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Improvements to the Range-Wide Genetic Baseline for Chum Salmon Through the Western Alaska Salmon Stock Identification Program (WASSIP) and PacSNP Collaboration

by

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Abstract

Chum salmon (*Oncorhynchus keta*) are important to the economy and culture of many communities in Western Alaska. The Western Alaska Salmon Stock Identification Program (WASSIP) was initiated as a means to determine stock of origin of chum and sockeye (*O. nerka*) salmon harvests in western Alaska fisheries. The foundation for this study was built through the North Pacific Anadromous Fish Commission (NPAFC) by the Working Group on Stock Identification Studies and through a United States/Japanese collaboration that coordinated and developed a DNA database for chum salmon based on SNPs “PacSNP”. WASSIP increased the baseline for chum salmon from 114 to 310 populations and from 60 to 95 SNPs selected from 188 SNPs. WASSIP also implemented novel quality control procedures for both laboratory and statistical analyses and developed statistical methods for handling linked loci. These data can serve as the springboard for collaborations among investigators from throughout the Pacific Rim to examine questions ranging from population structure, migratory behavior, stock-specific harvest, post-glacial colonization, and methods to select subsets of the data for specific research applications. Through PacSNP, the U.S. party is open to providing data and expertise in collaboration with scientists from other parties that will advance the use of these data for research on chum salmon.

Background on Western Alaska Salmon Stock Identification Program

Chum salmon (*Oncorhynchus keta*) are important to the economy and culture of many communities in Western Alaska. In addition to commercial fisheries throughout the area, chum salmon are extensively harvested in subsistence fisheries along the coast and in the Kuskokwim River, Yukon River, Norton Sound and Kotzebue Sound. Prior to the onset of spawning migrations, chum salmon from western Alaska and most other portions of the species range are distributed over vast areas of the Bering Sea and subarctic North Pacific Ocean (Quinn 2005; Meyers et al. 2007; Sato et al. 2009). The combination of life history, spawning migratory pathways and the complex geography of western Alaska creates potential for harvesting chum salmon populations originating from river systems throughout their range. While a majority of chum salmon harvest in western Alaska occurs in terminal and inriver fisheries, the harvest of nonlocal fish does occur.

As a means to determine stock of origin of chum and sockeye (*O. nerka*) salmon harvests in western Alaska, the Western Alaska Salmon Stock Identification Program (WASSIP) was initiated in 2006 as a collaborative effort among 11 stakeholder groups including the Alaska Department of Fish and Game (ADF&G) and 10 major regional fishery interests in the WASSIP study area. The program was designed to sample marine commercial and subsistence salmon fisheries in western Alaska from 2006 to 2009. The WASSIP study area included marine waters of ADF&G salmon management areas from Chignik (south Alaska Peninsula) to Kotzebue Sound (northwest Alaska; Figure 1), and genetic stock identification was to be used to estimate stock composition. Sockeye salmon captured in these fisheries are generally local

to western Alaska, narrowing the scope of the genetic baseline for this species to populations from western and southcentral Alaska. However, chum salmon from outside Alaska are known to occur in some marine fisheries along the Alaska Peninsula (Seeb et al. 2004), so it was necessary to have a comprehensive baseline of genetic data from representative populations across the North Pacific.

WASSIP was successfully completed and reported in 2012. Spanning more than eight years, WASSIP is the largest salmon genetics study ever attempted, analyzing more than 225,000 samples to determine stock-specific compositions, harvests, and harvest rates of sockeye and chum salmon in subsistence and commercial fisheries from Chignik to Kotzebue Sound. All reports can be accessed on the ADF&G website (<http://www.adfg.alaska.gov/index.cfm?adfg=wassip.reports>).

PacSNP Collaboration

Through the North Pacific Anadromous Fish Commission (NPAFC), genetic studies are coordinated by the Working Group on Stock Identification Studies with the goal to develop, standardize, and disseminate genetic databases among the parties. Beginning in the early 1990's large data sets were compiled using tissues sampled from spawning chum salmon in Washington, British Columbia, Alaska, Canada, Russia, Korea, and Japan. These data were collected by numerous agencies from around the Pacific Rim and have been used extensively by NPAFC in the Bering-Aleutian Salmon International Survey (BASIS) and other research to determine distribution and migration routes of salmon in the ocean. While early databases were based on allozyme markers (Kondzela et al. 2002; Seeb et al. 2004), subsequent data were developed using microsatellites (Beacham et al. 2009), mitochondrial DNA (mtDNA; Sato et al. 2004) and more recently single nucleotide polymorphisms (SNPs; Seeb et al. 2008, 2011a).

