

PHYLOGEOGRAPHY OF BOBWHITES

Damon L. Williford¹

Caesar Kleberg Wildlife Research Institute–Texas A&M University–Kingsville, TX 78363, USA

Randall W. DeYoung

Caesar Kleberg Wildlife Research Institute–Texas A&M University–Kingsville, TX 78363, USA

Leonard A. Brennan

Caesar Kleberg Wildlife Research Institute–Texas A&M University–Kingsville, TX 78363, USA

Fidel Hernández

Caesar Kleberg Wildlife Research Institute–Texas A&M University–Kingsville, TX 78363, USA

Rodney L. Honeycutt

Natural Science Division, Pepperdine University, Malibu, CA 90263, USA

ABSTRACT

Bobwhites (*Colinus* spp.) are a widely distributed genus of New World quails. Four species are recognized with a geographic range spanning the eastern United States to northern South America. The northern bobwhite (*C. virginianus*) historically occurred throughout much of the eastern United States and eastern Mexico with disjunct populations in Sonora and Cuba. The Yucatán bobwhite (*C. nigrogularis*) occurs in allopatric populations in Nicaragua and Honduras, and on the Yucatán Peninsula. The spot-bellied and crested bobwhites (*C. leucopogon* and *C. cristatus*) constitute a species complex with the spot-bellied bobwhite distributed from Guatemala to Costa Rica, and the crested bobwhite from Panama to northern Brazil. The 4 species exhibit substantial intraspecific variation, and up to 56 subspecies are recognized among *Colinus* largely on the basis of geographic distribution and male plumage coloration. However, relationships within and among species have not been studied in detail. We sampled museum study skins and obtained DNA sequences from mitochondrial control region and ND2 genes. We used concatenated sequences of control region and ND2 to investigate relationships among the bobwhite species, and the control region to assess the geographic distribution of genetic variation within each species. Maximum likelihood analysis of bobwhite phylogeny revealed *Colinus* is composed of two deeply divergent lineages, one clade of northern and Yucatán bobwhites and another of spot-bellied and crested bobwhites. The Yucatán bobwhite was genetically distinct from the northern bobwhite. The Yucatán bobwhite was composed of 2 distinct subclades, one confined to the Yucatán Peninsula and another occurring in Nicaragua. The genetic data showed the spot-bellied bobwhite is closely related to the crested bobwhite, but did not reveal clear support for 2 distinct species. The crested bobwhite was composed of 3 distinct lineages: a western clade that occurs in Panama and west of the northern Andes in Venezuela and Colombia, an eastern clade concentrated in Venezuela (east of the Andes), and a clade restricted to northern Brazil. We found 58 control region haplotypes, of which 29 were shared among ≥ 2 northern bobwhite subspecies and 5 haplotypes were especially geographically widespread. We found 16 haplotypes in the Yucatán bobwhite with 4 restricted to the Yucatán Peninsula and shared among the 3 subspecies found there, and 3 other haplotypes restricted to the Nicaraguan subspecies. The spot-bellied bobwhite did not share haplotypes with any of the 3 crested bobwhite subclades. We found little phylogeographic structure within the spot-bellied bobwhite, and 2 of the 5 haplotypes occurred across much of the species' range and were shared among the 6 subspecies. The crested bobwhite exhibited strong phylogeographic structure and a lack of shared haplotypes among subspecies. The 20 haplotypes of the crested bobwhite were distributed unevenly among its 3 clades: 2 haplotypes in the Brazilian clade, 6 in the eastern clade, and 12 in the western clade. The weak phylogeographic structure and geographically widespread haplotypes of the northern bobwhite suggests large effective population size and gene flow among subspecies. The deep phylogeographic breaks within the Yucatán bobwhite and the spot-bellied bobwhite-crested bobwhite complex may be due to changes in the availability of suitable habitat and geological events during the Pleistocene. The lack of geographically distinct groups within the northern bobwhite implies that many subspecies may not provide good management units. Our data support the continued recognition of the Yucatán bobwhite as a distinct species. The 2 intraspecific groups identified in the Yucatán and the 4 groups within the spot-bellied/crested bobwhite complex may each represent discrete management units. Further assessment of the phylogenetic relationships and the phylogeography of the bobwhite species is warranted to clarify the phylogeny of *Colinus*.

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¹E-mail: rook137@gmail.com