

Microsatellites, Allozymes, and SNPs Describe the Population Structure and Identify Spatial Distribution of Mixture Components of Sockeye Salmon in the Bering Sea

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Knowledge of stock-specific marine migration patterns of sockeye salmon *Oncorhynchus nerka* in the Bering Sea could provide insights into stock composition of international harvests and into factors affecting stock-specific early marine survival. Alaska Department of Fish and Game Gene Conservation Laboratory and National Marine Fisheries Service Auke Bay Laboratory (ABL) are collaborating to develop a Bering Sea baseline of genetic markers to be used to determine composition of stock mixtures caught on the high seas.

The baseline is composed of 166 collections extending from Northern Alaska Peninsula (8), through Bristol Bay (136; Fig. 1), north to Norton Sound (1) and west to the Kamchatka River and Kuril Lake drainages in Russia (23). Genotypes from 42 allozyme, eight microsatellite, and one single nucleotide polymorphism (SNP) loci were collected on approximately 100 fish per collection. Simulations using the Statistical Program to Analyze Mixtures (SPAM; Debevec et al. 2000) were used to identify reporting groups. High-seas collections from ABL Ocean Carrying Capacity (OCC) surveys were pooled regionally within years to attain approximately 400-fish samples. Initial stock composition estimates were made on these samples using allozymes in the 1999 and 2001 collections and using microsatellites and a SNP in some of the 2002 collections to identify patterns of stock distributions.

Simulation results produced 11 reporting groups which demonstrated high precision in estimating continent-of-origin, and distinguishing between North Alaska Peninsula, Bristol Bay and Norton Sound collections. Within Bristol Bay, collections from Kvichak Bay drainages south to Meshik River (eastern Bristol Bay) clustered together and separately from those from Nushagak Bay drainages east to the Kuskokwim Bay drainage (western Bristol Bay).

Within eastern Bristol Bay, each group of collections from drainages above obstacles to migration, such as rapids or falls, was a reporting group, but collections made from the remaining areas where unexpectedly homogeneous and produced a single reporting group (Fig. 2). Within western Bristol Bay collections, each major drainage was a reporting group (Fig. 3).

Results from 1999 surveys, which had the largest number of fish, are consistent with sequential migration along the North Alaska Peninsula whereby Bristol Bay drainage stocks enter the ocean at about the same time and then migrate south and east along the Alaska Peninsula (Figs. 4 and 5; Farley et al. 1999). Sampling design changed in 2000, so the pattern detected in 1999 was hard

Fig. 1. Locations of sites within nursery lake drainages where adult sockeye salmon were captured and tissues taken to resolve microsatellite, SNP and allozyme loci used to examine genetic relationships among populations spawning in drainages of Bristol Bay, Alaska.

