

Genomic assessment of a declining game bird reveals cryptic genetic structure and insights for population management

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Abstract

Population genomics applied to game species conservation can help delineate management units, ensure appropriate harvest levels, and identify populations needing genetic rescue to safeguard their adaptive potential. The ruffed grouse (*Bonasa umbellus*) is rapidly declining in much of the eastern USA due to a combination of forest maturation and habitat fragmentation. More recently, mortality from West Nile Virus may have affected connectivity of local populations; however, genetic approaches have never explicitly investigated this issue. In this study, we sequenced 54 individual low-coverage (~5X) grouse genomes to characterize population structure and assess migration rates across the landscape to identify potential barriers to gene flow. Surprisingly, we identified two genomic clusters with no clear geographic correlation, with large blocks of genomic differentiation associated with chromosomes 4 and 20, likely due to chromosomal inversions. After excluding these putative inversions from the data set, we found weak but non-significant signals of population subdivision. Estimated gene flow revealed reduced rates of migration in areas with extensive habitat fragmentation, while areas with more habitat continuity showed higher rates of genetic connectivity. Our findings provide a benchmark for wildlife managers to compare and scale the genetic diversity and structure of ruffed grouse populations in Pennsylvania and across the eastern USA, as well as reveal unexpected structural variation in the grouse genome that requires further study to understand its possible effects on individual fitness and population distribution.

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