2,120	5,777	1,791,400	2,468	106,615	433,829	2,340,089
1986	298	1,486	1,895	471,397	2	291,989	351,769	1,117,052
1987	290	2,019	5,163	792,964	380	16,982	443,019	1,258,508
1988	301	1,777	4,064	756,687	255	180,224	526,711	1,467,941
1989	305	1,350	2,758	1,744,505	0	199,235	455,163	2,401,661
1990	320	2,718	10,332	1,344,529	1	515,047	518,545	2,388,454
1991	334	2,025	4,473	1,548,930	12	619,137	772,705	2,945,257
1992	321	1,925	3,760	2,457,856	4	642,090	426,203	3,529,913
1993	327	2,262	9,466	2,973,744	1,233	81,136	532,247	3,597,826
1994	324	2,751	7,590	1,461,263	1,579	2,492,514	582,165	4,545,111
1995	332	3,635	14,747	2,105,321	6,042	178,635	537,433	2,842,178
1996	313	2,676	2,845	1,028,970	13,219	377,684	359,820	1,782,538
1997	292	3,174	5,811	1,628,181	560	605,937	322,325	2,562,814
1998	283	3,657	2,696	1,288,725	476	474,340	245,619	2,011,856
1999	277	2,114	3,051	1,375,399	2	30,539	245,306	1,654,297
2000	278	3,001	2,849	1,251,228	304	360,029	239,357	1,853,767
2001	128	270	345	150,632	2	39,251	48,350	238,580
2002	181	1,301	2,443	591,106	4	76,251	378,817	1,048,621
2003	177	1,170	1,323	453,147	153	217,900	282,438	954,961
2004	190	2,260	4,423	1,348,460	621	359,916	482,310	2,195,730
2005	190	2,344	3,055	1,004,395	1,919	1,654,959	427,830	3,092,158
2006	188	2,412	4,497	932,291	2,629	1,332,319	299,827	2,571,563
2007	185	2,650	4,636	1,589,840	1,633	267,528	297,539	2,161,176
2008	196	2,591	2,957	1,713,575	178	1,971,268	410,932	4,098,910
2009	216	2,852	3,836	1,167,918	203	2,248,555	696,775	4,117,287
2010	224	2,162	3,118	818,865	27	332,435	271,700	1,426,145
2011	211	2,279	3,464	1,359,441	124	723,135	423,335	2,509,499
2012	227	3,111	6,397	1,542,043	12	261,786	395,060	2,205,298
2013	219	2,567	2,237	1,562,849	299	304,022	399,058	2,268,465
2014	228	2,588	2,290	659,213	2,478	180,260	390,139	1,234,380
2015	227	2,636	44,389	1,115,504	20,193	573,104	178,715	1,931,905
2016	223	2,493	6,113	1,292,860	1,716	2,510,048	270,614	4,081,351
2017	226	2,326	4,955	1,956,065	43	1,714,307	640,891	4,316,261
2018	236	1,890	4,158	822,173	51	345,255	537,466	1,709,103
2019	236	1,996	10,049	630,888	3,681	9,021,357	549,072	10,215,047
2020	225	1,555	2,594	339,293	262	1,754,284	490,128	2,586,561
2021	229	1,898	3,188	3,541,620	86	4,038,219	1,168,601	8,751,714
2001–2020 Average	207	2,173	5,864	1,052,528	1,811	1,294,397	393,550	2,748,150
2011–2020 Average	226	2,344	8,665	1,128,033	2,886	1,738,756	427,448	3,305,787

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

Table 2.–Summary of stock-specific harvests of chum salmon in the June fishery of the South Alaska Peninsula in 2007-2009. Mean harvests summarize stock-specific harvests after temporal and area strata were summarized together into fishery strata (June fishery). Estimates include annual mean harvests, annual proportion of total harvest, average of annual proportions, and average of annual proportions applied to recent 10-year average harvests.

	June Fishery Mean Harvests			June Fishery Mean Proportion			
Reporting Group	2007	2008	2009	2007	2008	2009	June Average
Asia	60,760	117,171	178,693	0.20	0.29	0.26	0.25
Kotzebue Sound	1,349	4,154	2,791	0.00	0.01	0.00	0.01
Coastal W. AK	177,867	214,464	420,739	0.60	0.52	0.60	0.57
Upper Yukon River	3,752	6,914	1,612	0.01	0.02	0.00	0.01
Northern District	861	5,533	5,816	0.00	0.01	0.01	0.01
Northwestern District	2,492	13,760	31,034	0.01	0.03	0.04	0.03
South Peninsula	3,401	8,108	8,113	0.01	0.02	0.01	0.01
Chignik/Kodiak	4,889	13,186	16,075	0.02	0.03	0.02	0.02
East of Kodiak	42,183	27,620	31,931	0.14	0.07	0.05	0.08
Total	297,554	410,910	696,804	1.00	1.00	1.00	1.00

Note: Estimates of June Fishery Mean Harvests are sourced from Tables 122-124 from Munro et al. (2012), harvest and harvest rates by fishery, where area strata are rolled into fishery strata.

Table 3.–Summary of stock-specific harvests of chum salmon in the post-June fishery of the South Alaska Peninsula in 2007-2009. Mean harvests summarize stock-specific harvests after temporal and area strata were summarized together into fishery strata (post-June fishery). Estimates include annual mean harvests, annual proportion of total harvest, average of annual proportions, and average of annual proportions applied to recent 10-year average harvests.

