Molecular phylogenetic analysis of the white-crowned forktail Enicurus leschenaulti in Borneo

Abstract

Comparison of 1017 nucleotides of mitochondrial ND2 and ND3 DNA sequences of 26 individuals of white-crowned forktail Enicurus leschenaulti from SE Asia revealed multiple evolutionary lineages within Borneo. Montane birds were genetically homogeneous across localities, but diverged by more than 4.3% from all other samples. Lowland birds formed two distinct clades, one consisting of individuals from northern Borneo, and the other including individuals from western Borneo, as well as Sumatra and Malaya. Relationships among the subspecies were not well resolved. These findings indicate another example of montane and north Bornean endemicity, support the separation of the montane and lowland species, and define areas of conservation interest.