In 2008, United States and Japanese researchers met in Sapporo, Japan, at the National Salmon Resources Center for a two day meeting organized by the University of Washington and funded by the Gordon and Betty Moore Foundation, in order to discuss progress and development of a DNA database for chum salmon based on SNPs. SNPs are assayed using high-throughput technologies and are particularly appropriate for NPAFC applications because data can be easily transferred between laboratories and instrument platforms. The participants informally adopted the name PacSNP for the initiative which has since been expanded to include pink salmon (*O. gorbuscha*). At this meeting groundwork was laid for continued development of the baseline through SNP discovery and genotyping, designing joint projects and developing shared databases. An open invitation was and continues to be extended to all parties to participate in developing these open and shared databases.

Updated Baseline

Through collaborations made possible by the NPAFC and in coordination with colleagues in the PacSNP consortium (Seeb et al. 2008, Seeb et al. 2011), Alaska was able to prepare an initial baseline of genotypes from 60 SNPs measured in 114 populations from across the species range. However, while this baseline provided sufficient resolution for contemporary marine studies, it did not provide the resolution necessary for applications specific to western Alaska. Additional efforts were made to improve the resolution available with three objectives: 1) increase the number of populations included in the baseline, 2) discover and assay additional SNPs in these populations, and 3) refine the methods used to build the baseline. The first objective was met by increasing the number of populations from 114 to 310 (Table 1; Figure 2). While additional samples were added from across the range, most of the additional

populations were added to improve the coverage of western Alaska, the Alaska Peninsula, and south through the State of Washington. The second objective was met by increasing the number of SNPs from 60 to 188 (Seeb et al. 2011b; Petrou et al. 2013). A subset of 96 was chosen specifically for WASSIP from the full set of SNPs (DeCovich et al. 2012b). This subset was chosen in an attempt to gain the greatest resolution of western Alaska stocks while maintaining the representative value for marine studies in the North Pacific Ocean and the Bering Sea. The third objective was driven primarily by the need to handle the increased numbers of potentially linked loci (Dann et al. 2012), and as a byproduct of reanalyzing the baseline, novel quality control procedures for both laboratory and statistical analyses were implemented.

Invitation to Collaboration

The initial assessment of this baseline was reported in the context of WASSIP as an ADF&G Special Publication (DeCovich et al. 2012a); however, the scope of the analysis was limited to the specific questions applicable to that program. Population structure and resolution in mixed stock fisheries was only explored in-depth for chum salmon in western Alaska, leaving the remaining portions of the range grouped into large reporting regions. Analysis of the genetic structure of populations from the Alaska Peninsula and Kodiak Island has been published (Petrou et al. 2013, 2014), and populations in the eastern Pacific are currently being analyzed by members of the PACSNP collaboration.

These data can serve as the springboard for collaborations among investigators from throughout the Pacific Rim to examine questions ranging from population structure, migratory behavior, stock-specific harvest, post-glacial colonization, and methods to select subsets of the data for specific research applications. Through PacSNP, the U.S. party is open to providing data and expertise in collaboration with scientists from other parties that will advance the use of these data for research on chum salmon.

