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Phylogeny and biogeography of western Indian Ocean *Rousettus* (Chiroptera: Pteropodidae)

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We examined patterns of genetic variation in *Rousettus madagascariensis* from Madagascar and *R. obliviosus* from the Comoros (Grande Comore, Anjouan, and Mohéli). Genetic distances among individuals on the basis of 1,130 base pairs of the mitochondrial cytochrome *b* (*Cytb*) locus were estimated from specimens collected from 17 sites on Madagascar, 3 sites on Grande Comore, 3 sites on Anjouan, and 2 sites on Mohéli. We observed little variation in Madagascar and nearshore island samples (maximum 1.1%) and interisland Comoros samples (maximum 1.8%). In contrast, pairwise distances between different sampled sites on Madagascar and the Comoros varied from 8.5% to 13.2%. For 131 Malagasy animals, 69 unique haplotypes were recovered with 86 variable sites, and for 44 Comorian individuals, 17 unique haplotypes were found with 30 variable sites. No haplotype was shared between Madagascar and the Comoros, adding to previous morphological evidence that these 2 populations should be considered separate species. *Cytb* data showed that *Rousettus* populations of Madagascar (including nearshore islands) and the Comoros are respectively monophyletic and display no geographic structure in haplotype diversity, and that *R. madagascariensis* and *R. obliviosus* are strongly supported as sister to each other relative to other *Rousettus* species. Genotypic data from 6 microsatellite loci confirm lack of geographic structure in either of the 2 species. In pairwise tests of population differentiation, the only significant values were between samples from the Comoro Islands and Madagascar (including nearshore islands). Estimates of current and historical demographic parameters support population expansion in both the Comoros and Madagascar. These data suggest a more recent and rapid demographic expansion in Madagascar in comparison with greater population stability on the Comoros. On the basis of available evidence, open-water crossings approaching 300 km seem rarely traversed by *Rousettus*, and, if successful, can result in genetic isolation and subsequent differentiation. DOI: 10.1644/09-MAMM-A-283.1.

Key words: Comoros, cytochrome *b*, Madagascar, microsatellite, phylogeny, phylogeography, *Rousettus*, western Indian Ocean islands

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As currently configured, the pteropodid bat genus *Rousettus* Gray, 1921 is composed of 10 species distributed from southern Europe and the African continent (including offshore islands) eastward across portions of the Middle East, western Indian Ocean islands, mainland Asia, numerous islands to the east of the Sunda Shelf, Australia, and to the Solomon Islands (Simmons 2005). Across this vast geographical expanse certain taxa have broad distributions and others are localized, such as the western Indian Ocean island endemics *R. madagascariensis* G. Grandidier, 1928 on Madagascar and *R. obliviosus* Kock, 1978 in the Comoros Archipelago (Fig. 1). The Comoros, which are composed of 4 principal islands (Grande Comore, Anjouan, Mohéli, and Mayotte), have their origin as in situ volcanic islands of relatively recent geological age, with the youngest, Grande Comore, at 0.13–0.5 million years (Myr) and the oldest, Mayotte, at 7.7–15 Myr (Emerick and Duncan 1982; Nougier et al. 1986). Members of this genus are unknown from other islands in the western Indian Ocean such as the Seychelles and Mascarenes, but *R. aegyptiacus* (E. Geoffroy, 1810) occurs on nearshore and offshore islands of eastern and western Africa and the Arabian Peninsula (Bergmans 1994). On the basis of current taxonomy (Simmons 2005), the only other island endemics within the genus are *R. bidens* (Jentink, 1879) and *R. linduensis* Maryanto and Yani,

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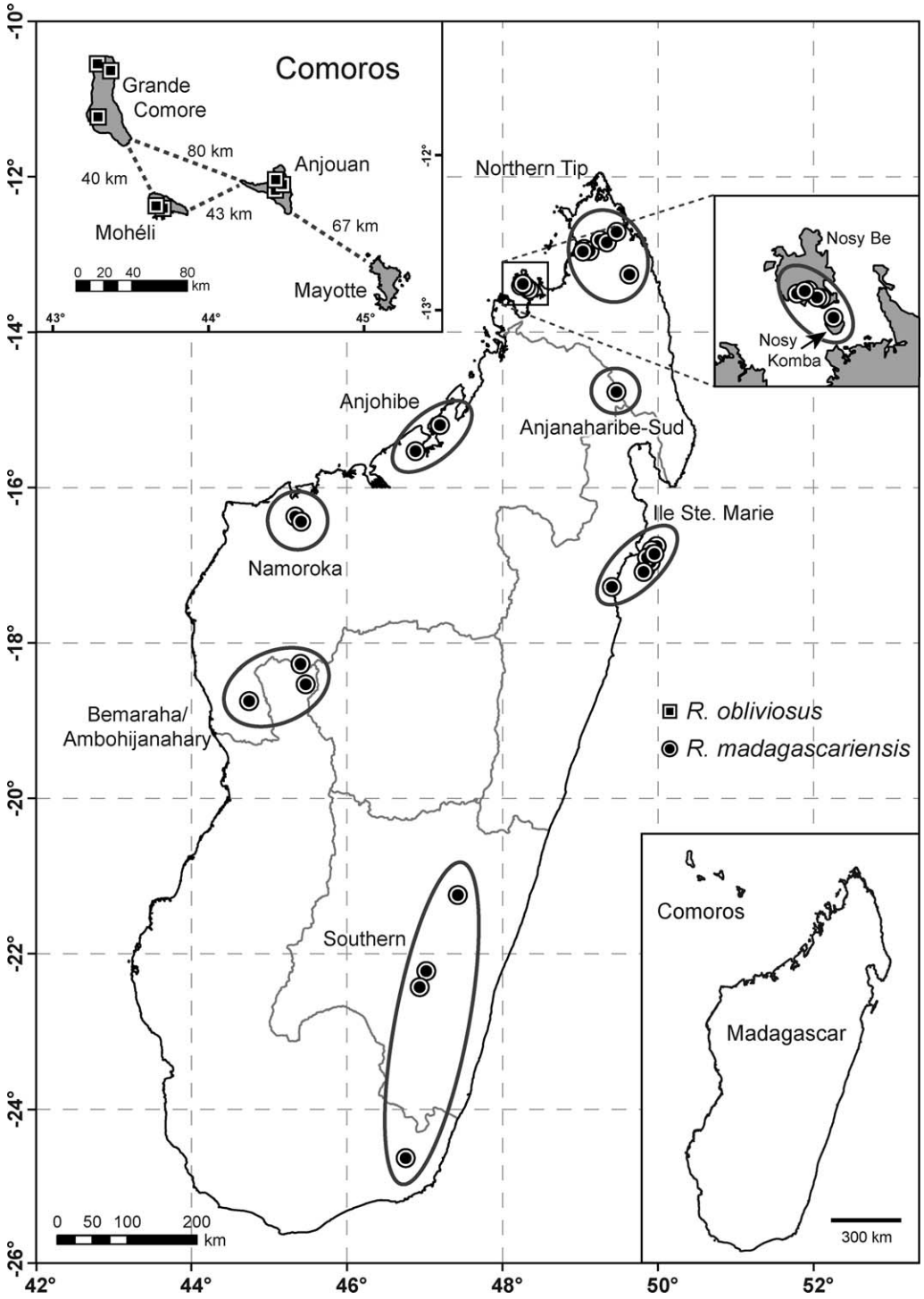


Fig. 1.—Map of principal collection localities on Madagascar and nearshore islands (Ile Sainte Marie, Nosy Komba, and Nosy Be) and in the Comoros Archipelago (Grande Comore, Anjouan, and Mohéli) of *Rousettus* specimens used in the current study.

2003 from Sulawesi. Hence, members of this genus have physical capacity to disperse considerable distances across ocean expanses, which in a few cases has led to island-specific endemics. However, on the basis of an extensive phylogenetic analysis, *R. bidens* is a member of a different subfamily of pteropodids bats, the Harpyionycterinae (Giannini et al. 2009).

Until recently, few details were available on natural history and distribution of *R. madagascariensis*; Dorst (1947) considered it rare. *R. obliviosus* was described by Kock (1978) on the basis of material collected in the late 19th century, and even until the early 1980s it was known only from the type series (Bergmans 1994). Subsequently, many aspects of distribution, natural history, and diet of these 40–75-g, frugivorous, and nonforest-dependent bats have been documented (Andrianaivoarivelo et al. 2009; Goodman et al. 2005, 2010; Louette 2004; MacKinnon et al. 2003; Racey et

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al. 2010; Razafindrakoto 2006; Sewall et al. 2003). On the basis of recent inventory work, both taxa are common, particularly in portions of Madagascar and the Comoros with caves, lava tubes, and rock crevices where they make their day roosts.

Systematic relationships of *R. madagascariensis* and *R. obliviosus* have been unresolved at subgeneric and species levels. *R. madagascariensis* previously was considered conspecific with *R. lanosus* Thomas, 1906 of eastern Africa (Hayman and Hill 1971; Kingdon 1974). *R. madagascariensis* has been shifted between subgenera *Rousettus* and *Stenonycteris* (Corbet and Hill 1991; Koopman 1994), and *R. obliviosus* has been placed in the subgenus *Rousettus* (Kock 1978). Further, these species have not been included in any explicit morphological phylogeny of the genus or pteropodid bats in general (Springer et al. 1995). Ambiguity of systematic relationships of *R. madagascariensis* and *R. obliviosus* is associated with their former rarity in museum collections (Bergmans 1977; Kock 1978) and lack of tissue samples for the latter species in genetic studies (Álvarez et al. 1999; Giannini and Simmons 2003; Juste et al. 1997, 1999; Kirsch et al. 1995).

