2011 Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative Project Final Product¹

45165 AYKSSI: Shared Chum Salmon Baseline Gap Analysis (904)

by:

A.J. Gharrett², M.R. Garvin², W. Templin³, N. Decovich³, C. Kondzela⁴, and J. Guyon⁴

²School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, 17101 Point Lena Loop Rd., Juneau, AK 99801

³Alaska Department of Fish and Game, Gene Conservation Laboratory, 333 Raspberry Road, Anchorage, AK 99518

⁴National Marine Fisheries Service, Auke Bay Laboratories, Ted Stevens Marine Research Institute, 17109 Point Lena Loop Rd., Juneau, AK 99801

August 2011

1 Final products of AYK Sustainable Salmon Initiative-sponsored research are made available to the Initiatives Partners and the public in the interest of rapid dissemination of information that may be useful in salmon management, research, or administration. Sponsorship of the project by the AYK SSI does not necessarily imply that the findings or conclusions are endorsed by the AYK SSI.

II. ABSTRACT:

This project funded the initiation of a collaborative effort among the Alaska Department of Fish and Game (ADF&G), NOAA Fisheries (NOAA), and the University of Alaska Fairbanks (UAF) (which will henceforth be referred to as the Team) to produce and improve the North Pacific Ocean chum salmon baseline for single nucleotide polymorphism (SNP) and microsatellite data. These data are central to applications of mixed stock analyses (MSA) for Alaskan stocks. During the project, we identified critical populations for which baseline data are missing or inadequate and to which we will add SNP (up to 54 populations for 6376 individuals) and microsatellite (30 populations for 2235 individuals) data. This project complements AKSSF project 44521 Shared Chum Baseline Development in which analysis of those populations will be completed and new informative SNP markers will be developed to improve delineation of western Alaska chum salmon populations. In addition, SNP data have been added for 13 key populations (n = 1235) by ADF&G and microsatellite data have been added for 13 (n = 1038) populations by NOAA. During the gap analysis, the Team chose a set of chum salmon populations that will be used by UAF to screen for new, informative SNP markers. UAF worked with ADF&G to extend their SNP analyses to resolve linkage phase in linked loci. UAF and NOAA acquired instrumentation that will be necessary for this and the complementary AKSSF project. By improving the chum salmon baseline, this research will assist both NOAA and ADF&G to better address western Alaska chum salmon management challenges.

Key Words: Bering Sea, chum salmon, genetic baseline, microsatellite, single nucleotide polymorphism (SNP), western Alaska

III. TABLE of CONTENTS:

| Cover Page | 1 |
|-------------------|---|
| Abstract | |
| Table of Contents | 3 |
| Introduction | 4 |
| Objectives | 5 |
| Methods | 6 |
| Results | 6 |
| Discussion | 7 |
| References | 8 |
| Deliverables | 9 |
| Project Data | 9 |
| Acknowledgments | |

List of Tables

| Table 1. | Ascertainment panel for SNP identification by UAF | 11 |
|-----------|-------------------------------------------------------------------------|----|
| | High priority target populations identified during gap analysis for SNP | |
| an | alysis by ADF&G | 12 |
| Table 3a. | High priority target populations identified during gap analysis for | |
| m | icrosatellite analysis by NOAA | 14 |
| Table 3b. | Secondary targets for microsatellite analysis by NOAA | 15 |
| Table 4. | Populations analyzed by ADF&G for 96 SNPs | 16 |
| | Populations analyzed at 13 microsatellite loci by NOAA | |
| | | |

List of Figures

| Figure 1. Locations of chum salmon populations for which SNP data exist or are | |
|---------------------------------------------------------------------------------|----|
| targets in this project (red), for which microsatellite data have been obtained | |
| by NOAA and UAF (light blue), and which are targets for microsatellite | |
| analysis in this project yellow) | 18 |

IV. INTRODUCTION:

This project addresses the following research question: Is it possible to improve resolution of mixed fishery analyses of chum salmon, particularly with respect to identifying contributors from Norton Sound, lower Yukon River, lower Kuskokwim River, and upstream northern Bristol Bay populations or areal aggregates of populations? Resolution ability depends on the extent of natural divergence among populations within areas and between areas as well as the quality of baseline available.

