Mitochromal Diversity and Morphological Variation of *Marmosa murina* (Didelphidae) in French Guiana

Cynthia Steiner* and François M. Catzeflis

Laboratoire de Paléontologie, Institut des Sciences de l’Évolution de Montpellier, Université Montpellier 2, Place Eugené Bataillon, Case Courrier 064, 34095 Montpellier Cedex 05, France

The murine mouse opossum *Marmosa murina* is a widely distributed species in tropical South America. In northeastern South America, authors propose the recognition of several subspecies, of which 2 might be found in French Guiana: a paler taxon (*M. murina murina*) inhabiting the narrow coastal strip and a darker one (*M. m. muscula*) occurring in the inner rainforests. We present here results of molecular analyses for 2 mitochondrial fragments (cytochrome-*b* gene and control region) and morphological examination of 3 external and 15 cranial measurements. These data support the presence of only 1 subspecies (*M. m. murina*) in French Guiana based on the absence of genetic structure and morphological divergence. Nevertheless, it appears that *M. murina* shows substantial morphometric variation across the Guianan shield with respect to the dental measurement M1–M4. This suggests that *M. murina* could be a differentiated taxon in the Guianas, likely comprising more than one biological entity.

Key words: control region, cytochrome *b*, French Guiana, *Marmosa murina*, morphological variation

The murine mouse opossum *Marmosa murina* (Didelphidae: Marsupialia) has a large distribution in tropical South America and lives in different habitats, including mature and secondary rainforests as well as disturbed zones (plantations, camps, gardens, and houses). The type locality of this species, originally given as “Asia, America” by Linnaeus (1758), was subsequently restricted to Surinam by Thomas (1911). *M. murina*, as currently understood, occurs in the Guianas, eastern Venezuela, Amazonian Ecuador, Peru, and Brazil from sea level to at least 1,365 m (Emmons and Feer 1997: map 13).

*Marmosa murina* is predominantly nocturnal and belongs to the trophic guild of arboreal omnivores (Voss et al. 2001). This small (25–50 g) opossum has uniformly warm brown dorsal fur with ventral fur that may be whitish, delicate salmon, seashell pink, yellowish or cream; its eye rings are large and prominent, and ears are large. Body fur extends along the tail for a short distance, not more than 10–15 mm (A. M. Husson, in litt.). The skull of *M. murina* has distinctly flared supraorbital ledges, with sharply pointed postorbital processes that are especially well developed in older individuals. The auditory bullae have a globular alisphenoid portion without an anteromedial process (Patton et al. 2000; Voss et al. 2001).

Some studies (Malcolm 1988, 1990; Ochoa 2000; Patton et al. 2000) have suggested that *M. murina* is a species generally rare within Amazonia, but Emmons and Feer (1997) consider it as an often-common marmosine. In French Guiana, the murine mouse opossum has a widespread distribution (Julien-Laferrière 1991) and is relative-
ly common, with large differences in abundance according to localities or years (in litt.).

Patton and Costa (2003) proposed that *M. murina* is a strongly differentiated taxon based on comparative molecular phylogeography. Traditional taxonomy lists 18 different names as synonyms (Gardner 1993), and this taxon likely comprises more than 1 biological species (Patton and Costa 2003). According to Tate (1933:90–97), 2 subspecies of *M. murina* are parapatrically distributed in Guyana, Surinam, and French Guiana. *M. murina murina* is said to occur from Brazilian Guiana (state of Amapá) to Guyana along the narrow coastal strip between the sea and the heavy rain forests of the hinterland; this form is allegedly replaced by the smaller darker *M. murina muscula* in the inner rainforests of the Guianan shield and eastern Amazonia (Tate 1933:90–97). However, Cabrera (1958) and Husson (1978) recognized only the former subspecies as occurring in the Guianas and northeastern Brazil. Voss et al. (2001) identified material off coastal French Guiana as *M. murina murina* but noticed some dorsal color difference between their paler specimens and a darker series of skins from Kar tabo, Guyana, which Tate (1933) had identified as *M. m. muscula*. Nevertheless, Voss et al. (2001:40) concluded that “it does not seem useful to recognize [these] subspecies as valid at the present time.”

