

**AN ASSESSMENT OF THE GENETIC STRUCTURE OF
AN URBAN COOPER'S HAWK POPULATION**

ANNUAL PROGRESS REPORT

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INTRODUCTION

The U.S. Fish and Wildlife Service has been coordinating a study of the population ecology of an urban population of Cooper's hawks (*Accipiter cooperii*) in Albuquerque, New Mexico since 2011, in collaboration with the New Mexico Department of Game and Fish and New Mexico State University (Millsap et al. 2014). A major objective of this study is to develop a detailed understanding of the demography and population ecology of a model raptor population to obtain insights into the population ecology of harder to study species of management concern, such as golden eagles (*Aquila chrysaetos*). We now have rigorous empirical estimates of the number of occupied Cooper's hawk nesting territories, reproductive success, survival rates, female dispersal, and spatially explicit estimates of prey density for each year of the study (Millsap et al. 2014, Lien et al. 2015, B. Millsap, unpubl. data). The study population is increasing, and the number of occupied nesting territories has increased from 40 in the first year of the study to 67 in 2014 to almost 80 in 2016.

As part of this study, mated pairs of Cooper's hawks are trapped, banded, and color-marked each year, and offspring are trapped, banded and radio-tagged from a subset of randomly selected nesting territories. In addition to being individually marked, standardized measurements are taken on each hawk, feathers (with calamus) are plucked, and a blood sample drawn. We now have tissue samples and feathers suitable for genetic and stable isotope analysis from nearly 450 Cooper's hawks of known breeding status and, for offspring, putative parentage based on the nest they fledged from.

As part of an extension of the demography study, we have initiated a study of the genetic structure, foraging ecology, and migration ecology of the Albuquerque Cooper's hawk study population. We hope to address important questions regarding the general ecology of Cooper's hawks, including: (1) what factors contribute to the high rates of extra-pair paternity observed in Cooper's hawks (Rosenfield et al. 2015), and how those factors may affect individual fitness and population growth; (2) what is the frequency and potential source of immigrants into the Albuquerque study population; (3) what factors, environmental or genetic, best explain migratory behavior in Cooper's hawks; and (4) what is the phylogeographic relationship of this population to others that have been genetically sampled (e.g., Sonsthagen et al. 2012). In addition, this study presents a valuable opportunity to compare and contrast genetic estimates of

population attributes (e.g., estimates of paternity certainty and of effective population size) with direct measures obtained through banding and radio telemetry.

PROJECT OBJECTIVES AND PRELIMINARY RESULTS

1. *Maintenance of a tissue/feather database:* We have hired an undergraduate technician to maintain a Cooper's hawk tissue and feather database in conjunction with an archive of similar samples from golden eagles. The samples are housed at the Department of Fish, Wildlife and Conservation Ecology (FWCE), New Mexico State University (NMSU) and the database currently has 176 entries. A number of samples have to be catalogued. We just received 53 samples from work that is being carried out this spring (2016), with more forthcoming, and we estimate that we currently have approximately 450 samples collected (B. Millsap, pers. comm.).

2. *Stable isotope analysis of food habits and migration patterns:* We are collaborating on a stable isotope analysis with Dr. Seth Newsome (Assoc. Director, Center for Stable Isotopes, University of New Mexico, Albuquerque, NM). Feathers from Cooper's hawks and remains of recovered prey will be assayed for stable isotopes of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) to assess the hawk's food habits. Carbon isotope signatures in an animal's tissue ultimately reflects the ratio of heavy to light carbon ($^{13}\text{C}/^{12}\text{C}$) found in plants. Plants have evolved different photosynthetic pathways and the proteins making up these pathways discriminate between the heavy and light isotopes to varying degrees resulting in different ratios of $^{13}\text{C}/^{12}\text{C}$ in plant tissues. Ratios of carbon are usually referred to as "delta-13 Carbon" ($\delta^{13}\text{C}$) and are expressed with respect to a standard in parts per thousand (‰). Grasses mostly have the C4 photosynthetic pathway and their $\delta^{13}\text{C}$ varies between -14 to -10‰ (Kelly 2000). In contrast, most shrubs have the C3 photosynthetic pathway and their $\delta^{13}\text{C}$ varies between -35 to -21‰ (Kelly 2000). Thus, primary consumers (i.e., herbivores) that are grazers can be distinguished from those that are browsers, and secondary consumers (i.e., carnivores or omnivores) that feed on one group of herbivores or the other can also be distinguished once fractionation among trophic levels is accounted for (Yeakel et al. 2009). Nitrogen, on the other hand, is discriminated during the formation of nitrogenous waste; ^{14}N is eliminated from an animal at greater rates than ^{15}N resulting in higher ratios of $^{15}\text{N}/^{14}\text{N}$ from tissues of animals at higher trophic tiers (i.e., $\delta^{15}\text{N}$ is higher in carnivores than in

herbivores). Thus, $\delta^{15}\text{N}$ can be used to determine an animal's trophic position (i.e., primary, secondary, or tertiary consumer). Carbon and nitrogen isotopic signatures can then be incorporated into mixing models to estimate the proportion of dietary sources (e.g., see Roemer et al. 2002, Newsome et al. 2009). The discrimination of heavy vs. light isotopes and their use in trophic ecology is actually more complicated than we have alluded to here, so we refer you to Kelly (2000) for a more thorough discussion.