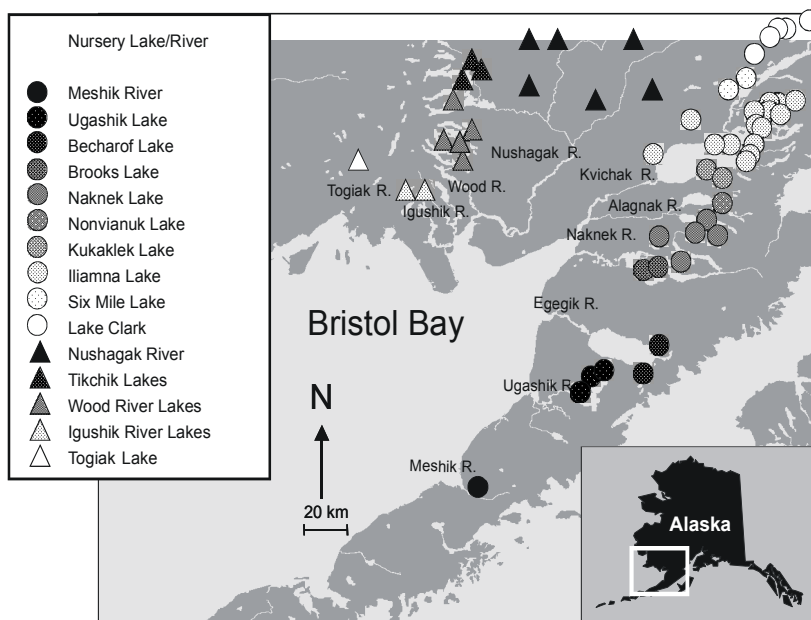


Fig. 2. Multidimensional scaling analysis of microsatellite and SNP data from sockeye salmon captured at 38 sites in Eastern Bristol Bay, Alaska. In 100% simulations, at least 89% were correctly allocated to each of the circled groupings using microsatellites and SNP and all circled groupings except Six Mile Lake using allozymes.

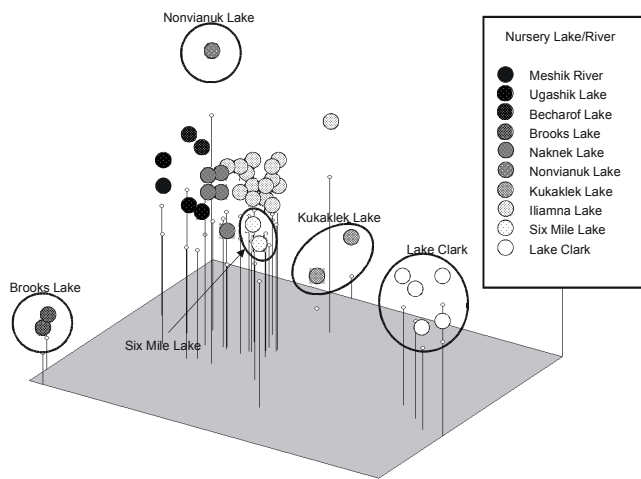


Fig. 3. Multidimensional scaling analysis of microsatellite and SNP data from sockeye salmon captured at 17 sites in Western Bristol Bay, Alaska. In 100% simulations, at least 89% were correctly allocated to each of the circled groupings using either microsatellite and SNP loci or allozymes.

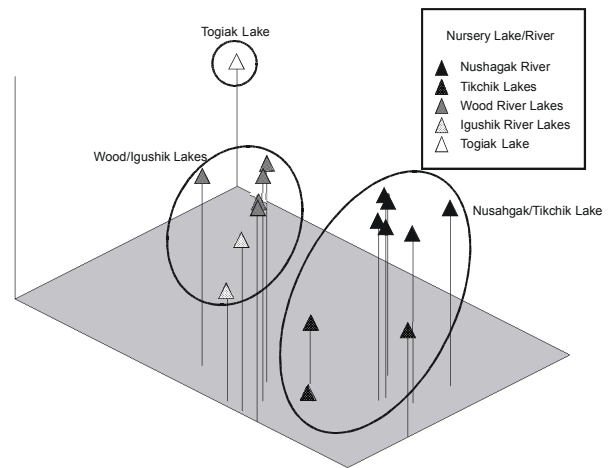


Fig. 4. Stock composition, using allozymes, of juvenile sockeye salmon captured in the Ocean Carrying Capacity project in July, 1999 from four transects. 'N' equals the number of fish included in the mixture sample.

