Using Molecular Genetics to Estimate Dispersal Rates Between Steller Sea Lion Rookeries

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Estimating dispersal rates between rookeries is important to understand past and future population dynamics of Steller sea lions (*Eumetopias jubatus*). Direct estimation of dispersal requires tracking many individuals throughout their lives. A quicker and less expensive method to indirectly estimate dispersal uses patterns of variation at selectively neutral genetic markers that reflect patterns of dispersal over time. We developed a case-specific simulation technique using mtDNA data to estimate dispersal rates. We found that acceptably precise estimates of dispersal required both high sample size (60-150 individuals per rookery) and relatively long mtDNA sequences (532 bp of control region). Estimated annual dispersal among rookeries in the Eastern stock, where numbers are increasing, ranged from 0.1% to 1% corresponding to 5 to 50 females dispersing each year, indicating that rookeries in Southeast Alaska are demographically connected. This agrees with independent evidence of the close historical relationships and evidence from branding studies of continued connectivity between rookeries in this region. Conversely, dispersal rates between rookeries in the Western stock, where numbers have declined dramatically, were about 0.01% corresponding to << 1 female per year. Such low levels of dispersal were surprising and indicate that neighboring rookeries are, in effect, demographically separate entities. These findings provide insight into the meta-population dynamics of sea lion populations and facilitate predictions on how depleted populations will recover.

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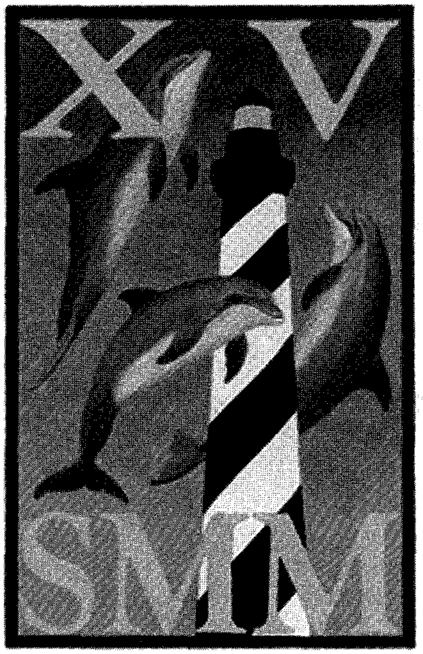

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