Given that Madagascar and the Comoros Archipelago are separated by about 300 km, molecular phylogenetic data are useful to decipher whether *R. madagascariensis* and *R. obliviosus* are sister taxa, therefore indicating a single continental origin of the 2 species, or show evidence of separate colonization events from continental areas. Further, such data allow for potentially contrasting phylogeographic patterns, with Madagascar being a large single island and the Comoros a series of small islands chained as an archipelago. Hence, this information should provide insight into the evolutionary history of members of this genus and their capacity and constraints to fly across expansive oceanic zones. Finally, *Rousettus* spp. are known to be reservoirs for a variety of different diseases and ectoparasites that could be important for domestic animals and humans (Calisher et al. 2006; Reeves et al. 2006). To interpret epidemiological patterns, explicit phylogenies and phylogeographic studies of regional members of the genus are needed. The purposes of our study, which uses molecular genetic data, are to determine if *R. madagascariensis* and *R. obliviosus* are true species and, if so, to examine possible sister-taxa relationships; unravel phylogeographic patterns within populations of these reputed taxa occurring on Madagascar and the Comoros; and examine patterns of population demographics within and among *Rousettus* populations in Madagascar and the Comoro Islands.

Materials and Methods

Sampling and deoxyribonucleic acid (DNA) extraction.—Since the early 1990s extensive chiropterological surveys have been conducted at numerous localities on Madagascar and nearshore islands (Ile Sainte-Marie, Nosy Be, and Nosy Komba), and in 2006 and 2007 fieldwork was conducted in the Comoros Archipelago (Fig. 1). Specimens referable to *R. madagascariensis* were collected from 17 sites on Madagascar and those to *R. obliviosus* from 3 different islands in the Comoro Islands (Grande Comore, Anjouan, and Mohéli). No evidence of the latter species was found on Mayotte. Voucher specimens are deposited in the Field Museum of Natural History (Chicago) and the Université d'Antananarivo, Département de Biologie Animale (Antananarivo, Madagascar). Small muscle samples from each collected individual were preserved in ethylenediaminetetra-acetic acid before specimen preparation. Research involving live animals followed the guidelines for the capture, handling, and care of mammals approved by the American Society of Mammalogists (Gannon et al. 2007). Genomic DNA was extracted using the DNeasy Blood and Tissue Kit (Qiagen, Valencia, California).

Sequence data collection.—The mitochondrial cytochrome *b* (*Cytb*) gene was selected to compare phylogenetic relationships of Comorian and Malagasy *Rousettus* to other Asiatic and African *Rousettus* spp. and to characterize the phylogeographic structure among individuals of *Rousettus* within these 2 island groups. We amplified the entire *Cytb* region for 44 samples of *R. obliviosus* and 131 samples of *R. madagascariensis* using polymerase chain reaction (PCR) with primers L14724 and H15915 (Irwin et al. 1991). PCR was done in a total volume of 20 μl with 1× buffer (100 mM Tris-HCl, pH 8.3, 500 mM KCl), 2.0 mM $MgCl_2$, 1 mM deoxynucleotide triphosphate (dNTP), 0.25 μM of each primer, 0.5 U of *Taq* polymerase, and 1 μl of template DNA. PCR cycles consisted of an initial denaturation at 95°C for 2 min, 30 cycles of 95°C for 30 s, 50°C for 45 s, and 72°C for 1 min 40 s, and a final extension at 72°C for 10 min. Samples were prepared for sequencing reactions by first incubating 5 μl of PCR product with 0.5 μl of ExoSAP-IT (USB Products, Cleveland, Ohio) and 1.5 μl of water at 37°C for 15 min followed by 80°C for 15 min. Cleaned PCR products were sequenced using primers used for amplification in a total volume of 5 μl (1× buffer, 1 μM primer, 0.2 μl of BigDye v3, and 0.5 μl of DNA template) and run on an ABI 3730xl DNA Analyzer capillary machine. Resulting sequences were checked by eye for errors and contigs were assembled in Sequencher 4.8 (GeneCodes, Ann Arbor, Michigan). Sequences were checked for stop codons and deposited in GenBank (accession numbers GU228597–GU228771; Appendix 1). To test monophyly of Malagasy and Comorian *Rousettus*, GenBank was searched for *Cytb* sequences of other members of this genus, which resulted in an additional 57 individuals.

Microsatellite data collection.—We genotyped 193 individuals from Madagascar and 43 individuals from the Comoros at 6 microsatellite loci designed for *R. leschenaultii* (Desmarest, 1820—Hua et al. 2006). For each locus, amplification by PCR using a fluorescently labeled forward primer was done in a total volume of 10 μl with 1× buffer, 2.0 mM $MgCl_2$, 0.4 mM dNTP, 0.1 μM each primer, 0.25 U *Taq* polymerase, and 0.1 μl of template DNA. Cycles consisted of an initial denaturation at 95°C for 2 min, followed by 36 cycles of 95°C for 30 s, 59°C (3 cycles), 56°C (3 cycles), or 50°C (30 cycles) for 30 s and 72°C for 1 min, followed by a final extension at 72°C for

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5 min. Fragments were run on an ABI 3730xl DNA Analyzer, and alleles were called and checked in GeneMarker (SoftGenetics, State College, Pennsylvania).

Haplotype alignment and phylogenetic analyses.—Haplotypes of *Cytb* for all samples were aligned by hand in the program MacClade (Maddison and Maddison 2003). Identical haplotypes were condensed using the program Collapse v1.2 (http://darwin.uvigo.es).

We partitioned our data set to account for rate variation among codon positions and used MrModeltest v2.3 (Nylander 2004) to determine the model of nucleotide sequence evolution that best fit each partition according to the Akaike information criterion. We estimated the phylogenetic relationship among haplotypes under a Bayesian framework using the program MrBayes v3.1.2 (Huelsenbeck and Ronquist 2001; Ronquist and Huelsenbeck 2003). A SYM+I+G model was applied to first position sites, a HKY+G model to second position sites, and a GTR+G model to third position sites. Analyses consisted of 3 independent runs each with 4 chains sampled every 100 generations for 5,000,000 generations. Convergence was verified by examining the trends in lnL scores within and across runs for all parameters. We discarded the first 5,001 trees as burn-in and estimated the 50% majority-rule consensus topology including branch lengths and posterior probabilities (PP) for each node.

Microsatellite data analysis.—We grouped individuals from the Comoros Archipelago by island and divided the Madagascar samples into 7 groups for a total of 10 putative populations. We tested for deviation from Hardy–Weinberg equilibrium (HWE) and linkage disequilibrium both within populations and globally using the program Genepop (Raymond and Rousset 1995). A Markov chain method (Guo and Thompson 1992) with 10,000 dememorization steps and 1,000 batches of 10,000 iterations per batch was used to determine the significance of each test after Bonferroni correction for multiple comparisons at $\alpha = 0.05$.

We used Fstat (Goudet 1995) to calculate observed heterozygosity (H_O), gene diversity (H_S), and overall F_{ST} for Madagascar samples, Comoros samples, and all samples together. We also estimated pairwise F_{ST} among population pairs in Fstat using 10,000 permutations of the data to determine significance after Bonferroni correction for multiple comparisons.

We used Bayesian assignment tests in Structure v2.2.3 (Pritchard et al. 2000) as an independent test of genetic structure that does not require prior assumptions of population delineation. Structure runs did not use population of origin as prior information and assumed correlated allelic frequencies among populations. We conducted 5 replicate runs at each K from $K = 1$ to 8 where K is the number of clusters. Each run consisted of 3.5 million generations sampled every 100 generations with the first 1.0 million steps tossed as burn-in. The best K was determined by calculating the posterior probability of each K and by examining the change in the ln L between runs. Additionally, we separately tested for evidence of population structure across individuals within the Comoros. Parameters for Comoros structure analyses were identical to those used for analysis of the entire data set; we ran 5 replicate runs at each K from $K = 1$ to 5.

Population demographics.—We tested for evidence of demographic expansion in the Comoros and Madagascar clades by examining the distribution of pairwise sequence differences (i.e., mismatch distribution—Rogers and Harpending 1992; Schneider and Excoffier 1999) and by calculating Fu's F_s statistic (Fu 1997) using the software Arlequin (Excoffier et al. 2005). For mismatch distribution tests, we used 10,000 simulations of the data to determine the null distribution of pairwise differences under a model of rapid population expansion. Significance of the F_s statistic was determined by simulating 10,000 random samples under a coalescent framework with the model of population equilibrium.

