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GENETIC STRUCTURE AND DIVERSITY IN SOUTH TEXAS BOBWHITES: IMPLICATIONS FOR CONSERVATION

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ABSTRACT

The northern bobwhite (*Colinus virginianus*) has experienced range-wide declines in population size and reductions in geographic range during the last century. Declines in northern bobwhite population size and geographic distribution continue to occur despite vigorous conservation and research efforts directed at sustaining and enhancing populations. Viable populations of northern bobwhite have persisted only in areas with large expanses of relatively contiguous habitat, such as southern Texas, parts of Oklahoma, Kansas, and areas in southern Georgia and northern Florida. The decline of northern bobwhite populations is often associated with changes in land-use practices, including proliferation of intensive agriculture and fire suppression, which have altered, removed, or fragmented northern bobwhite habitat. Typically, the effects of changes in land use on northern bobwhites are regional in scale, given the large geographic extent which current agricultural land-use practices, such as farming and timber production, occur. It is clear that precipitation and land use affect regional population trends, but consideration of northern bobwhite population dynamics has remained confined to the local scale. Thus, the specific manner in which land-use changes have affected populations of northern bobwhites is unknown. We investigated the genetics and population structure of northern bobwhites at the landscape scale to learn if bobwhites function as

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metapopulations. Dispersal and exchange in a metapopulation system are critical to the long-term maintenance of populations; if interrupted, the entire network of populations might collapse. We sampled hunter-harvested northern bobwhites during 2004 to 2007 from 24 sites in South Texas, a region containing large areas of contiguous habitat where populations of northern bobwhites have been relatively stable. We extracted DNA and used bi-parentally and maternally inherited genetic markers to compare genetic structure and diversity among populations. We genotyped 567 individuals at 7 DNA microsatellite loci and sequenced 353 bp of the mtDNA control region for 190 individuals. Genetic diversity was high for microsatellite loci and mtDNA haplotypes ($H_O = 0.58$; $H = 0.88$, respectively), and did not differ among populations. We observed little population structure across the geographic region (microsatellite $F_{ST} = 0.01$; mtDNA $\theta = 0.037$), and Fisher exact tests of population differentiation were not statistically significant. Spatial autocorrelation analysis of the microsatellite data set revealed a positive correlation between Moran's I and geographic distance out to >50 km. Our genetic data are surprising for an avian species that is considered relatively sedentary and a short-distance disperser. South Texas populations of northern bobwhites had high levels of genetic variation and were genetically similar across a broad region. Population genetics theory predicts that genetic diversity and similarity among local populations in a metapopulation are influenced by the rate of dispersal (gene flow). Life history theory predicts species with high turnover rates, such as northern bobwhite, should be good dispersers. The region-wide genetic similarity among populations of northern bobwhites implies dispersal may be more important in the population dynamics of the species than previous studies have indicated. We hypothesize that disruption of dispersal by habitat fragmentation may explain the overall decline of northern bobwhite populations in some regions. This may explain why patches of suitable habitat in fragmented landscapes go unoccupied by northern bobwhites. Our results lend additional support to recent calls for regional-scale management of this declining species.

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Key words: *Colinus virginianus*, dispersal, genetics, northern bobwhite, population structure