In addition to their use in food habits studies, stable isotopes can also be used to explore migration patterns (Bearhop et al. 2005) and they can be particularly useful when combined with genetic information to elucidate both breeding and wintering grounds of avian species (e.g., Chabot et al. 2012, Rundel et al. 2013). Isotopic ratios of hydrogen ($^2\text{H}/^1\text{H}$) and oxygen ($^{18}\text{O}/^{16}\text{O}$) in precipitation vary with latitude, with precipitation farther from the equator being less enriched in the heavier isotopes (Bowen and Revenaugh 2003). This pattern of enrichment occurs because water molecules containing the heavier isotopes weigh more, and it takes more energy to volatilize them into the atmosphere. Consequently, precipitation near the equator is more enriched with the heavy isotopes than precipitation farther away. As it rains, this isotopic signature is taken up by plants and then by the animals that eat them. For a nice review of the use of isotopes in avian studies, including the study of migration, see Inger and Bearhop (2008).

We recently had 28 feather samples analyzed for $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and for deuterium ($\delta^2\text{H}$ or δD). This initial analysis compared fledglings or 'Hatch-Year' (HY) birds to birds in their 'Second Year' (SY). Our purpose was to see if, in general, there was a difference in isotopic discrimination between young and older birds as isotopic signatures may vary between age classes owing to differences in physiology (Inger and Bearhop 2008). There was little difference in the mean isotopic signature of the two age classes (Table 1), but there was variation in this limited sample suggesting that both food habits and migration patterns can be explored. For

Table 1. A comparison of the $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and δD isotopic signatures (mean \pm SD) from the contour feathers of hatch year and second year Cooper's hawks captured in Albuquerque, NM between July 2013 and March 2016.

AGE	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$	δD
HATCH YEAR	-17.84 (0.80)	8.36 (0.63)	-68.74 (7.61)
SECOND YEAR	-17.04 (0.69)	8.67 (0.63)	-62.56 (7.92)

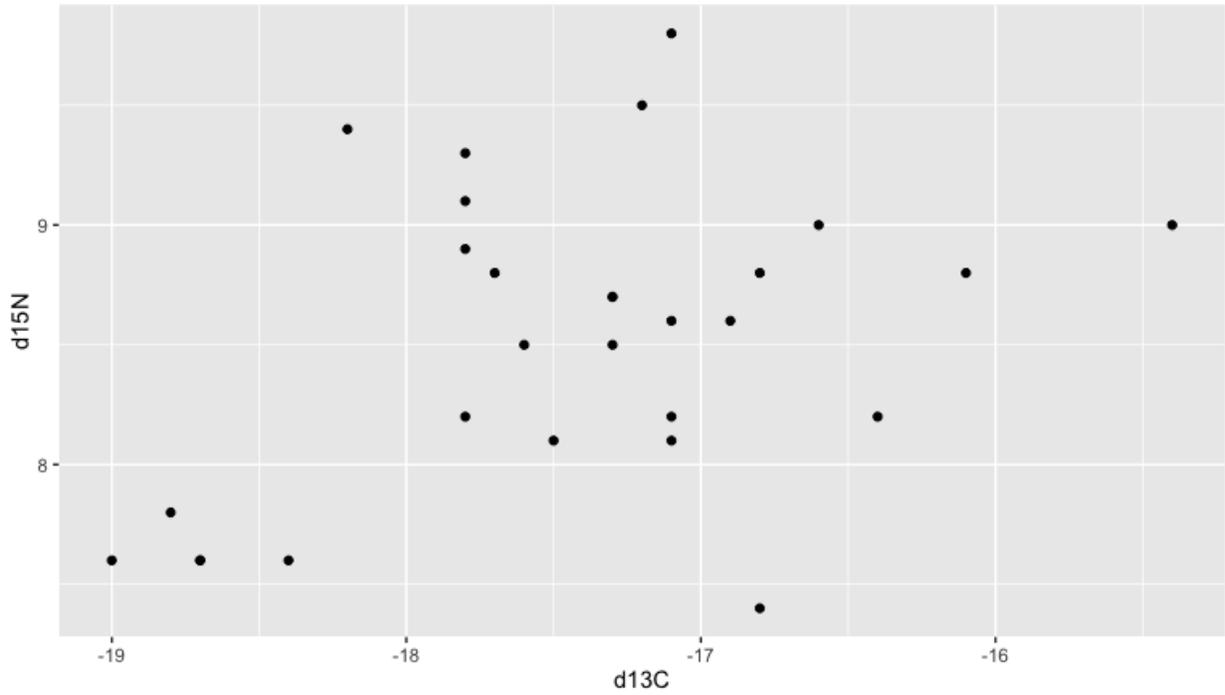


Figure 1. A plot of the $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ in the contour feathers of hatch year and second year Cooper's hawks captured in Albuquerque, NM between July 2013 and March 2016.