We used the program IM (Hey and Nielsen 2007) to estimate current and historical demographic parameters (current effective population sizes, ancestral effective population size, divergence time, migration rates, and splitting parameter) from the *Cytb* data for sister clades *R. obliviosus* and *R. madagascariensis*. Because we used a single mitochondrial locus, these data conform to assumptions of the IM model. We conducted multiple runs with 4 to 10 heated chains sampling every 10 steps after an initial burn-in of 1,000,000 generations. For each run, we noted effective sample sizes (ESS), mixing rates across heated chains, and plots of parameter trends throughout the run to ensure adequate exploration of likelihood space. We also compared marginal probability densities for parameter estimates across independent runs to verify convergence. The accepted IM run consisted of 8.8 million steps following initial burn-in with ESS greater than 80 for all parameters.

Synonymous and nonsynonymous substitution rates across coding regions of the mammalian mitochondrial genome are substantially different (Pesole et al. 1999). Thus, to approximate the mutation rate for the *Cytb* sequences used in our analyses, we calculated proportion of synonymous and nonsynonymous sites using DNAsp (Rozas et al. 2003) and determined an approximate overall rate for our *Cytb* data set (25.5% nonsynonymous sites, 74.5% synonymous sites) assuming an average rate of 1.8×10^{-3} substitution site^{-1} myr^{-1} and 27.4×10^{-3} substitutions site^{-1} myr^{-1} for nonsynonymous and synonymous sites, respectively (Pesole et al. 1999).

Results

Sequences results.—We recovered 1,130 base pairs (bp) of the *Cytb* locus for 175 newly sequenced individuals (Appendix 1). For these sequences, plus 57 *Cytb* sequences from other *Rousettus* spp. retrieved from Genbank (for a total of 232 sequences), we found 366 variable sites overall. We did not find any shared haplotypes among samples from the Comoros, Madagascar, or any individuals sampled from Genbank. For 131 animals from Madagascar, we recovered 69 unique

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Table 1.—Average pairwise distances of cytochrome *b* sequence data within 3 species of *Rousettus* from Madagascar, the Comoro Islands, and China.

	Uncorrected *P*	HKY+I+G
Comoros: *R. obliviosus*	0.005578	0.005775
Madagascar: *R. madagascariensis*	0.005382	0.005555
China: *R. leschenaultii*	0.007654	0.007983
Total data set	0.060776	0.102126
Madagascar: Comoros	0.062075	0.086758

haplotypes with 86 variable sites. For the Comoros we found 17 unique haplotypes and 30 variable sites among 44 individuals. Among 32 *R. leschenaultii* sequences retrieved from Genbank we recovered 27 unique haplotypes with 56 variable sites. The remaining Genbank sequences represented individuals sampled generally as singletons with no reference to geographic location of sampling, and thus similar statistics would not be meaningful.

Phylogenetic analysis of *Cytb* sequence data demonstrates that *Rousettus* populations from Madagascar display no geographic structure in haplotype diversity with respect to the main island and nearshore islands (Nosy Be, Nosy Komba, and Ile Sainte Marie; Fig. 2). A similar pattern was evident among interland comparisons within the Comoros Archipelago (Grande Comore, Anjouan, and Mohéli). Average pairwise genetic distances within and among putative species indicate a relatively deep divergence between Malagasy and Comorian *Rousettus*, represented by an average pairwise genetic distance that is at least 15 times larger between Madagascar and the Comoros Archipelago than within each island group (Table 1). Furthermore, within-island genetic distances were only slightly less than average genetic distance among all sequences from *R. leschenaultii*.

To test monophyly of Malagasy and Comorian *Rousettus* we performed a Bayesian phylogenetic analysis of the *Cytb* haplotype data. The resulting consensus phylogram (Fig. 2) demonstrates strong support for monophyly of all *Cytb* haplotypes in Madagascar and the Comoros, respectively. As with neighbor-joining analyses, no geographic structure to haplotypes within Madagascar and nearshore islands, or from 3 disjunct islands in the Comoros (Grande Comore, Anjouan, and Mohéli), is suggested.

Monophyly of all different western Indian Ocean *Rousettus* spp. included in this analysis was strongly supported. Although monophyly of *R. aegyptiacus*, *R. leschenaultii*, and the Malagasy/Comorian *Rousettus* also was strongly supported (i.e., PP = 1.0), *R. aegyptiacus* haplotypes were unresolved with respect to haplotype clades of sister species. *Rousettus madagascariensis* and *R. obliviosus* were strongly supported (i.e., PP = 0.99) as sisters to each other. It was not clear what species of *Rousettus* is sister to the Malagasy/Comorian clade, but the topology with the monophyletic group of *R. leschenaultii* haplotypes sister to the Malagasy/Comorian clade was supported by nearly 70% of trees in the posterior distribution.

Table 2.—Observed heterozygosity (H_O), gene diversity (H_S), and F_{ST} (with 95% *CI*) for all individuals and each species individually. Confidence intervals for F_{ST} were generated with 10,000 bootstrap replicates.

	H_O	H_S	F_{ST}
All	0.822	0.852	0.050 (0.026–0.083)
Madagascar (*R. madagascariensis*)	0.866	0.901	0.004 (0–0.009)
Comoros (*R. obliviosus*)	0.720	0.740	0.009 (−0.009–0.023)

Microsatellite results.—Microsatellite loci had between 14 and 25 alleles (average 17.5). We did not detect any deviation from HWE or any evidence of linkage after Bonferroni correction. Across all samples observed heterozygosity (H_O) was 0.817 and gene diversity (H_S) was 0.852. H_O and H_S were higher for *R. madagascariensis* in comparison with *R. obliviosus* (Table 2). F_{ST} across all samples was 0.050, but only 0.004 and 0.009 within *R. madagascariensis* and *R. obliviosus*, respectively. In pairwise tests of population differentiation, the only significant F_{ST} values were between samples from the Comoros and Madagascar + nearshore islands (Table 3). Between the Comoros and Madagascar groups the only nonsignificant values of F_{ST} involved populations with limited sampling. We did not find any significant genetic differentiation on the basis of F_{ST} within the Comoros or among Madagascar populations.

Likewise, Bayesian assignment tests across the entire data set found 2 genetic clusters, one corresponding to the Comoros species and the other corresponding to the Madagascar species. Tests focused within the Comoros clade did not recover additional genetic structure among islands, and average likelihood values from structure analyses did not differ across *K*.

Comparative demographic estimates of R. madagascariensis *on Madagascar and* R. obliviosus *in the Comoros*.—Fu's F_s statistic was significant for both the Comoros and Madagascar samples, supporting demographic expansion in each population. We also were unable to reject the hypothesis of demographic expansion on the basis of the mismatch distribution tests in either population despite a qualitatively multimodal distribution of pairwise sequence divergence among individuals from the Comoros (Fig. 3). Estimates of τ, the mutation-scaled time since expansion ($2\ \mu t$, where μ is the mutation rate), were larger for Comoros individuals in comparison with Madagascar individuals, but with wide 95% confidence intervals (*CI*s; $\tau_{\text{Comoros}} = 8.908$, $CI = 0.221$–14.293; $\tau_{\text{Madagascar}} = 3.996$, $CI = 1.893$–9.518). Estimates of current θ ($2\ \mu N$, where N is the effective population size) were 5.748 for the Comoros and nearly 5 times greater for Madagascar ($\theta_{\text{Madagascar}} = 26.836$).

Analysis of *R. obliviosus* and *R. madagascariensis Cytb* data under a model of isolation with migration in the program IM confirmed distinctiveness of each species and also suggested recent demographic expansion in *R. madagascariensis*. Estimates of migration between species approached zero, indicating no gene flow. The 90% highest probability density

