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Title: Phylogeography and Non-Invasive Molecular Monitoring of Coyote (*Canis latrans*) and Gray Fox (*Urocyon cinereoargenteus*) in Northern Virginia and the Eastern United States

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Abstract

Molecular tools allow us to answer ecological questions about some of the most intriguing animals, including North America's native gray fox (*Urocyon cinereoargenteus*) and Northern Virginia's recent colonist, the coyote (*Canis latrans*). This dissertation is divided into four independent chapters, cohered by the common theme of molecular ecology of North American canids. The first chapter details a phylogeographical study of the gray fox, a widespread, but understudied, canid species. Fossil and historic records indicate that gray foxes were not present in the Northeastern United States until well after the Pleistocene (c. 900AD). To test the hypothesis that gray foxes experienced a post-Pleistocene range expansion, I sequenced a variable portion of the mitochondrial control region from gray fox tissue samples representing the range of all three East coast subspecies. Phylogeographic analyses indicated no clear pattern of genetic structuring of gray fox haplotypes across most of the Eastern United States. However, when haplotype frequencies were subdivided into a "Northeastern" and a "Southern" region, I detected a strong signal of differentiation between the Northeast and the rest of the Eastern United States. Indicators of molecular diversity and tests for demographic expansion confirmed this division and suggested a recent expansion of gray foxes into the Northeast. My results support the hypothesis that gray foxes first colonized the Northeast during a historic period of hemisphere-wide warming, which coincided with the range expansion of deciduous forest. The second chapter describes a novel method to genetically identify canid species from scat (feces) found in the field. I used a short fragment of the mitochondrial control region that is a different length in kit fox (*Vulpes macrotis*), red fox (*V. vulpes*), gray fox, coyote, and dog (*C. familiaris*) to differentiate their scat without using multiple primer sets, real-time PCR, or restriction enzyme digestion. All canid species included are potentially sympatric at the study site utilized in the following two chapters (Marine Corps Base Quantico, MCBQ and adjacent Prince William Forest Park, PWFP) except the kit fox. I extensively tested

this technique using published and novel control region sequences and then applied it to two large scat data sets collected in California and Virginia (at MCBQ/PWFP). In the third chapter, I incorporate haplotype and genotype data obtained non-invasively from coyotes at MCBQ/PWFP into a regional analysis of patterns of coyote colonization across the Eastern United States. Coyotes have undergone a dramatic range expansion across North America since the early 19th century, colonizing east of the Mississippi River in two routes that have converged in the mid-Atlantic region in the past few decades. Notably, coyotes utilizing the Northern route of expansion show molecular evidence of admixture with the Great Lakes wolf (GLW). The study site at MCBQ/PWFP is located at the heart of the convergence of these two fronts. I screened scats collected at MCBQ/PWFP for species identification, then sequenced a hypervariable fragment of the mitochondrial control region to assign haplotype, and then used six microsatellite loci to identify individuals. I detected seven haplotypes (in 39 individuals), all of which have been previously reported in diverse surrounding geographic localities. Phylogeographic analyses indicated multiple sources of colonization of Northern Virginia and one common haplotype detected is of GLW origin, indicating the presence of admixed coyote/GLW individuals from the North. In the final chapter, I use the non-invasively collected genotype data to describe population demographics at MCBQ. I describe a population with low relatedness and minimal population genetic structure, reflective of the multiple geographic sources of colonization as described in the previous chapter. To estimate population density and size, I used a new class of spatially explicit capture-recapture models that address two key concerns of large carnivore demographic studies: violation of population closure and potentially sparse data sets. These models incorporate spatial data to eliminate the need for post hoc buffering and also use a Bayesian framework to effectively deal with a small sample size. Using this model, I estimated a population density and home range radius on par with other studies of coyotes in suburban areas. Collectively, these studies are a significant contribution to the development and usage of non-invasive molecular technology, as well as to our understanding of phylogeography and population genetics of North American canids.