	Post-June Fishery Mean Harvests			Post-June Fishery Mean Proportion			
Reporting Group	2007	2008	2009	2007	2008	2009	Post-June Average
Asia	40,672	40,716	17,582	0.12	0.14	0.02	0.09
Kotzebue Sound	401	476	1,164	0.00	0.00	0.00	0.00
Coastal W. AK	12,178	7,850	19,805	0.04	0.03	0.02	0.03
Upper Yukon River	424	252	288	0.00	0.00	0.00	0.00
Northern District	2,406	1,949	7,081	0.01	0.01	0.01	0.01
Northwestern District	7,877	8,177	9,439	0.02	0.03	0.01	0.02
South Peninsula	201,763	176,455	723,670	0.61	0.60	0.88	0.70
Chignik/Kodiak	49,068	37,181	40,854	0.15	0.13	0.05	0.11
East of Kodiak	18,184	18,694	5,399	0.05	0.06	0.01	0.04
Total	332,973	291,750	825,282	1.00	1.00	1.00	1.00

Note: Estimates of post-June Fishery Mean Harvests are sourced from Tables 125-127 from Munro et al. (2012), harvest and harvest rates by fishery, where area strata are rolled into fishery strata.

Table 4.–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 chum salmon harvests, 2022-2026.

	Harvest (10-yr avg)[a]						
Fishery (Districts)	June		July		August		Total
	Seine	Gillnet	Seine	Gillnet	Seine	Gillnet	
Unimak and Southwestern	171,705	65,841	173,381	20,489	51,547	19,975	502,938
Southeastern and South Central	251,280	13,079	166,791	35,000	92,597	18,447	577,194

	Design (# Temporal Strata x Sample Size)						
Fishery (Districts)	June		July		August		
	Seine	Gillnet	Seine	Gillnet	Seine	Gillnet	Total
Unimak and Southwestern	4 x 380	4 x 380 [b]	3 x 380	3 x 380 [b]	2 x 380	1 x 380 [b]	6,460
Southeastern and South Central	4 x 380	1 x 380 [c]	3 x 380	3 x 380 [c]	2 x 380	1 x 380 [c]	5,320

[a] Average harvest over ten years (2012 to 2021) if the area received effort and harvest by the gear type during that respective timeframe.

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

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

Table 5.– Source, observed heterozygosity (H_O), F_{IS}, and F_{ST} for the 96 single nucleotide polymorphism (SNP) markers used to analyze the population genetic structure of chum salmon in the WASSIP study area.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
Oke_ACOT-100	A	0.424	0.001	0.081
Oke_AhR1-78	B	0.477	-0.006	0.040
Oke_arf-319	C	0.352	-0.008	0.051
Oke_ATP5L-105	A	0.441	-0.009	0.034
Oke_azin1-90	A	0.404	-0.008	0.059
Oke_brd2-118	A	0.309	0.003	0.061
Oke_brp16-65	A	0.365	0.008	0.065
Oke_CATB-60	A	0.203	0.005	0.162
Oke_ccd16-77	A	0.415	-0.002	0.075
Oke_CD81-108	A	0.195	0.006	0.147
Oke_CD81-173	A	0.409	0.005	0.141
Oke_CKS1-94	A	0.379	0.002	0.047
Oke_CKS-389	D	0.387	0.003	0.088
Oke_Cr30[d]	A			0.200
Oke_Cr386[d]	A			0.527
Oke_ctgf-105	B	0.161	-0.005	0.047
Oke_DCXR-87	A	0.229	0.002	0.129
Oke_e2ig5-50	A	0.468	-0.013	0.046
Oke_eif4g1-43	A	0.371	-0.014	0.075
Oke_f5-71	A	0.369	-0.007	0.049
Oke_FANK1-166	A	0.311	-0.009	0.120
Oke_FBXL5-61	A	0.340	-0.003	0.105
Oke_gdh1-191	A	0.414	-0.015	0.067
Oke_gdh1-62[c]	A	0.390	-0.004	0.090
Oke_GHII-3129	B	0.220	0.007	0.146
Oke_glrx1-78	A	0.398	-0.007	0.032
Oke_GPDH-191	C	0.416	-0.007	0.068
Oke_GPH-105	B	0.464	-0.001	0.067
Oke_HP-182	B	0.330	-0.010	0.071
Oke_il-1racp-67	C	0.267	0.001	0.051
Oke_IL8r2-406	A	0.319	-0.003	0.045
Oke_KPNA2-87	B	0.180	-0.002	0.117
Oke_LAMP2-186	A	0.432	-0.006	0.107
Oke_mgll-49	A	0.460	0.002	0.065
Oke_MLRN-63	A	0.478	-0.014	0.036

-continued-

Table 5. Page 2 of 3.

