United States Bibliography in 2011-2012 for NPAFC Science Plan

by

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ABSTRACT

This bibliography contains original papers and documents published in 2011-2012 by United States scientists and their collaborators that address research priorities in the 2011 – 2015 NPAFC Science Plan.

BACKGROUND

During 2010, the Science Sub-Committee (SSC) of the North Pacific Anadromous Fish Commission (NPAFC) developed a new five-year Science Plan (2011-2015) (Anonymous 2010). The SSC identified an overarching research theme "Forecast of Pacific Salmon Production in the Ocean Ecosystems under Changing Climate" and five research components: 1) Migration and survival mechanisms of juvenile salmon in the ocean ecosystems; 2) Climate impacts on Pacific salmon production in the Bering Sea (BASIS) and adjacent waters; 3) Winter survival of Pacific salmon in the North Pacific Ocean; 4) Biological monitoring of key salmon populations; and 5) Development and application of stock identification methods and models for management of Pacific salmon.

The bibliography contains original papers and documents published during 2011-2102 by United States scientists and collaborators that address NPAFC research priorities. The bibliography also serves as a tool to review research efforts by the US during NPAFC annual meetings. The bibliography includes titles, authors, and abstracts for all articles.

Anonymous. 2010. North Pacific Anadromous Fish Commission Science Plan 2011-2015. NPAFC Doc. 1255. 34 pp. Committee on Scientific Research and Statistics (CSRS), North Pacific Anadromous Fish Commission, Suite 502, 889 West Pender Street, Vancouver, B. C., V6C 3B2 Canada. (Available at www.npafc.org).

BIBLIOGRAPHY
Component 1: Migration and Survival Mechanisms of Juvenile Salmon in the Ocean Ecosystems

Celewycz, A. G. and J. H. Moss. 2011. High seas salmonid coded-wire tag recovery data, 2011. NPAFC Doc. 1341. 24 pp. (Available at http://www.npafc.org).

Information on high seas recoveries of salmonids (*Oncorhynchus* spp.) tagged with codedwire tags (CWTs) has been reported annually to the International North Pacific Fisheries Commission (1981-1992) and to the North Pacific Anadromous Fish Commission (NPAFC, 1993-present). Data from these CWT recoveries are also reported into the Regional Mark Information System Database maintained by the Regional Mark Processing Center (RMPC, http://www.rmpc.org) of the Pacific States Marine Fisheries Commission (PSMFC). This document lists recovery data for 61 CWT salmonids that will be reported to PSMFC/RMPC for the first time. These 61 CWTs were recovered from the 2008, 2009, and 2010 U.S. groundfish trawl fishery in the Gulf of Alaska (41 Chinook salmon, *Oncorhynchus tshawytscha),* the 2009 and 2010 U.S. groundfish trawl fishery in the eastern Bering Sea- Aleutian Islands (13 Chinook salmon and 1 coho salmon *Oncorhynchus kisutch*), and from 2010 US research vessel operations in the Gulf of Alaska (3 Chinook salmon and 3 coho salmon,*)*. Recovery information is also presented for 9 new recoveries of Chinook salmon tagged with agency-only wire tags (not CWTs)

Echave, K., M. Eagleton, E. Farley, and J. Orsi. 2012. A refined description of EFH for Pacific salmon within the U.S. EEZ in Alaska. NOAA Tech. Memo NMFS-AFSC-236, 104 pgs. Available at http://www.afsc.noaa.gov/techmemos/nmfs-afsc-236.htm).

In 2005 the North Pacific Fishery Management Council used an improved analytical approach to identify essential fish habitat (EFH) for most species of groundfish and crab, however, due to the lack of available information, the entire U.S. Exclusive Economic Zone (EEZ; 200-nautical miles (nmi) from shore) for each of the five species of Pacific salmon was left intact as EFH. In order to better define EFH within the U.S. EEZ for Pacific salmon found in Alaska (Oncorhynchus spp.), we acquired catch, maturity, salinity, temperature, and station depth data for the Bering Sea and Gulf of Alaska from multiple data sources. We analyzed the influence of sea surface salinity (SSS), sea surface temperature (SST), and bottom depth on the distribution of Pacific salmon. Very few significant associations between catch and the three tested environmental variables were found to exist, indicating little to no relationship between species distribution and the three measures of habitat condition; however, many patterns were still evident. By calculating and mapping the coincidence of the 95% range of each environmental variable (SSS, SST, depth) for each of the five species at each maturity stage, our updated EFH descriptions reduce the area of designated EFH for Pacific salmon by 71.3% on average. Juvenile salmon EFH generally consists of the water over the continental shelf within the Bering Sea extending north to the Chukchi Sea, and over the continental shelf throughout the Gulf of Alaska and within the inside waters of the Alexander Archipelago. Immature and mature Pacific salmon EFH includes nearshore and oceanic waters, often extending well beyond the shelf break, with

fewer areas within the inside waters of the Alexander Archipelago and Prince William Sound. This has been the first time that salmon data sets from multiple surveys, agencies, and years have been accumulated and formatted for Pacific salmon distribution and habitat analysis. This study summarizes catches > 420,000 Pacific salmon sampled during 5,280 surface trawl and purse seine events in the Alaska EEZ from 1964 to 2009. Distribution was plotted for each salmon species and life history within the Alaska EEZ. To better describe salmon EFH, additional detailed habitat preference analysis was performed with available biophysical data from approximately 84% of the events. Not only will the database resulting from this project be of invaluable use for future research, but a much greater understanding of Pacific salmon distribution in the marine environment has been gained.

Larson, W.A., Utter F.M., Myers K.W, Templin W.D., Seeb J.E., Bugaev A.V., Seeb L.W. (2012) Single-nucleotide polymorphisms reveal distribution and migration patterns of Chinook salmon in the Bering Sea and North Pacific Ocean. *Canadian Journal of Fisheries and Aquatic Science* (accepted pending revision).

We genotyped Chinook salmon captured on the high seas for 43 single-nucleotide polymorphisms (SNPs) to investigate seasonal distribution and migration patterns in the Bering Sea and North Pacific Ocean. We analyzed 3 573 immature fish from 22 spatiotemporal strata; composition analyses were performed using genotype data from spawning stocks spanning the species range. Substantial variation in stock composition existed among spatial and seasonal strata. We constructed conceptual models of seasonal migration patterns based upon these data along with data available from previous tag, scale, and parasite studies. Our results indicate that stocks from western Alaska and Yukon River overwinter on the Alaskan continental shelf then travel to the middle and western Bering Sea during spring-fall. Stocks from California to Southeast Alaska are distributed in Gulf of Alaska year-round but a significant portion of this group migrates northward to the eastern Bering Sea during spring-fall. Proportions of Russian stocks increase when moving east to west in both the Bering Sea and North Pacific Ocean. These data can be incorporated into predictive models to better understand the impacts of fisheries and climate change on this valuable resource.

Seeb L.W., Seeb J.E., Habicht C., Farley E.V., Utter F.M. (2011) Single-nucleotide polymorphic genotypes reveal patterns of early juvenile migration of sockeye salmon in the Eastern Bering Sea. *Trans Am Fish Soc* **140**, 734-748.

We estimate patterns of nearshore migration in the eastern Bering Sea for out-migrating Bristol Bay sockeye salmon Oncorhynchus nerka in their first year at sea. Over 3,000 juveniles were collected during the late summer of 2005?2007 as part of the Bering?Aleutian Salmon International Survey and tested with a regional genetic baseline of 45 single-nucleotide polymorphisms. Population-specific and westward migrations from natal rivers were evident. Populations from Wood River and northwestward predominated in the northern latitudes of Bristol Bay and the eastern Bering Sea and populations from the Egegik River and southwestward in the southern latitudes, while the populations spawning at the head of Bristol Bay had the highest proportions in the middle latitudes. These patterns were stable across years, apparently unaffected by marine productivity and temperature. This continuum of marine

migratory patterns most likely reflects stable and population-specific adaptations to buffer the distribution of dynamically shifting marine resources. As monitoring continues, these juvenile surveys will accumulate information to refine predictions of the magnitude of adult returns to their respective rivers of origin and thereby assist in the management of this valuable resource.

