

Mito-communication

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Genetic–demographic models of population decline

Hoffmann et al. (2009) explore the relationship between population structure, genetic diversity and key demographic parameters (effective population size and growth rate) for the once heavily impacted Steller's sea lions (*Eumetopias jubatus*). The authors attempt to provide a broad understanding of this issue by integrating data from common, but seldom combined, molecular markers. Over 230 amplified fragment length polymorphism (AFLP) loci were jointly analysed with 13 microsatellite loci and 240 base pairs of mitochondrial DNA sequence data, which provided concordant evidence of population structure among the three previously identified Steller's sea lion stocks. Interestingly, AFLP and microsatellite data suggested differences in genetic diversity for these stocks while the mitochondrial DNA suggests equivalent estimates for all stocks, which underlines the importance of evaluating both nuclear and mitochondrial data whenever possible. The mitochondrial data alone would have painted a very different picture to the one suggested by evaluating all of the genetic data. One of the most interesting aspects of this analysis came about when the authors combined over 40 years of sea lion abundance data with genetic diversity estimates by constructing a series of general linear models. Using these models, the authors investigate the relationships between population size, population growth

rate and stock identity. Of the three analysed genetic markers, only microsatellite data supported a direct relationship between genetic diversity and population size, even when stock identity was included as a predictor variable in the models. This again underscores the importance of avoiding drawing conclusions from a single dataset, like the mitochondrial for instance. In addition, no meaningful relationships were detected between population growth rate and genetic diversity for any of the analysed markers. To further evaluate the usefulness of genetic data for assessing population size fluctuations, the authors evaluated the microsatellite data using tests for significant reductions in population size based on the proportion of alleles and heterozygosity lost during these events. This test provided weak, if any, evidence for the occurrence of a bottleneck to explain the loss in genetic diversity.

To address the lack of correlation found between genetic diversity and population size in the Steller's sea lions, the authors suggest that the temporal scale of the population size reductions may have been short enough to prevent a strong genetic signature in the diversity estimates. In addition, they postulate that ongoing gene flow among sea lion colonies would reduce the chance of independent demographic trajectories, and would in turn equalize genetic and demographic fluctuations. The results of this study highlight the importance of utilizing both mitochondrial and nuclear genetic

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data, in combination with different lines of evidence, to address the inherent complexities of population size decline and its resulting genetic signature in natural populations.

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References

- Hoffman JI, Dasmahapatra KK, Amos W, Phillips CD, Gelatt TS, Bickham JW. 2009. Contrasting patterns of genetic diversity at three different genetic markers in a marine mammal metapopulation. *Mol Ecol* 18:2961–2978.