Between 1997 and 2002, dramatic declines in chum salmon returns to western Alaska drainages prompted 15 disaster declarations by the governor of Alaska and federal agencies. Although there is no consensus as to the primary cause of the declines, climate change has affected both marine and freshwater habitats in Alaska and has altered run strengths of salmon populations along much of the Pacific Coast of North America. In addition, chum salmon are caught each year from the Bering Sea, Aleutian Islands, and Gulf of Alaska in both directed and non-directed fisheries. While average total escapements for chum salmon in western Alaska are estimated to exceed five million, both the pollock trawl fishery and salmon gillnet fisheries can capture substantial numbers of salmon. The Alaska Department of Fish and Game (ADF&G) manages the directed salmon fisheries and NOAA Fisheries (NOAA)manages the pollock fishery, which catches both Chinook and chum salmon as bycatch.

Chum salmon are a high priority species whose management has significant sociological, allocation, international treaty, and conservation implications. Sociological and allocation issues arise because many intercepted salmon will return to western Alaska river systems and rural Alaskans depend on them for subsistence. In addition, returns have generally declined in the last two decades. Many salmon returning to the Yukon River ascend to Canadian spawning grounds and are, consequently, counted as Canadian under the U.S./Canada Pacific Salmon Treaty. Conservation concerns result because migratory salmon from as far away as the Pacific Northwest move through the Bering Sea and Aleutian Islands (BSAI) and Gulf of Alaska (GOA). Consequently, both NOAA and ADF&G are concerned about chum salmon interceptions and are actively studying the chum salmon intercepted in the Bering Sea and near the Aleutian Islands.

Presently available baselines cannot adequately delineate among coastal western Alaska chum salmon stocks including stocks in Norton Sound, lower Yukon and Kuskokwim Rivers, and Bristol Bay. The baseline being developed by for immediate use in the Western Alaska Salmon Stock Identification Project (WASSIP) will have broad-scale resolution for estimating stock composition in nearshore salmon fisheries and potentially in the salmon bycatch of the Bering Sea pollock fisheries. However, the WASSIP baseline will not have comprehensive representation of chum salmon spawning aggregates necessary for application within more finescale regions, including within individual drainages in western Alaska. Filling the gaps in the baseline through data enhancement of the populations represented and providing additional informative genetic markers will improve resolution. This is an important issue for ADF&G because more fine-scale analyses will be necessary to provide information on the effects of harvest on local populations in more restricted fisheries (e.g., chum salmon harvests in Norton Sound).

This project expands upon previous Bering Sea Fishermen's Association (BSFA) supported work that was conducted by UAF in collaboration with NOAA to develop a microsatellite baseline and incorporate new SNP markers developed by UAF (*Developing DNA Markers for the Analysis of Bering Sea Chum Salmon*, funded separately). In addition, NOAA and UAF have recently applied this microsatellite baseline to bycatch and Bering-Aleutian Salmon International Survey (BASIS) samples. Whereas that work was able to resolve chum salmon origins to major geographic regions, it was inadequate to provide refined estimates, particularly among coastal Alaska and lower Yukon and Kuskokwim Rivers. ADF&G also conducts analyses that require similar delineation. This project began extending a genetic baseline that includes the markers that both ADF&G and NOAA use for their mixed-stock analyses. An essential portion of the overall task was to evaluate the data and samples that are available and to identify and fill gaps in the baseline in terms of data for particular markers, deficient sample sizes, and underrepresented geographic areas. Also, development of additional SNP markers is essential to establish a baseline that has the maximum ability to resolve major geographically distinct aggregates of chum salmon populations.

V. OBJECTIVES:

Objective 1: Conduct a gap analysis to identify deficiencies in the genetic sample locations, sample sizes, and sample quality for Bering Sea/North Pacific chum salmon populations, including identification of the specific populations that will be used in a SNP discovery panel.