Seeb L.W., Templin W.D., Sato S. *et al.* (2011) Single nucleotide polymorphisms across a species' range: implications for conservation studies of Pacific salmon. *Molecular Ecology Resources* **11**, 195-217.

Studies of the oceanic and near-shore distributions of Pacific salmon, whose migrations typically span thousands of kilometres, have become increasingly valuable in the presence of climate change, increasing hatchery production and potentially high rates of bycatch in offshore fisheries. Genetics data offer considerable insights into both the migratory routes as well as the evolutionary histories of the species. However, these types of studies require extensive data sets from spawning populations originating from across the species' range. Single nucleotide polymorphisms (SNPs) have been particularly amenable for multinational applications because they are easily shared, require little interlaboratory standardization and can be assayed through increasingly efficient technologies. Here, we discuss the development of a data set for 114 populations of chum salmon through a collaboration among North American and Asian researchers, termed PacSNP. PacSNP is focused on developing the database and applying it to problems of international interest. A data set spanning the entire range of species provides a unique opportunity to examine patterns of variability, and we review issues associated with SNP development. We found evidence of ascertainment bias within the data set, variable linkage relationships between SNPs associated with ancestral groupings and outlier loci with alleles associated with latitude.

Templin W.D., Seeb J.E., Jasper J.R., Barclay A.W., Seeb L.W. (2011) Genetic differentiation of Alaska Chinook salmon: the missing link for migratory studies. *Molecular Ecology Resources* **11**, 226-246.

Most information about Chinook salmon genetic diversity and life history originates from studies from the West Coast USA, western Canada and southeast Alaska; less is known about Chinook salmon from western and southcentral Alaska drainages. Populations in this large area are genetically distinct from populations to the south and represent an evolutionary legacy of unique genetic, phenotypic and life history diversity. More genetic information is necessary to advance mixed stock analysis applications for studies involving these populations. We assembled a comprehensive, open-access baseline of 45 single nucleotide polymorphisms (SNPs) from 172 populations ranging from Russia to California. We compare SNP data from representative populations throughout the range with particular emphasis on western and southcentral Alaska. We grouped populations into major lineages based upon genetic and geographic characteristics evaluated the resolution for identifying the composition of admixtures and performed mixed stock analysis on Chinook salmon caught incidentally in the walleye pollock fishery in the Bering Sea. SNP data reveal complex genetic structure within Alaska and can be used in applications to address not only regional issues, but also migration pathways, bycatch studies on the high seas, and potential changes in the range of the species in response to climate change.

Component 2: Climate Impacts of Pacific Salmon Production in the Bering Sea (BASIS) and Adjacent Waters

Farley, E.V. Jr. 2011. United States cruise plan for BASIS on the R/V *OSCAR DYSON*, August - September, 2011. NPAFC Doc. 1313. 2 pp. Auke Bay Laboratories, Ted Stevens Marine Research Institute, NMFS, NOAA, 17109 Pt. Lena Loop Road, Juneau, AK 99801-8626, U.S.A.

Scientists from the National Marine Fisheries Service (NMFS), Marine Ecosystem and Stock Assessment (MESA) Program, BASIS group will conduct a survey during Fall 2011 within the southeastern Bering Sea to provide key ecological data on the pelagic ecosystem. Primary objectives of the survey will be to: 1) collect biological information on ecologically important fish species and to 2) describe the physical and biological oceanographic conditions of the southeastern Bering Sea waters.

Moss, J.H. 2011. United States Cruise Plan for the Gulf of Alaska Project on the F/V NORTHWEST EXPLORER, July - October, 2011. NPAFC Doc. 1314. 3 pp. Auke Bay Laboratories, Ted Stevens Marine Research Institute, NMFS, NOAA, 17109 Pt. Lena Loop Road, Juneau, AK 99801-8626, U.S.A.

Scientists from the National Marine Fisheries Service (NMFS), Pacific Marine Enviornmental Laboratory, and the University of Alaska will conduct a survey during summer and Fall 2011 within the southestern and central Gulf of Alaska (GOA) to provide key ecological data on the pelagic ecosystem, examine oceanographic transport mechanisms, lower trophic level production, and age-0 marine fish and juvenile salmon distribution and condition. Primary objectives of the survey will be to: 1) collect biological information on ecologically important fish species and 2) describe the physical and biological oceanographic conditions of the GOA.

Murphy, J. M. 2011. United States Pelgic Trawl Survey on the Northern Bering Sea Shelf, August - October, 2011. NPAFC Doc.1316 4 pp. Auke Bay Laboratories, Alaska Fisheries Science Center, NOAA Fisheries, 17109 Pt. Lena Loop Road, Juneau, AK 99801-8626, U.S.A.

The survey will collect information on pelagic fish and oceanographic conditions in the coastal region of the northern Bering Sea shelf aboard the *F/V Bristol Explorer,* a chartered fishing vessel. The survey will begin 28 August in Nome, Alaska and end 22 September 2011 in Dutch Harbor, Alaska, for a total of 25 charter days.

Orsi, J.A., E.A. Fergusson, and M. V. Sturdevant. 2011. Recent harvest trends of pink and chum salmon in Southeast Alaska: Can marine ecosystem indicators be used as predictive tools for management? NPAFC international workshop on explanations for the high abundance of pink and chum salmon future trends. October 30-31, 2011, Nanaimo, BC. NPAFC Tech. Rep. No. 8:130-134. (no abstract)

Orsi, J., E. Fergusson, M. Sturdevant, and A. Wertheimer. 2011. Forecasting pink salmon harvest in Southeast Alaska. Pgs. 158-160 in: Ecosystems Considerations Report. North Pacific Fishery Management Council (S. Zador, Editor), 255 pages. Available: http://access.afsc.noaa.gov/reem/ecoweb/index.cfm (no abstract)

Orsi, J., E. Fergusson, M. Sturdevant, and A. Wertheimer. 2012, in press. Using ecosystem indicators from the Southeast Alaska Coastal Monitoring Project to forecast pink salmon harvest in Southeast Alaska. In: Ecosystems Considerations Report. North Pacific Fishery Management Council (S. Zador, Editor). Available: http://access.afsc.noaa.gov/reem/ecoweb/index.cfm (no abstract)

Sturdevant, M., E. Fergusson, and J. Orsi. 2011. Longterm zooplankton trends in Icy Strait, Southeast Alaska. Pgs. 140-142 in: Ecosystems Considerations Report. North Pacific Fishery Management Council (S. Zador, Editor), 255 pgs. Available: http://access.afsc.noaa.gov/reem/ecoweb/index.cfm (no abstract)

Sturdevant, M., J. Orsi, and E. Fergusson. 2012, in press. Longterm zooplankton and temperature trends in Icy Strait, Southeast Alaska. In: Ecosystems Considerations Report. North Pacific Fishery Management Council (S. Zador, Editor). Available: http://access.afsc.noaa.gov/reem/ecoweb/index.cfm (no abstract)

Sturdevant, M.V., J.A. Orsi, and E.A. Fergusson. 2012, in press. Diets and trophic linkages of epipelagic fish predators in coastal Southeast Alaska during a period of warm and cold climate years, 1997-2011. Marine and Coastal Fisheries.

