

## Even-Year Pink Salmon Pacific Rim Allozyme Baseline and Origin of Juveniles from Gulf of Alaska Coastal Waters, 2003

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Over the past two decades, even-year pink salmon have been collected and analyzed for allozyme variation from more than 150 river systems around the Pacific Rim. These studies have been accomplished by many individuals and laboratories. Most have been published as independent studies. This study combines data from those studies and unpublished data from North America. Where allele standardization was unavailable, alleles were pooled. The baseline used for simulations in this study attempted to maximize numbers of populations, balanced with a useful number of loci. The number of loci available across all populations was between 6 and 54. A series of analyses such as G-test, genetic distance, and multidimensional scaling was examined on baselines of varying numbers of populations and loci.

Simulations to estimate accuracy of stock allocations in a mixture were run using conditional maximum likelihood analysis. Using a baseline of 31 loci and 77 populations, the proportion (90% confidence interval) of regional simulated mixtures correctly assigned, when the expected is 100%, is as follows:

Magadan/Kamchatka, Russia	0.91 (0.85–0.95)
Japan/Sakhalin, Russia	0.95 (0.93–0.98)
Alaska/northern British Columbia	0.95 (0.94–0.97)
Snohomish River, Washington	0.93 (0.89–0.98)

Finer regional scale simulations of North American fish were less accurate:

Prince William Sound, Alaska	0.70 (0.58–0.85)
Little Susitna River, Alaska	0.85 (0.73–0.97)
Southeast Alaska	0.90 (0.80–0.97)
Northern British Columbia	0.64 (0.49–0.79)
Snohomish River, Washington	0.92 (0.87–0.99)

Three groups of juvenile pink salmon were collected ( $n = 781$ ) from the northern Gulf of Alaska, between Kodiak and Prince William Sound, by the Auke Bay Laboratory's Ocean Carrying Capacity program in July of 2003. Juveniles in the nearshore, mid-shelf, and offshore collections averaged 130, 142, 153 mm in length ( $p > 0.001$ ). Conditional maximum likelihood analysis using North American populations of the coastwide baseline allocated the regions of origin (with Standard Error) as follows (allocation to Asian populations was 0):

	<u>n</u>	<u>Susitna</u>	<u>P.W.S.</u>	<u>S.E. AK</u>	<u>Snoho</u>	<u>N. BC</u>
Nearshore	300	0	0.96 (0.89-1.0)	0.05 (0-0.11)	0	0
Mid-Shelf	241	0	0.43 (0.24-0.78)	0.54 (0.21-0.74)	0	0
Offshore	80	0.12 (0-.25)	0.58 (0.30-1.0)	0.27 (0-0.47)	0	0