A gap analysis has been completed that evaluated the SNP data available from ADF&G and UAF, the microsatellite data available from DFO and NOAA, as well as DNA and tissue samples available at ADF&G, NOAA, and those brought to UAF in July 2011 by collaborator Dr. V. Brykov (Russian Academy of Sciences). Note that Dr. Brykov traveled to Juneau with pollock catcher boat support. In addition, samples from populations that will be surveyed by UAF to identify new, informative SNPs have been determined and made available to UAF.

Objective 2: Add SNP and microsatellite data for key populations not in the baseline or fill in missing data types (SNP or microsatellite) in order to strengthen the coast-wide baseline for chum salmon. This project will focus on 10-12 populations.

Both microsatellite (NOAA) and SNP (ADF&G) laboratory analyses have been completed for the subset of samples that were to be analyzed for the AYKSSI portion of the overall baseline development. Several potential new SNP loci were identified during this project and their development begun. Analysis of the other samples identified during the gap analysis will continue under the associated AKSSF project.

VI. METHODS:

Objective 1:

Data are available from several sources including Department of Fisheries and Oceans Canada (DFO) (http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm/datadonnees/index-eng.htm), ABL, UAF, and ADF&G. The Team met several times to discuss how baseline information could be combined and made available for public use (effort still underway) and to identify gaps in the baseline either in terms of sample size or in geographic coverage. An inventory of archived tissue and DNA samples at ADF&G, NOAA, and UAF was compiled. Some samples have previously been provided by Russian collaborator Dr. V. Brykov (Russian Academy of Sciences) and he recently provided additional samples that would expand sample sizes and increase coverage. In addition, some samples may be available to ADF&G from DFO through NPAFC exchanges. The objective for the Team was to evaluate the available samples and choose ones that would be most effective in expanding the baseline. The SNP and microsatellite baselines have different gaps, and the Team met several times to identify the most important gaps. Another task was to identify a suite of about 12 populations for use in SNP discovery efforts by UAF. The goal was to choose populations that would emphasize western Alaska (Norton Sound, lower Yukon and Kuskokwim Rivers, and upstream Bristol Bay) populations but also include populations that are from geographically distinct locations to provide context and to improve the resolution of other regions.

<u>Objective 2</u>: Microsatellites are short repeated DNA sequences of variable length that are distributed throughout the genome. SNPs are simple single nucleotide changes in the DNA sequence. No available chum salmon genetic baseline adequately delineates chum salmon stocks from coastal northwestern Alaska and lower Yukon and Kuskokwim River populations. NOAA uses microsatellites both alone and combined with SNPs for chum salmon MSA, and ADF&G uses SNP data. However, SNPs are rapidly becoming the molecular marker of choice because they are abundant throughout the genome, simple to score, and easily transferrable among laboratories. If the SNP baseline develops sufficiently in the future, NOAA may focus entirely on that form of data; for now, microsatellites provide an important source of variation and both markers can be applied to MSA analyses. The target numbers of fish proposed for microsatellite and SNP analysis have been met. The entire project will include data collected with support from the complementary project supported by AKSSF. When the entire project is complete, available baseline data will be combined in a publicly available format.

VII. RESULTS:

Personnel from ADF&G, NOAA, and UAF met on 20 October 2010 to initiate an inventory of available samples, their archive locations, their status (tissues or DNA isolates), and the approximate quantities available.

Subsequently, the Team met in Anchorage on 7-9 February 2011 to compile information about the data, samples, and gaps in those holdings. From the inventory, particular populations were selected for SNP and microsatellite baseline analysis and a set of samples for which there are substantial amounts of sample were selected for SNP discovery. This effort established the

existing data that would be used to guide expansion and extension of the SNP and microsatellite baseline in the complementary AKSSF project. N. Decovich (ADF&G) and C. Kondzela (NOAA) share curation of that information. We also chose populations that would be screened for SNP discovery by UAF. Those populations simultaneously sample the species-wide genetic variation and focus on western Alaskan populations (Table 1). While he was in Anchorage, M. Garvin (UAF) presented information on the method that he developed to empirically resolve the linkage phase of linked SNP loci. Personnel from US Fish and Wildlife Service (USFWS) and US Geological Survey (USGS) attended those sessions.