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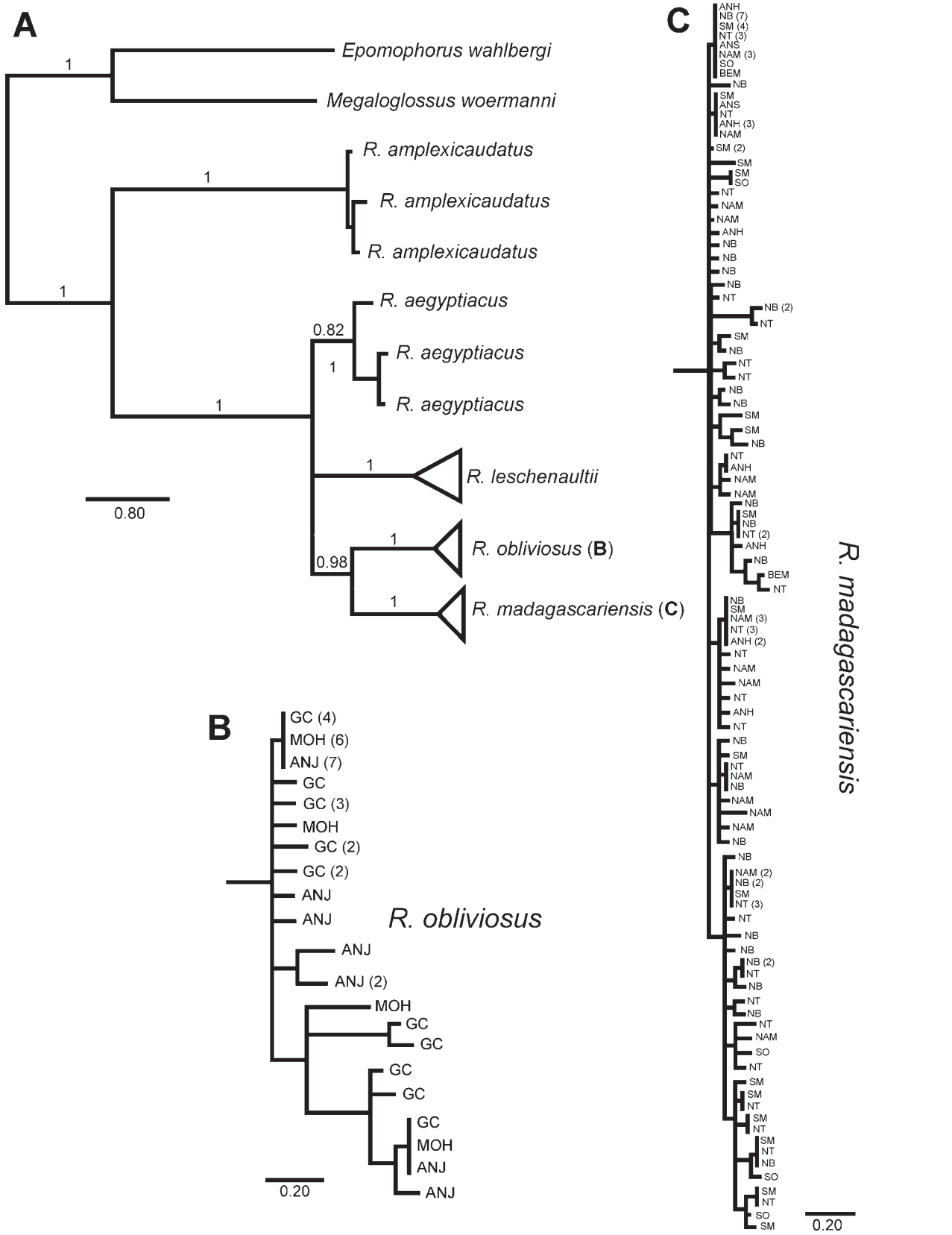


Fig. 2.—A) Bayesian consensus phylogram of *Rousettus* cytochrome *b* data. Branches of phylogram are labeled with posterior probability of bipartition, and scale bar for branches is provided below each tree. B) Detail of haplotype tree for samples of *R. obliviosus*. Tips of tree are labeled according to source islands: ANJ = Anjouan, MOH = Mohéli, and GC = Grande Comore. C) Detail of haplotype tree for samples of *R. madagascariensis*. Tips of tree are labeled according to source populations: ANH = Anjohibe, ANS = Anjanaharibe-Sud, NT = Northern Tip, NB = Nosy Be and Nosy Komba, SM = Ile Sainte Marie, BEM = Bemaraha/Ambohijanahary, NAM = Namoroka, and SO = Southern. Scale bar for branches is provided below each tree.

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TABLE 3.—F_{ST} pairwise values of *Rousettus madagascariensis* from Madagascar and *R. obliviosus* from the Comoros; sample size (n) is indicated in first column and significant values are in bold. The first 7 sites are from Madagascar and include the nearshore island of Ile Sainte Marie in the east and a nearshore island complex of Nosy Be and Nosy Komba in the northwest. The last 3 sites are from 3 different islands in the Comoros Archipelago.

	Southern	Bemaraha/ Ambohijanahary	Ile Ste. Marie	Namoroka	Anjohibe	Nosy Be/ Nosy Komba	Northern	Grande Comore	Anjouan
Southern (n = 5)									
Bemaraha/Ambohijanahary (n = 3)	0.007								
Ile Ste. Marie (n = 35)	0.0133	−0.025							
Namoroka (n = 26)	0.0098	−0.0087	0.0121						
Anjohibe (n = 12)	−0.0046	−0.0078	0.0025	0.0029					
Nosy Be/Nosy Komba (n = 70)	0.0241	−0.0104	0.0029	0.0101	0.0027				
Northern (n = 40)	0.0312	−0.0152	0.0002	0.0114	0.0026	−0.0002			
Grande Comore (n = 19)	0.0968	**0.1061**	**0.1158**	**0.1096**	**0.105**	**0.1224**	**0.1263**		
Anjouan (n = 13)	0.0957	0.1063	**0.1169**	**0.1092**	**0.1105**	**0.1274**	**0.1264**	0.0179	
Mohéli (n = 11)	0.1154	0.1201	**0.1273**	**0.1193**	**0.1098**	**0.1312**	**0.1322**	0.0015	0.0053

for the divergence time parameter ranged from 1.87 to 4.75 with a highest posterior probability at 2.93. Estimates of effective population size largely corroborated results of the mismatch distribution test. We found a greater effective population size in Madagascar ($\theta_{Madagascar} > \theta_{Comoros}$, PP = 1.0) and a strong signature of population expansion in *R. madagascariensis* postdivergence from *R. obliviosus* ($\theta_{Madagascar} > \theta_{Ancestral}$, PP = 0.998). However, evidence for postdivergence population expansion for *R. obliviosus* was weak ($\theta_{Comoros} > \theta_{Ancestral}$, PP = 0.068), and analyses indicated demographic stability and suggested that a much larger proportion of the predivergence ancestral population contributed to genetic diversity currently found in the Comoros populations.

Assuming an overall mutation rate of 8.3315×10^{-3} substitutions site^{-1} Myr^{-1}, mean time since expansion for the Comoros was 0.545 Myr (95% *CI* = 0.013–0.875 Myr) and for Madagascar was 0.245 Myr (95% *CI* = 0.116–0.583 Myr) on the basis of mismatch distribution analyses. Coalescent-based analyses of divergence time between Madagascar and the Comoros from IM suggested that the split occurred 0.358 Myr (90% HPD = 0.229–0.581 Myr).

DISCUSSION

Specific status of the Comorian Rousettus.—In his description of *R. obliviosus*, Kock (1978) made extensive comparisons with other species of *Rousettus*, including *R. aegyptiacus*, *R. leschenaultii*, *R.* (=*Lissonycteris*) *angolensis* (Bocage, 1898), and *R. lanosus* and found consistent morphological characters to diagnose this new species. Kock explicitly mentioned that he did not have access to material of *R. madagascariensis* and thus for many years it was unclear whether *R. obliviosus* and *R. madagascariensis* were synonyms. This is particularly important given that the Comoros and Madagascar are known to share a number of bat species (Goodman et al. 2009; Ratrimomanarivo et al. 2008, 2009; Weyeneth et al. 2008). Peterson et al. (1995) made cranial and dental comparisons to address this issue on the basis of measurements and figures in Kock (1978) and concluded that *obliviosus* was best considered a geographical form of *madagascariensis*. This was readdressed by Bergmans (1994), who was able to compare specimens of *R. madagascariensis* with *R. obliviosus*. He found a number of cranial characters that separate these taxa and concluded that *R. obliviosus* was specifically distinct from *R. madagascariensis*.

On the basis of molecular results we present herein, populations of *Rousettus* in Madagascar and Comoros, which are sister taxa, display 6.2–8.7% sequence divergence from one another and clearly form reciprocally monophyletic clades. If one applies the genetic species concept of Baker and Bradley (2006), which proposes that a genetic distance of greater than 5% between 2 populations may warrant their recognition as separate species, *R. madagascariensis* and *R. obliviosus* would be considered specifically distinct. Further, these 2 taxa do not share any common haplotypes. Hence, on the basis of these different lines of evidence, we consider *R. madagascariensis* and *R. obliviosus* distinct species.

Origin of Malagasy/Comorian Rousettus *spp.*—Several hypotheses have been proposed about origin of the genus *Rousettus* on the basis of phylogenetic inference, and centers of diversity pinpoint a southeastern Asian origin (Juste et al. 1999). Three separate routes have been suggested for western expansion of pteropodids into Africa, via a middle Asian–European–Gibraltar route, a middle-Asian, Middle Eastern route, and an Indian subcontinent–western Indian Ocean, east African route (Juste et al. 1999). Phylogenetic relationships presented herein on western Indian Ocean, African, and Asian *Rousettus* spp. are unresolved and hence do not provide clear support for any of these three hypotheses. In other studies with larger genetic data sets but not including *R. obliviosus* (Giannini and Simmons 2003, 2005), support exists for the Middle Eastern route with the Afrotropical clade composed of *R. aegyptiacus* + *R. madagascariensis* being the sister group to *R. leschenaultii*. Further geographic and species genetic sampling is needed, with the inclusion of new material of *R. obliviosus*, to have a greater resolution to phylogeny and patterns of colonization of this genus.

