

NORTHERN BOBWHITE POPULATION STRUCTURE AND DIVERSITY IN TEXAS AND THE GREAT PLAINS

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ABSTRACT

Many northern bobwhite (*Colinus virginianus*) populations have been experiencing severe declines. This decline is of concern to wildlife biologists, landowners, and legislators due to the popularity of this species as a game bird. Previous molecular genetic analyses for populations inhabiting intact habitats in South Texas indicate the northern bobwhite population in this region is genetically diverse with low population structure. We assessed whether landscape affects the population structure and diversity for northern bobwhite in Texas and the Great Plains. We extracted DNA from hunter-harvested northern bobwhites from 19 sites in South Texas from 2004 to 2010. We analyzed 7 microsatellites (Quail 5, 8, 9, 10, 11, 12, and 15). We used F_{ST} to measure genetic structure and AMOVA for genetic variation. We built 3 matrices to compare the genetic structure with the landscape. Geographic distances (km) between sample locations were ascertained using Google Earth. A matrix of barriers incorporated large water bodies and highways. We used the Biologist Ranking Information from the National Bobwhite Conservation Initiative for the third matrix to identify the number of different habitat patches a quail would need to cross from ranch to ranch. These matrices were compared to the genetic structure (pairwise F_{ST}), using Mantel tests with 10,000 permutations. We used partial Mantel tests to test the correlation of pairwise F_{ST} to combinations of distance and barriers, distance and habitat, and barriers and habitat. Overall F_{ST} was < 0.01 , suggesting low levels of population differentiation and AMOVA revealed most variation was within individuals. All Mantel tests had a positive correlation with genetic differentiation; however, barriers appear to be important factors for the observed genetic patterns.

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