

FEATURE ARTICLES

LOW GENETIC VARIABILITY IN THE GEOGRAPHICALLY WIDESPREAD ANDEAN CONDOR

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Abstract. We characterized DNA sequence variation in the mitochondrial control region and 12S ribosomal subunit for a sample of Andean Condors (*Vultur gryphus*) representing populations distributed throughout the species' extensive geographic range (Colombia to central Argentina and Chile). Domains II and III of the control region along with part of the 12S gene were sequenced from 38 individuals (956 base pairs in 30 individuals and 430–824 base pairs for an additional 8 individuals sampled from museum specimens), and Domain I was sequenced from five of these birds (400 base pairs). We identified a total of five haplotypes based on four variable sites distributed over Domains II and III of the control region and the 12S gene. An additional variable site was identified in Domain I. All changes were transitions and no more than three sites differed between any two individuals. Variation in the control region of condors was lower than for most other birds analyzed for these loci. Although low genetic variability is often associated with endangered megafauna, the condor example is notable because the species still maintains a substantial geographic range. Thus, low genetic variability may occur even in megafauna whose ranges have not been severely reduced over recent centuries. Our results therefore suggest that genetic data from geographically widespread megafauna provide important baseline data for assessing the relationship between genetic variability and its causes in other endangered species.

Key words: Andean Condor, *Vultur gryphus*, control region, *Cathartidae*, mitochondria.