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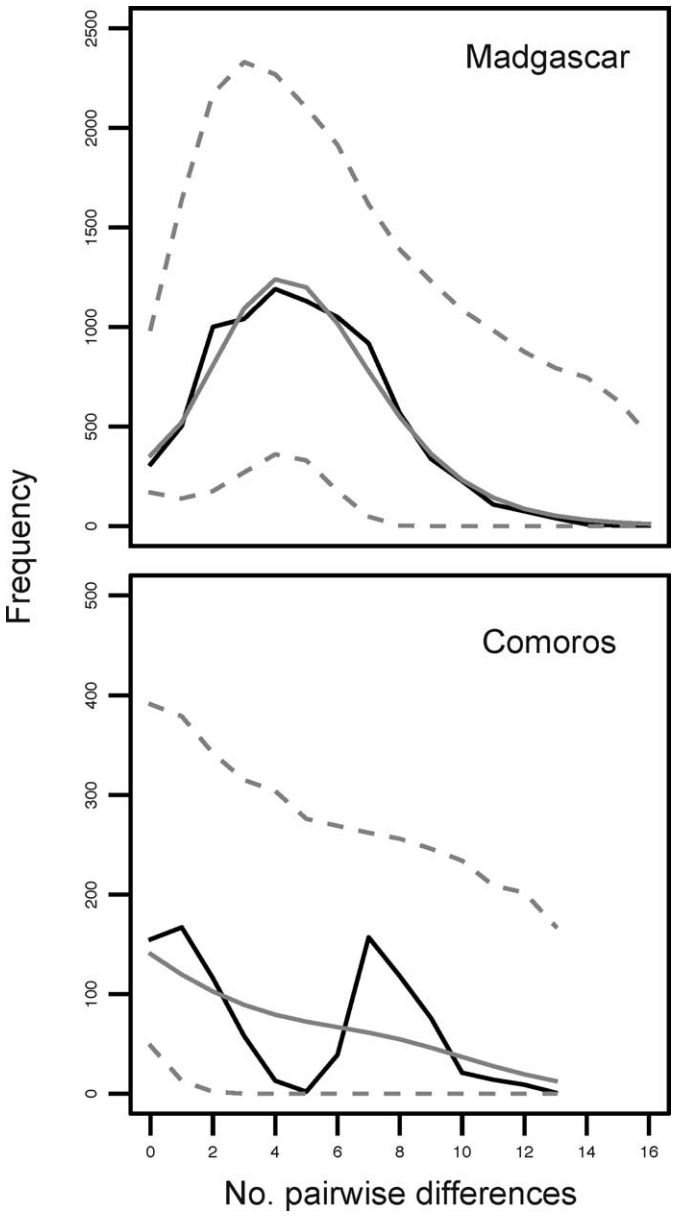


Fig. 3.—Mismatch distributions for *Rousettus madagascariensis* from Madagascar (top) and *R. obliviosus* from the Comoros (bottom). Empirical estimate of pairwise difference in solid black and simulated pairwise differences with 95% *CI* under a model of rapid demographic expansion in gray.

Phylogeography of Malagasy/Comorian Rousettus.—No clear phylogeographic structure was found in populations of *R. madagascariensis* on Madagascar or *R. obliviosus* in the Comoros. Across the approximately 1,600-km length of Madagascar individuals of *R. madagascariensis* from extreme ends of the island and across numerous biomes, and nearshore islands up to 13 km from the main island, demonstrated complete genetic mixing. Nothing is known about dispersal patterns of *R. madagascariensis*, but on the basis of genetic data presented here, dispersal movements are large scale. A possible explanation for this can be found in the unusual phenological patterns in fruiting of certain native plant genera, such as *Ficus* (Moraceae), resulting in a local paucity of food for frugivores during certain seasons, forcing obligate fruit-eating species to disperse (Goodman and Ganzhorn 1997). This potentially could explain lack of phylogeographic structure in *R. madagascariensis*. Even more striking is that a similar pattern of no phylogeographic structure was found in populations of *R. obliviosus* on Grande Comore, Anjouan, and Mohéli, with open-water distances separating these islands between 40 and 80 km.

Data presented herein on phylogeographic structure of *R. madagascariensis* and *R. obliviosus* have important implications outside the domain of their evolutionary history. Recent epidemiological work on *R. madagascariensis* sampled at Ankarana in northern Madagascar revealed presence of Tioman virus (Iehlé et al. 2007). Further, the other Malagasy members of the family Pteropodidae, *Eidolon dupreanum* (Pollen, 1866) and *Pteropus rufus* E. Geoffroy, 1803, tested positive for other *Paramyxoviridae* viruses (e.g., Hendra and Nipah), indicating that these diseases have circulated among these bat species. Given the genetic panmixia of *R. madagascariensis* across Madagascar, on the basis of the phylogeographic studies presented herein, Tioman virus isolated from this species likely is not restricted to the northern portion of the island. Further, numerous other viruses have been isolated from *Rousettus* spp. in Asia and Africa, signifying the potential importance of *R. madagascariensis* and *R. obliviosus* as reservoirs or vectors of different diseases. These include *Rhabdoviridae*—European bat lyssavirus 1 and Lagos bat virus; *Paramyxoviridae*—undetermined parainfluenzavirus; *Togaviridae* associated with the Chikungunya virus; *Filoviridae*—Marburg virus; *Flaviviridae—Flavivirus* Uganda S; *Coronaviridae*—severe acute respiratory syndrome coronavirus; and the unclassified viruses Yogue and Kasokero (Calisher et al. 2006; Kalunda et al. 1986; Kuzmin et al. 2008; Pavri et al. 1971; Towner et al. 2007, 2009; Wellenberg et al. 2002). Further, *Rousettus* ectoparasites (mites) are known to be vectors of pathogens such as *Rickettsia* (Reeves et al. 2006).

Dispersal distances and patterns of speciation within Rousettus.—Fruit bats of the family Pteropodidae, and specifically in this case members of the genus *Rousettus*, are strong fliers (Norberg 1981, 1994) and have broad distributions across a considerable portion of the Old World (Kirsch et al. 1995; Simmons 2005), including notably isolated islands in the western Indian Ocean. As witnessed by 4 of the 10 species in the genus being island endemics (Giannini et al. 2009), these animals have limited capacity to disperse across considerable oceanic distances. In certain cases these events are seemingly rare, having resulted in isolated populations that speciated, and in other cases they remain in contact with other island or continental populations (Bastian et al. 2001). To understand the importance of distance across water crossings as an isolation factor in different populations of *Rousettus* spp., we present here some examples that do not necessarily rely on the same genetic markers.

On Madagascar panmixia of haplotypes occurs in *R. madagascariensis*, with no clear phylogeographic structure.

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Samples were analyzed from 3 nearshore islands (Nosy Be, Nosy Komba, and Ile Sainte Marie), ranging from 2.5 to 13 km from the main island, and a significant number of shared haplotypes between these islands and the mainland indicate that this species easily traverses these water expanses. The direct distance from Madagascar to the nearest island in the Comoros, Mayotte (where the sister taxa *R. obliviosus* is unknown to occur), is 300 km and to Anjouan (where *R. obliviosus* does occur), 390 km. The latter volcanic island formed in situ about 3.7 Myr (Nougier et al. 1986). Given that *R. obliviosus* and *R. madagascariensis* are sister taxa and share no common haplotype, this distance of overwater dispersal is sufficiently great to have been a rare event that subsequently led to speciation. Within Grande Comore, Anjouan, and Mohéli, which are separated by a maximum distance of 80 km, no island-specific genetic structure at mitochondrial or nuclear markers is found, and these animals seemingly cross this water distance with some frequency.

Demographic analysis of mitochondrial data suggests that genetic diversity within each species has a relatively recent origin, within the last million years. Although our results are not conclusive, they also suggest that *R. madagascariensis* diverged from an established Comoros population. Data from a definitive sister species to this clade would help to test this hypothesis directly.

Distance from the African continent to the nearest of the Comoro Islands is about 300 km, the same distance from Madagascar to Mayotte. Further phylogenetic analyses are needed to determine if the *R. madagascariensis*/*obliviosus* group is sister to Asian *R. leschenaultii*, but if this relationship is upheld it would indicate that African *Rousettus* were unable to successfully colonize Madagascar or the Comoros across nearly equal distance over the water crossing of the Mozambique Canal.

Outside of western Indian Ocean a few similar comparisons for the genus *Rousettus* can be presented, such as the oceanic islands in the Gulf of Guinea (São Tomé and Príncipe), which are separated from the African mainland by a maximum of 280 km. As far as we are aware, genetic sequence data are not available from these populations, but on the basis of allozyme variation, populations occurring on São Tomé and Príncipe are different from those on the mainland, and they have been described as endemic subspecies, *R. aegyptiacus princeps* Juste and Ibañez, 1993 and *R. a. tomensis* Juste and Ibañez, 1993 (Juste and Ibañez 1993; Juste et al. 1996). For *R. amplexicaudatus* in the Philippines genetic distances for populations on islands of Luzon and Mindanao, on the basis of *Cytb* sequence data, were $<0.71\%$ across a minimal island-to-island distance of about 215 km (Bastian et al. 2001). In the intermediate area between Luzon and Mindanao other stepping-stone islands house *R. amplexicaudatus*. Sulawesi holds 3 species of *Rousettus*, including 2 endemics, and about 120 km of sea separate the coast of New Guinea and northern Sulawesi. Molecular phylogenetic data on the relationships and origins of these taxa are not available.