On 28 July 2011, the Team, including Dr. Brykov, met by teleconference to finalize the target populations for both SNP (Table 2) and microsatellite populations (Table 3 and Figure 1). These populations are the result of the gap analysis. Sufficient microsatellite data from Canadian populations exist for baseline applications for chum salmon caught in Alaskan waters. W. Templin will continue to pursue acquisition of Canadian samples that can be used to improve the SNP baseline.

One of the objectives of this AYKSSI project was to ensure that labs were adequately equipped to conduct the research proposed by these projects. To that end, UAF purchased two dual-head thermocyclers as replacements for defunct units, a thermal gradient thermal cycler, and a DNA scanner. All of those instruments are necessary for SNP development in the UAF lab. UAF also procured supplies and disposables necessary to conduct the work. Also, ADF&G purchased laboratory consumables to assay 1235 fish representing 13 collections of western Alaska chum salmon (Table 4) for a suite of 96 SNP loci. The SNP loci used were chosen as part of ADF&G's Western Alaska Salmon Stock Identification Program (WASSIP), and the data will be used to expand the current baseline. NOAA purchased a 384-well thermal cycler and a 384-block for a second thermal cycler and supplies with which they conducted microsatellite analyses at 13 microsatellite loci on 1038 fish from 12 populations (Table 5).

In anticipation of the SNP discovery effort, 100 DNA sequence targets have been chosen for SNP development by UAF. The first 40 of those have been screened. Each target is initially screened in a single DNA source, and if the amplification product is acceptable, it is then analyzed on pools of 5 individuals from 16 different populations. Out of the first 40 sequence targets, 13 primer sets have advanced to the TILLING process. The TILLING process has been completed for 9 of the targets, and all of the images collected for 7 of the targets. Four of those 7 show one or more potential SNP sites.

VIII. DISCUSSION:

This project was designed to identify gaps in the coastwide chum salmon baseline and identify populations that would be used throughout the SNP development process. The set of projects that include this AYK SSI project as well the current complementary and past AKSSF projects and support from the Bering Sea Aleutian Islands Pollock Intercooperative group (ICA) will improve and enhance the Bering Sea/North Pacific chum salmon baseline in order to provide greater resolution in MSA. An improved understanding of the natal origins of high seas intercepted salmon will help to quantify the problem and determine if some salmon stocks are preferentially

affected, thus assisting both NOAA and to better address western Alaska chum salmon management challenges.

The process initiated a joint effort by ADF&G, NOAA, and UAF, which has led to frequent intercourse and cooperation. Also, this project provided equipment and supplies necessary for the lab work entailed by the overall project. In addition, a subset of the target populations that were identified in the gap analysis have been analyzed for microsatellite or SNP variation and the search for new SNP loci has been initiated.

On or before completion of the complementary AKSSF project (44521), the resulting chum salmon genetic baseline data and molecular markers will be made available for public review and use either through peer-reviewed publications, agency reports, or web download. It is anticipated that results will be published in professional journals as warranted. Efforts will be made to coordinate results with the PacSNP consortium with the future goal of maintaining a single genetic baseline for chum salmon. Such a baseline may contain many markers of possibly many types (e.g., microsatellites, SNPs, mitochondrial, etc.) from which future researchers could select markers that best address their questions of interest.

