

LETTERS

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UNUSUAL NORTHERN GOSHAWK mtDNA HAPLOTYPE FOUND IN THE ROCKY MOUNTAINS

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The Northern Goshawk (*Accipiter gentilis*; hereafter “goshawk”) is a large forest raptor that is of management interest across the American West (Reynolds et al. 1992, Patla 2005, Dickson et al. 2014). When considering management objectives for any species, understanding dispersal rates is of critical importance. Since 2012, our research group has been studying goshawks to better understand gene flow and dispersal in the Northern Great Basin of western North America, and to place the goshawks in our study area within the biogeographical context set forth by Bayard de Volo et al. (2013). Previous work on goshawk dispersal conducted by Wiens et al. (2006) found that local natal dispersal distance of goshawks in the Kaibab Plateau of Arizona was 15 km (median distance; mean = 16.7 ± 1.2 km; range = 0.1–58.1 km). Breeding dispersal distance of adults within the northern Great Basin was 2.1–5.8 km (Bechard et al. 2006). However, Wiens et al. (2006) recorded juvenile movements as far as 442 km outside of their study area. With such dispersal potential and wildlife management interest, goshawks make a compelling species in which to study genetic diversity and structure.

We focused on a small and relatively isolated population of goshawks in south-central Idaho and northern Utah (Miller et al. 2014). We collected 36 genetic samples (either feathers or blood) from individual goshawks at nest sites (i.e., one mtDNA lineage per nest or two if both adult male and adult female were caught) in 2012, 2014, and 2015 to

evaluate the variation of mitochondrial DNA sequences (mtDNA haplotypes) and dispersal using microsatellite markers (S. Szarmach unpubl. data). In addition to our focused study in south-central Idaho, we collected a smaller sample ($n = 3$) of molted flight feathers from goshawks across Idaho. It was in this sampling across Idaho that we detected an H-haplotype usually found in the American Southwest (Bayard de Volo et al. 2013). Here we report this finding and discuss its significance within the context of our larger study.

To extract DNA from molted flight feathers we followed the extraction protocol outlined by Bayard de Volo et al. (2008). Then following the methods by Sonsthagen et al. (2004), we amplified a 450-base-pair fragment sequence from the the domain I control region of the mitochondrial DNA. Successful PCR amplications were purified using ExoSAPit (Affymetrix, Cleveland, OH, USA) and sequenced by Genewiz (Genewiz, Plainfield, NJ, USA). Sequences were reconciled using Phy-DE (Müller et al. 2005). A single individual was represented by a haplotype that matched with 100% identity to haplotype H (GenBank accession AY699835.1; Sonsthagen et al. 2004, Bayard de Volo et al. 2013) using a BLAST analysis (Altschul et al. 1990).

Previous research indicates that following the most recent glacial period, goshawks expanded within western North America from two primary refugia (Bayard de Volo et al. 2013). One refugium was in the “Pacific” (Cascade and Sierra Nevada Mountains) and the other in the “Southwest” (Colorado Plateau and the Jemez Mountains, NM; Bayard de Volo et al. 2013). Bayard de Volo et al. (2013) found several haplotypes specific to the Southwest refugium. One of these haplotypes, the H-haplotype, was found in low frequencies and was restricted to the Colorado Plateau and Arizona Sky Island populations. Interestingly,

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the H-haplotype that we detected was from a bird in central Idaho, near the town of Obsidian. This H-haplotype had not been previously described for goshawks in the Rocky Mountain region, and was not found in the other sampling in south-central Idaho (S. Szarmach unpubl. data).

There are a few possible explanations for the presence of the H-haplotype in the goshawks of the Idaho population. The first and most likely explanation is that this haplotype is not endemic to only the Southwest and Colorado Plateau, but occurs in the Rocky Mountains in low frequencies and was not detected by Bayard de Volo et al. (2013) with a sample size of 18 Rocky Mountain goshawks. In a recent genomic survey of goshawks, Geraldes et al. (2019) found there was weak genetic structuring from southeastern Alaska to New York with no clear separation of populations in a principal component analysis excluding Haida Gwaii. However, this study did not include goshawks from the Rocky Mountain regions of the United States or the American Southwest in their genomic dataset (Geraldes et al. 2019). The presence of a bird with this haplotype in Idaho may indicate that overall there is less genetic structure than previously thought. However, further study is needed.

A second explanation involves natal dispersal of individuals from surrounding populations. Female-mediated gene flow from the Arizona sky islands and Colorado Plateau may occur at a low rate (95% CI for number of female migrants per generation was 0–2 and 2–17, respectively; Bayard de Volo et al. 2013). Researchers on the Kaibab Plateau of northern Arizona hypothesized that the primary factors influencing goshawk natal dispersal were environmental conditions, competition for breeding opportunities, and avoidance of inbreeding (Wiens et al. 2006). Such factors may explain the presence of the H-haplotype in Idaho goshawks if its presence resulted from dispersal.

A third explanation is that the H-haplotype occurrence is the result of homoplasy. Overall, this explanation may be unlikely because the H-haplotype is two mutational steps away from the most common B-haplotype and one mutational step away from peripheral haplotypes G and M.

The presence of this H-haplotype in a goshawk in Idaho suggests continued study of the genetic structure of this species in the interior west of the United States may be warranted. Increased sampling with additional autosomal markers across this range will lead to a better understanding of changes in genetic structure on smaller scales, and reveal a more complete evolutionary history of the region. A better understanding of genetic structure, diversity, and dispersal could provide critical information for wildlife managers across the Northern Goshawk range.

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