Literature Cited

- Beacham, T. D., J. R. Candy, K. D. Le, and M. Wetklo. 2009. Population structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim, determined from microsatellite analysis. *Fishery Bulletin* 107:244–260.
- Dann, T. H., C. Habicht, J. R. Jasper, E. K. C. Fox, H. A. Hoyt, H. L. Liller, E. S. Lardizabal, P. A. Kuriscak, Z. D. Grauvogel, and W. D. Templin. 2012. Sockeye salmon baseline for the Western Alaska Salmon Stock Identification Project. Alaska Department of Fish and Game, Special Publication No. 12-12, 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. 2012a. Chum salmon baseline for the Western Alaska Salmon Stock Identification Program. Alaska Department of Fish and Game, Special Publication No. 12-26, Anchorage.
- DeCovich, N., J. R. Jasper, C. Habicht, and W. D. Templin. 2012b. Western Alaska Salmon Stock Identification Program Technical Document 23: Chum salmon SNP selection results. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-25, Anchorage.
- Kondzela, C. M., P. A. Crane, S. Urawa, N. V. Varnavskaya, V. Efremov, X. Luan, W. D. Templin, K. Hayashizaki, R. L. Wilmot, and L. W. Seeb. 2002. Development of a comprehensive allozyme baseline for Pacific Rim chum salmon. NPAFC Doc. 629. Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, AK, USA
- Meyers, K. W., N. W. Klovach, O. F. Gritsenko, S. Urawa, and T. C. Royer. 2007. Stock-specific distributions of Asian and North American salmon in the open ocean, Interannual changes, and oceanographic conditions. *North Pacific Anadromous Fish Commission. Bulletin No. 4*:159–177.
- Petrou, E. L., L. Hauser, R. S. Waples, J. E. Seeb, W. D. Templin, D. Gomez-Uchida and L. W. Seeb. 2013. Secondary contact and changes in coastal habitat availability influence the nonequilibrium population structure of a salmonid (*Oncorhynchus keta*). *Molecular Ecology* 22(23): 5848-5860.
- 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.
- Quinn, T. P. 2005. The behavior and ecology of Pacific salmon and trout. University of Washington Press, Seattle.
- Sato, S., S. Moriya, T. Azumaya, H. Nagoya, S. Abe, and S. Urawa. 2009. Stock distribution patterns of chum salmon in the Bering Sea and North Pacific Ocean during the summer and fall of 2002-2004. *North Pacific Anadromous Fish Commission Bulletin No. 5*:29–37.

- Sato, S., H. Kojima, J. Ando, H. Ando, R. L. Wilmot, L. W. Seeb, V. Efremov, L. LeClair, W. Buchholz, D-H. Jin, S. Urawa, M. Kaeriyama, and S. Abe. 2004. Genetic population structure of chum salmon in the Pacific Rim inferred from mitochondrial DNA sequence variation. *Environmental Biology of Fishes*, 69:37-50.
- Seeb, L. W., P. A. Crane, C. M. Kondzela, R. L. Wilmot, S. Urawa, N. V. Varnavskaya, and J. E. Seeb. 2004. Migration of Pacific Rim chum salmon on the high seas: Insights from genetic data. *Environmental Biology of Fishes* 69:21–36.
- Seeb, J. E., S. Abe., S. Sato, W. D. Templin, S. Urawa, K. I. Warheit, and L. W. Seeb. 2008. PACSNP: Progress on the development and standardization of single nucleotide polymorphisms (SNPs) baseline for genetic stock identification of chum salmon. NPAFC Doc. 1138. 10 pp.
- Seeb, J. E., C. E. Pascal, E. D. Grau, L. W. Seeb, W. D. Templin, T. Harkins, and S. B. Roberts. 2011b. Transcriptome sequencing and high-resolution melt analysis advance single nucleotide polymorphism discovery in duplicated salmonids. *Molecular Ecology Resources* 11(2):335-348.
- Seeb, L. W., W. D. Templin, S. Sato, S. Abe, K. Warheit, J. Y. Park, and J. E. Seeb. 2011a. Single nucleotide polymorphisms across a species' range: implications for conservation studies of Pacific salmon. *Molecular Ecology Resources* 11:195-217.

Table 1. Number of chum salmon populations analyzed for each area within regions of the Pacific Rim for the Western Alaska Salmon Stock Identification Program (WASSIP).

WASSIP Reporting Group	Nation	Region	Number of Populations	Population Numbers	Number of Individuals
Asia	Korea	Korea	1	1	192
Asia	Japan	Japan	15	2-16	1232
Asia	Russia	Russia	20	17-36	1613
Kotzebue Sound	U.S.	Kotzebue Sound	8	37-44	764
CWAK	U.S.	Norton Sound	14	45-58	1398
CWAK	U.S.	Yukon Coastal	16	59-74	1680
CWAK	U.S.	Kuskokwim	20	75-94	2061
CWAK	U.S.	Bristol Bay	14	95-108	1421
Upper Yukon	U.S.	Upper Yukon River	24	109-132	2328
Northern District	U.S.	North Alaska Peninsula	11	133-143	1349
Northwest District	U.S.	Northwest Alaska Peninsula	7	144-150	1002
South Peninsula	U.S.	South Alaska Peninsula	14	151-164	1910
Chignik/Kodiak	U.S.	Chignik Area and Kodiak Island	35	165-199	4375
East of Kodiak	U.S.	Cook Inlet	9	200-208	707
East of Kodiak	U.S.	Prince William Sound	7	209-215	2751
East of Kodiak	U.S.	Southeast Alaska	38	216-254	3915
East of Kodiak	Canada	British Columbia	27	255-280	2837
East of Kodiak	U.S.	Washington	30	281-310	2645
			310		34180