This study identifies important trophic links for epipelagic marine fish predators in Southeast Alaska to improve understanding of marine ecosystem dynamics in response to climate change. Fish predators can be viewed as autonomous samplers whose diets should integrate the available prey taxa commensurate with environmental conditions. We examined fish predators from annual (1997–2011) surveys conducted in May to September by the Southeast Coastal Monitoring (SECM) project of Auke Bay Laboratories in the marine waters of Southeast Alaska. This project has emphasized long-term monitoring of strait and coastal marine habitats used by juvenile Pacific salmon *Oncorhynchus* spp. and associated epipelagic fishes to understand how environmental variation affects the sustainability of salmon resources. From 1,295 surface trawl hauls, trophic links were identified for 2,473 fish representing 19 predator species, principally adult and immature salmon, immature walleye pollock *Theragra chalcogramma*, and spiny dogfish *Squalus acanthias*. The most common fish prey consumed were fish larvae, juvenile salmon, Pacific herring *Clupea pallasii*, capelin *Mallotus villosus*, walleye pollock, lanternfishes (Myctophidae), and Pacific sand lance *Ammodytes hexapterus*, whereas the most common invertebrate prey consumed were euphausiids, decapod larvae, pteropods, and amphipods. This study describes the degree of piscivory, incidence of juvenile salmon prey, and frequency and weight composition of prey in the diets of epipelagic fish predators, but it did not clearly detect an effect of warm-versus-cold climate years on the diets of key planktivorous or piscivorous

predators over the 15-year time series. Identifying the persistence of trophic links in epipelagic waters over time is important because climate-related changes in the upper water column have the potential to impact Southeast Alaska marine ecosystem dynamics and the productivity of important regional fisheries by altering key prey resources and trophic interactions.

Sturdevant, M., E. Fergusson, N. Hillgruber, C. Reese, J. Orsi, R. Focht, A. Wertheimer, and W. Smoker. 2012. Lack of trophic competition among wild and hatchery juvenile chum salmon during early marine residence in Taku Inlet, Southeast Alaska. Environ. Biol. Fishes 94:101-116. (Available: http://dx.doi.org/10.1007/s10641-011-9899-7)

Early marine trophic interactions of wild and hatchery chum salmon (*Oncorhynchus keta*) were examined as a potential cause for the decline in harvests of adult wild chum salmon in Taku Inlet, Southeast Alaska. In 2004 and 2005, outmigrating juvenile chum salmon were sampled in nearshore habitats of the inlet (spring) and in epipelagic habitat at Icy Strait (summer) as they approached the Gulf of Alaska. Fish were frozen for energy density determination or preserved for diet analyses, and hatchery stocks were identified from the presence of thermal marks on otoliths. We compared feeding intensity, diets, energy density, and size relationships of wild and hatchery stocks (n = 3123) across locations and weeks. Only hatchery fish feeding intensity was negatively correlated with fish abundance. In both years, hatchery chum salmon were initially larger and had greater energy density than wild fish, but lost condition in early weeks after release as they adapted to feeding on wild prey assemblages. Diets differed between the stocks at all inlet locations, but did not differ for hatchery salmon between littoral and neritic habitats in the outer inlet, where the stocks overlapped most. Both diets and energy density converged by late June. Therefore, if density-dependent interactions affect wild chum salmon, these effects must be very rapid because survivors in Icy Strait showed few differences. Our study also demonstrates that hatchery release strategies used near Taku Inlet successfully promote early spatial segregation and prey partitioning, which reduce the probability of competition between wild and hatchery chum salmon stocks.

Weitkamp, L. A., J. A. Orsi, K. W. Myers, and R. C. Francis. 2011. Contrasting early marine ecology of chinook salmon and coho salmon in Southeast Alaska: Insight into factors affecting marine survival. Marine and Coastal Fisheries 3:233-249.

To identify processes potentially contributing to the differential marine survival rates of Chinook salmon *Oncorhynchus tshawytscha* and coho salmon *O. kisutch* originating from Southeast Alaska, we compared the early marine ecology of the two species during the critical first summer in marine waters. We predicted that the higher survival rates for coho salmon relative to Chinook salmon were related to the larger size, faster growth, or different habitat or species associations of coho salmon. Our size and growth expectations were largely substantiated: juvenile coho salmon were larger than juvenile Chinook salmon and had faster length-based growth, although weight-based growth rates were similar. The most obvious difference was in their distributions. Juvenile coho salmon overlapped spatially and temporally with abundant juvenile pink salmon

O. gorbuscha and chum salmon *O. keta*, whereas juvenile Chinook salmon were geographically separated from other salmonids. This suggests that coho salmon benefited from a predation buffer that did not extend to Chinook salmon. Our results indicate that factors influencing marine survival of juvenile Chinook salmon and coho salmon in Southeast Alaska are attributable to species-specific differences in their early marine distribution patterns and species interactions.

Component 3: Winter Survival of Pacific Salmon in the North Pacific Ocean Ecosystem

Farley, E.V., A. Starovoytov, S. Naydenko. R. Heintz, M. Trudel, C. Guthrie, L. Eisner, and J.R. Guyon. 2011. Implications of a warming eastern Bering Sea for Bristol Bay sockeye salmon.

Overwinter survival of Pacific salmon (*Oncorhynchus sp.*) is believed to be a function of size and energetic status they gain during their first summer at sea. We test this notion for Bristol Bay sockeye salmon (*O. nerka*), utilizing data from large-scale fisheries and oceanographic surveys conducted during mid-August to September 2002 – 2008 and from February to March 2009. The new data presented in this paper demonstrate size-selective mortality for Bristol Bay sockeye salmon between autumn and their first winter at sea. Differences in the seasonal energetic signatures for lipid and protein suggest that these fish are not starving, but instead the larger fish caught during winter apparently are utilizing energy stores to minimize predation. Energetic status of juvenile sockeye salmon was also strongly related to marine survival indices and years with lower energetic status apparently are a function of density-dependent processes associated with high abundance of juvenile sockeye salmon. Based on new information regarding eastern Bering sea ecosystem productivity under a climate-warming scenario, we hypothesize that sustained increases in spring and summer sea temperatures may negatively affect energetic status of juvenile sockeye salmon, potentially resulting in increased overwinter mortality.

Component 4: Biological Monitoring of Key Salmon Population

Martinson E.C., Stokes H.H., Scarnecchia D.L. (2012) Use of juvenile salmon growth and temperature change indices to predict groundfish post age-0 yr class strengths in the Gulf of Alaska and Bering Sea. *Fish Oceanogr* **21**, 307-319.

Juvenile marine growth (SW1) of salmon and a new temperature change (TC) index were evaluated as ecosystem indicators and predictors for the post age- 0 year class strength (YCS) of groundfish in the Gulf of Alaska (GOA) and eastern Bering Sea (EBS). Our hypothesis was that SW1, as measured on the scales of adult Pacific salmon (*Oncorhynchus* spp.), is a proxy for ocean productivity on the continental shelf, a rearing area for young salmon and groundfish. Less negative TC index values are the result of a cool late summer followed by a warm spring, conditions favorable for groundfish YCS. In the GOA, SW1 was a positive predictor of age-1 pollock (*Theragra chalcogramma*), but not age-2 sablefish (*Anoplopoma fimbria*) YCS, indicating that the growth of the Karluk River sockeye salmon that enter Shelikof Strait is a proxy for ocean conditions experienced by age-0 pollock. Contrary to our hypotheses, the TC index was a negative predictor of GOA pollock YCS; and the SW1 a negative predictor of EBS

pollock and cod YCS since the 1980s. Recent fisheries oceanography survey results provide insight into possible mechanisms to support the inverse SW1 and YCS relationship. For the EBS, the TC index was a significant positive predictor for pollock and cod YCS, supporting the hypothesis that a cool late summer followed by a warm spring maximizes the over-wintering survival of pollock and cod (*Gadus macrocephalus*), especially since the 1980s. The TC and SW1 index showed value for the assessment of pollock and cod, but not sablefish.