French Guiana, with an area of approximately 85,000 km$^2$, is situated on the Precambrian base of the Guianan shield. The natural environment comprises mainly (90%) primary rainforests where the human impact has been and still is negligible. Only on a very narrow (1–5 km) coastal zone, where Quaternary marine sediments overlay the Precambrian base, does nonforest vegetation occur (mangroves, savannas, and coastal swamps—de Granville 1982).

In this article, we consider morphological (external and cranial) measurements and molecular markers (mitochondrial gene cytochrome *b* [Cyt* b*] and control region) for a series of specimens from different areas in French Guiana to determine if more than 1 form of *M. murina* occurs in this region. Patterns in genetic and morphometric variation as well as spatial structure appear congruent and complementary to address this question.

**MATERIALS AND METHODS**

**Molecular analyses.**—Partial sequences of mitochondrial Cyt* b* (820 base pairs) gene were obtained for 24 individuals of *M. murina* collected in the field from 11 localities in French Guiana (Fig. 1; Appendix I): 6 interior forest areas (Saül, Petit Saut, Saut Pararé, Nouragues, Trinité, Pic Matecho) and 5 coastal areas (Cayenne, Kourou, Macouria, Kaw, Iracoubo). To search for cryptic genetic structure among French Guianan *M. murina*, we next sequenced a 489-bp fragment of the fast-evolving mitochondrial control region (d-loop) for 16 individ-
nals from 10 different localities. We could not obtain a reliable d-loop sequence for all specimens sampled due to the presence of heteroplasmacy and of nuclear copies. The tissue samples are stored in the collection of mammal tissues of the Institut des Sciences de l’Évolution de Montpellier, France (Catzeflis 1991).

DNA was extracted from ethanol-preserved tissues using phenol–chloroform, proteinase K–ribonuclease methods (Sambrook et al. 1989). *Cytb* and d-loop were amplified by the polymerase chain reaction (Linnis et al. 1990) using the conserved primers MVZ05 and MVZ16 (Smith and Patton 1993) and L0 (Douzery and Randi 1997) and E3 (Huchon et al. 1999), respectively. *Cytb* and d-loop amplifications were performed in a thermocycler PTC-100 (MJ Research, Inc., Waltham, Massachusetts) with 30 cycles comprising denaturation at 94°C (30 s), annealing at 45°C for *Cytb* and 52°C for d-loop (1.5 min), respectively, and extension at 68°C (1.5 min for *Cytb* and 1 min for d-loop). Both strands of each mitochondrial fragment were sequenced using an automatic sequencer (ABI 310 Perkin Elmer, Applied Biosystems, Foster City, California) with Big Dye Terminator Cycle Polymerase. Internal primers H8 (5′-CCTCAG-AATGATATTGTCCCTC-3′) and L13 (5′-TC-TTCCATGAGGACAAATTC-3′) were used for *Cytb* sequencing.

Sequence alignment of *Cytb* and d-loop fragments and substitution pattern analyses were performed using MUST (Philippe 1993) software. Two *M. murina* sequences from Peru (Loreto) were added to assess the extent of French Guiana genetic diversity as compared with a distant locality from the species range. Out-group taxa were *Micoureus demerarae* (*n* = 2 individuals), *Marmosops parvidens* (*n* = 2), *Philander opossum* (*n* = 1), and *Didelphis albiventris* (*n* = 1; European Molecular Biology Laboratory–GenBank accession numbers AJ486978–AJ487009 for *Cytb* and AJ487087–AJ487103 for d-loop sequences). Phylogenetic relationships were analyzed by maximum parsimony and maximum likelihood methods. Distance matrices were generated from the Kimura 2-parameters estimator using the neighbor-joining algorithm in MUST (Philippe 1993).

Maximum parsimony and maximum likelihood trees were obtained with PAUP version 4.0 b8 (Swofford 1998) using heuristic searches with 100 random addition sequences of taxa using the tree bisection–reconnection branch swapping option. Maximum likelihood trees were calculated using general time-reversible model. The shape parameter of the gamma distribution, λ, and rates of substitution matrix were estimated using maximum likelihood method. Support for internal nodes was assessed by bootstrap analyses (Felsenstein 1985), with 1,000 and 200 replicates for maximum parsimony and maximum likelihood methods, respectively. Estimates of haplotypic (h) and nucleotide (H) diversity between individuals were calculated through DnaSP version 3.0 (Rozas and Rozas 1999).