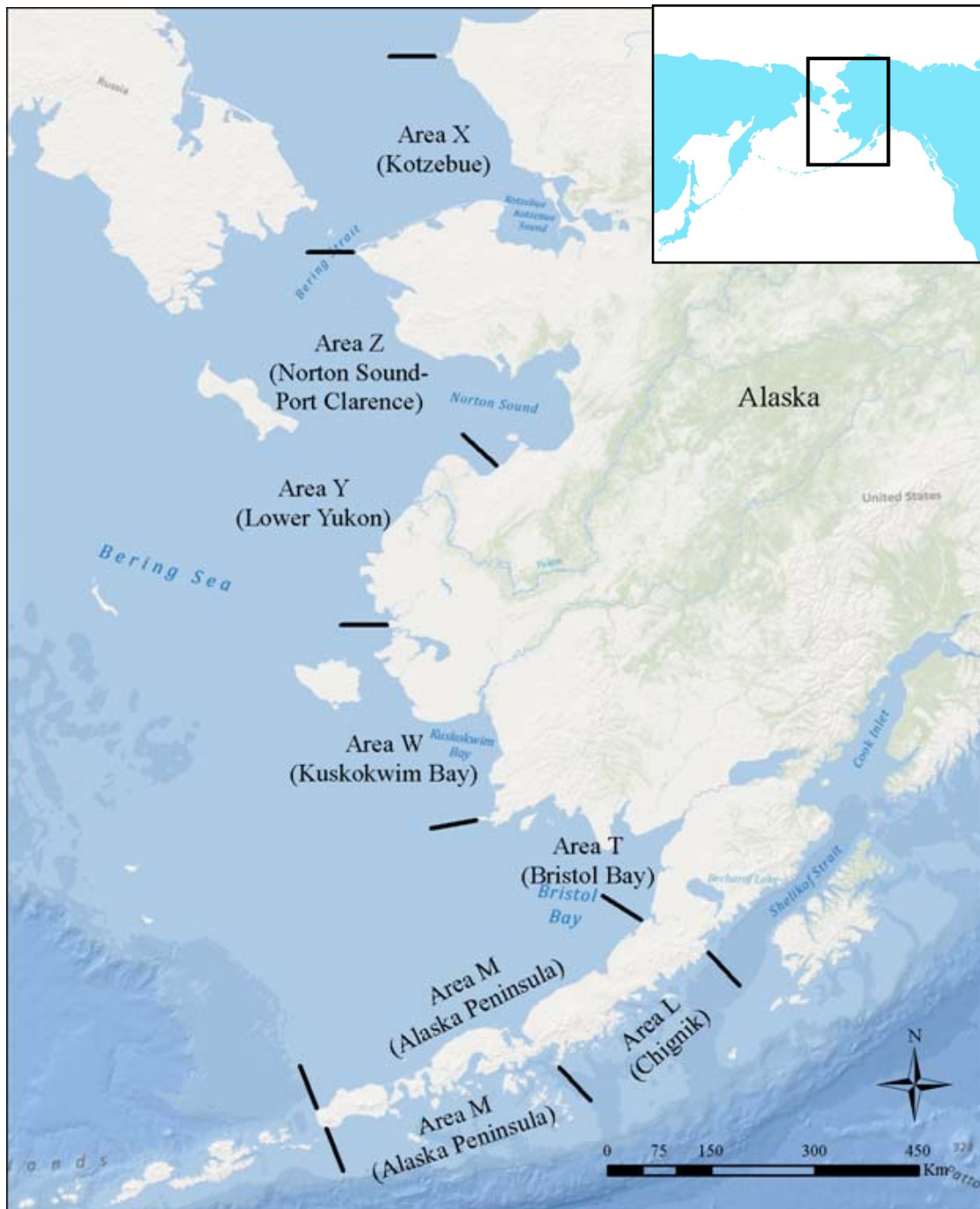


Figure 1.—Western Alaska Stock Identification Program (WASSIP) study area including Alaska Department of Fish and Game salmon management areas where sockeye and chum salmon were sampled to estimate stock-specific harvests and harvest rates.