Murphy, J. M. and Rutecki Thomas, L. 2011. Comparison of pelagic fishing gear in coastal waters of southeastern Alaska. NPAFC Doc. 1328. 11 pp. Auke Bay Laboratories, Alaska Fisheries Science Center, National Marine Fisheries Service, 17109 Pt. Lena Loop Road, Juneau, AK 99801-8626, U.S.A.

During August1998 scientists from the Auke Bay Laboratory conducted a study in the coastal waters of southeastern Alaska to compare a rope trawl modified for fishing at the surface with a floating gillnet of variable mesh size for sampling juvenile sablefish(*Anoplopoma fimbria*) and juvenile salmon (*Oncorhynchus* spp.). Species composition, catches, and average fish size differed between the rope trawl and gillnet catches. A total of 257 fish and squid representing 11 species was captured with rope trawl gear, whereas gillnet sampling resulted in the capture of 89 fish representing six species. Nearly twice as many species were present in rope trawl catches than gillnet catches and this difference is believed to reflect higher selectivity in gillnet sampling gear. Although juvenile salmon catch was higher using the rope trawl, juvenile sablefish catch was higher using the gillnet. Average fork lengths of juvenile salmon were higher in gillnet catches. Average fork length of juvenile sablefish was higher in rope trawl catches, but the difference in length between gear types was not significant.

Nelson, P.A. and R. Narita, 2011. Incidental catches of salmonids by U.S. groundfish fisheries in the Bering Sea/Aleutian Islands and the Gulf of Alaska, 1990-2011. NPAFC Doc. 1359. 11 pp. Fisheries Monitoring and Analysis Div., Alaska Fish. Sci. Cent., NMFS, NOAA, U.S. Dep. Commerce, 7600 Sand Point Way NE, Seattle, WA 98115-0070. (Available at http://www.npafc.org).

This report presents the estimated incidental catches of Pacific salmonids in U.S. groundfish fisheries off Alaska for 1977 through September 15, 2011. Estimated annual incidental samon catches (all species combined) through September 15, 2011, were 87,550 salmon in the Bering Sea/Aleutian Islands (BSAI) and 12,271 salmon in the Gulf of Alaska (GOA).
In the U.S. groundfish fisheries in the BSAI, annual estimated numbers of Chinook salmon (Onchorhynchus tshawytscha) have ranged from 8,223 (year 2000) to 129,5567 (year 2007) and the annual average weight has ranged from 2.82 kg in 2007 to 5.21 kg in 1995. Annual estimated numbers of non-Chinook salmon have ranged from 14,965 in 2010 to 709,391 in 2005. Chum salmon (Onchorhynchus keta) typically account for over 95% of the non-Chinook salmon catch. The annual average chum salmon weight has ranged from 2.07 kg in 1993 to 3.43 kg in 1995.
In the U.S. groundfish fisheries in the Gulf of Alaska, annual estimated numbers of Chinook salmon have ranged from 8,430 in 2009 to 54,631 in 2010 and the annual average weight has ranged from 2.28 kg in 2010 to 4.60 kg in 1991. Annual estimated numbers of non-Chinook salmon have ranged from 1,860 in 2010 to 64,792 in 1995. Chum salmon typically account for over 95% of the non-Chinook salmon catch. The annual average chum salmon weight has ranged

from 2.16 kg in 1993 to 4.87 kg in 1999. Incidental catches of Pacific salmonids in foreign and joint venture groundfish fisheries off Alaska are presented for 1977-1990. The last joint venture operations took place in 1990 in the Bering Sea/Aleutian Islands, with an incidental catch of 152 salmon.

Nishimura, G., and M. Sturdevant. 2011. Portable winch technology for use on smaller vessels. Sea Technology (July):21-24. Available: http://www.sea-technology.com/features/2011/0711/portable_winch.php (no abstract)

Orsi, J.A, M. V. Sturdevant, E. A. Fergusson, W. R. Heard, and E. V. Farley. 2011. Southeast Alaska Coastal Monitoring (SECM) Survey Plan for 2011. NPAFC Doc. 1300. 15 pp. (Available at http://www.npafc.org).

The Southeast Coastal Monitoring (SECM) project was initiated in 1997 by the Alaska Fisheries Science Center, Auke Bay Laboratories, to study the habitat use and early marine ecology of juvenile (age-0) Pacific salmon (*Oncorhynchus* spp.) and associated epipelagic ichthyofauna in Southeast Alaska. SECM surveys are conducted off government and chartered research vessels in the vicinity of Icy Strait (58° N, 135°W) and sample fish, zooplankton, nutrients/chlorophyll, and physical water properties using a surface trawl, plankton nets, and an oceanographic profiler. In 2011 SECM research surveys are scheduled to continue at 13 core stations in Icy Strait during four monthly intervals from late May to late August and also at four stations in the Gulf of Alaska. This 2011 SECM survey plan reflects what was accomplished at the inception of the project in 1997, and this additional survey year will extend the biophysical time series to 15 years.

Orsi, J. A., E. A. Fergusson, M. V. Sturdevant, W. R. Heard, and E. V. Farley, Jr.. 2011. Annual Survey of Juvenile Salmon, Ecologically-Related Species, and Environmental Factors in the Marine Waters of Southeastern Alaska, May August 2010. NPAFC Doc. 1342, 87 pp. (Available at http://www.npafc.org).

Juvenile Pacific salmon (*Oncorhynchus* spp.), ecologically-related species, and associated environmental (biophysical) data were collected from the marine waters of the northern region of southeastern Alaska in 2010. This annual survey, conducted by the Southeast Coastal Monitoring (SECM) project, marks 14 consecutive years of systematically monitoring how juvenile salmon utilize in marine ecosystems, and was implemented to identify the relationships among biophysical parameters that influence habitat use, marine growth, predation, stock interactions, and year-class strength of juvenile salmon. This report also contrasts the 2010 findings with selected biophysical parameters from the prior 13 sampling years. Up to 13 stations were sampled in epipelagic waters monthly, totaling 21 sampling days, from May to August. Fish, zooplankton, surface water samples, and physical profile data were typically collected during daylight at each station using a surface rope trawl, conical and bongo nets, a water sampler, and a conductivity-temperature-depth profiler. Surface (3-m) temperatures and salinities ranged from approximately 9 to 14 ºC and 17 to 32 PSU from May to August. More than 39,000 fish, representing 26 taxa, were captured in 67 rope trawl hauls fished from June to August. Juvenile salmon comprised about 97% of the total fish catch. Juvenile pink (*O. gorbuscha*), chum (*O. keta*), sockeye (*O. nerka*), and coho (*O. kisutch*) salmon occurred in 71-87% of the trawls, while

juvenile Chinook salmon (*O. tshawytscha*) occurred in 9% of the hauls. Unusually high numbers of juvenile salmon were captured in strait habitat in both June and July, although CPUE was greatest in June for all species except sockeye salmon. Coded-wire tags were recovered from 15 juvenile coho salmon and one juvenile Chinook salmon from hatchery and wild stocks originating in southeastern Alaska and Washington. Alaska enhanced stocks were also identified by thermal otolith marks from 67% of the chum and 16% of the sockeye salmon examined. Onboard stomach analysis revealed predation on highly abundant juvenile salmon by adult coho salmon, a common predator, and adult pink salmon, a rare predator. Biophysical measures from 2010 differed from prior years, in many respects. May integrated (20-m) temperature anomalies were generally positive and salinity anomalies were generally negative; in particular, the positive May temperature anomaly was the highest on record. Zooplankton monthly total densities were near longterm averages, reversing the trend for strongly positive anomalies over the past four years. For juvenile pink, chum, and sockeye salmon, low condition residuals in June were followed by small size and low energy density in July. Regional biophysical data from SECM are used in conjunction with basin-scale biophysical parameters to forecast pink salmon harvest in southeastern Alaska. Longterm monitoring of key stocks of juvenile salmon, on seasonal and interannual time scales, will enable researchers to understand how growth, abundance, and ecological interactions affect year-class strength of salmon and to better understand their roles in North Pacific marine ecosystems.

