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 compared 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-HARCERODE, MEREDITH J. HAMILTON, AND GERARDO CEBALLOS

Harvest mice (genus Reithrodonomys) are small rodents affiliated with the Neotomine/Peromyscine complex. Historically two subgenera (Reithrodonomys and Aporodon) have been recognized (Howell, 1914; Hooper, 1952) with Reithrodonomys 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 (Reithrodonomys gracilis, R. mexicanus, and R. microdon) are paraphyletic and likely are composed of multiple unrecognized species. Given the physiographic 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 Reithrodonomys were collected near Filo de Caballo, Guerrero, Mexico. Based on external morphological traits, these specimens closely resembled Reithrodonomys 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 mitochondrial cytochrome-b gene were obtained and compared to sequences obtained from 11 species of Reithrodonomys.

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), Reithrodonomys sumichrasti (n = 3; two of which were collected sympatrically with the R. microdon-like specimens), Reithrodonomys mexicanus (n = 5), Reithrodonomys gracilis (n = 1), Reithrodonomys fulvescens (n = 2), Reithrodonomys megalotis (n = 2), Reithrodonomys zacatecus (n = 2), Reithrodonomys humulis (n = 1), Reithrodonomys raviventris (n = 2), and Reithrodonomys 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-
measurements 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 (Genta; 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 *Osgoodomyys 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-bisection-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 invariant 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 (breath 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>
<thead>
<tr>
<th>Character</th>
<th>Taxon</th>
<th><em>R. m. albilabris</em> (n = 1)</th>
<th><em>R. m. microdon</em> (n = 2)</th>
<th><em>R. m. wagneri</em> (n = 2)</th>
<th><em>R. bakeri</em> (n = 4)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total length</td>
<td></td>
<td>187.0</td>
<td>182.5 (180-185)</td>
<td>171.0 (169-173)</td>
<td>176.7 (165-185)</td>
</tr>
<tr>
<td>Tail length</td>
<td></td>
<td>117.0</td>
<td>125 (112-113)</td>
<td>102.0 (101-103)</td>
<td>100.5 (94-107)</td>
</tr>
<tr>
<td>Hindfoot</td>
<td></td>
<td>20.0</td>
<td>21.0 (21-21)</td>
<td>19.0 (19-19)</td>
<td>18.5 (17-19)</td>
</tr>
<tr>
<td>Ear</td>
<td></td>
<td>—</td>
<td>14.0 (14)</td>
<td>17.0 (16.5-17.5)</td>
<td>18.0 (17-19)</td>
</tr>
<tr>
<td>Length of skull</td>
<td></td>
<td>22.4</td>
<td>22.5 (22.4-22.5)</td>
<td>21.9 (21.6-22.1)</td>
<td>21.7 (21.4-22.4)</td>
</tr>
<tr>
<td>Zygomatic breadth</td>
<td></td>
<td>11.5</td>
<td>11.0 (10.7-11.2)</td>
<td>11.1 (11.0-11.1)</td>
<td>10.4 (9.9-11.1)</td>
</tr>
<tr>
<td>Breadth of braincase</td>
<td></td>
<td>11.4</td>
<td>11.0 (10.9-11.0)</td>
<td>10.8 (10.6-10.9)</td>
<td>11.2 (10.7-11.5)</td>
</tr>
<tr>
<td>Depth of cranium</td>
<td><em>R. m. albilabris</em></td>
<td>8.8</td>
<td>8.9 (8.7-9.1)</td>
<td>8.3 (8.3-8.3)</td>
<td>8.3 (7.9-8.6)</td>
</tr>
<tr>
<td>Interorbital breadth</td>
<td><em>R. m. microdon</em></td>
<td>3.6</td>
<td>3.7 (3.7-3.7)</td>
<td>3.5 (3.4-3.6)</td>
<td>3.7 (3.7-3.8)</td>
</tr>
<tr>
<td>Breadth of rostrum</td>
<td><em>R. m. wagneri</em></td>
<td>4.2</td>
<td>4.0 (4.0-4.0)</td>
<td>3.9 (3.8-3.9)</td>
<td>3.8 (3.7-3.9)</td>
</tr>
<tr>
<td>Length of rostrum</td>
<td><em>R. bakeri</em></td>
<td>8.0</td>
<td>8.2 (8.0-8.4)</td>
<td>7.8 (7.6-7.9)</td>
<td>8.3 (7.9-8.5)</td>
</tr>
<tr>
<td>Length of palate</td>
<td></td>
<td>3.5</td>
<td>3.4 (3.3-3.4)</td>
<td>3.6 (3.5-3.6)</td>
<td>4.1 (4.0-4.3)</td>
</tr>
<tr>
<td>Length of molar toothrow</td>
<td></td>
<td>3.2</td>
<td>3.3 (3.2-3.3)</td>
<td>3.1 (3.0-3.1)</td>
<td>3.3 (3.1-3.5)</td>
</tr>
<tr>
<td>Length of incisive foramen</td>
<td></td>
<td>4.1</td>
<td>4.3 (4.2-4.4)</td>
<td>4.2 (4.0-4.3)</td>
<td>4.2 (3.9-4.3)</td>
</tr>
<tr>
<td>Breadth of zygomatic plate</td>
<td></td>
<td>1.2</td>
<td>1.3 (1.3-1.3)</td>
<td>1.4 (1.4-1.4)</td>
<td>1.5 (1.4-1.6)</td>
</tr>
<tr>
<td>Breadth of mesopterygoid fossa</td>
<td></td>
<td>1.5</td>
<td>1.7 (1.6-1.8)</td>
<td>1.6 (1.5-1.6)</td>
<td>1.9 (1.8-2.0)</td>
</tr>
</tbody>
</table>
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. zacatecensis*) 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 sites. 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. zacatecensis* differ by an average genetic distance of 8.47%, *R. montanus* and *R. riviventer* 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 Reithrodonomys. 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.

