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Estimating Population Size of Mexican Wolves Noninvasively (Arizona)

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Monitoring wolf abundance is a significant problem confronting biologists coordinating the recovery of the Mexican wolf (*Canis lupus baileyi*) population in the Blue

Figure 1. A female Mexican wolf (*Canis lupus baileyi*) from the population in the Blue Range Wolf Recovery Area in Arizona and New Mexico. Researchers use radiotelemetry to monitor noninvasively. Photo courtesy of USFWS

Range Wolf Recovery Area (BRWRA) in Arizona and New Mexico (Figure 1). Thus far, radiotelemetry has been a satisfactory method. However, collaring and tracking more wolves in the expanding population is expensive. The development of a cost-effective method to estimate Mexican wolf populations will assist the long-term management and recovery of wolves.

We are attempting species and individual identification using DNA extracted from wolf scat because scat is both readily available and easy to collect (Putman 1984). Progress in contemporary molecular genetics has made noninvasive genetic sampling of an animal population possible (Goossens et al. 2000, Prugh et al. 2005). The ability to identify an individual through DNA amplification of a scat sample allows us to treat reoccurrences of a genotype in additional samples as marked recaptures. Mark-recapture models may then be used to estimate population size based on collected genotypes. We are currently developing appropriate laboratory, sampling, and field protocols to collect scat and conduct a genetic mark-recapture study of Mexican wolves in a portion of the BRWRA.

We tested our ability to identify individual Mexican wolves in the lab by collecting scat and blood from eight captive wolves at the Sevilleta National Wildlife Refuge in New Mexico. We stored scat samples in 50-ml centrifuge tubes along with silica beads to act as a desiccant (1:4 scat to silica beads by volume), using filter paper barriers to prevent silica dust from embedding itself on the surface of the scat. We extracted DNA from surface scrapings of scat following the protocol for human DNA analysis from stool samples (QIAGEN 2007). We have successfully amplified 10 canid specific microsatellite markers (Ostrander et al. 1993) in the Sevilleta samples. These markers allowed us to obtain individual genotypes for all eight wolves. We are in the process of cross-checking genotypes obtained from scat against those obtained from blood.

We have demarcated a compact study area within the BRWRA comprising approximately 2,500 km² in the Apache Sitgreaves National Forest in Arizona. The Interagency Field Team, which coordinates the recovery project, is using radiotelemetry to monitor wolves in the study area and knows precisely how many wolves exist there. The study area is occupied by four packs (Paradise, Hawk's Nest, Bluestem, and Rim) whose territories are contiguous with each other. Furthermore, there are no unoccupied regions within the study area that could be colonized during the duration of the study. Therefore, this study area presents us with an opportunity to use radiotelemetry estimates as a baseline to evaluate the precision and accuracy of our technique.

Wolves are known to travel along existing roads, trails, and waterways and often deposit scat along these pathways (Mech 1970). Consequently, we have laid out eight approximately 60-km transects, some of which intersect two or three pack territories, along Forest Service roads in the study area. The total length of all transects is approximately 500 km. All transects are navigable by four-wheel drive, high-clearance vehicles. After first clearing all transects of scat, teams of two volunteers in vehicles driven at speeds not exceeding 20 km/h surveyed these transects on two consecutive weekends in September 2007 and collected all observed canid scats—a total of 52 samples. These transects will be surveyed again in a similar manner for three consecutive weekends in November 2007, February 2008, and April 2008.

We will use mark-recapture modeling to analyze the encounter histories generated by genotyping collected scat. However, two of the four packs are known to occupy territory outside the study area. Thus some wolves are likely to have a much higher capture probability than others, leading to low-biased population estimates under the usual model assumption that all animals have an equal probability of capture. We will attempt to overcome this difficulty by logging the distance between scat location and the edge of the study area. We will use this individual covariate to explain the variation in capture rates between individuals. The primary collection events will be modeled using a Huggins-type population estimation model (Huggins 1989), which allows for individual covariates such as average distance to the edge of the study area. The data will be analyzed using the robust design in Program MARK (White and Burnham 1999) that allows for the trading of information between primary capture periods and simultaneously allows us to estimate survival rates. We will evaluate the effectiveness of our method by determining if the confidence interval for estimated population size contains the actual population size in each sampling period.

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