Orsi, J. A., E. A. Fergusson, M. V. Sturdevant, W. R. Heard, and E. V. Farley, Jr. 2012, in press. Annual Survey of Juvenile Salmon, Ecologically-Related Species, and Biophysical Factors in the Marine Waters of Southeastern Alaska, May–August 2011. NPAFC Doc. 1428. 104 pp. (Available at http://www.npafc.org).

Juvenile Pacific salmon (Oncorhynchus spp.), ecologically-related species, and associated biophysical data were collected from the marine waters of the northern region of southeastern Alaska in 2011. This annual survey, conducted by the Southeast Coastal Monitoring (SECM) project, marks 15 consecutive years of systematically monitoring how juvenile salmon utilize marine ecosystems during a period of climate change. The survey was implemented to identify the relationships among biophysical parameters that influence habitat use, marine growth, prey fields, predation, stock interactions, and year-class strength of juvenile salmon. This report also contrasts the 2011 findings with selected biophysical factors from the prior 14 sampling years. Up to 13 stations were sampled monthly in epipelagic waters from May to August (total of 21 sampling days). Fish, zooplankton, surface water samples, and physical profile data were typically collected during daylight at each station using a surface rope trawl, conical and bongo nets, a water sampler, and a conductivity-temperature-depth profiler. Surface (3-m) temperatures and salinities ranged from approximately 6 to 14 ºC and 15 to 32 PSU from May to August across inshore, strait, and coastal habitats. A total of 6,640 fish and squid, representing 27 taxa, were captured in 96 rope trawl hauls fished from June to August. Juvenile salmon comprised approximately 78% of the total fish catch. Juvenile pink (O. gorbuscha), chum (O. keta), sockeye (O. nerka), and coho (O. kisutch) salmon occurred in 42-80% of the hauls by month and habitat, while juvenile Chinook salmon (O. tshawytscha) occurred in ≤ 17% of the hauls. Abundance of juvenile salmon was relatively low in 2011; peak CPUE occurred in straits in June for chum salmon and in August for all other species. Coded-wire tags were recovered from 10 coho salmon and 6 Chinook salmon from hatchery and wild stocks originating in southeastern Alaska

and Washington. Alaska enhanced stocks were also identified by thermal otolith marks from 60%, 21%, and 5% of chum, sockeye, and coho salmon examined, respectively. Predation on juvenile salmon was observed in 3 of 9 species examined. Biophysical measures from 2011 differed from prior years, in many respects. Compared to the 15-yr longterm mean values, temperature anomalies were negative, salinity anomalies were positive, zooplankton density was low, and condition residuals were negative for juvenile pink, chum, and sockeye salmon. The SECM juvenile salmon stock assessment and biophysical data are used in conjunction with basin-scale biophysical data to forecast pink salmon harvest in southeastern Alaska. Longterm seasonal monitoring of key stocks of juvenile salmon and associated ecologically-related species, including fish predators and prey, will enable researchers to understand how growth, abundance, and interactions affect year-class strength of salmon in marine ecosystems.

Sturdevant, M., G. Nishimura, and J. Orsi. 2011. Sidewinder: Description of a new block winch for deploying instruments at sea. Marine and Coastal Fish. 3:317-323.

We describe a new electric winch design and its functionality for conducting research operations off different-sized vessels. Currently, several small oceanographic winches are available for deploying research instruments and nets, but they are typically heavy, noisy, semi-permanently mounted to the deck, hydraulically operated, and not readily transferable between vessels. The limitation of winch portability between vessels, in particular, has been exacerbated by the increasing use of a variety of chartered vessels to conduct state and federal agency and university research. To address these challenges, we developed a relatively lightweight (70 kg), portable block-design winch that is spooled with 400 m of plasma line, powered by two 12-V marine batteries, and operated by a remote control box on a pendant equipped with a joystick. The 2.2-kW drive produces 100 kg of line pull at speeds of 0 to 2.0 m/s. The pendant includes digital displays for line speed, scope, and angle as well as an emergency stop. Nicknamed the "Sidewinder," this winch is quiet, can be operated by one person, and is suspended outboard from a davit or crane boom, increasing available deck space and relocating all lines safely away from vessel personnel. On vessels to 50 m in length the Sidewinder has been successfully tested for deploying small gear such as conductivity– temperature–depth profilers and large BONGO plankton nets that require specific deployment d retrieval speeds and line angles. To ensure safe operation, vessel support features such as the power system and davit working load capacity should be considered when the Sidewinder is custom-built.

Wertheimer, A. C., J. A. Orsi, E. A. Fergusson, and M. V. Sturdevant. 2011. Forecasting Pink Salmon Harvest in Southeast Alaska from Juvenile Salmon Abundance and Associated Environmental Parameters: 2010 Returns and 2011 Forecast. NPAFC Doc. 1343. 20 pp. (Available at http://www.npafc.org).

The Southeast Alaska Coastal Monitoring (SECM) project has been sampling juvenile salmon (*Oncorhynchus* spp.) and associated environmental parameters in northern Southeast Alaska (SEAK) annually since 1997 to better understand effects of environmental change on salmon production. A pragmatic application of the annual sampling effort is to forecast the abundance of adult salmon returns in subsequent years. Since 2004, juvenile peak salmon catch per unit effort

(CPUE) from SECM, adjusted for highly-correlated environmental parameters, has been used to forecast harvest of adult pink salmon (*O. gorbuscha*) in SEAK. The 2010 forecast of 26.8 M fish was 15% higher than the actual harvest of 23.4 M fish. Six forecasts produced over the period 2004-2010 have been within 0-17% of the actual harvest, with an average forecast deviation of 7.9%. However, the forecast for 2006 did not follow this pattern. The simple CPUE forecast model indicated a downturn in the harvest, but the prediction was 209% higher than the actual harvest. These results show that the CPUE information has great utility for forecasting year class strength of SEAK pink salmon, but additional information may be needed to avoid "misses" such as the forecast for the 2006 return. For the 2011 forecast, model selection included a review of ecosystem indicator variables and considered additional environmental parameters to improve the simple single-parameter CPUE forecast model. The single parameter model was selected as the "best" forecast model for 2011. Juvenile pink salmon CPUE in northern SEAK accounted for 82% of the variability in annual harvest of SEAK pink salmon over the period 1997-2010. The 2011 forecast from this model, using juvenile salmon data collected in 2010, was 56.2 M fish, with an 80% bootstrap confidence interval of 47-62 M fish. Over the past seven years, the use of the SECM time series of CPUE data and associated environmental parameters has largely been successful in forecasting year-class strength of pink salmon in SEAK.

Wertheimer, A. C., J. A. Orsi, E. A. Fergusson, and M. V. Sturdevant. 2012, in press. Forecasting Pink Salmon Harvest in Southeast Alaska from Juvenile Salmon Abundance and Associated Biophysical Parameters: 2011 Returns and 2012 Forecast. NPAFC Doc. 1414, Rev.1.   23 pp. (Available at http://www.npafc.org).

