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A NEW SPECIES OF *REITHRODONTOMYS* FROM GUERRERO, MEXICO

Editor's Comment: This paper describes a new species of harvest mouse (*Reithrodontomys*) from a rather remote area in southern Mexico. Three specimens were collected from a cloud forest region of Guerrero, Mexico and tentatively were identified as *Reithrodontomys microdon*. At a later date, DNA sequences from the mitochondrial cytochrome *b* gene were obtained, analyzed, and compare to all available sequences of *Reithrodontomys*. The level of sequence divergence between these samples and representatives of *R. Microdon* were of the magnitude that is normally seen between recognized species of *Reithrodontomys*. Eventually, additional information (samples from surrounding areas, morphology, karyology, and biogeography) supported the idea that an undescribed species of *Reithrodontomys* was present in southern Mexico. However, without the initial DNA sequences, the uniqueness of these samples would have been unnoticed, catalogued as *R. microdon*, and curated accordingly. We wonder how often samples are treated in a routine fashion, only to realize that we have overlooked something "neat" at a later date? Situations such as these reinforce the necessity of collecting multiple data sets and emphasize the value of tissue collections.

RDB
Associate Editor

Front cover: Photograph of *Reithrodontomys bakeri* collected near Filo de Caballo, Mexico.

A New Species of *Reithrodontomys* from Guerrero, Mexico

Robert D. Bradley, Francisca Mendez-Harclerode, Meredith J. Hamilton, and Gerardo Ceballos

Harvest mice (genus *Reithrodontomys*) are small rodents affiliated with the Neotomine/Peromyscine complex. Historically two subgenera (*Reithrodontomys* and *Aporodon*) have been recognized (Howell, 1914; Hooper, 1952) with *Reithrodontomys* typically distributed from the United States to southern Mexico, and *Aporodon* occurring throughout central Mexico, Central America, and northern South America. Although numerous studies have commented on the systematic relationships within the genus (Arellano et al., 2003; Arnold et al., 1983; Bell et al., 2001; Carleton, 1980; Hood et al., 1984; Hooper, 1952; Nelson et al., 1984; Robbins and Baker, 1980), several systematic relationships remain enigmatic, especially within the subgenus *Aporodon*. For example, Arenallo et al. (2003) demonstrate that three species of *Aporodon* (*Reithrodontomys gracilis*, *R. mexicanus*, and *R. microdon*) are paraphyletic and likely are composed of multiple unrecognized species. Given the physiogeographic characteristics of southern Mexico and Central America and potential for isolation and differentiation of taxa in this region (Hooper, 1952; Sullivan et al. 2000), the findings of Arenallo et al. (2003) are not surprising. Instead, it appears that a substantial systematic re-evaluation is in order.

In July 2000, three individuals of the genus *Reithrodontomys* were collected near Filo de Caballo, Guerrero, Mexico. Based on external morphological traits, these specimens closely resembled *Reithrodontomys microdon* and tentatively were identified as such. In addition, karyologic data were compared to karyotypes of *R. microdon*. Following the collection of these individuals, additional specimens resembling *R. microdon* were collected near Omiltemi, Guerrero (approximately 25 km E Filo de Caballo). These collecting sites are located approximately 240 km south from the nearest recorded population of *R. microdon*, represented by *R. m. wagneri* from Distrito Federal, Mexico. Two other subspecies of *R. microdon* (*albilabris* and *microdon*) are known from Oaxaca and Chiapas, but represent even more distant localities (320 and 700 km to the east and southeast, respectively). Given the geographic location of the samples from Guerrero and the parapatric distribution of the three subspecies of *R. microdon* (Hall, 1981), it seemed unlikely that the samples from Guerrero were affiliated with *R. microdon*. To further investigate the correct taxonomic assignment of these specimens, nucleotide sequences from the mitochrondrial cytochrome-*b* gene were obtained and compared to sequences obtained from 11 species of *Reithrodontomys*.

Methods and Materials

Sampling.—Previously unreported specimens from Filo de Caballo (n = 3) and Omiltemi, Guerrero (n = 2) form the basis of this study. For comparative purposes, specimens of *R. microdon albilabris* (n = 1), *R. microdon microdon* (n = 1), *Reithrodontomys sumichrasti* (n = 3; two of which were collected sympatrically with the *R. microdon*-like specimens), *Reithrodontomys mexicanus* (n = 5), *Reithrodontomys gracilis* (n = 1), *Reithrodontomys fulvescens* (n = 2), *Reithrodontomys megalotis* (n = 2), *Reithrodontomys zacatecus* (n = 2), *Reithrodontomys humulis* (n = 1), *Reithrodontomys raviventris* (n = 2), and *Reithrodontomys montanus* (n = 1), were included. Eleven of these sequences were from Bell et al. (2001) or Arellano (1999); the remaining sequences were generated in this study. Specimen numbers, collection localities, and GenBank accession numbers are listed in Appendix I.