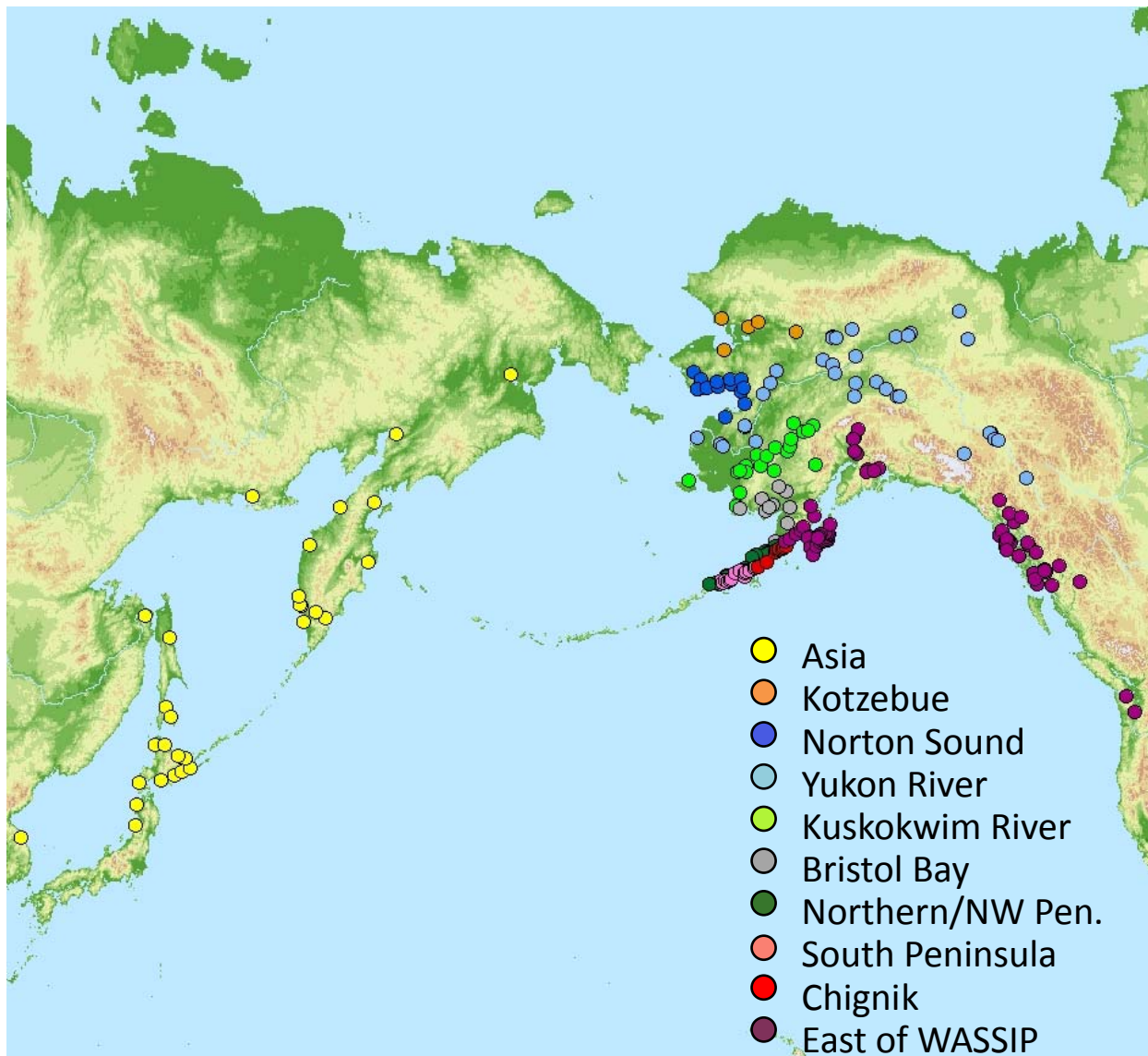


Figure 2.—The location and regional reporting group affiliation of 310 populations of chum salmon included in final baseline analyses for WASSIP. Populations are colored by membership in the reporting regions used for WASSIP (Table 1).