Assay	Source[a]	HO	FIS	FST
Oke_Moesin-160	C	0.118	0.002	0.043
Oke_nc2b-148	A	0.405	0.011	0.084
Oke_ND3-69[d]	A			0.526
Oke_NUPR1-70	A	0.360	0.000	0.069
Oke_pgap-111	A	0.426	-0.006	0.070
Oke_*pgap*-92[c]	A	0.377	-0.006	0.076
Oke_PPA2-635	B	0.316	0.000	0.128
Oke_psmd9-57	A	0.184	0.000	0.033
Oke_rab5a-117	A	0.355	-0.001	0.133
Oke_ras1-249	B	0.423	-0.005	0.091
Oke_RFC2-618	C	0.168	-0.002	0.304
Oke_RH1op-245	C	0.163	0.001	0.123
Oke_RS27-81	A	0.297	-0.005	0.016
Oke_RSPRY1-106	A	0.250	0.001	0.108
Oke_serpin-140	C	0.440	0.002	0.072
Oke_slc1a3a-86	A	0.390	0.003	0.092
Oke_sylc-90	A	0.395	-0.001	0.059
Oke_TCP1-78	B	0.182	-0.008	0.081
Oke_Tf-278	B	0.371	-0.015	0.171
Oke_thic-84	A	0.451	-0.007	0.089
Oke_U1002-262	A	0.420	0.000	0.131
Oke_U1008-83	A	0.154	-0.015	0.097
Oke_U1010-251	A	0.294	0.020	0.137
Oke_U1012-241	A	0.460	-0.013	0.087
Oke_U1015-255	A	0.336	0.005	0.085
Oke_U1016-154	A	0.457	-0.012	0.036
Oke_U1017-52	A	0.391	-0.028	0.068
Oke_U1018-50	A	0.138	-0.002	0.114
Oke_U1021-102[b]	A	0.354	0.010	0.068
Oke_U1022-139[b]	A	0.344	-0.002	0.097
Oke_U1023-147	A	0.444	-0.001	0.098
Oke_U1024-113	A	0.160	-0.001	0.053
Oke_U1025-135	A	0.073	0.021	0.076
Oke_u200-385	C	0.463	-0.006	0.067
Oke_U2006-109	A	0.446	-0.001	0.027
Oke_U2007-190	A	0.432	-0.007	0.099

-continued-

Table 5. Page 3 of 3.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
Oke_U2011-107	A	0.227	-0.012	0.095
Oke_U2015-151	A	0.162	-0.005	0.152
Oke_U2025-86	A	0.467	-0.002	0.062
Oke_U2029-79	A	0.416	0.002	0.134
Oke_U2031-37	A	0.205	0.006	0.075
Oke_U2032-74	A	0.212	-0.003	0.043
Oke_U2034-55	A	0.349	0.005	0.116
Oke_U2035-54	A	0.175	-0.003	0.126
Oke_U2037-76	A	0.143	0.006	0.038
Oke_U2041-84	A	0.426	0.007	0.030
Oke_U2043-51	A	0.208	0.001	0.083
Oke_U2048-91	A	0.451	-0.002	0.095
Oke_U2050-101	A	0.158	0.006	0.048
Oke_U2053-60	A	0.465	-0.005	0.062
Oke_U2054-58	A	0.234	-0.002	0.073
Oke_U2056-90	A	0.478	0.000	0.041
Oke_U2057-80	A	0.363	-0.009	0.102
Oke_U212-87	C	0.077	0.012	0.087
Oke_U217-172	C	0.462	-0.015	0.054
Oke_U302-195	B	0.191	-0.043	0.134
Oke_U502-241	B	0.238	-0.002	0.351
Oke_U504-228	B	0.412	-0.013	0.097
Oke_U506-110	B	0.268	0.010	0.203
Oke_U507-286	B	0.475	-0.016	0.054
Oke_U509-219	B	0.457	-0.008	0.060
Oke_U1021-102_U1022-139[b]		-	0.000	0.065
Oke_Cr30_Cr386_ND3-69[d]		-	0.000	0.437
Overall		0.331	-0.003	0.086

Note: Weir and Cockerham estimates of F_{ST} (1984) are also provided for the 2 sets of linked loci combined as composite phenotypes. Statistics for each marker are based on the 310 populations within the area.

Note: Overall summary statistics are estimates from the final marker set; overall H_O is the average across loci and overall F_{IS} and F_{ST} are estimated following Weir and Cockerham (1986).

[a] A=International Program for Salmon Ecological Genetics at the University of Washington (Petrou 2012); B=Elfstrom et al. 2007; C=Smith et al. 2005[a]; and D=Smith et al. 2005[b].

[b] These nuclear SNPs were combined into haplotypes and treated together as a single locus: "*Oke_U1021-102_U1022-139".*

[c] These SNPs were dropped due to linkage.

[d] These mitochondrial SNPs were kept for consistency with other coastwide baselines, and were combined into a haplotype *a priori*, without being subject to the same criteria as nuclear SNPs. See discussion for details. Combined locus: "*Oke_Cr30_Cr386_ND3-69*".

Table 6.– Geographic boundaries of the reporting groups defined for use in mixed stock analysis of chum salmon for 2007-2009 fisheries in the Western Alaska Salmon Stock Identification Program (WASSIP). Most of these groups will be used as a starting point for definition of reporting groups for mixed stock analysis of chum salmon harvests from South Peninsula fisheries in 2022-2026.