**Morphological methods.**—We examined 29 adult specimens of *M. murina* from 8 localities in French Guiana (3 coastal sites and 5 localities from inner forests; Fig. 1; Appendix I). Specimens were aged using the dental criteria suggested by Tribe (1990). Fifteen cranial measurements were taken as defined by Patton et al. (2000) and Voss et al. (2001): condylobasal length, total cranial length, zygomatic breadth, braincase breadth, mastoid breadth, anterior interorbital constriction, posterior interorbital constriction, rostral length, rostral width, length of upper canine to 4th molar, length of upper molars (M1–M4), palatal length, palatal width, occipital condylic breadth, and tympanic bullar width. We also measured the length of medial caudal-scale hair (average length of medial caudal-scale hair in proximal, middle, and distal dorsal parts of the tail) and length of lateral caudal-scale hairs, and we counted the number of caudal scales per 0.5 cm (average number of caudal scales on proximal, middle, and distal dorsal parts of the tail).

To test for the presence of 2 morphological units in French Guiana, we compared populations in terms of cranial variables using multivariate analysis of variance (MANOVA) as implemented in the STATISTICA (1993) software package (StatSoft, Inc., Tulsa, Oklahoma). The same approach was used to understand the morphometric variation of *M. murina* over a more extensive area (Guianian shield) considering dental measurement M1–M4 for 12 adult individuals from Surinam (3 localities; Appendix I), 22 from Amapá, Brazil (3) and 20 from the southeastern part of Venezuela (17).

**RESULTS**

**Molecular.**—Twenty-six sequences from *M. murina* were obtained for the *Cytb* gene.
French Guianan individuals (24 sequences from 11 localities) were characterized by 14 haplotypes, with a high haplotypic diversity ($h = 0.8 \pm 0.1$) in contrast to a low nucleotide diversity ($I = 0.01$). Numbers of variable and parsimony-informative sites were very low, 25 and 10, respectively. The average divergence (Kimura 2-parameters estimator) between French Guianan haplotypes is $1.2 \pm 0.9\%$. The Cytb maximum parsimony and maximum likelihood ($-\ln L = 3378.24, \lambda = 0.33$) analyses showed a similar topology (Fig. 2), separating $M. murina$ into 2 clades: the 2 individuals from Peru and the 24 animals from French Guiana differing by an average of $8.7\%$ substitutions. The 14 French Guianan haplotypes show no apparent genetic segregation between coastal and inner rainforest localities. Identical sequences were found in different localities, such as Cayenne (coastal), Kaw (coastal), and Pic Matécho (inner forests). The 8 individuals from Nouragues (inner forests) locality revealed 4 different haplotypes differing by an average of $0.4\%$ substitutions. The highest genetic divergence ($3.9\%$) was measured between the localities of Kaw (coastal swamps) and Petit Saut (inner forests).

When $D. albiventris$ and $P. opossum$ are designed as out-group, $M. demerarae$ is the sister-taxon of $M. murina$, in agreement with the results—based on nuclear gene IRBP—of Jansa and Voss (2000). The 2 Peruvian $M. murina$ are sisters to a monophyletic group of French Guianan sequences (Fig. 2).

The 16 French Guianan $M. murina$ d-loop sequences comprise only 5 closely related haplotypes (less than for the same sampling of Cytb, where those 16 animals are represented by 9 haplotypes). Maximum parsimony and maximum likelihood phylogenetic analyses of d-loop fragments do not evidence phylogeographic relationships among French Guiana individuals (trees not shown). The most divergent individuals (1.5%) are those from Nouragues (inner forests) and Macouria (coastal) on the one hand and Nouragues and Iracoubo (coastal) on the other.

D-loop haplotypic diversity ($h = 0.7 \pm 0.1$) appears similar to that for Cytb ($h = 0.9 \pm 0.1$), whereas nucleotide diversity is higher for the control region ($I = 0.099$ and $0.0091$, respectively). Nevertheless, the 2 mitochondrial fragments have a similar variability for French Guianan animals: 16 d-loop (482-bp length) sequences with 17 polymorphic (14 parsimony-informative) sites, as compared with 24 Cytb (820-bp length) sequences with 44 polymorphic (17 parsimony-informative) sites.

