

FEATURE ARTICLES

**GEOGRAPHICAL STRUCTURE OF GENETIC VARIATION IN THE MALAGASY SCOPS-OWL INFERRED FROM MITOCHONDRIAL SEQUENCE DATA**

JÉRÔME FUCHS<sup>1,2,6</sup>, JEAN-MARC PONS<sup>1,2</sup>, ERIC PASQUET<sup>1,2</sup>, MARIE JEANNE RAHERILALAO<sup>3,4</sup>, AND STEVEN M. GOODMAN<sup>3,5</sup>

<sup>1</sup>UMR5202 "Origine, Structure et Evolution de la Biodiversité", Département Systématique et Evolution, Muséum National d'Histoire Naturelle, 55, Rue Buffon, 75005 Paris, France

<sup>2</sup>Service Commun de Systématique Moléculaire, IFR CNRS 101, Muséum National d'Histoire Naturelle, 43, rue Cuvier, 75005 Paris, France

<sup>3</sup>WWF, BP 738, Antananarivo (101), Madagascar

<sup>4</sup>Département de Biologie Animale, Université d'Antananarivo, BP 906, Antananarivo (101), Madagascar

<sup>5</sup>Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605

Manuscript received 6 July 2006; accepted 11 January 2007.

<sup>6</sup> E-mail: [fuchs@mnhn.fr](mailto:fuchs@mnhn.fr)

*Abstract.* A recent taxonomic revision of the Malagasy Scops-Owl (*Otus rutilus*) recognized two distinct endemic species on the island based on plumage, vocal, and morphological characters: *O. rutilus* (sensu stricto) from eastern humid forest formations and *O. madagascariensis* from western dry forest areas. An evaluation of these characters calls into question their validity for taxonomic studies, as they may be ecologically linked. To independently assess the two-species hypothesis, we used sequence data from 1449 base pairs (bp) of mitochondrial DNA (mtDNA) from 34 scops-owls obtained across the range of these two putative species. Nineteen haplotypes were detected, four of which were shared by more than one individual. Maximum sequence divergence was 0.6% (mean = 0.24%). While the most common haplotype was shared by 10 individuals originating from different eastern and western localities, 12 haplotypes were exclusive to *O. rutilus* and five to *O. madagascariensis*. An analysis of molecular variance showed significant partitioning of the genetic variability between *O. rutilus* and *O. madagascariensis*. The estimate of the divergence time between populations associated with the names *O. rutilus* and *O. madagascariensis* was 8070 years BP. Based on haplotype frequencies and sequence divergence, we conclude that there are two populations of *Otus* on Madagascar that started to diverge in recent geological time following an ecological parapatric model, perhaps associated with Quaternary climatic shifts. Using these results, it is inappropriate to recognize two species of *Otus* on Madagascar.

*Key words:* coalescent analyses, Madagascar, mitochondrial DNA, *Otus*, phylogeography, two-species hypothesis.