Successful/failed reporting groups	Start point	Stop point
Asia	Western end of species range	US/Russia border
Kotzebue Sound	Point Hope	Cape Prince of Wales
Coastal Western Alaska (CWAK)	Cape Prince of Wales (excluding Upper Yukon River)	Cape Menshikof
Upper Yukon River	Fall-run populations in Koyukuk River drainage and all populations in Tanana River drainage	Canadian Headwaters
Northern District	Cape Menshikof	Moffit Point
Northwest District	Moffit Point	Cape Sarichef
South Peninsula	Scotch Cap	Kupreanof Point
Chignik/Kodiak	Kupreanof Point (including Kodiak Island)	Cape Douglas
East of Kodiak	Cape Douglas	Eastern end of species range

FIGURES

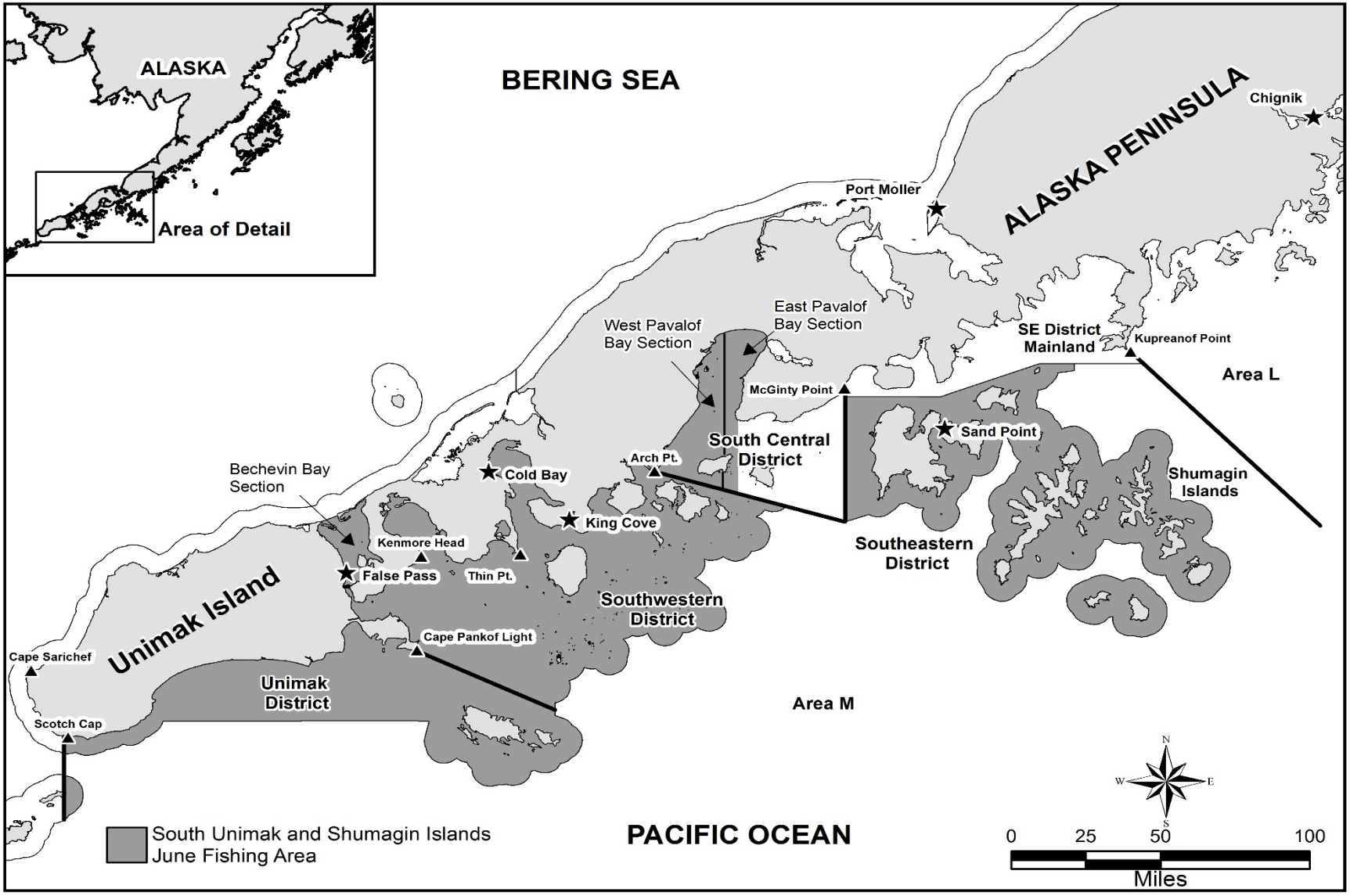


Figure 1.– Map of the South Alaska Peninsula Management Area and the locations of the South Unimak and Shumagin Islands June fisheries.