If the hypothesis presented herein that *R. leschenaultii* is the sister group to *R. madagascariensis*/*obliviosus* is correct and that the ancestor of the latter group arrived in the Madagascar region via stepping-stone islands from the Indian subcontinent region (Juste et al. 1999), this would have involved dispersal across considerable distances: southern India to the Maldives (Malé), where no species of *Rousettus* has been recorded (Bates and Harrison 1997), is about 425 km; from the Maldives to the granitic Seychelles, also where no species of *Rousettus* has been recorded (Goodman and Gerlach 2007), is about 2,000 km; and then from the granitic Seychelles to northern Madagascar, an additional 800 km. This complete trajectory is over 3,200 km. However, if *R. aegyptiacus* is the closest species to the *madagascariensis*/*obliviosus* group, the distances of 300–400 km that separate the African continent from Madagascar and the Comoros are more reasonable for members of this genus to cross. Clearly, further molecular genetic work is needed, particularly with samples from east of the Sunda Shelf and Australia, to understand the evolutionary and speciation history of this genus across a much broader geographical scale.

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Literature Cited

Álvarez, Y., J. B. Juste, E. Tabares, A. Garrido-Pertierra, C. Ibáñez, and J. M. Bautista. 1999. Molecular phylogeny and morphological homoplasy in fruitbats. Molecular Biology and Evolution 16:1061–1067.

Andrianaivoarivelo, A. R., et al. 2009. Characterization of 22 microsatellite marker loci in the Madagascar rousette (*Rousettus madagascariensis*). Conservation Genetics 10:1025–1028.

Baker, R. J., and R. D. Bradley. 2006. Speciation in mammals and the genetic species concept. Journal of Mammalogy 87:643–662.

Bastian, S. T., Jr., K. Tanaka, R. V. P. Anunciado, N. G. Natural, A. C. Sumalde, and T. Namikawa. 2001. Phylogenetic relationships among megachiropteran species from the two major islands of the Philippines, deduced from DNA sequences of the cytochrome *b* gene. Canadian Journal of Zoology 79:1671–1677.

Bates, P. J. J., and D. L. Harrison. 1997. Bats of the Indian subcontinent. Harrison Zoological Museum, Sevenoaks, Kent, United Kingdom.

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BERGMANS, W. 1977. Notes on new material of *Rousettus madagascariensis* Grandidier, 1829 (Mammalia, Megachiroptera). Mammalia 41:67–74.

BERGMANS, W. 1994. Taxonomy and biogeography of African fruit bats (Mammalia, Megachiroptera). 4. The genus *Rousettus* Gray, 1821. Beaufortia 44:79–126.

CALISHER, C. H., J. E. CHILDS, H. E. FIELD, K. V. HOLMES, AND T. SCHOUNTZ. 2006. Bats: important reservoir hosts of emerging viruses. Clinical Microbiology Reviews 19:531–545.

CORBET, G. B., AND J. E. HILL. 1991. A world list of mammalian species. 3rd ed. Oxford University Press, New York.

DORST, J. 1947. Les chauves-souris de la faune Malgache. Bulletin du Muséum National d'Histoire Naturelle, série 2, 19:306–313.

EMERICK, C. M., AND R. A. DUNCAN. 1982. Age progressive volcanism in the Comores Archipelago, western Indian Ocean and implications for Somali plate tectonics. Earth and Planetary Science Letters 60:415–428.

EXCOFFIER, L., G. LAVAL, AND S. SCHNEIDER. 2005. Arlequin ver. 3.0: an integrated software package for population genetics data analysis. Evolutionary Bioinformatics 1:47–50.

FU, Y.-X. 1997. Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. Genetics 147:915–925.

GANNON, W. L., R. S. SIKES, AND THE ANIMAL CARE AND USE COMMITTEE OF THE AMERICAN SOCIETY OF MAMMALOGISTS. 2007. Guidelines of the American Society of Mammalogists for the use of wild mammals in research. Journal of Mammalogy 88:809–823.

GIANNINI, N. P., F. C. ALMEIDA, AND N. B. SIMMONS. 2009. Phylogenetic relationships of Harpyionycterine megabats (Chiroptera: Pteropodidae). Bulletin of the American Museum of Natural History 331:183–204.

GIANNINI, N. P., AND N. B. SIMMONS. 2003. A phylogeny of megachiropteran bats (Mammalia: Chiroptera: Pteropodidae) based on direct optimization analysis of one nuclear and four mitochondrial genes. Cladistics 19:496–511.

GIANNINI, N. P., AND N. B. SIMMONS. 2005. Conflict and congruence in a combined DNA morphology analysis of megachiropteran bat relationships (Mammalia: Chiroptera: Pteropodidae). Cladistics 21:411–437.

GOODMAN, S. M., ET AL. 2005. The distribution and conservation of bats in the dry regions of Madagascar. Animal Conservation 8:153–165.

GOODMAN, S. M., AND J. GANZHORN. 1997. Rarity of figs (*Ficus*) on Madagascar and its relationship to a depauperate frugivore community. Revue d'Ecologie 52:321–329.

GOODMAN, S. M., AND J. GERLACH. 2007. Chiroptera. Pp. 105–109 in Terrestrial and freshwater vertebrates of the Seychelles Islands (J. Gerlach, ed.). Backhuys Publishers, Leiden, The Netherlands.

GOODMAN, S. M., ET AL. 2009. The use of molecular and morphological characters to resolve the taxonomic identity of cryptic species: the case of *Miniopterus manavi* (Chiroptera: Miniopteridae). Zoologica Scripta 38:339–363.

GOODMAN, S. M., N. WEYENETH, Y. IBRAHIM, I. SAÏD, AND M. RUEDI. 2010. A review of the bat fauna of the Comoro Archipelago. Acta Chiropterologica 12:117–141.

GOUDET, J. 1995. Fstat (version 1.2): a computer program to calculate F-statistics. Journal of Heredity 86:485–486.

GUO, S. W., AND E. A. THOMPSON. 1992. Performing the exact test of Hardy–Weinberg proportion for multiple alleles. Biometrics 48:361–372.

HAYMAN, R. W., AND J. E. HILL. 1971. The mammals of Africa; an identification manual. Part 2. Order Chiroptera. Smithsonian Institution Press, Washington, D.C.

HEY, J., AND R. NIELSEN. 2007. Integration within the Felsenstein equation for improved Markov chain Monte Carlo methods in population genetics. Proceedings of the National Academy of Sciences 104:2785–2790.

HUA, P. Y., J. P. CHEN, M. SUN, B. LIANG, S. Y. ZHANG, AND D. H. WU. 2006. Characterization of microsatellite loci in fulvous fruit bat *Rousettus leschenaulti*. Molecular Ecology Notes 6:939–941.

HUELSENBECK, J. P., AND F. RONQUIST. 2001. MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17:754–755.

IEHLE, C., ET AL. 2007. Henipavirus and tioman virus antibodies in pteropodid bats, Madagascar. Emerging and Infectious Diseases 13:159–161.

IRWIN, D. M., T. D. KOCHER, AND A. C. WILSON. 1991. Evolution of the cytochrome *b* gene of mammals. Journal of Molecular Evolution 32:128–144.

JUSTE, J., Y. ÁLVAREZ, E. TABARES, A. GARRIDO-PERTIERRA, C. IBÁÑEZ, AND J. M. BAUTISTA. 1999. Phylogeography of African fruitbats (Megachiroptera). Molecular Phylogenetics and Evolution 13:596–604.

JUSTE, J., AND C. IBÁÑEZ. 1993. Geographic variation and taxonomy of *Rousettus aegyptiacus* (Mammalia: Megachiroptera) in the islands of the Gulf of Guinea. Zoological Journal of the Linnean Society 107:117–129.

JUSTE, J. B., C. IBÁÑEZ, AND A. MACHORDOM. 1997. Evolutionary relationships among the African fruit bats: *Rousettus egyptiacus*, *R. angolensis*, and *Myonycteris*. Journal of Mammalogy 78:766–774.

JUSTE, J. B., A. MACHORDOM, AND C. IBÁÑEZ. 1996. Allozyme variation of the Egyptian Rousette (*Rousettus egyptiacus*; Chiroptera Pteropodidae) in the Gulf of Guinea (West-Central Africa). Biochemical Systematics and Ecology 24:499–508.

KALUNDA, M., ET AL. 1986. Kasokero virus: a new human pathogen from bats (*Rousettus aegyptiacus*) in Uganda. American Journal of Tropical Medicine and Hygiene 35:387–392.

KINGDON, J. 1974. East African mammals: an atlas of evolution in Africa. Vol. II Part A (insectivores and bats). Academic Press, London, United Kingdom.

KIRSCH, J. A., T. F. FLANNERY, M. S. SPRINGER, AND F. J. LAPOINTE. 1995. Phylogeny of the Pteropodidae (Mammalia: Chiroptera) based on DNA hybridisation, with evidence for bat monophyly. Australian Journal of Zoology 43:395–428.

KOCK, D. 1978. A new fruit bat of the genus *Rousettus* Gray 1821, from the Comoro Islands, western Indian Ocean (Mammalia: Chiroptera). Pp. 205–216 in Proceedings of the Fourth International Bat Research Conference (R. J. Olembo, J. B. Castelino, and F. A. Mutere, eds.). Kenya Literature Bureau, Nairobi, Kenya.

KOOPMAN, K. F. 1994. Chiroptera: systematics. Pp. 1–217 in Handbook of zoology (J. Niethammer, H. Schliemann, and D. Starck, eds.). Walter de Gruyter, Berlin, Germany. Vol. 8.

KUZMIN, I. V., ET AL. 2008. Lagos bat virus in Kenya. Journal of Clinical Microbiology 46:1451–1461.

