

A GENETIC APPROACH TO ESTIMATE RIVER OTTER ABUNDANCE IN MISSOURI

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ABSTRACT

Extirpated from Missouri by the 1930s, river otters (*Lontra canadensis*) were reintroduced by the Missouri Department of Conservation (MDC) from 1982-1992. Since the reintroductions, concerns over the legitimacy of otter trapping and the predator's effects on sport fish populations have sparked controversy. The MDC responded by increasing efforts to monitor river otter populations, using latrine site counts to measure relative abundance across several rivers in Missouri. However, the actual number of otters represented by these counts was unknown. To address this question, I extracted DNA from scat samples collected along 8 rivers in the winter and spring of 2009, using 10 microsatellite markers plus sexing markers to estimate the number and sex of otters. I then developed a model to estimate population size from latrine site index variables, observing that the number of scats per latrine and the density of active latrines across the river best predicted population size. I then used the genotypes to calculate the genetic diversity of the otter populations, evaluate the distribution of genotype clusters across the landscape, and track otter movements between latrines. Unexpected genetic similarities indicated that otters translocated to different areas may have come from the same source populations. Overall, this project has demonstrated the utility of genetic methods for estimating otter abundance, provided insight into the genetic diversity of the populations, and presented a model for inexpensive monitoring of river otter populations in the future.