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## Western Alaska Salmon Stock Identification Program (WASSIP): Cooperation Among Stakeholders to Improve Understanding of Alaska Fisheries



Map of Alaska with inshore and marine waters included in the WASSIP study highlighted in blue and ADFG salmon management areas.

The Western Alaska Salmon Stock Identification Program (WASSIP) is a unique collaboration among stakeholders and scientists to address long-standing questions about harvest patterns of chum and sockeye salmon in western Alaska fisheries. Born from frustration with widely divergent regulatory decisions based on limited and controversial data, WASSIP created a framework for representatives from affected stakeholders in western Alaska to collectively design a scientific study to address critical information gaps in a highly contentious commercial and subsistence fishing environment.

While engaged in the largest salmon genetics study ever conducted (collecting over 325,000 samples), we established a process where representatives of major regional fishery interests accepted responsibility for the design of scientific investigations that would inform regulatory decisions they must live with. Spanning more than eight years, WASSIP analyzed more than 225,000 tissues to determine stock-specific compositions, harvests, and harvest rates of sockeye and chum salmon in subsistence and commercial fisheries across a vast region of By Erica Chenoweth, Eric Volk, and Bill Templin Alaska Department of Fish and Game (ADFG)

> coastal western Alaska, including statemanaged marine and inshore waters on both sides of the Alaska Peninsula, Bristol Bay, the lower portions of the Yukon and Kuskokwim River drainages, Norton Sound, up around the east side of the Bering Strait to Point Hope, and Kotzebue Sound.

WASSIP's origins date back to the 1990s, when stakeholders and fishery regulators became acutely aware of the need for improved science-based information to better understand catch composition of diverse fisheries in western Alaska, so that informed decisions on allocations could be made.



Naknek gillnet sockeye salmon fishery in Bristol Bay. Photo credit: © ADFG used with permission

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Picking salmon from the net on the Alaska Peninsula. Photo credit: Gene Conservation Laboratory, Lisa Fox, ADFG

Of particular concern to chum fishermen in the Arctic, Yukon, and Kuskokwim regions and to sockeye fishermen in Bristol Bay were catches of chum and sockeye salmon in regulatory Area M, on the North and South Alaska Peninsula. It was widely assumed that fisheries in Area M were intercepting excessive levels of salmon bound for distant regions. Previous tagging and genetic studies for sockeye and chum salmon provided some useful information, but study limitations and a lack of comprehensive sampling hindered their utility.

Following the Area M Alaska Board of Fisheries meeting in 2004, tensions boiled over leading to pointed discussions among ADFG leadership and stakeholders to envision the kind of study that would provide the necessary fishery-specific information to understand stock-specific impacts from the many fisheries in western Alaska. Recent advances in genetic stock identification (GSI) provided a practical method for wide-scale salmon stock discrimination and the means to effectively address these questions.

In 2004, the ADFG and affected stakeholders began drafting proposals to rally financial resources and create a study design. In 2005, the federal government pledged financial support if a unified study design was agreed upon by all stakeholders. For more than a year, the fledgling group embarked on intense discussions to gain consensus on a plan. In 2006, a second advisory panel meeting was held, where elements of a draft Memorandum of Understanding (MOU) were discussed at length, and eighteen months later, an acceptable MOU was signed and adopted.





Subsistence users around Alaska. Photo credit: © ADFG used with permission



Advisory Panel representatives and ADFG staff at meeting in Anchorage, Alaska, fall 2012 (left) WASSIP results and presentation methods are discussed (right) Photo credits: Gene Conservation Laboratory, ADFG.

The challenge of reaching these agreements among many stakeholders with widely divergent interests should not be minimized. Signatories to WASSIP represent major fisheries interests and stakeholder groups, including local governments, corporations, and fishermen associations. The 10 signatory groups other than ADFG were Bristol Bay Native Association, Bering Sea Fishermen's Association, Yukon River Drainage Fisheries Association, Lake and Peninsula Borough, Association of Village Council Presidents, Kawerak Incorporated, Tanana Chiefs Conference, Aleut Corporation, Aleutians East Borough, and Concerned Area M Fishermen. WASSIP began with federal funding, which provided for just a single year of sampling in 2006.

The hard-won WASSIP MOU forms the foundation and framework of the program. It established the tripartite structure for WASSIP consisting of the (1) Advisory Panel (11 signatories, including Alaska Department of Fish and Game), (2) ADFG (department staff in genetics, stock assessment, and biometrics), and



Spring 2012 WASSIP Advisory Panel meeting. Photo credit: Gene Conservation Laboratory, ADFG

(3) an expert technical committee.

Advisory Panel members reviewed and approved elements of the study plan and, in addition, played a direct and tangible role in the development of specific technical and programmatic components. ADFG technical staff was responsible for all analyses and reporting.

The technical committee was composed of four internationally recognized scientists in the fields of genetics, population dynamics, biometrics, and salmon life history and migration. These were Drs. Milo Adkison from the University of Alaska, Robin Waples from NOAA Fisheries, and Tom Quinn and Bruce Weir from the University of Washington. They provided an independent source of critical technical insight into all methods and analyses that are the foundation of WASSIP data.

It was further stipulated that samples would be analyzed as a complete set; no analyses would begin until three years of samples had been collected and approved for both species; and no reporting of results would occur until all analyses for both species were complete. All project decisions were made by consensus; all meetings were open to the public; and all information was publically available.