<table>
<thead>
<tr>
<th>Comparison</th>
<th>% Sequence Divergence</th>
</tr>
</thead>
<tbody>
<tr>
<td>within Filo de Caballo, Guerrero</td>
<td>0.18%</td>
</tr>
<tr>
<td>within Omiltemi, Guerrero</td>
<td>0.62%</td>
</tr>
<tr>
<td>Filo de Caballo versus Omiltemi</td>
<td>3.89%</td>
</tr>
<tr>
<td>Filo de Caballo and Omiltemi versus R. m. albilabris</td>
<td>11.26%</td>
</tr>
<tr>
<td>Filo de Caballo and Omiltemi versus R. m. microdon</td>
<td>11.26%</td>
</tr>
<tr>
<td>R. m. albilabris versus R. m. microdon</td>
<td>11.07%</td>
</tr>
<tr>
<td>R. megalotis versus R. zacatecae</td>
<td>8.47%</td>
</tr>
<tr>
<td>R. raviveniris versus R. montanus</td>
<td>13.01%</td>
</tr>
<tr>
<td>R. cherri versus R. microdon</td>
<td>11.33%</td>
</tr>
<tr>
<td>R. cherri versus R. m. albilabris</td>
<td>11.47%</td>
</tr>
<tr>
<td>R. mexicanus versus R. gracilis</td>
<td>13.51%</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th>Position</th>
<th>Sample/Taxon</th>
<th>Guerrero</th>
<th>R. m. albilabris</th>
<th>R. m. microdon</th>
<th>R. mexicanus cherri</th>
</tr>
</thead>
<tbody>
<tr>
<td>42</td>
<td>Isoleucine</td>
<td>Leucine</td>
<td>Valine</td>
<td>Valine</td>
<td>Valine</td>
</tr>
<tr>
<td>118</td>
<td>Alanine</td>
<td>Leucine</td>
<td>Valine</td>
<td>Valine</td>
<td>Valine</td>
</tr>
<tr>
<td>224</td>
<td>Phenylalanine</td>
<td>Phenylalanine</td>
<td>Tyrosine</td>
<td>Tyrosine</td>
<td></td>
</tr>
<tr>
<td>238</td>
<td>Threonine</td>
<td>Valine</td>
<td>Phenylalanine</td>
<td>Valine</td>
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<tr>
<td>363</td>
<td>Leucine</td>
<td>Isoleucine</td>
<td>Phenylalanine</td>
<td>Isoleucine</td>
<td>Isoleucine</td>
</tr>
</tbody>
</table>

The occurrence of different species, 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 allogene study of Arenal et al., (2003) who found samples of R. microdon from Guatemala and Chiapas to be paraphyletic with R. temirostris. 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/Oriltemi, Guerrero, (although not ne-
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 spe-
cies 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, col-
lected 20 July 2000. Original number, Robert D. Bra-
dley 1121, TK number 93372 identifies karyotype and 
tissue samples deposited in the Natural Science Re-
search Laboratory, Museum of Texas Tech Univer-
sity. 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 particu-
larly 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 differ-
ences. 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 in the field (in millimeters) by R. D. Bradley: 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 tooththrow -- 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/Oriztemi 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 (Pseudoeurycea ahuizotl, P. mixcotli, P. teotepec, P. tendingho, P. tlahuizol, Thorius granulos, T. infernales, T. orientalensis), frogs (Eleutherodactylus oaxacanus, E. saltator, Rana oaxacana), lizards (Anolis oaxacanus), snakes (Geophis oaxacanus), 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 Omitzemi rabbit, Sylvilagus insularis (Adler, 1996; Ceballos and Navarro, 1991; Ceballos and Oliva, in press; Hanken et al. 1999; Vega Luna and Llorente, 1993).


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Specimens Examined.—Specimen identification numbers (TK: Museum of Texas Tech University; BYU: Brigham Young University; IBUNAM: Instituto de Biología, 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.

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

*Reithrodonotmys fulvescens.*—Oklahoma: McIntosh County; 3.1 mi E Dustin (TK 23469, AF176257); MEXICO: Jalisco: Mescócuco (TK 93018, AY294626).

*Reithrodonotmys graciosus.*—MEXICO: Yucatán: Laguna Beacanchen (FN 30426, AY293817).

*Reithrodonotmys humulis.*—Oklahoma: Pottawatomie County; 3 mi E Tecumseo (TK 26505, AF176258).

*Reithrodonotmys 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).

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

*Reithrodonotmys mexicanus cherri.*—COSTA RICA: San José: SW Poas (LSUMZ 25165, AY293820; LSUMZ 25376, AY293821).

*Reithrodonotmys microdon.*—MEXICO: Chiapas: Cerro Tzontzehuit (BYU 14476, AY293818); Oaxaca: Cerro Zempoaltepec (IBUNAM 35252, AY293819).

*Reithrodonotmys montanus.*—Texas: Castro County; 5.5 mi S, 2.5 mi W Dimmit (TK 32314, AF176250).

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

*Reithrodonotmys sumichrasti.*—MEXICO: Oaxaca: 3 mi N Suchítepepex (TK 20994, AF176256); Guerrero: Filo de Caballo (TK 93363, AY293811), (TK 93354; AY293810).

*Reithrodonotmys zacateceae.*—MEXICO: Durango: 3.8 mi W Coyotes, UTM 13-2634281-465908 (TK 72369, AF176251); 12 Km E Ojitós, UTM 13-2775718-385011 (TK 70989, AF176252).
A NEW SPECIES OF REITHRODONTOMYS FROM GUERRERO MEXICO

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