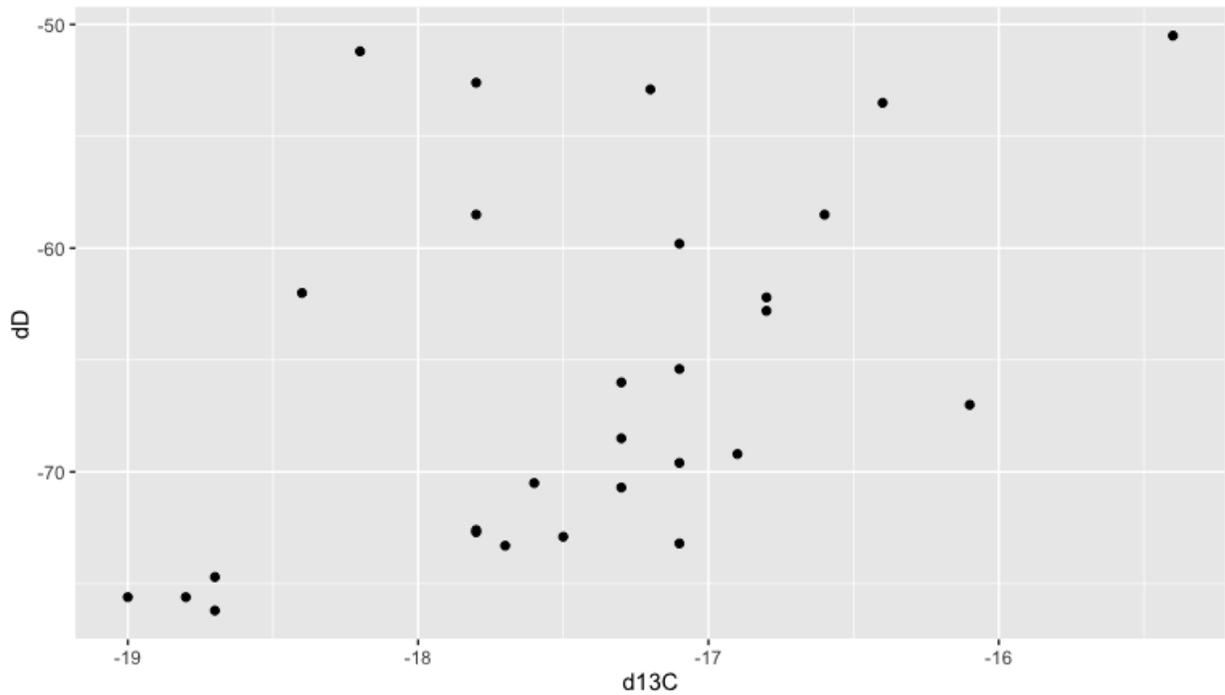


Figure 2. A comparison of the δD and $\delta^{13}\text{C}$ in the contour feathers of hatch year and second year Cooper's hawks captured in Albuquerque, NM between July 2013 and March 2016.

example, there were 6 samples that had $\delta^{13}\text{C}$ values less than -18 and four of these samples had $\delta^{15}\text{N}$ values less than 8, which may reflect a dietary difference compared to the other samples. These samples came from nesting territories that have access to natural vegetation and the hawks could be feeding on avian species existing in these habitat remnants (e.g., quail). The other samples are from territories that reflect more of an urban setting and these individuals typically forage on human commensals including doves, pigeons, sparrows and other passerines that may rely more on human subsidies such as bird feeders (Lien et al. 2015, B. Millsap, pers. comm.)

3. Development of genetic tools for describing phylogeographic structure and exploring the evolution of Cooper's hawks: Sonsthagen et al. (2012) conducted the only phylogeographic analysis of Cooper's hawks to date with genetic samples from 3 populations in the mid-west United States (Wisconsin, Minnesota, and North Dakota) and one population from British Columbia, Canada. To our knowledge, there have been no other assessments of the genetic structure of Cooper's hawks. We recently developed a collaboration with Dr. Ron Van Den Bussche (Associate Vice President for Research, Oklahoma State University, Stillwater, OK) who will be sequencing the genome of the Cooper's hawk, a first for this species, and developing a SNP (single nucleotide polymorphism) chip that can be used to elucidate phylogeographic patterns, explore the mating system, and search for the genetic underpinnings of migration in Cooper's hawks. This past week, we collected a blood sample for the genomic analysis and have sent that to Dr. Van Den Bussche to begin this aspect of our research.

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