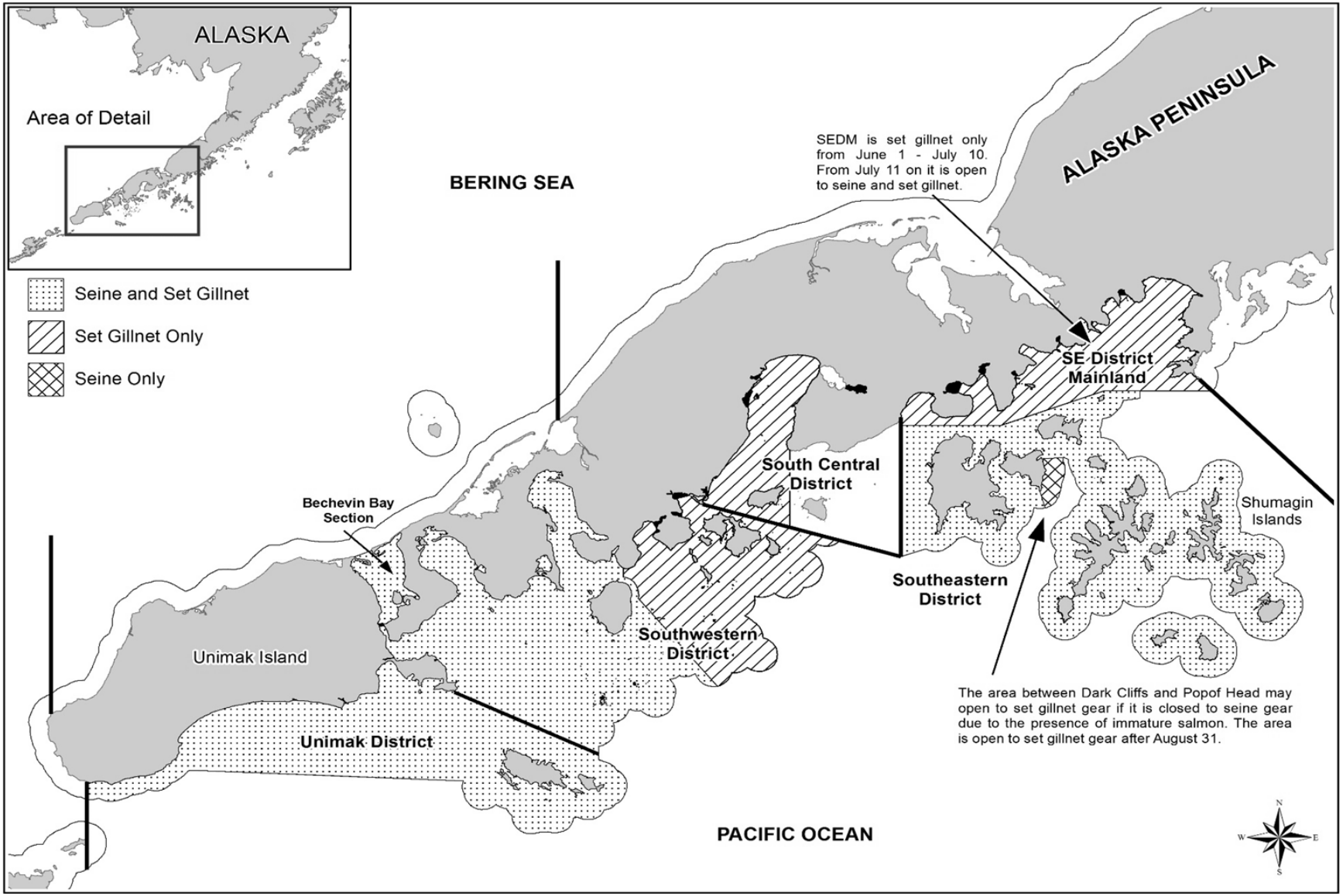


Figure 2.– Map depicting the locations of June South Alaska Peninsula fisheries for purse seine and set gillnet gear.