Phylogenetic analyses for concatenated Cytb and d-loop sequences of $M. murina$ are presented in Fig. 3, with a Peruvian individual used to root the tree of 13 French Guiana haplotypes. The concatenated data matrix has 1,239 sites, of which 47 are polymorphic and 29 are parsimony-informative for French Guianan animals. Only 1 single clade is robustly supported, namely, the association between 2 coastal individuals (Macouria, Iracoubo). All other relationships are poorly supported, and the average divergence (Kimura 2-parameters estimator) between French Guianan animals is low: $0.8 \pm 0.5\%$. An identical haplotype is shared by coastal (Kaw, Cayenne) and inner-forest (Pic Matecho) localities. The average amount of substitutions among the 5 coastal localities is higher ($1.2 \pm 0.4\%$) than the one measured among the 5 inner forests localities ($0.4 \pm 0.3\%$).

Morphological data.—For French Guiana murine opossums (29 specimens), we did not find significant differences between the samples from coastal localities ($n = 15$) and the animals from inner-forest localities ($n = 14$) for most cranial measurements (MANOVA analysis: Wilks’ lambda = 0.21, $P = 0.11$; Table 1). Only the cranial measurement rostral width and the number of caudal scales per 0.5 cm showed significant differences between the 2 regions ($P = 0.02$ and $P = 0.04$, respectively), with the inner-forests individuals being smaller and having more caudal scales.
Fig. 2.—Maximum likelihood tree ($-\ln L = 3378.24; \lambda = 0.33$) of cytochrome-\textit{b} sequences (820 pb) for 16 \textit{Marmosa murina} individuals and 6 other didelphids. Bootstrap values are indicated along the branches for maximum parsimony (italic) and maximum likelihood methods. Sequences of \textit{Marmosops}, \textit{Didelphis}, and \textit{Philander} were used to root the tree. Specimens from coastal localities are in italics.

Side-by-side comparisons of some animals caught in coastal ($n = 10$) and inner-forest ($n = 10$) localities did not show differences in any external characters, including those mentioned by Tate (1933:94–97) for recognizing both subspecies: dorsal color (paler in \textit{M. m. muscula}), feet (larger and stronger in \textit{M. m. murina}), and pelage (longer in \textit{M. m. muscula}).

MANOVA analyses for length of M1–M4 showed highly significant differences among the 4 regions (Wilks’ lambda = 0.53, $P \ll 0.001$). It appears that Venezuelan individuals have larger molars in comparison with those from Surinam, French Guiana, and Amapá (Fig. 4).

**DISCUSSION**

**Genetic structure.**—For northeastern South America, Tate (1933) recognized several subspecies in \textit{M. murina}, of which 2 possibly co-occur in French Guiana: a paler taxon (\textit{M. murina murina}) inhabiting the narrow coastal strip and a darker one (\textit{M. m. muscula}) occurring in the inner rainforests. The absence of significant genetic structure in 2 fast-evolving mitochondrial sequences (\textit{Cytb}, control region) among the
samples from both the coastal and the inner-forest localities does not support Tate’s hypothesis, at least for French Guiana. Our results are more in agreement with the recent revision made by Voss et al. (2001) recognizing—by morphological criteria only—1 subspecies (M. m. murina) in French Guiana and neighboring regions.

The apparent lack of genetic structure could be the consequence of an extensive gene flow occurring among French Guianan populations or of a recent origin of all these populations from a common ancestral gene pool that might have been confined in a Pleistocene refuge during the last glaciation period (22,000–10,000 years ago). Our current knowledge does not allow us to distinguish between these 2 nonexclusive explanations accounting for the absence of genetic structure of French Guianan populations. The hypothetical refuge was perhaps limited to the northeast by the Kaw mountains and to the south by the Inini-Camopi mountains (de Granville 1982).

In French Guiana, Catzeflis and Lavergne (1998) also showed the absence of genetic structure for another didelphid marsupial, Didelphis marsupialis, using microsatellite markers. However, clear genetic structuring was found for another mouse opossum, M. demerarae (Patton et al. 2000) in western Amazonia, along the Rio Juruá basin of Brazil. There was a strong separation of geographical samples inhabiting upper versus lower parts of the river. This genetic dichotomy was also observed in several other nonvolant small mammals, coinciding with a geological structure termed the Iquitos Arch (Brazil; Patton et al. 2000: 267–277).

The small size of French Guiana (about 85,000 km²) is not necessarily the cause of the genetic homogeneity observed in M. murina. In the same geographic area we have previously discovered, using the same molecular markers, a stronger genetic structuring for an echimyid rodent, Proechimys cuvieri (Steiner and Catzeflis 2000).

