

POPULATION GENETICS OF MIDCONTINENT SANDHILL CRANES

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Abstract: The Midcontinent Sandhill Crane Population is comprised of 3 subspecies, lesser (*Grus canadensis canadensis*), Canadian (*G. c. rowani*), and greater (*G. c. tabida*) sandhill cranes. In conjunction with the USGS Northern Prairie Wildlife Research Center, we studied the extent of genetic variation between and within each race of the Midcontinent Sandhill Crane Population. DNA was extracted from 150 feather and dried blood samples collected from 1995–99 from sandhill cranes in the Platte River Valley, central Nebraska. Parsimony and maximum likelihood analysis of the mtDNA D-loop sequences (ca 675 bp amplified using PCR) from 29 sandhill cranes and 3 other species revealed 2 distinct clades within *G. canadensis*. Using known morphological data, these 2 clades represent *G. c. canadensis* and *G. c. tabida*. Birds measured as *G. c. rowani* proved indistinguishable from either *canadensis* or *tabida* and are therefore included in both clades. Genetic divergence was 6.6% to 9.4% between the 2 subspecies: 0.1% to 6.0% within *G. c. canadensis* and 0.1% to 6.1% within *G. c. tabida*. From the sequence data, PCR-RFLP analysis was conducted on all 150 sandhill cranes using 5 restriction enzymes. PCR-RFLP revealed 16 haplotypes but was still able to differentiate only 2 subspecies. Based on the levels of mtDNA D-loop variation observed, this marker will be useful for genetic monitoring of these subspecies. In addition, the ability to use feather samples for genetic analysis will facilitate monitoring of cranes in the wild and make museum specimens useful as well.

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