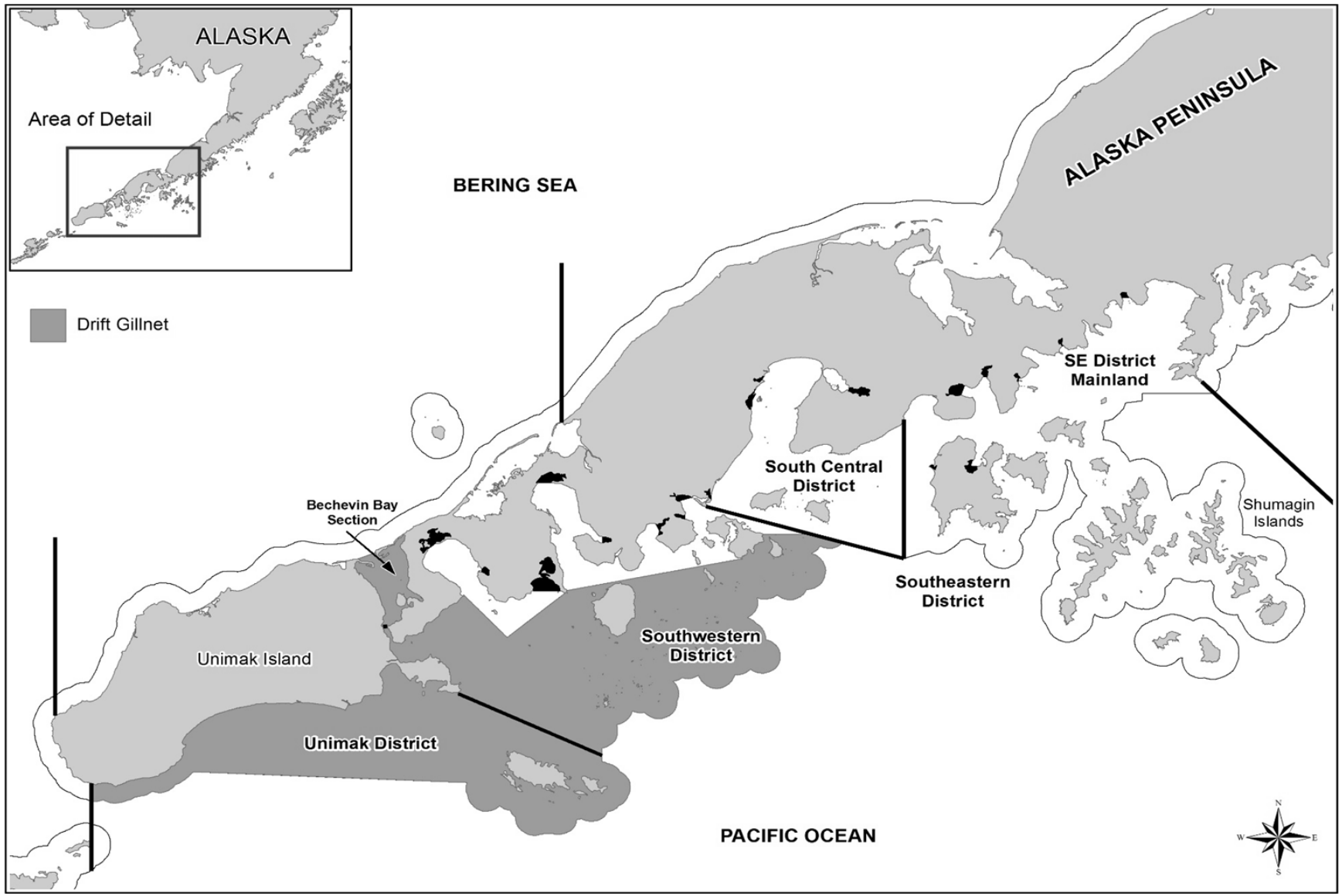


Figure 3.– Map depicting the locations of June South Alaska Peninsula fishery for drift gillnet gear.

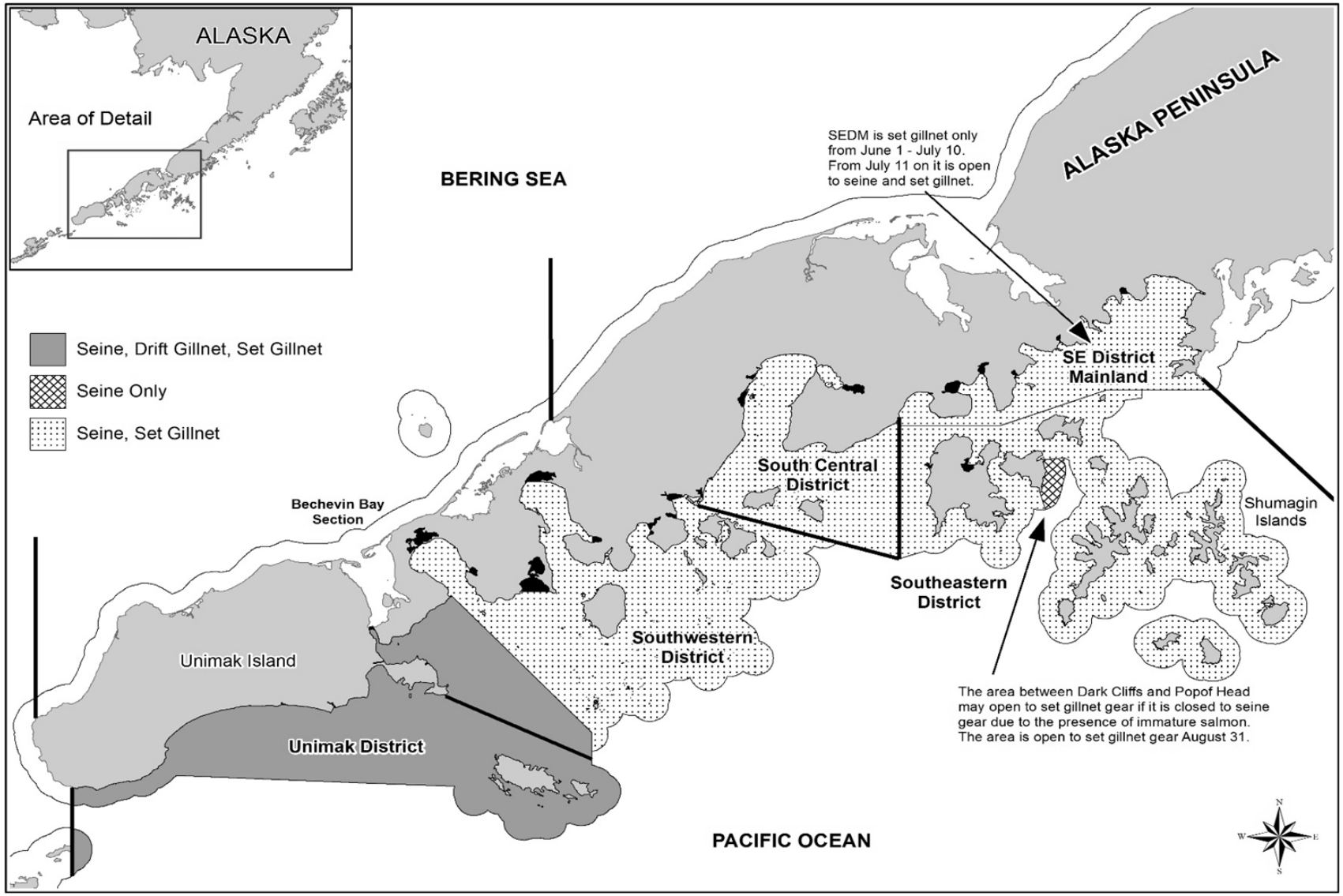


Figure 4.– Map depicting the locations of post-June South Alaska Peninsula fisheries and permitted gear types.