Sequences divergence.—The genetic homogeneity (Kimura 2-parameters distances and nucleotidic diversities) between French Guiana individuals suggests a recent origin of the M. murina population. The high h and low P are compatible with a rapid population growth from an ancestral population with small N, provided the time was sufficient for the recovery of haplotypes variation via mutation yet too short for an accumulation of large sequence differences (Avise 2000).

Whereas our results emphasize genetic homogeneity, Patton and Costa (2003) made observations across the Amazonian basin and along coastal Brazil showing that samples currently identified as M. murina on morphological criteria comprise 4 distinctive geographic clades, each markedly divergent from the other. Samples from central-west Amazonia are strongly differ-
Table 1.—Average values for 15 cranial and 3 external morphological measurements among Marmosa murina from 2 locations in French Guiana: coastal (n = 15 individuals) versus inner-forest (n = 14 localities). Linear measurements are in mm. MANOVA analysis was performed for all measurements. Significant differences (P < 0.05) are marked with asterisks.

<table>
<thead>
<tr>
<th>Morphometric characters</th>
<th>Coastal</th>
<th>Inner-forests</th>
<th>Mean square effect</th>
<th>Mean square error</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Condylobasal length</td>
<td>32.03</td>
<td>31.36</td>
<td>3.25</td>
<td>4.08</td>
<td>0.38</td>
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<tr>
<td>Total cranial length</td>
<td>33.76</td>
<td>32.93</td>
<td>4.95</td>
<td>3.81</td>
<td>0.26</td>
</tr>
<tr>
<td>Zygomatic breadth</td>
<td>18.78</td>
<td>18.09</td>
<td>3.50</td>
<td>1.58</td>
<td>0.15</td>
</tr>
<tr>
<td>Braincase breadth</td>
<td>12.41</td>
<td>12.29</td>
<td>0.10</td>
<td>0.39</td>
<td>0.61</td>
</tr>
<tr>
<td>Mastoid breadth</td>
<td>9.00</td>
<td>8.88</td>
<td>0.10</td>
<td>0.21</td>
<td>0.49</td>
</tr>
<tr>
<td>Anterior interorbital constriction</td>
<td>5.58</td>
<td>5.51</td>
<td>0.04</td>
<td>0.22</td>
<td>0.69</td>
</tr>
<tr>
<td>Posterior interorbital constriction</td>
<td>6.04</td>
<td>6.36</td>
<td>0.73</td>
<td>0.19</td>
<td>0.06</td>
</tr>
<tr>
<td>Rostral length</td>
<td>12.29</td>
<td>11.68</td>
<td>2.68</td>
<td>1.42</td>
<td>0.18</td>
</tr>
<tr>
<td>Rostral width</td>
<td>5.52</td>
<td>5.16</td>
<td>0.91</td>
<td>0.16</td>
<td>0.02*</td>
</tr>
<tr>
<td>Length of upper canine to 4th molar</td>
<td>13.03</td>
<td>12.94</td>
<td>0.06</td>
<td>0.34</td>
<td>0.68</td>
</tr>
<tr>
<td>Length of upper molars</td>
<td>6.58</td>
<td>6.64</td>
<td>0.03</td>
<td>0.06</td>
<td>0.47</td>
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<td>Palatal length</td>
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<td>17.15</td>
<td>1.01</td>
<td>1.13</td>
<td>0.35</td>
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<td>Palatal width</td>
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<td>10.03</td>
<td>0.83</td>
<td>0.21</td>
<td>0.06</td>
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<tr>
<td>Occipital condyle breadth</td>
<td>6.95</td>
<td>6.89</td>
<td>0.03</td>
<td>0.10</td>
<td>0.59</td>
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<tr>
<td>Tympanic bullar width</td>
<td>11.00</td>
<td>10.89</td>
<td>0.09</td>
<td>0.20</td>
<td>0.52</td>
</tr>
<tr>
<td>Length of medial caudal hairs</td>
<td>0.40</td>
<td>0.45</td>
<td>0.01</td>
<td>0.00</td>
<td>0.07</td>
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<tr>
<td>Length of lateral caudal hairs</td>
<td>0.29</td>
<td>0.26</td>
<td>0.01</td>
<td>0.00</td>
<td>0.07</td>
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<tr>
<td>Number of caudal scales</td>
<td>11.26</td>
<td>12.11</td>
<td>7.42</td>
<td>1.67</td>
<td>0.04*</td>
</tr>
</tbody>
</table>

Morphology.—The absence of morphological variation among French Guianan samples of M. murina individuals supports the molecular results in suggesting the presence of only 1 subspecies in this region. Similarly, Husson (1978) could not find any significant differences between Surinamese specimens from the coastal plains and those from the inner forests.