IX. REFERENCES:

Resources for explanations of SNP methods

- Garvin, M.R., and A.J. Gharrett. 2007. DEco-TILLING: An inexpensive method for SNP discovery that reduces ascertainment bias. Mol. Ecol. Notes. 7:735-746.
- Garvin, M.R., and A.J. Gharrett. 2010. Application of SNP markers to chum salmon *Oncorhynchus keta*: Discovery, genotyping, and linkage phase resolution. J. Fish Biol. 77:2137–2162.
- Garvin, M.R., K. Saitoh, D.Y. Churikov, V.A. Brykov, and A.J. Gharrett. 2010. Single Nucleotide Polymorphisms in chum salmon (*Oncorhynchus keta*) mitochondrial DNA derived from restriction site haplotype information. Genome 53:501-507.
- Garvin, M.R., K. Saitoh, and A.J. Gharrett. 2010. Application of Single Nucleotide Polymorphisms to Non-model species: A Technical Review. Mol. Ecol. Res. 10:915-934.

Examples of applications

- (ADF&G) Alaska Department of Fish and Game. 2011. ADF&G Division of Commercial Fisheries, The Western Alaska Salmon Stock Identification Project (WASSIP). <u>http://www.adfg.alaska.gov/index.cfm?adfg=wassip.main</u>
- Beacham, T.D., B. Spilsted, K.D. Le, and M. Wetklo. 2008. Population structure and stock identification of chum salmon (*Oncorhynchus keta*) from British Columbia determined with microsatellite DNA variation. Can. J. Zool. 86:1002–1014.
- Beacham, T.D., S Sato, S. Urawa, K.D. Le, and M. Wetklo, 2008. Population structure and stock identification of chum salmon *Oncorhynchus keta* from Japan determined by microsatellite DNA variation. Fish. Sci. 74:983-994.
- Flannery B.G., T.D. Beacham, J.R. Candy, R.R. Holder, G.F. Maschmann, E.J. Kretschme, and J.K. Wenburg. 2010. Mixed-Stock Analysis of Yukon River chum salmon: application and validation in a complex fishery. N. Amer. J. Fish. Manage..30:1324-1338.

X. DELIVERABLES:

Coordination of efforts and collaboration among ADF&G, NOAA, and UAF (the Team) was one of the objectives of this project. To that end, we met formally on 20 October 2010, 7-9 March 2011, and 28 July 2011. However, substantial telephone and email correspondence took place to iron out small details, exchange information, and to coordinate efforts. In particular, C. Kondzela (NOAA), N. Decovich (ADF&G), and M. Garvin (UAF) communicated frequently. In addition during the 7-9 February meeting in Anchorage, M. Garvin presented his methods for resolving linkage phase in linked SNPs to both ADF&G and USFWS.

Periodic reports were a semiannual report in October (before most participants had received funding from their agencies), a completion report in April 2011, and this final product.

XI. PROJECT DATA:

This project was designed to identify gaps in the baseline and identify populations that would be used throughout the screening process. No specific reports or products were anticipated at the conclusion of this stage of the project. A primary objective of the overarching program, however, is to make data generally available. The time frame for that will be at the termination of the complementary AKSSF project.

XII. ACKNOWLEDGEMENTS:

This project is one facet of a larger project that includes support from AKSSF (project 44521 Shared Chum Baseline Development) and the Bering Sea Aleutian Islands Pollock Intercooperative group (ICA) which is made up of all the pollock cooperatives and includes Pollock Conservation Cooperative (catcher-processors), High Seas Catchers' Cooperative (Catcher vessels that deliver to catcher-processors), Mothership Fleet Cooperative (catcher vessels that deliver to motherships), Akutan Catcher Vessel Association (an inshore cooperative), Northern Victor Fleet Cooperative (an inshore cooperative), Peter Pan Fleet Cooperative (an inshore cooperative), Unalaska Cooperative (an inshore cooperative), UniSea Fleet Cooperative (an inshore cooperative), and Westward Fleet Cooperative (an inshore cooperative). Dr. V. Brykov provided Russian chum samples and will be a collaborator in subsequent baseline development and analyses. We appreciate the guidance and support of Dr. J. Spaeder.

XIII. PRESS RELEASE:

Scientists to track Bering Sea salmon with genetic markers.