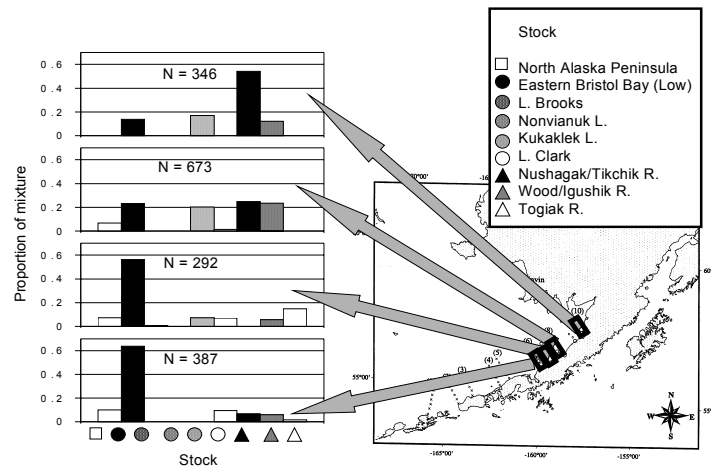
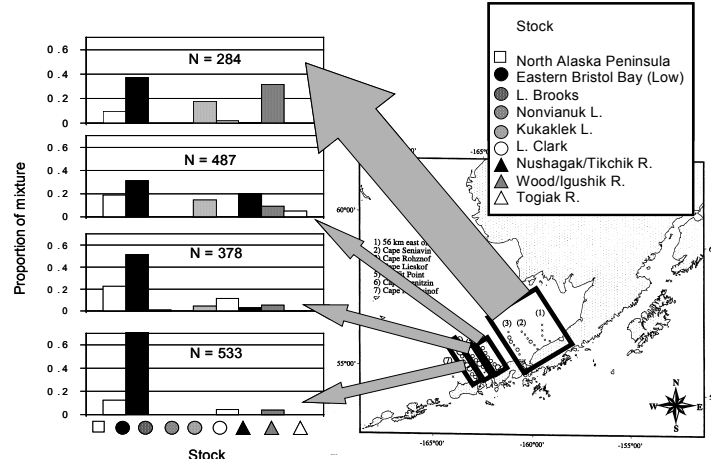


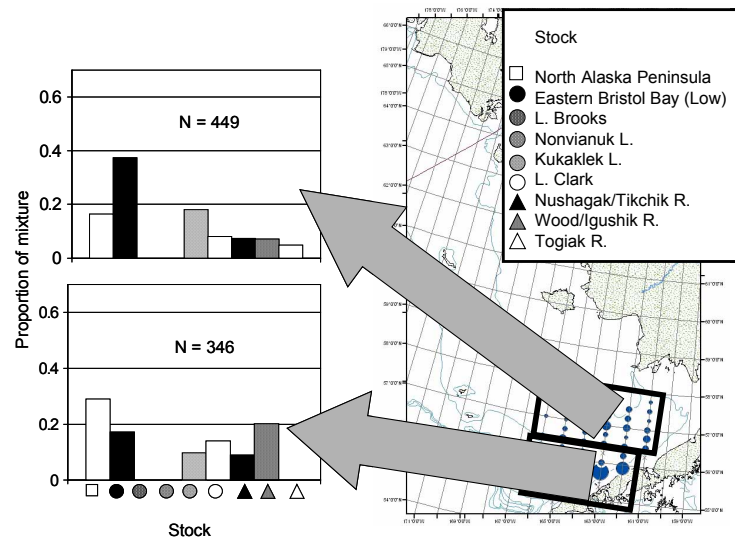
Fig. 5. Stock composition, using allozymes, of juvenile sockeye salmon captured in the Ocean Carrying Capacity project in September, 1999 from four transect groups. 'N' equals the number of fish included in the mixture sample.



to compare with later years (Farley *et al.* 2000, 2001 and 2002). In 2001, only enough samples were taken to produce two estimations of stock composition: 1) near shore and 2) offshore (Farley *et al.* 2001). Near shore estimates indicated relatively higher numbers of North Alaska Peninsula stocks, while offshore estimates indicated relatively more eastern Bristol Bay stocks (Fig. 6). Only enough samples were analyzed in 2002 to produce a single stock composition estimate, so no patterns could be identified (data not shown).

We plan to collect genotypes for allozyme, microsatellite and SNP loci on all the OCC samples from 1999 to 2002. We plan to collect genotypes from microsatellite and SNP loci from the 2003 OCC samples and the Bering Aleutian Salmon International Survey samples from 2003 and 2004. Adding the DNA markers will produce more precise estimates of stock composition and completing the remaining samples will allow for better interpretation of migration patterns. In addition, we are screening an additional five microsatellite loci in the full baseline to determine if eastern Bristol Bay drainage stocks below obstacles to migration can be separated into more reporting groups.

Fig. 6. Stock composition, using allozymes, of juvenile sockeye salmon captured in the Ocean Carrying Capacity project in August, 2001 for two sets of collections, those north and south of 56.5°N. 'N' equals the number of fish included in the mixture sample.



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