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PHYLOGEOGRAPHY OF SCALED QUAIL

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ABSTRACT

Scaled quail (*Callipepla squamata*) are distributed over much of the Chihuahuan Desert in the United States and south into central Mexico. Four subspecies have been described based on slight variations in coloration and body size, but the distinctiveness of the subspecies is unknown. We conducted a range-wide phylogeographic analysis of scaled quail based on the mitochondrial control region (D-loop). Our objectives were to: (1) ascertain the overall genetic diversity, (2) examine the phylogeographic structure of the scaled quail, and (3) examine the genetic distinctiveness of its 4 subspecies. We obtained D-loop sequences from 190 hunter-harvested wings and 38 museum specimens. Haplotype diversity ($Hd = 0.386$) and nucleotide diversity ($\pi = 0.002$) were relatively low. We found 16 D-loop haplotypes, 5 of which were shared by 2 or more subspecies. Haplotype A (carried by 178 individuals) was most widespread and occurred in nearly every population. Analysis of molecular variance revealed that most of the genetic variation in scaled quail occurred within populations rather than among subspecies. The low levels of genetic diversity probably reflect a historically restricted distribution within the Chihuahuan Desert, and wide geographic distribution of some haplotypes implies expansion from a single refugium. Our data indicate the scaled quail subspecies probably do not represent historically independent units. Phenotypic-based subspecies should not be used as proxies for management units if preserving genetic diversity and evolutionary potential is a goal of management, unless molecular data demonstrate the subspecies represent genetically distinct entities. Our data support viewing the entire species as a single management unit.

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