

FEATURE ARTICLES

**POPULATION DIVERGENCE TIMES AND HISTORICAL DEMOGRAPHY IN RED KNOTS AND DUNLINS**

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*Abstract.* We employed Bayesian coalescent modeling of samples of mitochondrial control region sequences in two species of shorebird, Red Knots (*Calidris canutus*) and Dunlins (*Calidris alpina*) to estimate evolutionary effective population size, population divergence times, and time to most recent common ancestor of genes in the samples. The gene trees for the two species contrast sharply: knot haplotypes were connected in a shallow, star phylogeny whereas Dunlin haplotypes were related in a deeper bifurcating genealogy. Divergence times of populations representing all six subspecies of knots are estimated to have occurred within the last 20 000 (95% CI: 5600–58 000) years, and evolutionary effective population sizes of females are small ( $N_{ef} = 2000–14\ 000$ ). We hypothesized that breeding knots were restricted to unglaciated regions of Eurasia during the last glacial maximum, and gradually expanded eastwards into Alaska, the high Canadian Arctic and Greenland as the ice melted. Population divergence times in Dunlins are much older (58 000–194 000 ybp) and effective population size has historically been higher in major lineages ( $N_{ef} = 12\ 000–44\ 000$ ). We conclude that Dunlin populations were not severely reduced in size in the last 200 000 years, and major lineages have differentiated under restricted gene flow for a much longer time than knots. Knots present a snapshot of genetic evolution in the last 20 000 years, whereas Dunlins display patterns of genetic evolution over an order of magnitude longer time frame.

*Key words:* *Calidris alpina*, *Calidris canutus*, *coalescent theory*, *control region*, *mitochondrial DNA*, *phylogeography*.