The Southeast Alaska Coastal Monitoring (SECM) project has been sampling juvenile salmon (*Oncorhynchus* spp.) and associated environmental parameters in northern Southeast Alaska (SEAK) annually since 1997 to better understand effects of environmental change on salmon production. A pragmatic application of the annual sampling effort is to forecast the abundance of adult salmon returns in subsequent years. Since 2004, juvenile peak salmon catch per unit effort (CPUE) from SECM, adjusted for highly-correlated environmental parameters, has been used to forecast harvest of adult pink salmon (*O. gorbuscha*) in SEAK. Remarkably, the 2011 forecast of 56.2 M fish was only 5% lower than the actual harvest of 59.0 M fish. Seven of eight forecasts produced over the period 2004-2011 have been within 0-17% of the actual harvest, with an average forecast deviation of 7%. The forecast for 2006 was the exception; while the simple CPUE model indicated a downturn in harvest, the prediction still overestimated the harvest by 209%. These results show that the CPUE information has great utility for forecasting year class strength of SEAK pink salmon, but additional information may be needed to avoid "misses" such as the forecast for the 2006 return. For the 2012 forecast, model selection included a review of ecosystem indicator variables and considered additional environmental parameters to improve the simple single-parameter CPUE forecast model. A two-parameter model, including May temperature data as well as juvenile CPUE, was selected as the "best" forecast model for 2012. The 2012 forecast from this model, using juvenile salmon data collected in 2011, was for 18.8 M fish, with an 80% bootstrap confidence interval of 13-25 M fish.

Component 5: Development and Applications of Stock Identification Methods and Models for Management of Pacific Salmon

Ackerman M.W., Habicht C., Seeb L.W. (2011) Single-nucleotide polymorphisms (SNPs) under diversifying selection provide increased accuracy and precision in mixed-stock analyses of sockeye salmon from the Copper River, Alaska. *Trans Am Fish Soc* **140**, 865-881.

Genetic markers are increasingly being used to ascertain the population of origin of individuals or mixtures of individuals in complex aggregations of Pacific salmon Oncorhynchus spp. Multilocus genotype data from single-nucleotide polymorphisms (SNPs) are especially useful for admixture analyses. Single-nucleotide polymorphisms can be discovered in nonmodel organisms with relative ease and can be characterized in the coding and regulatory regions of the genome influenced by selection. Those influenced by diversifying selection may show atypically high levels of differentiation among populations and thus be particularly valuable for genetic stock identification in cases where neutral loci show little difference among populations of interest. We identified four SNP loci from a panel of 42 as candidates for diversifying selection (referred to here as nonneutral SNPs) in sockeye salmon O. nerka from the Copper River and adjacent coastal drainages in south-central Alaska. We evaluated the information content of the four nonneutral loci for use in genetic stock identification and assessed their ability to improve the accuracy and precision of composition estimates. The average measure of informativeness for assignment (In) for neutral loci was 0.019, and the average In for nonneutral loci was 0.064. A simulation-based approach indicated that the addition of the nonneutral SNP loci to a neutral marker panel provided significantly higher resolution in the assignment of individuals to their populations of origin than would have been accomplished by adding an equal number of neutral loci. Nonneutral SNP loci improved the ability to identify the origin of individual fish and to estimate the composition of Pacific salmon populations in mixed fisheries.

Ackerman M.W., Templin W.D., Seeb J.E., Seeb L.W. (2012) Landscape heterogeneity and local adaptation define the spatial genetic structure of Pacific salmon in a pristine environment. Conservation Genetics (revisions accepted).

Identifying the spatial distribution of genetic variation across the landscape is an essential step in informing species conservation. Comparison of closely related and geographically overlapping species can be particularly useful in cases where landscape may similarly influence genetic structure. Congruent patterns among species highlight the importance that landscape heterogeneity plays in determining genetic structure whereas contrasting patterns emphasize differences in species-specific ecology and life-history or the importance of species-specific adaptation to local environments. We examined the interacting roles of demography and adaptation in determining spatial genetic structure in two closely related and geographically overlapping species in a pristine environment. Using single nucleotide polymorphism (SNP) loci exhibiting both neutral and putative adaptive variation, we evaluated the genetic structure of sockeye salmon in the Copper River, Alaska; these data were compared to existing data for Chinook salmon from the same region. Overall, both species exhibited patterns of isolation by distance; the spatial distribution of populations largely determined the distribution of genetic variation across the landscape. Further, both species exhibited largely congruent patterns of

within- and among-population genetic diversity, highlighting the role that landscape heterogeneity and historical processes play in determining spatial genetic structure. Potential adaptive differences among geographically proximate sockeye salmon populations were observed when high F_{ST} outlier SNPs were evaluated in a landscape genetics context. Results were evaluated in the context of conservation efforts with an emphasis on reproductive isolation, historical processes, and local adaptation.

Celewycz, A. G., E. A. Fergusson, J. H. Moss, and V. J. Tuttle. 2012, in press. High seas
       salmonid coded-wire tag recovery data, 2012. NPAFC Doc. 1415. 37 p. (Available:
       http://www.npafc.org).

Information on high seas recoveries of salmonids (*Oncorhynchus* spp.) tagged with coded-wire tags (CWTs) has been reported annually to the International North Pacific Fisheries Commission (1981-1992) and to the North Pacific Anadromous Fish Commission (NPAFC, 1993-present). Data from these CWT recoveries are also reported to the Regional Mark Processing Center (RMPC, http://www.rmpc.org) of the Pacific States Marine Fisheries Commission (PSMFC) for inclusion into their Regional Mark Information System Database. This document lists recovery data for 279 CWT salmonids that will be reported to PSMFC/RMPC for the first time. These 279 CWTs were recovered from the 2011 and 2012 U.S. groundfish trawl fishery in the Gulf of Alaska (13 Chinook salmon, *O. tshawytscha)*, the 2011 and 2012 U.S. groundfish trawl fishery in the eastern Bering Sea-Aleutian Islands (4 Chinook salmon), the 2010 and 2011 at-sea Pacific hake (*Merluccius productus*) trawl fishery in the Northern Pacific Ocean off Washington/Oregon (WA/OR, 220 Chinook salmon and 2 coho salmon, *O. kisutch)*, the 2011 West Coast trawl fishery off WA/OR/CA (15 Chinook salmon), and from 2011 U.S. trawl research in the Gulf of Alaska (3 Chinook salmon, 21 coho salmon, and 1 sockeye salmon, *O. nerka*). Recovery information is also presented for 5 new recoveries (4 Chinook salmon and 1 sockeye salmon) of salmon tagged with agency-only wire tags (not CWTs).

Creelman E.K., Hauser L., Simmons R.K., Templin W.D., Seeb L.W. (2011) Temporal and
       geographic genetic divergence: characterizing sockeye salmon populations in the Chignik
       Watershed, Alaska, using single-nucleotide polymorphisms. *Trans Am Fish Soc* **140**,
       749-762.

The high fidelity of Pacific salmon Oncorhynchus spp. to their natal spawning habitat often results in genetically divergent populations. Management and conservation of the natural variation within species is critical for maintaining robust populations. The Chignik watershed, Alaska, supports highly productive populations of sockeye salmon Oncorhynchus nerka that vary in return timing and spawning locations among breeding populations, presenting challenges to the management of commercially exploited stocks. We describe the genetic structure of the sockeye salmon populations spawning in the Chignik watershed using 45 single-nucleotide polymorphisms from 2,013 individuals representing 19 collections of spawning adults. From

these data we estimated within-population statistics and among-population divergence, detected loci in linkage disequilibrium and loci that are F ST outliers, and tested loci for potential use in mixed-stock assessments. The results indicate significant genetic structure among the sockeye salmon populations in the Chignik watershed at both spatial and temporal scales. This structuring can be largely explained by putative evidence of selection at two markers and the differences in spawn timing between populations. Genetic structure determined at geographic and temporal levels provides a basis for application in the conservation of this resource and the management of commercial and subsistence fisheries.