Morphometric analyses.—Four standard, external measurements were recorded from specimen tags and 12 cranial measurements were taken with dial calipers for the specimens from Filo de Caballo, Guerrero (n = 3) and Omiltemi, Guerrero (n = 1). Measurements followed the diagnostic characteristics listed in Hooper (1952). Measurements for *R. m. albilabris* (n = 1), *R. m. microdon* (n = 2), and *R. m. wagneri* (n = 2) were obtained from Hooper (1952) and included for comparison. A one-way analysis of variance (ANOVA) was conducted on external and cranial mea-

surements to test for significant differences among taxa.

Karyotypic analyses.—Karyotypes were prepared under field conditions for the specimens from Filo de Caballo following the methods of Baker and Qumsiyeh (1988). A minimum of five chromosomal spreads were examined per specimen to obtain a diploid number (2n) and fundamental number (FN) of autosomal arms.

Sequence data.—Mitochondrial DNA was extracted from frozen liver samples (0.1g) and purified using the Wizard Miniprep kit (Promega®; Madison, Wisconsin). For some specimens (Omiltemi, Guerrero) skin clips were used as a DNA source and genomic DNA was isolated using the PureGene kit (Gentra; Minneapolis, Minnesota). The complete cytochrome-*b* gene (1,143 bp) was amplified from all individuals. The following polymerase chain reaction (PCR) parameters were modified as described by Saiki et al. (1988): 27--40 cycles of 95° C denaturation (1 min), 50° C annealing (1 min), 72° C extension (2 min), and 1 final 72° C extension cycle (7 min). Primers utilized in the PCR reactions were MVZ05 of Smith and Patton (1993) and L14724 of Irwin et al. (1991). The resulting PCR product was purified using the QIAquick PCR purification kit (Qiagen®, Valencia, California). The following 6 primers were used in cycle sequencing reactions to amplify fragments on the forward and reverse strands, respectively: CWE1, SIG270, 400R, 400F, 700H, 700L, 752R, and P3 (Bradley et al., 2000; Peppers and Bradley, 2000; Tiemann-Boege et al., 2000). Cycle sequencing was conducted using the ABI Prism dRhodamine or BigDye Version 2.0 or 3.0 terminator ready reaction mixes (PE Applied Biosystems®, Foster City, California) and samples were analyzed on an ABI Prism 310 automated sequencer (PE Applied Biosystems®, Foster City, California). Sequencher 3.1.1 software (Gene Codes, Ann Arbor, Michigan) was used to align and proof nucleotide sequences. All cytochrome-*b* sequences obtained in this study are deposited in GenBank and accession numbers listed in Appendix I.

Nucleotide sequence analyses.—Nucleotide sequences for *Osgoodomys banderanus* and *Peromyscus boylii* were obtained from Tiemann-Boege et al. (2000) and were used as outgroup taxa in all analyses. Likelihood, parsimony, and Bayesian methods (described below) were used to generate hypotheses concerning phylogenetic relationships of taxa. The variable nucleotide positions within the data set were treated as unordered, discrete characters with four possible states; A, C, G, or T.

Parsimony analyses (PAUP*; Swofford, 2002) were performed using equally-weighted characters. The heuristic search and the tree-bissection-reconnection options were used to obtain the most parsimonious tree(s). All phylogenetically uninformative characters were excluded from these analyses. Bootstrap analysis (Felsenstein, 1985) with 1,000 iterations and Bremer decay indices (Bremer, 1994; Eriksson, 1997) were used to assess nodal support. In addition, nucleotide sequences were translated into amino acids using MacClade (version 3.04, Maddison and Maddison, 1992) and subsequently analyzed using the maximum parsimony option of PAUP.

Fifty-six maximum likelihood models were examined using MODELTEST (Version 3.06; Posada and Crandall, 1998) in order to determine the model of DNA evolution best fitting the data. The GTR+I+G model was identified as being most appropriate for this data set. A maximum likelihood analysis was conducted in PAUP* using the GTR+I+G model and the following parameters: base frequencies (A = 0.3118, C = 0.2995, G = 0.1129, T = 0.2758), rates of substitution (A-C = 5.08, A-G = 20.54, A-T = 6.15, C-G = 1.49, C-T = 68.38, G-T = 1.00), proportion of invariable sites (I = 0.5703) and gamma distribution (G = 1.5516).

