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GENETIC STRUCTURE OF NORTHERN BOBWHITE IN THE ROLLING PLAINS

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ABSTRACT

The recent declines in northern bobwhite quail populations in the Rolling Plains of Texas have raised concerns about habitat connectivity and gene flow. In addition, bobwhites have several life history traits that make them likely to display high levels of spatial genetic structure including low survival, high reproductive rates, and low dispersal rates. To determine if populations within the Rolling Plains have limited gene flow, we investigated the genetic structure of northern bobwhites within the ecoregion. Blood samples were collected at 16 ranches, encompassing 22 million acres, between February 2010 and April 2013. Bobwhites were also samples at a ranch in South Texas to serve as an outgroup. Samples ($n = 647$) were genotyped at 14 microsatellite loci that averaged 19.00 ± 5.07 alleles per loci. Global Fst indicated significant genetic structure ($p = 0.001$) between ranches with no isolation by distance signal ($p = 0.079$). Program STRUCTURE, however, indicated many ($n = 30$) overlapping subpopulations with no ranch constituting a single subpopulation and individuals from the outgroup ranch were included in 11 subpopulations. It appears that bobwhites within the Rolling Plains have few restrictions to gene flow and dispersal is not limited by the dominant habitat, xeric rangeland. These results suggest that populations in the Rolling Plains are not in danger of becoming isolated nor are bottlenecks present due to the recent decline.

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