

FEATURE ARTICLES

GENE FLOW AND GENETIC CHARACTERIZATION OF NORTHERN GOSHAWKS BREEDING IN UTAH

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Abstract. Adult movement and natal dispersal data demonstrate that Northern Goshawks (*Accipiter gentilis*) are able to travel over long distances, suggesting a large functional population. However, these data are unable to determine whether these movements contribute to gene flow among adjacent breeding areas. We used eight microsatellite DNA loci and mitochondrial DNA control-region sequence data to assess population structure of Northern Goshawks breeding in Utah. Goshawks had moderate levels of genetic variation at microsatellite loci (observed heterozygosity = 50%), similar to levels found in other medium-sized, highly mobile birds. Overall estimates of interpopulation variance in microsatellite alleles ($F_{ST} = 0.011$) and mtDNA haplotypes ($\Phi_{ST} = 0.126$) were low and not significantly different from zero. Pairwise population comparisons using microsatellite markers revealed no differentiation among sampled sites, indicating that the functional population extends beyond Utah. However, pairwise population analyses of mtDNA uncovered a single case of differentiation between goshawks inhabiting Ashley National Forest, in northeastern Utah, and Dixie National Forest, in southwestern Utah. Low levels of population structuring observed in mtDNA between the two forests may be due to the smaller effective population size sampled by mtDNA, a cline of haplotypes across the West, or the presence of a contact zone between *A. g. atricapillus* and goshawks of southern Arizona and the Mexican Plateau.

Key words: *Accipiter gentilis*, gene flow, microsatellite loci, Northern Goshawk, population structure