

FEATURE ARTICLES

CONSERVATION PRIORITIES FOR RESPLENDENT QUETZALS BASED ON ANALYSIS OF MITOCHONDRIAL DNA CONTROL-REGION SEQUENCES

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*Abstract.* The Resplendent Quetzal (*Pharomachrus mocinno*) is a threatened bird species classified into two putative subspecies (*P. m. mocinno* and *P. m. costaricensis*) and distributed in cloud forests of seven countries in Mesoamerica. Because the birds are rare, tissue samples are difficult to obtain, but we analyzed genetic diversity in 25 quetzals from five countries based on 255 bp of domain I of the control region of mitochondrial DNA. Eight haplotypes were detected. Nucleotide diversity for Mexico (*P. m. mocinno*: 0.0021) and Panama (*P. m. costaricensis*: 0.0026) were low, and did not differ from the values estimated for other birds species irrespective of whether they were endangered. A haplotype tree rooted with the Pavonine Quetzal (*P. pavoninus*) recovered two reciprocally monophyletic clades corresponding to each subspecies, so we propose that each subspecies be considered as an evolutionarily significant unit for conservation planning. A minimum spanning network showed the number of genetic differences separating haplotypes within subspecies was small relative to the number of substitutions among them, indicating strong population subdivision ( $F_{ST} = 0.37$ ). In spite of the limited sampling we propose that in conservation practice Mexico–Guatemala, Nicaragua, El Salvador, and Panama be considered preliminarily as independent conservation management units since they each have unique haplotypes. Additionally, these countries should construct international agreements to protect the natural vegetation corridors among cloud forests of Mesoamerica and to curtail the illegal trade of quetzals.

*Key words:* evolutionarily significant units, Mesoamerica, mitochondrial DNA, management units, *Pharomachrus mocinno*.