

Should I stay or should I go? Dispersal, colonization and mate choice in Steller sea lions

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Mate choice and the decision to disperse or not have major implications for individual fitness, group structure, population dynamics and genetic subdivision. Understanding these processes is essential in the management of perturbed populations where dispersal and (re)colonization are key elements of population recovery and viability. Such behaviors, however, are especially challenging to study in marine mammals. We used genetic data and observations of marked animals to study the mechanisms of mate choice, individual transfer and rookery formation in three metapopulations of Steller sea lions that exhibited differing trends. Analysis of large numbers of sea lion pups from 28 rookeries for mtDNA variation (control region; n=1,840), and microsatellite polymorphism (16 loci; n=820) revealed a general pattern of female-mediated philopatry ($F_{st \text{ mtDNA}}=0.1$) and male-mediated gene flow ($F_{st \text{ nDNA}}=0.003$). Unexpectedly, new rookeries were colonized by breeding females from both a declining (endangered) as well as increasing metapopulation. Paternity and assignment tests revealed that the original female colonists had mated successfully with bulls from their natal metapopulation. Subsequent cohorts exhibited greater mixing with many females choosing males from a different source metapopulation. The temporal dimension provided by genetics indicated that these colonization events are rare because colonists dispersed across a strong evolutionary-scale boundary. These findings establish a new paradigm in mate choice and dispersal in marine mammals. Density-dependent processes, limited migration distance and conspecific attraction are all implicated in the pattern of rookery formation. In addition to reducing birth and increasing death rates, this study demonstrates that resource limitation may trigger an exodus of breeding animals from declining populations, with substantial impacts on distribution and patterns of genetic variation. When emigration events are found to be rare in the evolutionary history of a population, it raises suspicions that the causative factors behind the decline are also rare or of larger magnitude than normally occur.

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