# Fishing for population structure in North Pacific seals: challenges, pitfalls and solutions

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The analysis of population genetic structure traditionally consists of: (A) testing explicit hypothesis, such as genetic differentiation among breeding groups, and (B) inference about what genetic heterogeneity means in terms of historical relationships or the level of contemporary gene flow or dispersal. Both have proven difficult in several North Pacific seal species such that the analysis of population subdivision is often reduced to a fishing exercise driven primarily by sampling limitations, and often applying incorrect approaches, insufficient markers and inappropriate stratification regimes. Drawing on extensive datasets of Pacific harbor seals (*Phoca vitulina*, n=1,449), spotted seals (*P. largha*, n=244), bearded seals (*Erignathus barbatus*, n=160) and ribbon seals (*P. fasciata*, n=33) for mtDNA and up to 16 microsatellite markers, we conducted a critical analysis of a broad array of approaches for investigating population subdivision. Genetic differentiation was found in harbor, spotted and bearded seals at a number of spatial scales, indicative of restricted dispersal at range of temporal scales. Five key findings affected our ability to reveal underlying patterns of dispersal and gene flow: (1) Sampling regime. Seals were often sampled opportunistically, e.g. on migration or during long-distance foraging trips, limiting our ability to characterize baseline populations. (2) High mtDNA diversity (He0.92) in all species indicated large historical population sizes but severely limited statistical power in frequency-based analysis. (3) Small sample size limited information content and increased uncertainty in parameter estimation. (4) Recent common ancestry, asymmetric dispersal and changing population size indicated that equilibrium-based methods may not be appropriate. (5) Most currently available analysis methods, including model-based clustering, gene frequency and coalescent-based methods, are informative only when there s substantial genetic differentiation, which was not always the case for the species investigated. By contrast, individual-based analyses, including genotypic assignment tests and relatedness estimation were relatively assumption free and dealt with contemporary time frames relevant to management. These approaches are yielding fresh insight into breeding and dispersal behavior in harbor seals in Alaska and need to be applied to other species. Such methods, however, are sample intensive and require coordinated, directed sampling where the genetic research is integrated into broader ecological studies.

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