A Bayesian approach (Huelsenbeck and Ronquist, 2001) was used for a comparison to the likelihood method and to develop clade probabilities (support values). This analysis used the GTR+I+G model with no prior assignments of parameters. In this analysis, the following options were employed: four Markov chains, 1,000,000 generations, and sample frequency = every 100th generation. Following an inspection of likelihood scores, the first 100 trees were discarded and the program was rerun using the remaining stable likelihood values. A consensus tree (50% majority rule) was constructed from remaining trees.

The Kimura two-parameter model of evolution (Kimura, 1980) was used to calculate genetic distances. Distance values then were used to compare levels of genetic divergence among taxa of *Reithrodontomys* following the suggestions of Bradley and Baker (2001).

RESULTS

Morphometrics.—The four external and 12 cranial measurements (Table 1) were subjected to a one-way ANOVA. This analysis revealed significant differences ($P < 0.05$) for one external (length of ear) and three cranial measurements (breadth of rostrum, length of palate, and breadth of mesopterygoid fossa) among the specimens from Filo de Caballo/Omiltemi, Guerrero and representatives of the three subspecies of *R. microdon*. Of these four characters, the specimens from Filo de Caballo/Omiltemi, Guerrero were significantly smaller than *R. m. albilabris* and *R. m. microdon* for breadth of rostrum, larger than *R. m. albilabris*, *R. m. microdon*, and *R. m. wagneri* for length of palate and breadth of mesopterygoid fossa, and larger than *R. m. microdon* for length of ear. The specimens from Filo de Caballo/Omiltemi, in general, were smaller in size for most measurements compared to *R. m. albilabris* and *R. m. microdon*, and were most similar in size to *R. m. wagneri*. Compared to *R. m. wagneri*, the specimens from Filo de Caballo/Omiltemi (although not necessarily statistically significant) possessed a larger ear, longer and broader rostrum at the distal end (Table 1), longer palate, longer molar toothrow, broader zygomatic plate, and greater breadth across mesopterygoid fossa.

Karyotypic data.—The three specimens from Filo de Caballo possessed an identical karyotype of 2n = 52 and a FN = 50. This results in a fully acrocentric autosomal complement. The X and Y chromosomes also are acrocentric in morphology.

Sequence data.—The three analyses (parsimony, likelihood, Bayesian) produced nearly identical topologies and similar support values for most clades. The topologies obtained from the parsimony and Bayesian

Table 1.—Selected measurements (in mm) for specimens of Reithrodontomys microdon *and* R. bakeri. *Measurements for* R. microdon *(*albilabris, microdon, *and* wagneri *are from Hooper (1952). All measurements are presented as means and ranges are in parentheses.*

Character	Taxon			
	R. m. albilabris (n = 1)	*R. m. microdon* (n = 2)	*R. m. wagneri* (n = 2)	*R. bakeri* (n = 4)
Total length	187.0	182.5 (180-185)	171.0 (169-173	176.7 (165-185)
Tail length	117.0	112.5 (112-113)	102.0 (101-103)	100.5 (94-107)
Hindfoot	20.0	21.0 (21-21)	19.0 (19-19)	18.5 (17-19)
Ear	—	14.0 (14)	17.0 (16.5-17.5)	18.0 (17-19)
Length of skull	22.4	22.5 (22.4-22.5)	21.9 (21.6-22.1)	21.7 (21.4-22.4)
Zygomatic breadth	11.5	11.0 (10.7-11.2)	11.1 (11.0-11.1)	10.4 (9.9-11.1)
Breadth of braincase	11.4	11.0 (10.9-11.0)	10.8 (10.6-10.9)	11.2 (10.7-11.5)
Depth of cranium	8.8	8.9 (8.7-9.1)	8.3 (8.3-8.3)	8.3 (7.9-8.6)
Interorbital breadth	3.6	3.7 (3.7-3.7)	3.5 (3.4-3.6)	3.7 (3.7-3.8)
Breadth of rostrum	4.2	4.0 (4.0-4.0)	3.9 (3.8-3.9)	3.8 (3.7-3.9)
Length of rostrum	8.0	8.2 (8.0-8.4)	7.8 (7.6-7.9)	8.3 (7.9-8.5)
Length of palate	3.5	3.4 (3.3-3.4)	3.6 (3.5-3.6)	4.1 (4.0-4.3)
Length of molar toothrow	3.2	3.3 (3.2-3.3)	3.1 (3.0-3.1)	3.3 (3.1-3.5)
Length of incisive foramen	4.1	4.3 (4.2-4.4)	4.2 (4.0-4.3)	4.2 (3.9-4.3)
Breadth of zygomatic plate	1.2	1.3 (1.3-1.3)	1.4 (1.4-1.4)	1.5 (1.4-1.6)
Breadth of mesopterygoid fossa	1.5	1.7 (1.6-1.8)	1.6 (1.5-1.6)	1.9 (1.8-2.0)