LOUETTE, M. 2004. Mammifères. Pp. 65–87 in La faune terrestre de l'archipel des Comores (M. Louette, D. Meitre, and R. Locqué, eds.). Musée royal de l'Afrique centrale, Tervuren, Belgium.

MACKINNON, J. L., C. E. HAWKINS, AND P. A. RACEY. 2003. Pteropodidae, fruit bats. Pp. 1299–1302 in The natural history of Madagascar (S. M. Goodman and J. P. Benstead, eds.). University of Chicago Press, Chicago, Illinois.

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MADDISON, D. R., AND W. P. MADDISON. 2003. MacClade 4: analysis of phylogeny and character evolution. Version 4.06. Sinauer Associates, Sunderland, Massachusetts.

NORBERG, U. M. 1981. Allometry of bat wings and legs and comparison with bird wings. Philosophical Transactions of the Royal Society London, B. Biological Sciences 292:359–398.

NORBERG, U. M. 1994. Wing design, flight performance and habitat use in bats. Pp. 205–239 in Ecological morphology: integrative organismal biology (P. C. Wainwright and S. M. Reilly, eds.). University of Chicago Press, Chicago, Illinois.

NOUGIER, J., J. M. CANTAGREL, AND J. P. KARCHE. 1986. The Comores Archipelago in the western Indian Ocean: volcanology, geochronology and geodynamic setting. Journal of African Earth Sciences 5:135–145.

NYLANDER, J. A. A. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Sweden.

PAVRI, K. M., K. R. P. SINGH, AND F. B. HOLLINGER. 1971. Isolation of a new parainfluenza virus from a frugivorous bat, *Rousettus leschenaulti*, collected at Poona, India. American Journal of Tropical Medicine and Hygiene 20:125–130.

PESOLE, G., C. GISSI, A. DE CHIRICO, AND C. SACCONE. 1999. Nucleotide substitution rate of mammalian mitochondrial genomes. Journal of Molecular Evolution 48:427–434.

PETERSON, R. L., J. L. EGER, AND L. MITCHELL. 1995. Chiroptères. Faune de Madagascar 84:1–204.

PRITCHARD, J. K., M. STEPHENS, AND P. DONNELLY. 2000. Inference of population structure using multilocus genotype data. Genetics 155:945–959.

RACEY, P. A., S. M. GOODMAN, AND R. K. B. JENKINS. 2010. The ecology and conservation of Malagasy bats. Pp. 369–404 in Island bats (T. H. Fleming and P. A. Racey, eds). University of Chicago Press, Chicago, Illinois.

RATRIMOMANARIVO, F. H., S. M. GOODMAN, W. T. STANLEY, N. HOOSEN, P. J. TAYLOR, AND J. LAMB. 2008. Morphological and molecular variation in *Mops leucostigma* (Chiroptera: Molossidae) of Madagascar and the Comoros: phylogeny, phylogeography and geographic variation. Mitteilungen aus dem Hamburgischen Zoologischen Museum 105:57–101.

RATRIMOMANARIVO, F. H., S. M. GOODMAN, W. T. STANLEY, T. NAIDOO, P. J. TAYLOR, AND J. LAMB. 2009. Geographic and phylogeographic variation in *Chaerephon leucogaster* (Chiroptera: Molossidae) of Madagascar and the western Indian Ocean islands of Mayotte and Pemba. Acta Chiropterologica 11:25–52.

RAYMOND, M., AND F. ROUSSET. 1995. Genepop (Version 1.2)—population-genetics software for exact tests and ecumenicism. Journal of Heredity 86:248–249.

RAZAFINDRAKOTO, N. 2006. Etude comparative du régime alimentaire de *Pteropus rufus* Tiedemann, 1808 et de *Rousettus madagascariensis* Grandidier, 1928 (Pteropodidae) dans le district de Moramanga. Mémoire Diplôme d'Etudes Approfondies, Département de Biologie Animale, Université d'Antananarivo, Antananarivo, Madagascar.

REEVES, W., A. DOWLING, AND G. DASCH. 2006. Rickettsial agents from parasitic Dermanyssoidea (Acari: Mesostigmata). Experimental and Applied Acarology 38:181–188.

ROGERS, A. R., AND H. HARPENDING. 1992. Population growth makes waves in the distribution of pairwise genetic differences. Molecuar Biology and Evolution 9:552–569.

RONQUIST, F., AND J. P. HUELSENBECK. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19:1572–1574.

ROZAS, J., J. C. SÁNCHEZ-DELBARRIO, X. MESSEGUER, AND R. ROZAS. 2003. DnaSP, DNA polymorphism analyses by the coalescent and other methods. Bioinformatics 19:2496–2497.

SCHNEIDER, S., AND L. EXCOFFIER. 1999. Estimation of past demographic parameters from the distribution of pairwise differences when the mutation rates vary among sites: application to human mitochondrial DNA. Genetics 152:1079–1089.

SEWALL, B. J., E. F. GRANEK, AND W. J. TREWHELLA. 2003. The endemic Comoros Islands fruit bat *Rousettus obliviosus*: ecology, conservation, and Red List status. Oryx 37:344–352.

SIMMONS, N. B. 2005. Order Chiroptera. Pp. 312–529 in Mammal species of the world: a taxonomic and geographic reference, 3rd ed. (D. E. Wilson and D. M. Reeder, eds.). Johns Hopkins University Press, Baltimore, Maryland.

SPRINGER, M. S., L. J. HOLLAR, AND J. A. KIRSCH. 1995. Phylogeny, molecules versus morphology, and rates of character evolution among fruitbats (Chiroptera: Megachiroptera). Australian Journal of Zoology 43:557–582.

TOWNER, J. S., ET AL. 2007. Marburg virus infection detected in a common African bat. PLoS ONE 2(8):e764.

TOWNER, J. S., ET AL. 2009. Isolation of genetically diverse Marburg viruses from Egyptian fruit bats. PLoS Pathog 5(7):e1000536.

WELLENBERG, G. J., L. AUDRY, L. RØNSHOLT, W. H. M. VAN DER POEL, C. J. M. BRUSCHKE, AND H. BOURHY. 2002. Presence of European bat lyssavirus RNAs in apparently healthy *Rousettus aegyptiacus* bats. Archives of Virology 147:349–361.

WEYENETH, N., S. M. GOODMAN, W. T. STANLEY, AND M. RUEDI. 2008.The biogeography of *Miniopterus* bats (Chiroptera: Miniopteridae) from the Comoro Archipelago inferred from mitochondrial DNA. Molecular Ecology 17:5205–5219.

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APPENDIX I

Museum number, species, locality, and GenBank numbers of specimens used in this study. Museums holding this material include the Field Museum of Natural History (FMNH) and the Université d'Antananarivo Département de Biologie Animale (UADBA). Abbreviations used in locality names include: PN = Parc National, RNI = Réserve Naturelle Intégrale, RS = Réserve Spéciale, SF = Station Forestière.

Museum number	Species	Province/ island	Locality	GenBank accession number
FMNH 179237	*R. madagascariensis*	Antsiranana	Andlavakarano (Andavadrano)	GU228684
FMNH 179319	*R. madagascariensis*	Antsiranana	Andlavakarano (Andavadrano)	GU228685
FMNH 172678	*R. madagascariensis*	Antsiranana	Antsahabe River, near village of Ankijabe	GU228639
FMNH 172679	*R. madagascariensis*	Antsiranana	Antsahabe River, near village of Ankijabe	GU228640
FMNH 179320	*R. madagascariensis*	Antsiranana	Campement Matsaborymadio	GU228686
FMNH 188555	*R. madagascariensis*	Antsiranana	Nosy Be	GU228693
FMNH 188556	*R. madagascariensis*	Antsiranana	Nosy Be	GU228694
FMNH 188558	*R. madagascariensis*	Antsiranana	Nosy Be	GU228695
FMNH 188559	*R. madagascariensis*	Antsiranana	Nosy Be	GU228696
UADBA SMG-15185	*R. madagascariensis*	Antsiranana	Nosy Be	GU228697
UADBA SMG-15186	*R. madagascariensis*	Antsiranana	Nosy Be	GU228698
UADBA SMG-15187	*R. madagascariensis*	Antsiranana	Nosy Be	GU228699
UADBA SMG-15188	*R. madagascariensis*	Antsiranana	Nosy Be	GU228700
FMNH 188561	*R. madagascariensis*	Antsiranana	Nosy Be	GU228701
FMNH 188562	*R. madagascariensis*	Antsiranana	Nosy Be	GU228702
FMNH 188564	*R. madagascariensis*	Antsiranana	Nosy Be	GU228703
FMNH 188613	*R. madagascariensis*	Antsiranana	Nosy Be	GU228704
FMNH 188614	*R. madagascariensis*	Antsiranana	Nosy Be	GU228705
FMNH 188615	*R. madagascariensis*	Antsiranana	Nosy Be	GU228706
UADBA SMG-15201	*R. madagascariensis*	Antsiranana	Nosy Be	GU228707
FMNH 187670	*R. madagascariensis*	Antsiranana	Nosy Be	GU228597
FMNH 187675	*R. madagascariensis*	Antsiranana	Nosy Be	GU228598
FMNH 187676	*R. madagascariensis*	Antsiranana	Nosy Be	GU228599
FMNH 187684	*R. madagascariensis*	Antsiranana	Nosy Be	GU228600
FMNH 187690	*R. madagascariensis*	Antsiranana	Nosy Be	GU228601
FMNH 187693	*R. madagascariensis*	Antsiranana	Nosy Be	GU228602
FMNH 187698	*R. madagascariensis*	Antsiranana	Nosy Be	GU228603
FMNH 187699	*R. madagascariensis*	Antsiranana	Nosy Be	GU228604
FMNH 187701	*R. madagascariensis*	Antsiranana	Nosy Be	GU228605
FMNH 187702	*R. madagascariensis*	Antsiranana	Nosy Be	GU228606
FMNH 187703	*R. madagascariensis*	Antsiranana	Nosy Be	GU228607
UADBA SMG-15239	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228708
UADBA SMG-15240	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228709
UADBA SMG-15241	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228710
FMNH 188629	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228711
FMNH 188630	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228712
FMNH 188631	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228713
FMNH 188632	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228714
UADBA SMG-15250	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228715
FMNH 188622	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228716
FMNH 188623	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228717
FMNH 188624	*R. madagascariensis*	Antsiranana	Nosy Komba	GU228718
FMNH 178790	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228673
FMNH 178791	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228674
FMNH 178792	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228675
FMNH 178793	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228676
FMNH 178795	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228677
FMNH 178796	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228678
FMNH 178797	*R. madagascariensis*	Antsiranana	RS d'Analamerana, Grotte de Bazaribe	GU228679
FMNH 154287	*R. madagascariensis*	Antsiranana	RS d'Anjanaharibe-Sud, Marolakana River	GU228633
FMNH 176268	*R. madagascariensis*	Antsiranana	RS d'Ankarana, 3.5 km SE Andrafiabe (village)	GU228672
FMNH 176262	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228668
FMNH 176263	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228669
FMNH 176264	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228670
FMNH 176265	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228671
FMNH 172997	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228641
FMNH 172998	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228642
FMNH 172999	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228643