Everett M.V., Grau E.D., Seeb J.E. (2011) Short reads and nonmodel species: exploring the complexities of next-generation sequence assembly and SNP discovery in the absence of a reference genome. *Molecular Ecology Resources* **11**, 93-108.

How practical is gene and SNP discovery in a nonmodel species using short read sequences? Next-generation sequencing technologies are being applied to an increasing number of species with no reference genome. For nonmodel species, the cost, availability of existing genetic resources, genome complexity and the planned method of assembly must all be considered when selecting a sequencing platform. Our goal was to examine the feasibility and optimal methodology for SNP and gene discovery in the sockeye salmon (Oncorhynchus nerka) using short read sequences. SOLiD short reads (up to 50 bp) were generated from single- and pooled-tissue transcriptome libraries from ten sockeye salmon. The individuals were from five distinct populations from theWood River Lakes and Mendeltna Creek, Alaska. As no reference genome was available for sockeye salmon, the SOLiD sequence reads were assembled to publicly available EST reference sequences from sockeye salmon and two closely related species, rainbow trout (Oncorhynchus mykiss) and Atlantic salmon (Salmo salar). Additionally, de novo assembly of the SOLiD data was carried out, and the SOLiD reads were remapped to the de novo contigs. The results from each reference assembly were compared across all references. The number and size of contigs assembled varied with the size reference sequences. In silico SNP discovery was carried out on contigs from all four EST references; however, discovery of valid SNPs was most successful using one of the two conspecific references.

Everett M.V., Miller M.R., Seeb J.E. (2012) Meiotic maps of sockeye salmon derived from massively parallel DNA sequencing. *BMC Genomics* (revised version accepted).

Meiotic maps are a key tool for comparative genomics and association mapping studies. Next-generation sequencing and genotyping by sequencing are speeding the processes of SNP discovery and the development of new genetic tools, including meiotic maps for numerous species. Currently there are limited genetic resources for sockeye salmon, *Oncorhynchus nerka*. We develop the first dense meiotic map for sockeye salmon using a combination of novel SNPs found in restriction site associated DNA (RAD tags) and SNPs available from existing expressed sequence tag (EST) based assays. We discovered and genotyped putative SNPs in 3,430 RAD tags. We removed paralogous sequence variants leaving 1,672 SNPs; these were combined with 69 EST-based SNP genotypes for mapping. The map contained 29 male and female linkage groups, consistent with the haploid chromosome number expected for sockeye salmon. The female map contains 1,057 loci spanning 4896 cM, and the male map contains 1,121 loci spanning 4,148 cM. Regions of conservation with rainbow trout and synteny between the RAD

based rainbow trout linkage map and the sockeye salmon linkage map were established. Using RAD sequencing and tradition EST-based SNP assays we successfully generated the first high density linkage map for sockeye salmon.

Gomez-Uchida D., Seeb J., Smith M., Habicht C., Quinn T., Seeb L. (2011) Single nucleotide polymorphisms unravel hierarchical divergence and signatures of selection among Alaskan sockeye salmon (*Oncorhynchus nerka*) populations. *BMC Evolutionary Biology* **11**, 48.

Disentangling the roles of geography and ecology driving population divergence and distinguishing adaptive from neutral evolution at the molecular level have been common goals among evolutionary and conservation biologists. Using single nucleotide polymorphism (SNP) multilocus genotypes for 31 sockeye salmon (Oncorhynchus nerka) populations from the Kvichak River, Alaska, we assessed the relative roles of geography (discrete boundaries or continuous distance) and ecology (spawning habitat and timing) driving genetic divergence in this species at varying spatial scales within the drainage. We also evaluated two outlier detection methods to characterize candidate SNPs responding to environmental selection, emphasizing which mechanism(s) may maintain the genetic variation of outlier loci.RESULTS:For the entire drainage, Mantel tests suggested a greater role of geographic distance on population divergence than differences in spawn timing when each variable was correlated with pairwise genetic distances. Clustering and hierarchical analyses of molecular variance indicated that the largest genetic differentiation occurred between populations from distinct lakes or subdrainages. Within one population-rich lake, however, Mantel tests suggested a greater role of spawn timing than geographic distance on population divergence when each variable was correlated with pairwise genetic distances. Variable spawn timing among populations was linked to specific spawning habitats as revealed by principal coordinate analyses. We additionally identified two outlier SNPs located in the major histocompatibility complex (MHC) class II that appeared robust to violations of demographic assumptions from an initial pool of eight candidates for selection. First, our results suggest that geography and ecology have influenced genetic divergence between Alaskan sockeye salmon populations in a hierarchical manner depending on the spatial scale. Second, we found consistent evidence for diversifying selection in two loci located in the MHC class II by means of outlier detection methods; yet, alternative scenarios for the evolution of these loci were also evaluated. Both conclusions argue that historical contingency and contemporary adaptation have likely driven differentiation between Kvichak River sockeye salmon populations, as revealed by a suite of SNPs. Our findings highlight the need for conservation of complex population structure, because it provides resilience in the face of environmental change, both natural and anthropogenic.

Gomez-Uchida D., Seeb James E., Habicht C., Seeb Lisa W. (2012) Allele frequency stability in large, wild exploited populations over multiple generations: insights from Alaska sockeye salmon (*Oncorhynchus nerka*). *Can J Fish Aquat Sci* **69**, 916-929.

We genotyped nuclear and mitochondrial single nucleotide polymorphisms (SNPs) in six paired archived and contemporary collections of Alaskan sockeye salmon (Oncorhynchus nerka) to evaluate the stability of allele frequencies over 25–42 years (4.9–8.4 generations). First, our results show that temporal changes were dramatically (between 40- and 250-fold) smaller than

spatial differences in allele frequencies when based on nuclear SNPs. Second, the magnitude of temporal change was consistent with a model of genetic drift: (i) SNPs with high levels of differentiation (large θ) and candidates for diversifying selection were not more likely to show significant temporal changes than small-θ SNPs; and (ii) the fraction of single-locus significant tests was consistent with theoretical predictions relating sample size and the annual number of breeders (Nb). Third, estimates of Nb were bound by infinitely large upper 95% confidence intervals, except for one paired collection with unique life-history attributes of both a smoltification phase and generation time shorter than the other paired collections. Use of multigenerational SNP data sets seems a safe practice in management of Alaska sockeye salmon that could be extended to other large, wild aquatic populations.

Hauser L., Baird M., Hilborn R., Seeb L.W., Seeb J.E. (2011) An empirical comparison of SNPs and microsatellites for parentage and kinship assignment in a wild sockeye salmon (*Oncorhynchus nerka*) population. *Molecular Ecology Resources* **11**, 150-161.

Because of their high variability, microsatellites are still considered the marker of choice for studies on parentage and kinship in wild populations. Nevertheless, single nucleotide polymorphisms (SNPs) are becoming increasing popular in many areas of molecular ecology, owing to their high-throughput, easy transferability between laboratories and low genotyping error. An ongoing discussion concerns the relative power of SNPs compared to microsatellites— that is, how many SNP loci are needed to replace a panel of microsatellites? Here, we evaluate the assignment power of 80 SNPs (HE = 0.30, 80 independent alleles) and 11 microsatellites (HE = 0.85, 192 independent alleles) in a wild population of about 400 sockeye salmon with two commonly used software packages (Cervus3, Colony2) and, for SNPs only, a newly developed software (SNPPIT). Assignment success was higher for SNPs than for microsatellites, especially for parent pairs, irrespective of the method used. Colony2 assigned a larger proportion of offspring to at least one parent than the other methods, although Cervus and SNPPIT detected more parent pairs. Identification of full-sib groups without parental information from relatedness measures was possible using both marker systems, although explicit reconstruction of such groups in Colony2 was impossible for SNPs because of computation time. Our results confirm the applicability of SNPs for parentage analyses and refute the predictability of assignment success from the number of independent alleles.