Nevertheless, across the Guianan shield, it appears that M. murina shows some morphometric variation for the length of upper molars (M1–M4). Dental measurements are often used in discriminating similar species of rodents and marsupials (e.g., M. demerarae and M. regina—Patton et al. 2000; P. cuvieri and P. cayennensis—Catzeulis and Steiner 2000). Morphometric variation of M1–M4 might suggest the presence of more than 1 biological entity in the Guiana shield.

Fig. 4.—Comparison of length of M1–M4 toothrow for samples from 4 regions in the Guianan shield: Surinam (Sur), Venezuela (Ven), French Guiana (Gui), and Amapá (Ama). Plots indicate mean, SE (rectangle), and SD (vertical line). Samples from Surinam and French Guiana each differed significantly from samples from Venezuela and Amapá (P < 0.05).
Voss et al. (2001), comparing the sub-specific taxa of *M. murina* from Venezuela (*klagesi, duidae and roraimae*) and Guyana (*chloe*), recognized subtle differences in fur color, fur length, and pelage texture. Further morphometric and molecular studies across the Guianan shield are necessary to test the homogeneity of *M. murina* and the hypothesis of Patton and Costa (2003) that this is a strongly differentiated taxon that quite likely comprises more than one biological species. Combined approaches are also necessary to address the validity of sub-specific taxa, such as *M. murina roraimae* Tate (1931), *M. m. klagesi* Allen, (1900), or *M. m. madeirensis* Cabrera (1913).

**RESUMEN**

La comadreja ratona *M. murina* es una especie ampliamente distribuida en la región tropical de América del Sur. Algunos autores proponen la existencia de varias subespecies sobre el Escudo Guyanes, con 2 de ellas probablemente presentes en Guyana francesa: una de aspecto más claro (*M. murina murina*) habitando la estrecha franja continental costera y un taxon más oscuro (*M. murina muscula*) distribuido al interior del bosque tropical. Nuestro trabajo presenta los resultados de los análisis moleculares de 2 marcadores mitocondriales (cytochrome b y region de control) y de la revisión morfológica de medidas craniales (15 caracteres) y externas (3). Estos datos señalan la presencia de una sola subespecie (*M. murina murina*) en Guyana francesa basado en la ausencia de estructuración genética y de variación morfológica. Sin embargo, *M. murina* parece presentar una importante variación morfológica sobre el Escudo Guyanes con respecto a la talla de los molares superiores (M1–M4). Estos resultados sugieren que *M. murina* es un taxón bien diferenciado sobre el Escudo Guyanés comprendiendo posiblemente mas de una entidad biológica.

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**LITERATURE CITED**


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APPENDIX I

Specimens examined.—The 106 specimens of Marmosa murina and other didelphids examined for molecular or morphological analysis (or both) belong to the following collections: MNHN = Muséum National d’Histoire Naturelle (Paris, France); ISEM = Institut des Sciences de l’Évolution de Montpellier, France; TTU = Texas Tech University (Lubbock, Texas); FMNH = Field Museum of Natural History (Chicago, Illinois); EBRG = Estación Biológica Rancho Grande (Maracay, Venezuela); MCUSB = Museo de Ciencias de la Universidad Simón Bolívar (Caracas, Venezuela); MHNLS = Museo de Historia Natural La Salle (Caracas, Venezuela); USNM = National Museum of Natural History (Washington, D.C.). Symbols represent the specimens sequenced only for Cytb gene (A) or for both Cytb and d-loop fragments (B) and
French Guiana specimens examined for both genes and morphology (C) or for Cytb gene and morphology (D).


*Micoureus demerarae.*—FRENCH GUIANA: Nouragues, ISEM V-972A, ISEM V-888A.

*Marmosops parvidens.*—FRENCH GUIANA: St. Eugène, MNHN 1998-1830A.

*Philander opossum.*—FRENCH GUIANA: Trinité, MNHN 2000-216A.

*Didelphis albiventris.*—FRENCH GUIANA: Petit Saut, MNHN 2000-217A.