

FEATURE ARTICLES

LACK OF SPATIAL GENETIC STRUCTURE AMONG NESTING AND WINTERING KING EIDERS

JOHN M. PEARCE^{1,5}, SANDRA L. TALBOT¹, BARBARA J. PIERSON¹,
MARGARET R. PETERSEN¹, KIM T. SCRIBNER², D. LYNNE DICKSON³ AND
ANDERS MOSBECH⁴

¹*U.S. Geological Survey, Alaska Science Center, 1011 E. Tudor Rd., Anchorage, AK 99503*

²*Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI 48824*

³*Canadian Wildlife Service, Edmonton, AB T6B 2X3, Canada*

⁴*National Environmental Research Institute, Department of Arctic Environment, Frederiksborgvej 399, DK4000 Roskilde, Denmark*

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⁵E-mail: john_pearce@usgs.gov

Abstract. The King Eider (*Somateria spectabilis*) has been delineated into two broadly distributed breeding populations in North America (the western and eastern Arctic) on the basis of banding data and their use of widely separated Pacific and Atlantic wintering areas. Little is known about the level of gene flow between these two populations. Also unknown is whether behavioral patterns common among migratory waterfowl, such as site fidelity to wintering areas and pair formation at these sites, have existed for sufficient time to create a population structure defined by philopatry to wintering rather than to nesting locations. We used six nuclear microsatellite DNA loci and cytochrome *b* mitochondrial DNA sequence data to estimate the extent of spatial genetic differentiation among nesting and wintering areas of King Eiders across North America and adjacent regions. Estimates of interpopulation variance in microsatellite allele and mtDNA haplotype frequency were both low and nonsignificant based on samples from three wintering and four nesting areas. Results from nested clade analysis, mismatch distributions, and coalescent-based analyses suggest historical population growth and gene flow that collectively may have homogenized gene frequencies. The presence of several unique mtDNA haplotypes among birds wintering near Greenland suggests that gene flow may now be more limited between the western and eastern Arctic, which is consistent with banding data.

Key words: gene flow, King Eider, microsatellites, mitochondrial DNA, population genetic differentiation, seaduck, *Somateria spectabilis*.