analyses were identical, whereas the likelihood analysis differed in the placement of the sample of *R. m. microdon* from Chiapas, Mexico. Given the similarity in tree topologies among the three analyses, only the Bayesian topology with clade probability values is shown and discussed (Fig. 1). Three clades were apparent; one clade contained all members of the subgenus *Reithrodontomys* (except *R. fulvescens*), the second clade contained members referable to the subgenus *Aporodon*, and the third clade contained *R. fulvescens*. The specimens from Guerrero (Filo de Caballo and Omiltemi) were embedded in the *Aporodon* clade. Specifically, these five samples formed a clade that was sister to the sample of *R. m. microdon* from Chiapas. This clade then formed a sister relationship with the samples of *R. mexicanus* from Costa Rica before including the sample of *R. m. albilabris* from Oaxaca. Bayesian support values (Fig. 1) were 100 for the clade containing the Guerrero samples, but were substantially lower in supporting the remaining clades.

Genetic distances (Table 2), estimated using the Kimura two-parameter model (Kimura, 1980), averaged 0.18% among the three specimens from Filo de Caballo and 0.62% between the two specimens from Omiltemi. Specimens from these two populations differed by an average genetic distance of 3.89%; whereas they differed from *R. m. albilabris* and *R. m. microdon* by 11.26% and 10.16%, respectively. Comparisons between other sister species of *Reithrodontomys* included in this study ranged from 8.47% (*R. megalotis* and *R. zacatecae*) to 13.51% (*R. mexicanus* and *R. gracilis*).

Parsimony analysis of amino acids revealed that the specimens from Filo de Caballo and Omiltemi, Guerrero differed from closely related taxa of *Reithrodontomys* at five amino acid cites. These codon positions and corresponding amino acids are listed in Table 3.

Given the initial hypothesis that the Guerrero samples were affiliated with *R. microdon* and the fact that *R. m. albilabris* and *R. m. microdon* were paraphyletic in the parsimony and Bayesian analyses, these taxa were constrained to form a monophyletic group. The Shimodaira and Hasegawa test (1999) was used to test for significance between this topology (constrained) and that generated in the likelihood analysis (unconstrained). The likelihood value obtained from the constrained tree was worse (but not significantly) than that obtained from the unconstrained tree.

DISCUSSION

Given that the samples from Guerrero formed a sister relationship to *R. m. microdon* in the parsimony and Bayesian analyses, it may seem appropriate to refer these samples to *R. m. microdon*. However, the large genetic distances (10.16% and 11.26%) between the samples from Guerrero and those of *R. microdon* from Chiapas and Oaxaca were equal to or greater than genetic distances between other recognized species of *Reithrodontomys* (Table 2). For example, *R. megalotis* and *R. zacatecae* differ by an average genetic distance of 8.47%, *R. montanus* and *R. raviventris* by 13.01% and *R. mexicanus* and *R. gracilis* by 13.51%. Bradley and Baker (2001) discuss circumstances under which DNA sequences may be used to identify situations where a previously unrecognized species may be suspected. This premise was constructed on the basis of the genetic species concept (Dobzhansky, 1950) and appears useful, especially with sequences from the mitochondrial cytochrome-*b* gene. Baker et al. (2002) furthered this approach in naming a new species of *Carollia* (*C. sowelli*) that was first recognized based on DNA sequence differences. It appears that a similar situation presents itself with the samples of *Reithrodontomys* from Guerrero.

To eliminate the possibility that the samples from Guerrero were not representative of a new taxon, several hypotheses were tested. First, cranial characters were examined and based on the position of the interorbital constriction, these specimens clearly belong to the subgenus *Aporodon*. Likewise the chromosomal data is characteristic of members of the subgenus *Aporodon*. These traits, plus the affiliation of the samples from Guerrero with *Aporodon* in the phylogenetic analyses, eliminated any connection to the sub-