APPENDIX A. CHUM SALMON GENETICS SAMPLING

Adult Finfish Tissue Sampling for DNA Analysis

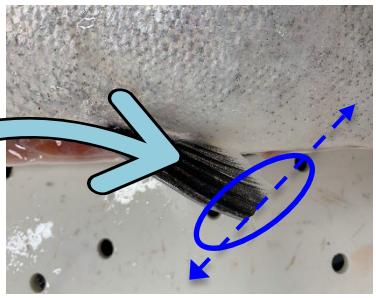
ADF&G Gene Conservation Lab, Anchorage

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.
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
Judy Berger: 907-267-2175
Freight code: _____

Appendix A2.–Chum Genetics Sampling Form example.

Species: Chum

Harvest Date: _____ Sample Date: _____

Sampling Location: _____ Gear: _____

Stat areas: _____

Scale Card: _____ Whatman Card: _____

Fish #1 M F Length	Fish #2 M F Length	Fish #3 M F Length	Fish #4 M F Length	Fish #5 M F Length	Fish #6 M F Length	Fish #7 M F Length	Fish #8 M F Length	Fish #9 M F Length	Fish #10 M F Length
Fish #11 M F Length	Fish #12 M F Length	Fish #13 M F Length	Fish #14 M F Length	Fish #15 M F Length	Fish #16 M F Length	Fish #17 M F Length	Fish #18 M F Length	Fish #19 M F Length	Fish #20 M F Length
Fish #21 M F Length	Fish #22 M F Length	Fish #23 M F Length	Fish #24 M F Length	Fish #25 M F Length	Fish #26 M F Length	Fish #27 M F Length	Fish #28 M F Length	Fish #29 M F Length	Fish #30 M F Length
Fish #31 M F Length	Fish #32 M F Length	Fish #33 M F Length	Fish #34 M F Length	Fish #35 M F Length	Fish #36 M F Length	Fish #37 M F Length	Fish #38 M F Length	Fish #39 M F Length	Fish #40 M F Length

Comments:

Note:

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

January 18, 2006

-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.

January 18, 2006

Source: Washington State Department of Fish and Wildlife.

Position Salmon

Place the salmon on its right side (the head should face toward the left).

Measure the length

Adult salmon length is measured from mid-eye to tail fork because the shape of the salmon's snout changes as it approaches sexual maturity. 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. Flatten and spread the tail against the board with your right hand. Read and record the mid-eye to tail fork length to the nearest millimeter. Please look at Figure 1.

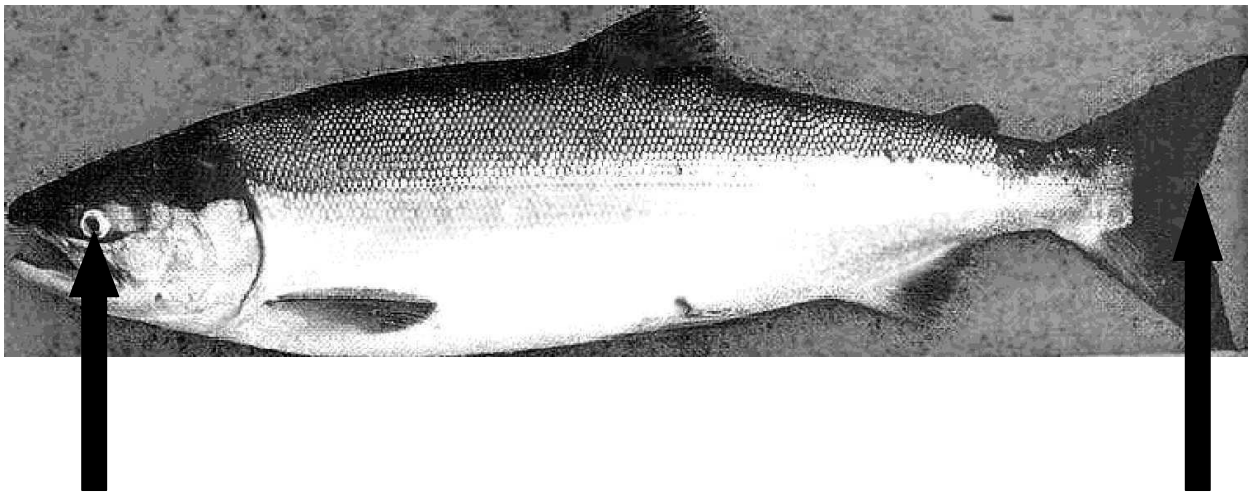


Figure 1.–Measure fish length from mid-eye to tail fork.

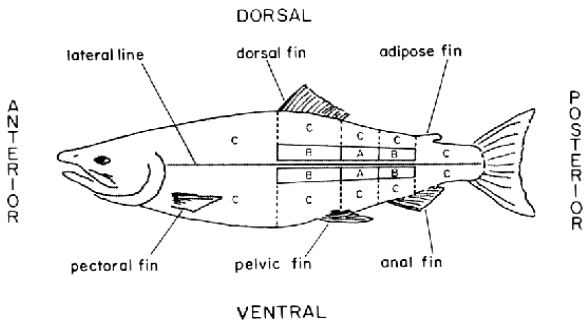
Sex

The determination of the sex of the fish is typically done by examining external characteristics of the salmon.