Fisheries geneticists of the National Oceanic and Atmospheric Administration (NOAA), Alaska Department of Fish and Game, and University of Alaska Fairbanks have been collaborating to improve baselines of genetic data that can be used to determine the geographic origins of chum salmon caught on the high seas. In the past decade, chum salmon abundance declined in many western Alaska systems; and, although their numbers have increased recently, scientists are still seeking to understand the causes of their decline. Each year, immature chum salmon that are pasturing in the Bering Sea are intercepted in commercial fisheries that target other marine species. During the period of decline, there has also been a dramatic change in climate and oceanographic conditions. Fishery scientists know little about the routes that salmon from

different geographical regions take on the high seas or where salmon from particular streams are at a given time. To understand the influences of changes in the marine environment and to avoid incidental catches, we need to know the answers to questions such as: "Are fish from different rivers and different geographic areas found in different areas of the Bering Sea?"; "Do the locations of fish from a stream change seasonally?"; and "Do their locations change from year to year?". The genetic data that have been obtained will go a long way toward answering these questions.

| Region | Population | n |
|---------------------|---------------------------|-----|
| Russia | Hairusova River | 40 |
| | Ossora River | 40 |
| | Oklan River | 40 |
| | Kanchalan River | 40 |
| Norton Sound | Tubutulik River | 40 |
| | Unalakleet River | 40 |
| Cook Inet | Willow Creek | 40 |
| Yukon summer | Gisasa River | 40 |
| | Otter Creek (Anvik River) | 40 |
| Kuskokwim summer | Salmon River | 40 |
| | Goodnews North Fork | 40 |
| western Bristol Bay | Togiak River | 40 |
| | Stuyahok River (Nushagak) | 40 |
| Southeast Alaska | Harding River | 40 |
| N British Columbia | Stagoo Creek | 40 |
| Washington | Grovers Creek Hatchery | 40 |
| - | <u>·</u> | 640 |

Table 1. Ascertainment panel for SNP identification by UAF.

| Region | Population | п |
|------------------------|--------------------------------------------|-----|
| Kotzebue Sound | Kobuk River | 197 |
| Norton Sound | American River | 202 |
| | Eldorado River | 199 |
| | Fish River | 100 |
| | Fish River | 50 |
| | Fish River | 30 |
| | Kwiniuk River | 100 |
| | Niukluk River | 103 |
| | Nome River | 130 |
| | Pikmiktalik | 197 |
| | Pilgrim River | 200 |
| | Snake River | 200 |
| | Tubutulik River | 59 |
| Yukon - Lower (Alaska) | East Fork Andreafsky River | 100 |
| | Atchuelinguk River | 100 |
| | Beaver Creek - Anvik | 120 |
| | Swift River - Anvik | 100 |
| | Rodo River | 78 |
| | California Creek | 100 |
| | Gisasa River | 100 |
| | Gisasa River | 293 |
| | Tolstoi Creek | 100 |
| | Melozitna River - Melozi Hot Springs Creek | 146 |
| Yukon - Upper (Alaska) | Henshaw Creek | 268 |
| | Clear Creek | 100 |
| | Jim River | 57 |
| | Toklat River (Sushana River) | 100 |
| | Delta River | 100 |
| | Clearwater Creek - Tanana River | 80 |
| | Sheenjek River | 64 |
| | Fishing Branch | 100 |

Table 2. High priority target populations identified during gap analysis for SNPS.

Table 2 continued.