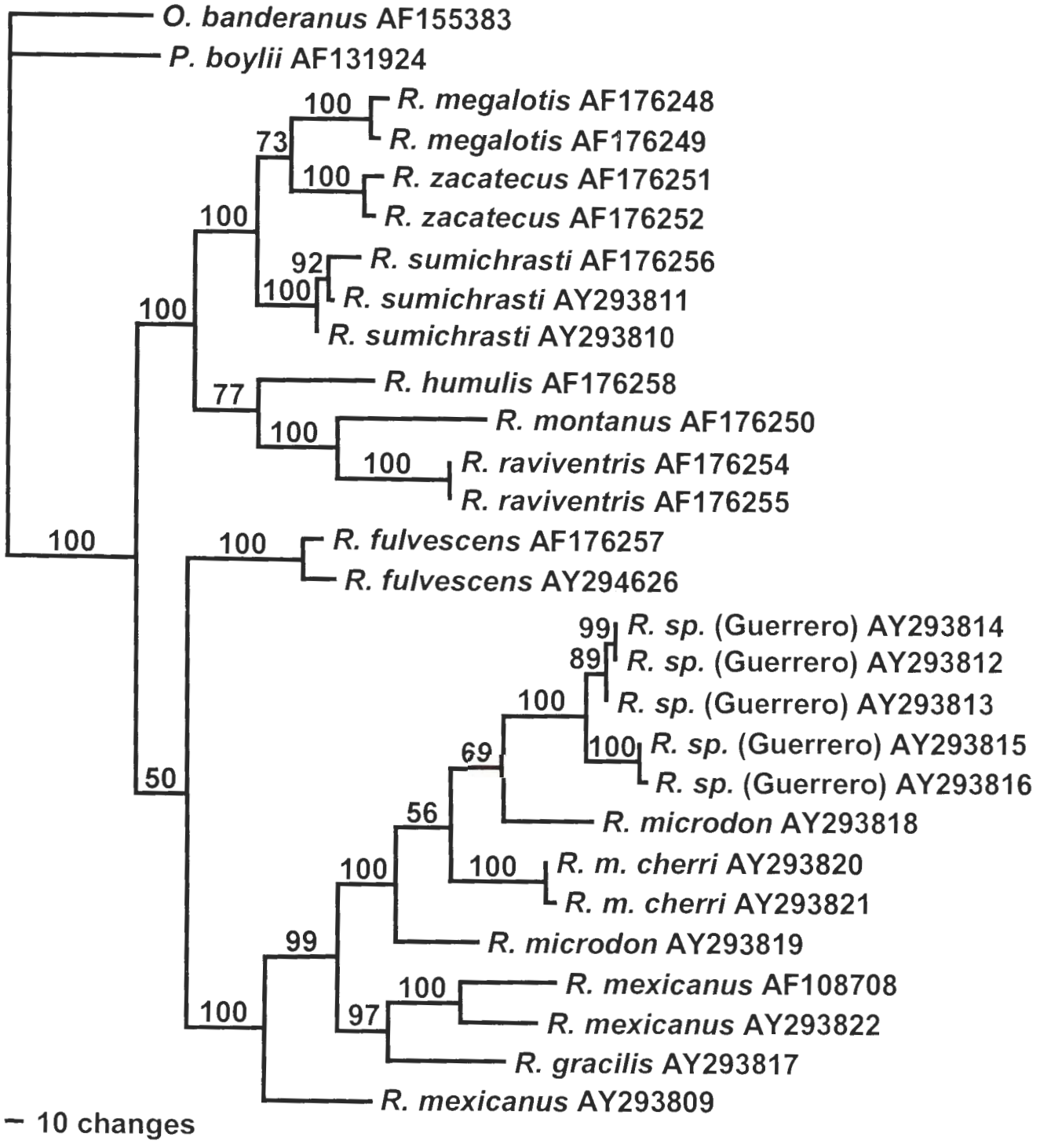

Figure 1.—Phylogenetic tree generated from the Bayesian analyses of 26 taxa of *Reithrodontomys*. *Osgoodomys banderanus* and *Peromyscus boylii* were used as the outgroup taxa. Clade probability values are listed above branches.

Table 2.—Sequence divergence values obtained from the Kimura two-parameter (Kimura, 1980) model of evolution. Values are provided for selected representatives of Reithrodontomys.

Comparison	% Sequence Divergence
within Filo de Caballo, Guerrero	0.18%
within Omiltemi, Guerrero	0.62%
Filo de Caballo versus Omiltemi	3.89%
Filo de Caballo and Omiltemi versus *R. m. albilabris*	11.26%
Filo de Caballo and Omiltemi versus *R. m. microdon*	11.26%
R. m. albilabris versus *R. m. microdon*	11.07%
R. megalotis versus *R. zacatecae*	8.47%
R. raviventris versus *R. montanus*	13.01%
R. cherri versus *R. microdon*	11.53%
R. cherri versus *R. m. albilabris*	11.47%
R. mexicanus versus *R. gracilis*	13.51%

Table 3.—Comparison of amino acid differences among samples of R. microdon albilabris, R. m. microdon, R. mexicanus cherri, *and those from Guerrero (Filo de Caballo and Omiltemi). Position refers to the amino acid position downstream from the start codon.*

Position	Sample/Taxon			
	Guerrero	*R. m. albilabris*	*R. m. microdon*	*R. mexicanus cherri*
42	Isoleucine	Leucine	Valine	Valine
118	Alanine	Leucine	Valine	Valine
224	Phenyalanine	Phenyalanine	Tyrosine	Tyrosine
238	Threonine	Valine	Isoleucine	Valine
363	Leucine	Isoleucine	Isoleucine	Isoleucine

genus *Reithrodontomys*. Second, the combination of phylogenetic relationships based on the differences in DNA sequences, genetic distances, amino acids, geographic distribution, and morphology eliminated the possibility of affiliations with all members of *Aporodon* except *R. microdon*.

