

Genetic Population Structure of Alaska Eulachon

Genetic variation was assayed at 14 microsatellite loci to investigate the genetic population structure of Alaska eulachon. Alaska eulachon have high levels of genetic diversity and relatively large effective population sizes (N_e), although a large variance in reproductive success is likely responsible for a low N_e / N ratio. Eulachon exhibit a low degree of genetic divergence ($G_{ST} = 0.005$) that is structured by broad-scale geographic regions. Overall, there is a significant correlation between genetic and geographic distance, suggesting that gene flow is geographically restricted and follows an isolation-by-distance (IBD) model, with geographic distance explaining 28% of the genetic variation. However, closer analysis reveals an absence of IBD within regions and that gene flow is primarily restricted by geographic distance between regions. The demographic independence of the regions warrants separate management regimes. However, it may be prudent to take a precautionary approach and conserve potential spawning habitat throughout the geographical range of eulachon because of high gene flow and variable use of rivers for spawning.

Key Words: eulachon, genetic population structure, genetic diversity, effective population size.

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