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Simulations of the Odd-Year Pink Salmon (*Oncorhynchus gorbuscha*) Genetic Baseline to Determine Accuracy and Precision of Stock Composition Estimates, and Mixture Analysis of Juveniles from the Bering Sea

by

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Simulations of the Odd-Year Pink Salmon (*Oncorhynchus gorbuscha*) Genetic Baseline to Determine Accuracy and Precision of Stock Composition Estimates, and Mixture Analysis of Juveniles from the Bering Sea

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Abstract

Allozyme data was analyzed for 90 odd-year pink salmon populations from a broad range of the Pacific Rim. Results indicated structure exists among regions. Southern Asia populations (Japan, Sakhalin and Kuril Islands) differ significantly from northern populations (Kamchatka and the sea of Okhotsk). There are only two small river systems from western Alaska in the baseline. They appear to be genetically similar to stocks from Kamchatka. Multidimensional scaling analyses reveal a gradation of genetic differentiation among British Columbia, Southeast Alaska and central Alaska.

Simulations of the baseline reflect results indicated by the structure. In simulations with 100% expected results, southern Asia is distinguished with 94% accuracy. Western Alaska is not genetically distinct (68%) from Kamchatka, though estimates may improve with increased representation from western Alaska. Because of a continuum of structure exhibited throughout central and southeast Alaska and British Columbia, 100% expected simulations produce results with about 75% accuracy by region. Estimates by region are improved with an increased number of loci. Further investigation may reveal more localized structure.

A collection of 286 pink juveniles from the eastern Bering Sea were analyzed to determine their region of origin. Results indicated a mixture of sizes and genomes. Log likelihood estimates suggest approximately 42% of the individuals are from Kamchatka and 44% from Norton Sound, with the rest misallocated to Prince William Sound or Japan. While the results appear consistent with the expected, the standard error around these estimates is large and improvements to the baseline and/or additional markers will be needed before it can be accurately applied.

Introduction

Little is known about the marine ecology and migration of pink salmon. Pink salmon are a key indicator species for ocean environments because of their short and specific 2-year life span and alternate brood years. In 2004 and 2005, pink salmon returns increased significantly to regions surrounding the Bering Sea. Even historically small odd-brood year runs experienced explosive returns. The Nome River in western Alaska supported an escapement of 11,000 pinks in 2003; in 2005, the escapement swelled to 285,000 (ADFG Fishery Data Series No. 05-24).

Over the past two decades, odd-year pink salmon have been collected and analyzed for allozyme variation from more than 110 river systems around the Pacific Rim. Here we begin to examine stock structure, and investigate the accuracy and precision of stock composition estimates. In 2004, pink juvenile salmon were collected from the Bering Sea and analyzed for stock composition.

Methods

This study combines published data from Hawkins et al. 2002, and unpublished data from North America. An array of population structure analyses such as homogeneity tests and cluster analysis was conducted on a varying number of populations and loci. Initial analyses, such as multidimensional scaling, were done using 80 populations and 39 loci. All loci could not be reliably scored for all populations, thus the baseline used for simulations in this study was constructed with a maximum number of populations (90) balanced with a useful number of loci (30). Simulations of 100% composition from each of six regions were run using a conditional maximum likelihood method (SPAM 3.7) that used a simulated mixture size of 300. 90% confidence intervals were estimated from 1000 bootstrap iterations. Simulations of 25% composition from each of four regions closest to the Bering Sea were also calculated to ascertain accuracy of a mixture from the Bering Sea.

In 2004, juvenile pink salmon were collected from the eastern Bering Sea ($n=286$) on the US BASIS survey. Samples were processed from eight stations between latitude 59.5N - 62.5N and longitude 167.0W - 172.0W (Fig. 1). Fork length (mm) and weight (g) were recorded and muscle, heart, liver and eye were retained for allozyme analysis. Protein electrophoretic procedures were followed as in Hawkins et al. 2002 and stock estimates of this mixture were determined using the same 30 loci in the baseline (SPAM 3.7).

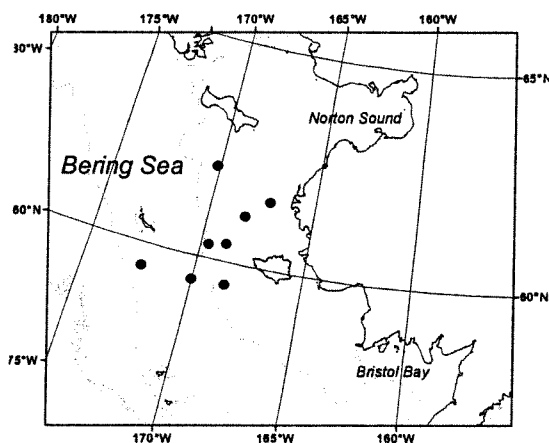


Fig. 1. Location of juvenile pink salmon caught in the Bering Sea in 2004.