In evaluating the hypothesis that the taxonomic status of samples from Guerrero are representative of *R. microdon*, two approaches were taken. First, the samples were compared genetically (sequences from the cytochrome-*b* gene) to two of the three subspecies of *R. microdon* (*albilabris* and *microdon*). The magnitude of genetic divergence between these samples (10.16% and 11.26%) precludes a logical affiliation to *R. microdon*. In fact, the differences between *R. m. albilabris* and *R. m. microdon*, and their apparent paraphyly in the parsimony and Bayesian analyses, suggest that they may represent different species. A similar situation was reported in the allozyme study of Arenallo et al., (2003) who found samples of *R. microdon* from Guatemala and Chiapas to be paraphyletic with *R. tenuirostris*. Although it is beyond the scope of this project, it appears that perhaps as many as three unrecognized species exist within *R. microdon*. Obviously, further research is needed to address these findings.

We were unsuccessful in generating DNA sequences from bone samples for the third subspecies (*R. m. wagneri*); therefore external and cranial characteristics were compared between specimens from Guerrero and the sample of *R. m. wagneri*; as well as to samples of *R. m. albilabris* and *R. m. microdon*. Although samples sizes were extremely low, the specimens from Filo de Caballo/Omiltemi, Guerrero, typi-

cally were smaller compared to *R. m. albilabris* and *R. m. microdon* (significantly smaller for breadth of rostrum). However, they were significantly larger than *R. m. albilabris*, *R. m. microdon*, and *R. m. wagneri* for length of palate and breadth across mesopterygoid fossa, and larger than *R. m. microdon* for length of ear. Compared to *R. m. wagneri*, the specimens from Filo de Caballo/Omiltemi, Guerrero, (although not necessarily statistically significant) possessed a larger ear, longer and broader rostrum at the distal end, longer palate, longer molar toothrow, broader zygomatic plate, and greater breadth across mesopterygoid fossa (Table 1).

Based on differences in nucleotide sequences, morphology, and distribution we conclude that the samples from Guerrero represent an undescribed species of *Reithrodontomys*. Below, we provide a formal description of this new taxon.

Reithrodontomys bakeri, New Species

Holotype.—Adult male, skin, skull, and skeleton, Museum of Texas Tech University, TTU 82790, from Mexico, Guerrero, 4 mi SSW Filo de Caballo, collected 20 July 2000. Original number, Robert D. Bradley 1121, TK number 93372 identifies karyotype and tissue samples deposited in the Natural Science Research Laboratory, Museum of Texas Tech University. Paratypes include one male (TTU 82791, TK 93373) and one female (TTU 82192, TK 93374).

Distribution.—Montane regions in central Guerrero at elevations greater than 2,150 m particularly in pine-oak habitats associated with cloud forests (Figure 2). Currently known only from Filo de Caballo and Omiltemi, Guerrero. May occupy other montane regions in central Guerrero, but appears to be restricted in distribution.

Diagnosis.—Member of the subgenus *Aporodon*, resembling *R. microdon* in size and coloration. Initial diagnosis was based on nucleotide sequence differences. Differs genetically (mitochondrial cytochrome-*b* gene) from *R. m. albilabris* and *R. m. microdon* by 10.16% and 11.26% sequence divergence, respectively and at five amino acid positions.

Morphologically, *R. bakeri* differs from *R. m. wagneri* in having a slightly larger ear, longer and broader rostrum (distally), longer palate, longer molar toothrow, broader zygomatic plate, and greater breadth of mesopterygoid fossa (Fig. 3 and Table 1). Selected measurements were compared to those reported in Hooper (1952).

