

FEATURE ARTICLES

**INTRASPECIFIC PHYLOGEOGRAPHY AND ADAPTIVE DIVERGENCE IN THE
WHITE-HEADED WOODPECKER**

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Abstract. This study uses mitochondrial DNA (mtDNA) to examine the phylogeography of the White-headed Woodpecker (*Picoides albolarvatus*), one of the least-studied woodpeckers in North America. A mismatch distribution and calculation of Tajima's *D* indicate that the overall phylogeographic history of the species is characterized by a recent range expansion that probably occurred after the start of the Pleistocene. In addition, a nested clade phylogeographic analysis indicates that additional processes such as allopatric fragmentation and restricted gene flow have influenced the evolutionary history of this species. Traditionally, the White-headed Woodpecker has been split into two subspecies whose distributions meet in the northern part of the Transverse Ranges in California. The two subspecies differ morphologically, with the southern subspecies having a larger bill in proportion to its body size than the northern subspecies. Geographical variation in mtDNA is concordant with a division at the Transverse Ranges that corresponds to the morphological variation seen between the two subspecies. An analysis of molecular variance indicates that 27% of the genetic variation results from differences between the northern and southern subspecies. Furthermore, birds in the northern part of the range differ from those in the southern part of the range by at least one base substitution. These results agree with the hypothesis that the larger bill of the southern subspecies is the result of recent local adaptation to feeding on the large cones of Coulter pines (*Pinus coulteri*).

Key words: bill morphology, evolutionarily significant unit, nested clade phylogeographic analysis, phylogeography, *Picoides albolarvatus*, subspecies, White-headed Woodpecker.