

## AFSC/ABL: Sockeye salmon allozyme baseline - 1982-1990

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Genetic data were collected and prepared with the use of protein electrophoresis from 52 spawning locations in southeastern Alaska and northern British Columbia. Genetic relationships were examined from principal components analysis and unrooted trees constructed from genetic distances between collections. These descriptive analyses suggest a geographic basis to genetic divergence among populations. This geographic basis was confirmed using log-likelihood-ratio analysis and analyses of variance. Three groups of populations were observed: one from systems that drain into the inside waters of northern and central southeast Alaska; another from the far southeastern islands (including Prince of Wales Island); and the third in systems of the southern inside waters. Although the geographic structure was a statistically significant component of the overall genetic structure, gene diversity analysis indicates that only about 4.7% of the total genetic variability was attributable to genetic differences among those regions, whereas about 8.4% of the total was due to differences among populations within each region. The other 87.0% of the variation occurred, on average, within each collection.