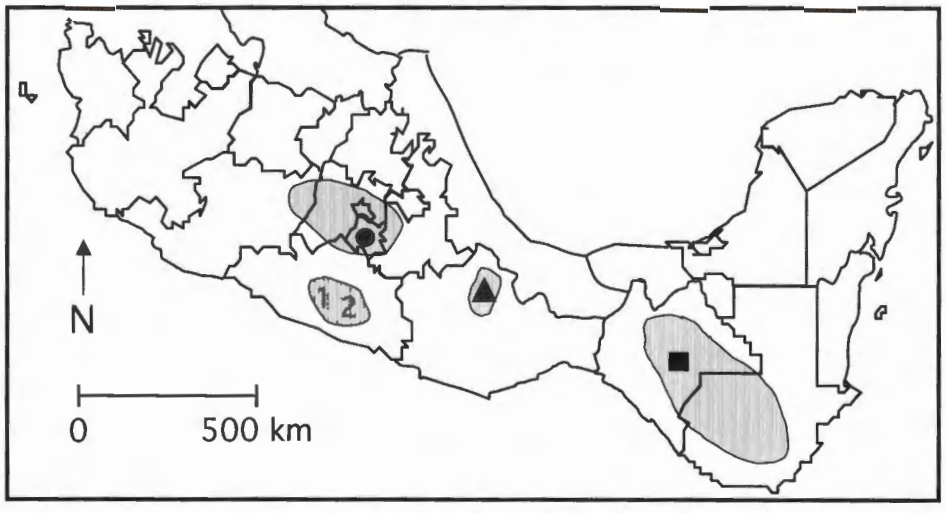

Figure 2.—Geographic distribution of taxa examined in this study. Closed triangle = Reithrodontomys microdon albilabris, closed square = *R. m. microdon*, closed circle = *R. m. wagneri*, 1= *Reithrodontomys bakeri* from Filo de Caballo, Guerrero, and 2 = *R. bakeri* from Omiltemi, Guerrero.

Figure 3.–Dorsal, ventral, and lateral view of the skull and lower jaw of the holotype of *Reithrodontomys bakeri* (TTU 100001; TK 93372) from Filo de Caballo, Guerrero. Scale bar = 1cm. Drawing by Michael W. Nickell.

Description of coloration is based on a comparison to Ridgway's color standards (Ridgway, 1912). Dorsal pelage is Sanford's Brown at tips and Blackish Plumbeous at base; sides are Tawny; ventor pelage is White at tips and Blackish Plumbeous at base; feet possess a Black stripe extending from the ankles to toes; tail is uniform in color (Deep Neutral Gray), scantily haired at base and more heavily haired at tip; ears are Deep Neutral Gray, and vibrissae are Black.

Selected Measurements.—External measurements of holotype taken in the field (in millimeters) by R. D. Bradley are: total length -- 185; tail length -- 107; hindfoot -- 19; and ear -- 18. Cranial measurements were taken using dial calipers and are: length of skull -- 22.4; zygomatic breadth -- 11.1; breadth of braincase -- 11.5; depth of cranium -- 8.6; interorbital breadth -- 3.7; breadth of rostrum -- 3.7; length of rostrum -- 8.5; length of palate -- 4.3; length of molar toothrow -- 3.5; length of incisive foramen -- 4.3; breadth of zygomatic plate -- 1.6; and breadth of mesopterygoid fossa -- 2.0 (see also Table 1).

Karyologic Data.—The karyotype of *R. bakeri* is similar to that reported for other members of the subgenus *Aporodon* (Carleton and Myers, 1979; Rogers et al., 1983; Hood et al., 1984). Specifically, *R. bakeri* has a diploid number (2n) = 52 and a fundamental number (FN) = 50, resulting in a fully acrocentric autosomal complement. The X and Y chromosomes also are acrocentric in morphology.

Etymology.—It is our pleasure to name this species after Dr. Robert J. Baker. Dr. Baker has played a major role in investigating chromosomal evolution, systematics, and molecular evolution in *Reithrodontomys*. Through his tutelage, many of his former graduate students gained valuable research experiences by examining systematic and evolutionary questions affiliated with members of this genus. Through his efforts, our knowledge of *Reithrodontomys* has been increased and it seems appropriate to name this taxon accordingly.

Biogeography.—The discovery of a new *Reithrodontomys* species in the Filo de Caballo/Omiltemi region is somewhat expected on biogeographic grounds. The Sierra Madre del Sur in Guerrero is a large and isolated mountain range, which has maintained its temperate cloud, pine, and oak forest for millions of years. Several analysis of the mammalian and other vertebrate faunas of mountain ranges in southern Mexico and Central American supports the hypothesis that the Sierra Madre del Sur is one of the most isolated (Carleton et al., 2002). One outcome of such a long isolation is the presence of a large number of endemic species of flora and fauna (Ceballos and Navarro, 1991; Luna Vega and Llorente, 1993). There are many endemic vertebrates including plethodontid salamanders *(Pseudoerycea ahuitzotl, P. mixcoatl, P. teotepec, P. tenchalli, P. tlahcuiloh, Thorius grandis, T. infernales, T. omiltemi),* frogs *(Eleutherodactylus omiltemanus, E. saltator, Rana omiltemana)*, lizards (*Anolis omiltemanus*), snakes (*Geophis omiltemanus*), 20 species and subspecies of birds (whose geographic ranges generally include regions in Oaxaca), and mammals such as a subspecies of flying squirrel, *Glaucomys volans guerreroensis*, and the Omiltemi rabbit, *Sylvilagus insonus* (Adler, 1996; Ceballos and Navarro, 1991; Ceballos and Oliva, in press; Hanken et al. 1999; Vega Luna and Llorente, 1993).