An important expectation for WASSIP stakeholders was increasing public trust through an interactive process and ensuring that results were disseminated in an open and understandable way. In addition to public meetings, the primary mechanism for disseminating information was the <u>WASSIP website</u>, where agendas, meeting minutes, and documents (including final reports, data files, posters, and maps) were posted and remain accessible today. A highlight of the website is the availability of technical documents, which trace the development of methods and techniques between ADFG, the Advisory Panel, and the expert technical committee, both in their original white paper form and in a more complete and readily citable report form.



Pelvic fin held out to show the axillary process on ocean bright salmon. The tissue is non-lethally sampled for genetic analysis. Photo credit: © ADFG used with permission



Dockside genetics sampling. Photo credit: © ADFG used with permission

From 2007 to 2009, WASSIP was fully funded by the State of Alaska and continued comprehensive sampling for both species. Agreement was reached on various technical components of the study, such as selection and development of genetic markers to increase stock resolution, methods to build the genetic baselines (the spawning stocks sampled to characterize genetic stock structure), and the best way to report results. For example, while Asian stocks of chum salmon are harvested in some western Alaska fisheries and Asian populations were included in the genetic baseline, the main concern of WASSIP was to describe the harvest of local western Alaska stocks. Therefore all Asian populations were reported as a single stock. Likewise, all North American populations from east of Kodiak Island were reported as a single stock. Further resolution is possible, but the decision was made to gain the greatest precision and accuracy for stocks important to WASSIP. For sockeye salmon, the scope of the baseline was even more specific and included only one group outside of the WASSIP area, described simply as "East of WASSIP".

Another early and important decision was to use single nucleotide polymorphisms (SNPs) as the marker type for the project due to the potential for high throughput analysis. ADFG was able to draw on an archive of tissues, DNA, and genetic markers available from throughout the ranges of both species made possible by collaborative research among U.S. scientists and scientists from Korea, Japan, Russia, and Canada. As an example, the collaboration made possible through PacSNP allowed for the development of the initial range-wide SNP baseline for chum salmon (See Seeb et al. 2008, Templin et al. 2012, Templin et al. 2014, and Seeb et al. 2011). The main goal of WASSIP was to better understand the impact of all western Alaska fisheries on each of the two species and stocks of interest. In order to meet this overarching goal, genetic baselines were expanded, commercial and subsistence fisheries were sampled over several years to characterize temporal and spatial variability in stock contributions, and methods were explored and refined to maximize our capacity for stock discrimination in these fisheries. Meeting these lofty goals required an unprecedented level of effort on the part of all WASSIP



Gene Conservation Laboratory members often had to utilize helicopter transportation for baseline sampling. Photo credit: © ADFG used with permission



Dockside genetics sampling (upper left), sampling chum salmon (upper right), collecting fishery samples into a deep-well plate (lower left), and collecting baseline samples into a bulk sample bottle (lower right). Photo credit: Gene Conservation Laboratory, ADFG

## participants.

Complete WASSIP results are contained in nine reports. The foundation for the study is presented in the first five reports documenting fishery sampling, establishing genetic baselines for each species, and estimating stock-specific escapements for each species. Results of mixed-stock fishery analyses are contained in two reports for each species: one documenting estimated stock compositions from genetic analyses and one providing estimates of stock-specific harvest numbers and harvest rates for chum and sockeye salmon in WASSIP fisheries. The last two reports for each species are closely connected. The stock composition of fishery catches shows the percentage of harvest represented by various stocks in WASSIP fisheries. These stock percentages were applied to the number of fish harvested in the fisheries to determine stock-specific harvest numbers. Stock-specific harvest numbers for each WASSIP fishery were divided by the total run for each stock to determine harvest rates. It was essential that stock composition, harvest, and harvest rate results for each species be considered together to gain a complete understanding and full context of study results. All results are accessible on the WASSIP website (see http://www. adfg.alaska.gov/index.cfm?adfg=wassip.reports)



Lab staff working on extractions and genotyping. Photo credits: Gene Conservation Laboratory, ADFG



Sockeye salmon genetic baseline populations (39,205 sockeye salmon, 294 populations, 96 SNPs) and sockeye salmon genetic baseline structure. Genetic baselines are used to estimate the contribution of each stock to WASSIP catches.

While results from the study cannot address all questions surrounding fishery impacts on chum and sockeye salmon stocks across this vast geography, WASSIP provided opportunity for representatives of major regional fishery interests to collaborate with technical experts on design of scientific studies to inform regulatory decision making.

The results of this large and comprehensive effort will serve as a springboard for continued collaborative investigations on these species both within Alaska and throughout the Pacific Rim, thereby increasing our knowledge of population structure, migratory behavior,



Chum salmon genetic baseline populations (32,817 chum salmon, 310 populations, 96 SNPs) and chum salmon genetic baseline structure. Genetic baselines are used to estimate the contribution of each stock to WASSIP catches.

## stock-specific harvests, and post-glacial colonization. *References*

Templin W.D., C. Habicht, L.W. Seeb, J. E. Seeb, and E.C. Volk. 2014. Improvements to the range-wide genetic baseline for chum salmon through the Western Alaska Salmon Stock Identification Program (WASSIP) and PacSNP collaboration. NPAFC Doc. 1533. 8 pp. Alaska Department of Fish and Game. (Available at http://www.npafc.org.)

Templin, W.D., C. Habicht, L.W. Seeb, S. Sator, S. Abe, K. Warheit, J.Y. Park, J.E. Seeb. 2012. <u>Improved genetic</u> <u>stock identification of chum salmon through the PacSNP</u> <u>collaboration</u>. NPAFC Technical Report No. 8:49.