| Region | Population | n |
|-----------------------------|-------------------------------------------------|------|
| Kuskokwim-Goodnews-Kanektok | Kanektok River | 100 |
| | Kwethluk River | 100 |
| | Tuluksak River | 100 |
| | Holokuk River | 62 |
| | Kogrukluk River | 75 |
| | Kogrukluk River | 50 |
| | George River | 100 |
| | Talawitsuk River | 100 |
| | Takotna River - Set B (4th of July Creek) | 100 |
| | Big River | 100 |
| | South Fork Kuskokwim | 100 |
| Nushagak | Muklung River | 100 |
| Alagnak | Alagnak River | 84 |
| Bristol Bay | Pumice Creek, (King Salmon River, Ugashik Bay). | 100 |
| Chignik | Rudy's Creek | 97 |
| | Smokey Hollow | 172 |
| North Alaska Peninsula | Plenty Bear Creek | 50 |
| | Shoe Creek | 204 |
| | Joshua Green - N. Peninsula | 80 |
| | Blue Violet Creek - Meshik | 75 |
| | Russel Creek | 100 |
| Kodiak/Afognak Islands | American River | 100 |
| | Coxcomb Creek | 41 |
| | Dog Salmon Creek | 65 |
| | Olds River | 103 |
| Susitna | Spink Creek - Mouth | 23 |
| | Spink Creek - Mouth | 22 |
| Yentna | Lake Creek | 100 |
| | | 6376 |

| Region | Location | n |
|---------------------------------------------|-----------------------------------------|-----|
| Primorye | Narva | 51 |
| Sakhalin Island | Udarnitsa (hatchery) (SE) | 48 |
| | Kalininka (hatchery) (SW) | 90 |
| | Langry | 50 |
| Magadan | Kulkuty River (near Magadan) | 49 |
| West Kamchatka | Utka (SW) | 40 |
| | Palana(NW) | 50 |
| | Belogolovaya (NW) # | 50 |
| East Kamchatka | Kamchatka (CE) | 80 |
| Northeast Russia | Anadyr | 33 |
| Nunivak Island, Alaska | Mekoryuk River | 96 |
| South Bristol Bay, Alaska | Wiggly Creek (Cinder River-King Salmon) | 96 |
| North Alaska Peninsula and Aleutian Islands | Lawrence Valley Creek | 96 |
| | Peterson Lagoon | 96 |
| Southwest Alaska Peninsula | Foster Creek (Balboa Bay) | 96 |
| Southeast Alaska Peninsula | Wide Bay - Kialagvik River | 96 |
| Cook Inlet | Susitna River (Slough 11) | 96 |
| | Willow Creek | 96 |
| Kodiak/Afognak Island | Kitoi Bay (hatchery) | 96 |
| | Big Sukhoi | 96 |
| | Gull Cape Creek | 96 |
| Prince William Sound, Alaska | Wally Noerenberg (hatchery) (W) | 96 |
| Admiralty Island, Alaska | Green's Creek (NW) | 48 |
| Chichagof Island, Alaska | Spasski (N) | 96 |
| Baranof Island, Alaska | Hidden Fall (hatchery) (E) | 96 |
| | Medvejie (hatchery) (W) | 96 |
| west Prince of Wales Island, Alaska | Coco Harbor | 48 |
| | Port Real Marina | 48 |
| Southeast Alaska, northern mainland | Sanborn Creek | 96 |
| Southeast Alaska, southern mainland | Herman River | 14 |
| | | 223 |

Table 3a. High priority target populations identified during gap analysis for microsatellite analysis by NOAA.

| Region | Location | n |
|------------------------------------------------|------------------------------------|------|
| Kurile Islands | Reidovaya River | 82 |
| Sakhalin Island | Naiba (hatchery) (SE) | 96 |
| West Kamchatka | Kol (SW) | 48 |
| East Kamchatka | Kichiga (NE) | 50 |
| | Rusakova (NE) | 29 |
| Lower Yukon, summer run, Alaska | Kaltag | 48 |
| Kuskokwim-Goodnews-Kanektok | Holokuk River (mid) | 48 |
| | Kogrukluk (mid) | 48 |
| | Tatlawiksuk (mid) | 48 |
| | Tuluksak River (lower) | 96 |
| North and Central Bristol Bay, Alaska | Osviak River | 96 |
| | Alagnak River (Kvichak drainage) | 48 |
| South Bristol Bay, Alaska | Meshik River (Plenty Bear and Brai | 48 |
| Southeast Alaska Peninsula | Rudy's Creek | 96 |
| | Bear Bay Creek | 96 |
| Cook Inlet | Little Susitna | 96 |
| Kodiak/Afognak Island, Alaska | Kizhuyak | 48 |
| - | Russian River | 96 |
| Chichagof Island, Alaska | Kennell Creek (E) | 48 |
| Baranof Island, Alaska | Lover's Cove (SE) | 31 |
| | Saook (N) | 96 |
| east Prince of Wales Island, Alaska | Karta | 48 |
| | Lagoon Creek | 48 |
| Southeast Alaska, northern mainland | Well's Bridge | 48 |
| Southeast Alaska, southern mainland | King | 96 |
| | Wilson | 10 |
| North coast, British Columbia | Khutzeymateen River | 48 |
| Central Coast, British Columbia | Snootli River | 96 |
| Vancouver Island, west coast, British Columbia | Sooke | 48 |
| | Conuma | 96 |
| Fraser River, British Columbia | Alouette River | 96 |
| | - | 2026 |