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Appendix I.—Continued.

Museum number	Species	Province/ island	Locality	GenBank accession number
FMNH 173000	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228644
FMNH 173001	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228645
FMNH 177383	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228629
FMNH 177384	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte des Chauves-souris	GU228630
FMNH 183863	*R. madagascariensis*	Antsiranana	RS d'Ankarana, Grotte Milaintety	GU228631
FMNH 169703	*R. madagascariensis*	Antsiranana	RS d'Ankarana, near Andrafiabe Cave	GU228637
FMNH 162064	*R. madagascariensis*	Fianarantsoa	9 km NE Ivohibe, 6.5 km ESE Angodongodona	GU228636
FMNH 187600	*R. madagascariensis*	Fianarantsoa	Ambodiamontana	GU228692
FMNH 151705	*R. madagascariensis*	Fianarantsoa	PN d'Andringitra	GU228632
FMNH 179289	*R. madagascariensis*	Mahajanga	Grotte d'Anjohibe	GU228681
FMNH 179290	*R. madagascariensis*	Mahajanga	Grotte d'Anjohibe	GU228682
FMNH 179294	*R. madagascariensis*	Mahajanga	Grotte d'Anjohibe	GU228683
FMNH 184008	*R. madagascariensis*	Mahajanga	Grotte d'Ankelimahogo	GU228687
FMNH 184009	*R. madagascariensis*	Mahajanga	Grotte d'Ankelimahogo	GU228688
FMNH 184010	*R. madagascariensis*	Mahajanga	Grotte d'Ankelimahogo	GU228689
FMNH 184011	*R. madagascariensis*	Mahajanga	Grotte d'Ankelimahogo	GU228690
FMNH 184012	*R. madagascariensis*	Mahajanga	Grotte d'Ankelimahogo	GU228691
FMNH 169679	*R. madagascariensis*	Mahajanga	PN de Bemaraha, Foret d'Andranogidro	GU228638
FMNH 175759	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228646
FMNH 175760	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228647
FMNH 175761	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228648
FMNH 175762	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228649
FMNH 175763	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228650
FMNH 175765	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228651
FMNH 175766	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228652
FMNH 175897	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228653
FMNH 175898	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228654
FMNH 175899	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228655
FMNH 175900	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228656
FMNH 175901	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228657
FMNH 175903	*R. madagascariensis*	Mahajanga	RNI de Namoroka, along Ampandra River	GU228658
FMNH 175767	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228659
FMNH 175768	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228660
FMNH 175769	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228661
FMNH 175770	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228662
FMNH 175771	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228663
FMNH 175772	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228664
FMNH 175773	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228665
FMNH 175774	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228666
FMNH 175775	*R. madagascariensis*	Mahajanga	RNI de Namoroka, near source of Mandevy River	GU228667
FMNH 187720	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228608
FMNH 187721	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228609
FMNH 187722	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228610
FMNH 187723	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228611
FMNH 187724	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228612
FMNH 187725	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228613
FMNH 187727	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228614
FMNH 187728	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228615
FMNH 187729	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228616
FMNH 187730	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228617
FMNH 187731	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228618
FMNH 187732	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228619
FMNH 187733	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228620
FMNH 187735	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228621
FMNH 187736	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228622
FMNH 187737	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228623
FMNH 187738	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228624
FMNH 187739	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228625
FMNH 187741	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228626
FMNH 187742	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228627
FMNH 187743	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228628
FMNH 188656	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228719
FMNH 188657	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228720

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APPENDIX I.—Continued.

Museum number	Species	Province/ island	Locality	GenBank accession number
FMNH 188658	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228721
FMNH 188659	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228722
FMNH 188660	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228723
FMNH 188661	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228724
FMNH 188662	*R. madagascariensis*	Toamasina	Ile Sainte Marie	GU228725
FMNH 179197	*R. madagascariensis*	Toamasina	SF de Tampolo	GU228680
UADBA ZR-157	*R. madagascariensis*	Toliara	Ambohijanahary Mountain	GU228726
FMNH 194598	*R. madagascariensis*	Toliara	Ambohijanahary Mountain	GU228727
FMNH 156610	*R. madagascariensis*	Toliara	PN d'Andohahela, 8 km NW Eminiminy	GU228634
FMNH 156611	*R. madagascariensis*	Toliara	PN d'Andohahela, 8 km NW Eminiminy	GU228635
FMNH 194230	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228753
FMNH 194231	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228728
FMNH 194232	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228754
FMNH 194233	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228755
FMNH 194234	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228729
FMNH 194236	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228730
FMNH 194238	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228731
FMNH 194240	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228732
FMNH 194241	*R. obliviosus*	Grande Comore	Nyamaoui Panga [=Panga Chilamouinani], near Fassi	GU228733
FMNH 194305	*R. obliviosus*	Grande Comore	above Boboni, on trail towards La Convalescence	GU228734
FMNH 194306	*R. obliviosus*	Grande Comore	above Boboni, on trail towards La Convalescence	GU228735
FMNH 194307	*R. obliviosus*	Grande Comore	above Boboni, on trail towards La Convalescence	GU228756
FMNH 194308	*R. obliviosus*	Grande Comore	above Boboni, on trail towards La Convalescence	GU228757
FMNH 194313	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228758
FMNH 194314	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228759
FMNH 194315	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228760
FMNH 194316	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228761
FMNH 194317	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228736
FMNH 194318	*R. obliviosus*	Anjouan	Grotte de Mangamitsano, between Bambao and Col de Patsi	GU228737
FMNH 194320	*R. obliviosus*	Anjouan	Grotte de Hapira, near Limbi along Trondroni River	GU228762
FMNH 194322	*R. obliviosus*	Anjouan	Grotte de Hapira, near Limbi along Trondroni River	GU228763
FMNH 194438	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228738
FMNH 194439	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228739
FMNH 194440	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228740
FMNH 194441	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228741
FMNH 194442	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228742
FMNH 194443	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228764
FMNH 194444	*R. obliviosus*	Anjouan	Lac de Dzialande	GU228765
FMNH 194458	*R. obliviosus*	Mohéli	Ouallah I	GU228743
FMNH 194459	*R. obliviosus*	Mohéli	Ouallah I	GU228766
FMNH 194460	*R. obliviosus*	Mohéli	Ouallah I	GU228744
FMNH 194461	*R. obliviosus*	Mohéli	Ouallah I	GU228767
FMNH 194462	*R. obliviosus*	Mohéli	Ouallah I	GU228768
FMNH 194463	*R. obliviosus*	Mohéli	Ouallah I	GU228769
FMNH 194530	*R. obliviosus*	Mohéli	Ouallah I	GU228770
FMNH 194464	*R. obliviosus*	Mohéli	near Ouallah I, along Akomodjou River	GU228745
FMNH 194465	*R. obliviosus*	Mohéli	near Ouallah I, along Akomodjou River	GU228746
FMNH 194466	*R. obliviosus*	Mohéli	near Ouallah I, along Akomodjou River	GU228747
FMNH 194539	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228748
FMNH 194540	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228749
FMNH 194541	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228750
FMNH 194542	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228751
FMNH 194543	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228752
FMNH 194544	*R. obliviosus*	Grande Comore	Panga Milembeni, near village of Dimadjou	GU228771

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