McGlauflin M.T., Schindler D.E., Seeb L.W., Smith C.T., Habicht C., Seeb J.E. (2011) Spawning habitat and geography influence population structure and juvenile migration timing of sockeye salmon in the Wood River Lakes, Alaska. *Trans Am Fish Soc* **140**, 763-782.

The strict homing of sockeye salmon Oncorhynchus nerka results in reproductively isolated populations that often spawn in close proximity and share rearing habitat. High spawning fidelity enables these populations to adapt to local conditions, resulting in a wide range of life history characteristics and genetic variation within individual watersheds. The Wood River system in southwestern Alaska provides a pristine, well-studied system in which to examine fine-scale population structure and its influences on juvenile life histories. Adult sockeye salmon spawn in lake beaches, rivers, and small tributaries throughout this watershed, and juveniles rear in five nursery lakes. We genotyped 30 spawning populations and 6,066 migrating smolts at 45 single

nucleotide polymorphism loci, two of which are candidates for positive selection in the study system. We show that there is significant genetic structure (F ST = 0.032) in the Wood River lakes and that divergence is generally related to spawning rather than nursery habitat (hierarchical analysis of molecular variance; P < 0.05). Four groups of populations were identified based on genetic structure and used to determine the composition of unknown mixtures of migrating smolts using a Bayesian modeling framework. We demonstrate that smolt migration timing is related to genetic structure; stream and river populations dominate catches in early June, while beach spawners and the populations in Lake Kulik are more prevalent from mid-June to early September. Age-2 smolts are primarily produced by the Lake Kulik and beach spawning populations, showing that genetic differences may reflect divergent freshwater and migration life history strategies. These results indicate that local adaptation to spawning habitat influences genetic divergence in the Wood River lakes, affecting both adult and juvenile life stages of sockeye salmon.

Oxman, D.S. and R. Josephson. 2011. Proposed thermal marks for brood year 2011 salmon in Alaska. NPAFC Doc. 1318, Rev. 1. 7 pp. Alaska Dept. Fish and Game, Juneau, Alaska, 99811, USA. (Available at www.npafc.org).

In Alaska, mass-marking of salmon using otolith thermal marking is an effective research and management tool applicable to a variety of situations. For brood year 2011, approximately 60 million sockeye, 800 million pink salmon, 586 million chum, 9 million coho, and 7 million Chinook salmon will be marked at 22 different hatcheries using 77 thermal marks.

Oxman, D.S. and R.P. Josephson. 2011. Releases of otolith marked salmon from Alaska in 2009. NPAFC Doc. 1327. 5pp. Alaska Dept. Fish and Game, Juneau, Alaska. 99801

In Alaska, mass-marking of salmon using otolith thermal marking is an effective research and management tool for a variety of situations. This document reports the otolith mark patterns applied to hatchery-raised salmon stocks released in Alaska during 2010. It includes five species of salmon from brood years 2008 through 2010. Release numbers, mark patterns, and release locations are summarized.

Seeb J.E., Pascal C.E., Grau E.D. *et al.* (2011) Transcriptome sequencing and high-resolution melt analysis advance single nucleotide polymorphism discovery in duplicated salmonids. *Molecular Ecology Resources* **11**, 335-348.

Until recently, single nucleotide polymorphism (SNP) discovery in nonmodel organisms faced many challenges, often depending upon a targeted-gene approach and Sanger sequencing of many individuals. The advent of next-generation sequencing technologies has dramatically improved discovery, but validating and testing SNPs for use in population studies remain labour intensive. Here, we detail a SNP discovery and validation pipeline that incorporates 454 pyrosequencing, high-resolution melt analysis (HRMA) and 5¢ nuclease genotyping. We generated $4.59 \cdot 10^8$ bp of redundant sequence from transcriptomes of two individual chum salmon, a highly valued species across the Pacific Rim. Nearly 26 000 putative SNPs were

identified—some as heterozygotes and some as homozygous for different nucleotides in the two individuals. For validation, we selected 202 templates containing single putative SNPs and conducted HRMA on 10 individuals from each of 19 populations from across the species range. Finally, 5¢ nuclease genotyping validated 37 SNPs that conformed to Hardy–Weinberg equilibrium expectations. Putative SNPs expressed as heterozygotes in an ascertainment individual had more than twice the validation rate of those homozygous for different alleles in the two fish, suggesting that many of the latter may have been paralogous sequence variants. Overall, this validation rate of $37 / 202$ suggests that we have found more than 4500 templates containing SNPs for use in this population set. We anticipate using this pipeline to significantly expand the number of SNPs available for the studies of population structure andmixture analyses as well as for the studies of adaptive genetic variation in nonmodel organisms.

Smith M.J., Pascal C.E., Grauvogel Z.A.C., Habicht C., Seeb J.E., Seeb L.W. (2011) Multiplex preamplification PCR and microsatellite validation enables accurate single nucleotide polymorphism genotyping of historical fish scales. *Molecular Ecology Resources* **11**, 268-277.

Incorporating historical tissues into the study of ecological, conservation and management questions can broaden the scope of population genetic research by enhancing our understanding of evolutionary processes and anthropogenic influences on natural populations. Genotyping historical and low-quality samples has been plagued by challenges associated with low amounts of template DNA and the potential for pre-existing DNA contamination among samples. We describe a two-step process designed to (i) accurately genotype large numbers of historical low-quality scale samples in a high-throughput format and (ii) screen samples for pre-existing DNA contamination. First, we describe how an efficient multiplex preamplification PCR of 45 single nucleotide polymorphisms (SNPs) can generate highly accurate genotypes with low failure and error rates in subsequent SNP genotyping reactions of individual historical scales from sockeye salmon (Oncorhynchus nerka). Second, we demonstrate how the method can be modified for the amplification of microsatellite loci to detect pre-existing DNA contamination. A total of 760 individual historical scale and 182 contemporary fin clip samples were genotyped and screened for contamination. Genotyping failure and error rates were exceedingly low and similar for both historical and contemporary samples. Pre-existing contamination in 21% of the historical samples was successfully identified by screening the amplified microsatellite loci. The advantages of automation, low failure and error rates, and ability to multiplex both the preamplification and subsequent genotyping reactions combine to make the protocol ideally suited for efficiently genotyping large numbers of potentially contaminated low-quality sources of DNA.

Storer C.G., Pascal C.E., Roberts S.B., Templin W.D., Seeb L.W., Seeb J.E. (2012) Rank and order: evaluating the performance of SNPs for individual assignment in sockeye salmon. *PlosOne*. (accepted pending revision).

Single nucleotide polymorphisms are valuable tools for ecological and evolutionary studies. In non-model species, the use of SNPs has been limited by the number of markers available.

However, new technologies and decreasing technology costs have facilitated the discovery of a constantly increasing number of SNPs. With hundreds or thousands of SNPs potentially available, there is interest in comparing and developing methods for evaluating SNPs to create panels of high-throughput assays that are customized for performance, research questions, and resources. Here we use five different methods to rank 43 new SNPs and 71 previously published loci for sockeye salmon: F_{ST}, informativeness (I_n), average contribution to principal components (LC), and the locus ranking programs BELS and WHICHLOCI. We then tested the performance of these different ranking methods by creating 48- and 96-SNP panels of the top-ranked loci for each method and used empirical and simulated data to obtain the probability of assigning individuals to the correct population using each panel. All 96-SNP panels performed similarly and better than the 48-SNP panels except for the 96-SNP BELS panel. Among the 48-SNP panels, panels created from F_{ST}, I_n, and LC ranks performed better than panels formed using the top-ranked loci from the programs BELS and WHICHLOCI. The application of ranking methods to optimize panel performance will become more important as more high-throughput assays become available.