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Addresses of authors:

ROBERT D. BRADLEY

Department of Biological Sciences and Museum
Texas Tech University
Lubbock, Texas 79409-3131
e-mail: robert.bradley@ttu.edu

MEREDITH J. HAMILTON

Department of Zoology
Oklahoma State University
Stillwater, OK 74078
e-mail: mjh@okstate.edu

FRANCISCA MENDEZ-HARCLERODE

Department of Biological Sciences
Texas Tech University
Lubbock, Texas 79409
e-mail: francisca.m.mendez-harclerode@ttu.edu

GERARDO CEBALLOS

Laboratorio de Conservación y Manejo de Vertebrados
Instituto de Ecología
Universidad Nacional Autónoma de México
A.P. 70-275 Ciudad Universitaria
04510 México D. F. México
e-mail: gceballo@miranda.ecologia.unam.mx

APPENDIX I

Specimens Examined.--- Specimen identification numbers (TK: Museum of Texas Tech University; BYU: Brigham Young University; IBUNAM: Instituto de Biologia, Universidad Autónoma de Mexico; LSUMZ: Louisiana State University, Museum of Zoology; JLP: Museum of Vertebrate Zoology, or FN: Royal Ontario Museum); ICN: Instituto de Ciencias Naturales, Universidad Nacional de Colombia; and GenBank accession numbers (AF or AY) are listed in parentheses after the taxon name. All localities are in the United States unless otherwise denoted.

Reithrodontomys bakeri.---MEXICO: Guerrero: Filo de Caballo (TK 93374, AY293814; TK 93372, AY293812; TK 93373, AY293813); Omiltemi (IBUNAM 40380, AY293815; IBUNAM 40381, AY293816).

Reithrodontomys fulvescens.---Oklahoma: McIntosh County; 3.1 mi E Dustin (TK 23469, AF176257); MEXICO: Jalisco: Mesconcitos (TK 93018, AY294626).

Reithrodontomys gracilis.---MEXICO: Yucatán: Laguna Becanchen (FN 30426, AY293817).

Reithrodontomys humulis.---Oklahoma: Pottawatomie County; 3 mi E Tecumseh (TK 26505, AF176258).

Reithrodontomys megalotis.---Texas: Lubbock County; Lubbock Lake Landmark State Historical Park (TK 22460, AF176248); Castro County; 5.5 mi S, 2.5 mi W Dimmit (TK 32283, AF176249).

Reithrodontomys mexicanus.---COLOMBIA: Risaralda: La Pastora, Reserva Ucumarí (ICN 16579, AF108708); MEXICO: Veracruz: Teocelo (BYU 15439, AY293822); Oaxaca: Llano de las Flores (TK 93156, AY293809).

Reithrodontomys mexicanus cherri.---COSTA RICA: San José: SW Poas (LSUMZ 25165, AY293820; LSUMZ 25376, AY293821).

Reithrodontomys microdon.---MEXICO: Chiapas: Cerro Tzontzehuits (BYU 14476, AY293818); Oaxaca: Cerro Zempoaltepec (IBUNAM 35252, AY293819).

Reithrodontomys montanus.---Texas: Castro County; 5.5 mi S, 2.5 mi W Dimmitt (TK 32314, AF176250).

Reithrodontomys raviventris.---California: Sonoma County; Mount of Tolay Creek (TK 24662, AF176254); Alameda County; 2.5 mi W Newark Slough (TK 13714, AF176255).

Reithrodontomys sumichrasti.---MEXICO: Oaxaca: 3 mi N Suchixtepex (TK 20994, AF176256); Guerrero: Filo de Caballo (TK 93363, AY293811), (TK 93354; AY293810).

Reithrodontomys zacatecae.---MEXICO: Durango: 3.8 mi W Coyotes, UTM 13-2634281-465908 (TK 72369, AF176251); 12 Km E Ojitos, UTM 13-2775718-385011 (TK 70989, AF176252).

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Museum of Texas Tech University
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(806)742-2442

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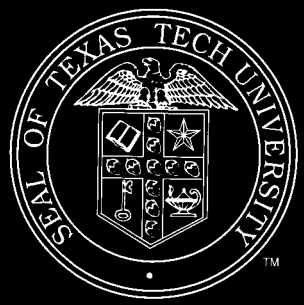
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