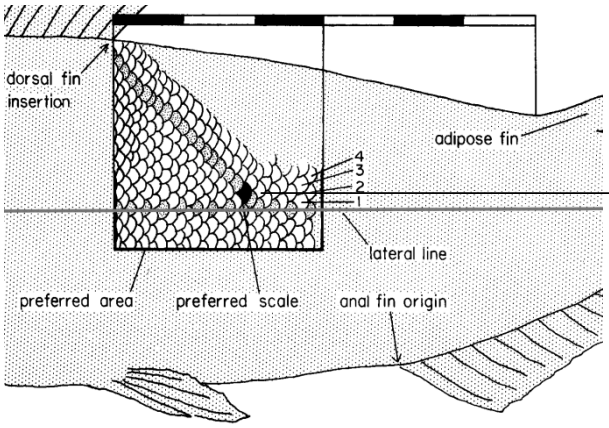
Remove the preferred scale and place on scale card

The preferred scale is located 2 rows up from the lateral line, on a diagonal from the insertion (posterior) of the dorsal fin toward the origin of the anal fin (Figure 2). Remove all silver from the scale. Samplers should be careful to make sure that the scale is not flipped over before it is placed on the scale card. The preferred scale should be properly placed on a labeled scale (gum) card (Figures 2 and 3). If sampling commercial catch, write the date the fish were caught on the card (not the sampling date).

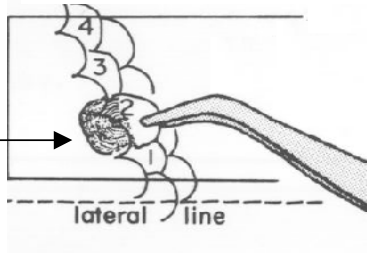
-continued-

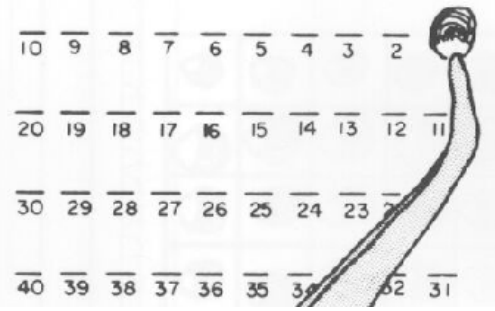


Area A is the preferred area. If scales on the left side are missing, try the right side. Area B is the second choice if there are no scales in Area A on either side of the fish. Area C designates non-preferred areas.



Do not turn scale over.

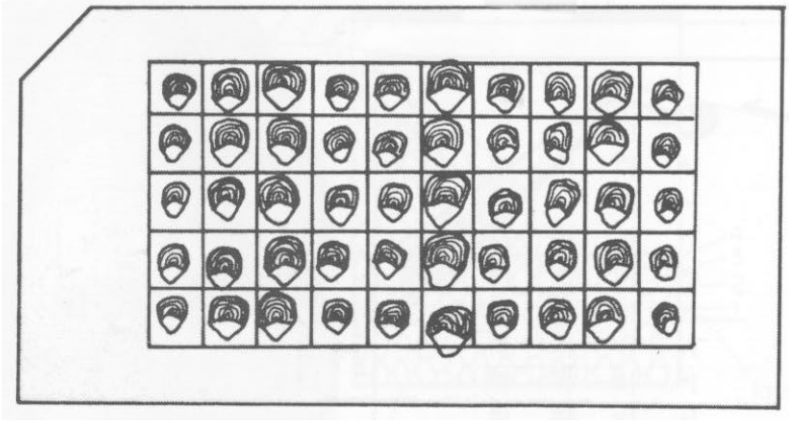




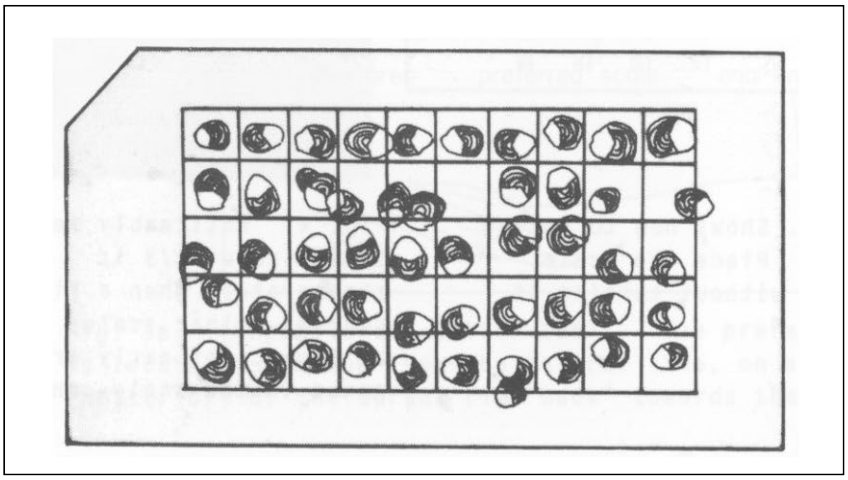
The preferred scale in the diagram is solid black. It is located 2 rows up from the lateral line, on a diagonal from the insertion (posterior) of the dorsal fin "back" toward the origin of the anal fin.

Figure 2.–Removal and placement of the preferred salmon scale onto the scale card.

-continued-



The scales are all correctly oriented on the card in the same direction, with the anterior portion of the scale pointed toward the top of the card and the posterior portion (which is that portion of the scale held in the forceps) pointed toward the bottom of the card.



The scales are incorrectly oriented in different directions. This increases the time spent to age samples.

Figure 3.–Scale orientation on scale card.