Table 3b. Secondary targets for microsatellite analysis by NOAA.

| Table 4. Populations analyzed by ADF&G for 96 SNPs. |
|-----------------------------------------------------|
|-----------------------------------------------------|

| Region | Population | n |
|----------------|---------------------------|------|
| Kotxebue Sound | Inmachuk River | 95 |
| | Selby Slough | 95 |
| Norton Sound | Fish River | 95 |
| | Pikmiktalik River | 95 |
| | Snake River | 95 |
| Lower Yukon | Black River | 95 |
| | Kaltag River | 95 |
| | Nulato River | 95 |
| | Tozitna River | 95 |
| Kuskokwim | Kisaralik River - (Set F) | 95 |
| | Stony River - Early | 95 |
| | Necons River | 95 |
| Nunivak Island | Mekoryuk River - Set C | 95 |
| | | 1235 |

| Region | Location | n |
|-----------------------------|-------------------------|------|
| Kuskokwim-Goodnews-Kanektok | Aniak River | 95 |
| | Oskawalik 1994 | 58 |
| | Stony River early | 95 |
| | Stony River late | 56 |
| | Holokuk River | 42 |
| | Kogrukluk River | 59 |
| | Tatlawiksuk River | 57 |
| | Salmon River | 96 |
| | George River | 96 |
| | Takotna River | 96 |
| | Big River | 96 |
| | S. Fork Kuskokwim River | 96 |
| | Windy River | 96 |
| | - | 1038 |

Table 5. Populations analyzed at 13 microsatellite loci by NOAA.

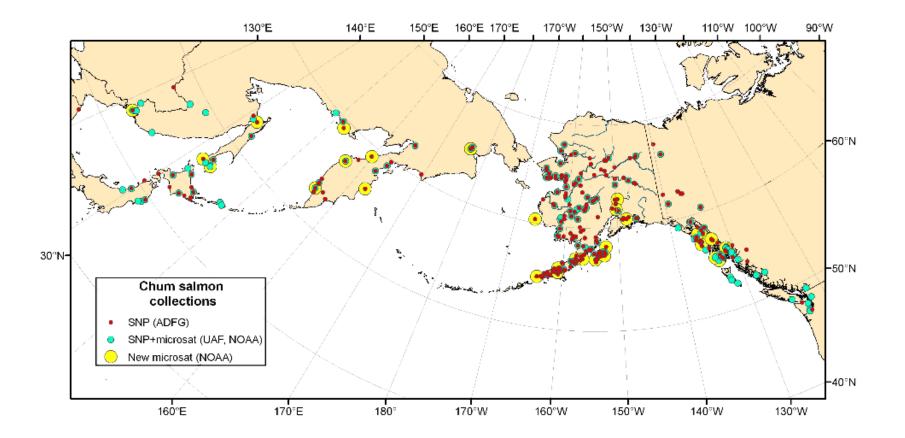


Figure 1. Locations of chum salmon populations for which SNP data exist or are targets in this project (red), for which microsatellite and SNP data have been obtained by NOAA and UAF (light blue), and which are targets for microsatellite analysis in this project (yellow).