Results and Discussion

Tests of homogeneity and multidimensional scaling indicate genetic heterogeneity exists among odd-year pink salmon of the Pacific Rim (Fig.2). Populations from southern Asia (Japan, Sakhalin and Kuril Islands) cluster together and significantly differ from populations in northern Russia, the Okhotsk Sea and Kamchatka (Hawkins et al., 2002). British Columbia, southeast Alaska and central Alaska populations form a distinct group with a north-south gradation of structure. Western Alaska fish are genetically similar to northern Russia populations, a pattern also evident in even-year populations (Noll et al., 2001). However, the western Alaska region is greatly under-represented in the baseline, containing only 83 individuals from two rivers near Nome in Norton Sound,

Alaska. Pink salmon populations from Bristol Bay, the Alaska Peninsula and the Aleutian Islands are not represented.

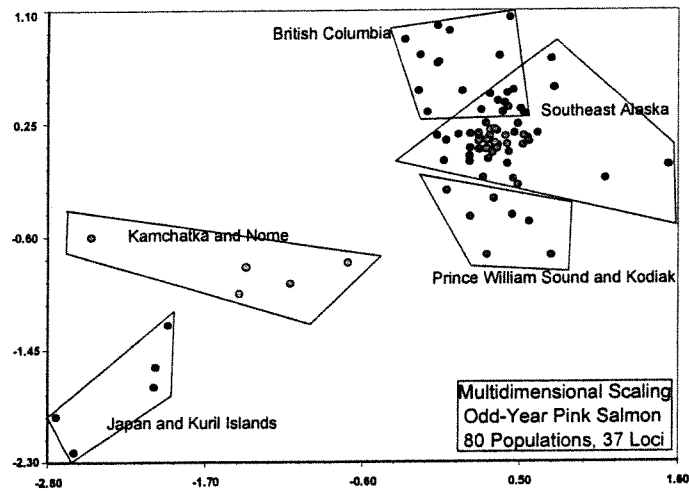


Figure 2. Multidimensional scaling of 80 odd-year pink salmon populations, using 37 loci.

Simulations of 100% composition of the six regions are consistent with the multidimensional scaling results (Table 1). Because of a continuum of structure exhibited throughout central and southeast Alaska and British Columbia, 100% expected simulations produce results with about 75% accuracy by region. The majority of misallocation among these three regions is assigned to adjacent regions. Estimates by region are improved with an increased number of loci. However, populations missing data at these loci must be excluded. Further investigation may reveal more localized structure, and more useful information for stock identification.

Table 1. Simulations (and standard deviation) for each region and percent misallocation by region, read horizontally. Estimates in bold were theoretically expected to be 100%.

Region	BC	SE	PW/KD	wAK	Kam	Jap/Sak/Kur
British Columbia	.72 (.09)	.24	.01	.01	.01	.01
Southeast Alaska	.09	.83 (.09)	.05	.01	.01	.01
PWS/Kodiak	.02	.23	.70 (.09)	.01	.03	.01
Western Alaska	.01	.04	.02	.68 (.11)	.20	.05
Kamchatka	.01	.04	.02	.05	.83 (.07)	.05
Japan/Sakhalin/Kurils	.01	.01	0	.01	.03	.94 (.04)

Because western Alaska is under-represented in the baseline, and 100% estimates show a heavy bias assigned to Asian stocks, a simulated mixture of four regions, with an expected composition of 25% for each region was estimated. The results show that theoretically, a mixture estimate would underestimate western Alaska with a mixture estimate of 17% (.08) and overestimate the other regions: northern Asia with an estimate of 29% (.09), central Alaska 27% (.05) and southern Asia 27% (.07).

Results of the pink salmon juvenile mixture analysis suggest that in addition to the presumed presence of western Alaska fish, some northern Russian stocks are also present on the eastern Bering Sea shelf (Table 2). While the mixture estimates approximate an expected result, the standard errors around the estimate are large. Average length and weight of individuals in this mixture supports the presence of fish from multiple sources. The three easternmost hauls yielded significantly larger fish: 20cm in length and 85g as compared to the other five hauls: 17cm and 50g.

Table 2. Mixture estimate for 286 Bering Sea pink Juveniles captured in 2004.

<u>Estimate</u>	<u>Region</u>
.42(.24)	Kamchatka
.44(.23)	Western Alaska
.06(.10)	Prince William Sound
.08(.14)	Japan

While the current allozyme baseline has a level of misallocation higher than we would like using six geographic regional groupings, there is some strong population structure with a geographic basis, which may be better described with DNA markers such as microsatellite or SNP loci. We recommend that additional collections be taken from representative pink salmon populations from the Bering Sea coast of Alaska to improve baseline coverage. Closing the gaps in the baseline will be necessary to improve mixed stock estimates used to better understand migration of juvenile pink salmon in the Bering Sea.

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