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Original investigation

A new species of *Eumops* (Chiroptera: Molossidae) from southeastern Brazil and Bolivia

Renato Gregorin[a,b,*], Ligiane Martins Moras[b], Luis Hernán Acosta[d,e], Karina Lobão Vasconcellos[a], José Luis Poma[d], Fabrício Rodrigues dos Santos[c], Roberto Carlos Paca[d]

[a] *Departamento de Biologia, Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil*
[b] *Programa de Pós-Graduação em Zoologia, Departamento de Zoologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil*
[c] *Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil*
[d] *Museo de Historia Natural Noel Kempff Mercado, Universidad Autónoma Gabriel René Moreno, Santa Cruz de la Sierra, Bolivia*
[e] *Programa de Pós-Graduação em Biodiversidade Biologia e Conservação Nos Trópicos, Universidade Federal de Alagoas, Maceió, Alagoas, Brazil*

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ABSTRACT

Eumops is the most speciose and morphologically diverse genus of Neotropical molossid bats presently encompassing 16 species. Here were described a new species in the genus based on three specimens from southeastern Bolivia and Brazil. A combined phylogenetic analysis using Cytochrome *b* gene sequences and morphological data revealed that the specimens form a sister-group of *Eumops perotis* + *Eumops trumbulli* and are 7.9% diverged from *E. perotis* at Cytochrome *b*. Three morphological autapomorphies, the shape of rostrum and the position and size of first upper premolar, distinguish new species from *E. perotis* and *E. trumbulli*. The combination of morphological and molecular characters justifies the description of a new species.

Introduction

The last two decades of bat systematics have seen many novelties and controversies such as the placement of bats into Laurasiatheria (Springer et al., 2004) instead of Archonta (Wible and Novacek, 1988), description of new and important fossils from Messel (Germany) and Wyoming (United States) (Simmons et al., 2008), paraphyly of microbats (Teeling et al., 2002), and new classificatory arrangements within very diversified families like Phyllostomidae (Baker et al., 2000), Emballonuridae (Lim, 2007), and Molossidae (Ammerman et al., 2012; Gregorin and Cirranello, 2015). Among molossids, *Eumops* is the most diverse New World genus with high levels of inter- and intraspecific variation on external, cranial, dental, and penis morphology, karyotype, biochemistry, and molecular genetics (e.g., Brown, 1967; Dolan and Honneycutt, 1978; Freeman, 1979; Staaden and Jones, 1997; Gregorin, 2003; Morielle-Versute et al., 1996; McDonough et al., 2008; Bartlett et al., 2013; Medina et al., 2014). In the most comprehensive taxonomic review for the genus and based on the application of Biological Species Concept Eger (1977) recognized nine species and 12 subspecies totalizing 16 taxa for the species-group in *Eumops*. Recent descriptions of new species (e.g., *Eumops wilsoni* Baker et al., 2009 and *Eumops chiribaya* Medina et al., 2014) and revisionary studies recognizing many taxa at the species level (e.g., *Eumops floridanus*, *Eumops ferox*, *Eumops delticus*, and *Eumops nanus*—Timm and Genoways, 2004; Eger, 2008; McDonough et al., 2008) resulted in the recognition of 16 species. Those noteworthy revisions were carried out in a phylogenetic frame and used morphological and molecular data to satisfy some criteria for delimiting species in an integrative approach (Padial et al., 2010; Heller et al., 2014).

Additionally, this taxonomic diversity has supported several phylogenetic and phenetic hypotheses of relationships (Eger 1977; Dolan and Honneycutt, 1978; McDonough et al., 2008; Gregorin,

* Corresponding author at: Departamento de Biologia, Universidade Federal de Lavras, Lavras, Minas Gerais, Caixa Postal 3037, CEP 37200-000, Brazil.
E-mail addresses: rgregorin@dbi.ufla.br (R. Gregorin), ligimoras@gmail.com (L.M. Moras), l.jubatus096@gmail.com, lacosta@museonoelkempff.org (L.H. Acosta), lobaobio@gmail.com (K.L. Vasconcellos), jose_luispoma@hotmail.com (J.L. Poma), fsantos@icb.ufmg.br (F.R. dos Santos), robertocarlospaca@gmail.com (R.C. Paca).

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2009; Baker et al., 2009; Bartlett et al., 2013; Medina et al., 2014), and has provided support for numerous solid taxonomic decisions.

A recent phylogenetic analysis based on a combined analysis of a single mitochondrial DNA gene (Cytochrome *b*) and morphological characters (Medina et al., 2014), split *Eumops* into two clades: one clade of small-sized species (*Eumops hansae*, *Eumops bonariensis*, and relatives) and another clade grouping medium-size (*Eumops maurus*, *Eumops auripendulus*, *Eumops glaucinus*, and relatives) and large-sized species (*Eumops dabbenei*, *Eumops underwoodi*, *Eumops perotis*, and relatives) in agreement with previous hypotheses (e.g., Dolan and Honneycutt, 1978; Bartlett et al., 2013). This suggests that large size evolved twice in *E. dabbenei* + *E. underwoodi*, and *E. perotis* + *E. trumbulli*. Considering the variation already described and the old age of diversification for the genus with fossil record from La Venta, Colombia (Czaplewski, 1997) diversity within *Eumops* is regarded as underestimated (Medina et al., 2014). Part of this problem stems from the difficulty in capturing individuals of *Eumops* in the field and thus available samples for some species are poorly represented in collections (e.g., *E. maurus*, *E. dabbenei*, *E. wilsoni*, *E. nanus*, and *E. hansae*) or known only by the holotype (*E. chiribaya*).

Here we describe a new species based on three specimens of *Eumops* from southeastern Bolivia and Brazil, which present an exclusive set of morphological characteristics that distinguish them from any species hitherto known from *Eumops*. We performed a phylogenetic analysis of the genus based on both morphological and mitochondrial Cytochrome *b* gene data in order to ascertain the level of divergence of our specimens and we describe a new species based on the high divergence presented in both of our datasets.

Material and methods

Material examined

We reviewed 303 specimens housed in 15 institutions: Coleção de Mamíferos da Universidade Federal de Lavras, Lavras (CMUFLA), Museo de Historia Natural de la Universidad Nacional de San Agustín, Arequipa (MUSA), Museu de Zoologia da Universidade de São Paulo, São Paulo (MZUSP), American Museum of Natural History, New York (AMNH), Laboratório de Chiroptera, Universidade Estadual Paulista, São José do Rio Preto (DZSJRP), The Field Museum, Chicago (FMNH), Museum of Comparative Zoology, Harvard University, Boston (MCZ), Museum of Vertebrate Zoology, University of California, Berkeley (MVZ), Royal Ontario Museum, Toronto (ROM), Texas Cooperative Wildlife Research Collection, Texas A&M University (TCWC), Coleção de Chiroptera, Universidade Federal Rural do Rio de Janeiro, Seropédica (ALP), Museum of Zoology, University of Michigan, Ann Harbor (UMMZ), Natural History Museum, London (BMNH), Museo de Historia Natural Noel Kempff Mercado, Santa Cruz, Bolivia (MNKM), Colección Boliviana de Fauna, La Paz, Bolivia (CBF), and National Museum of Natural History, Smithsonian Institution, Washington D.C. (USNM). We only examined adult specimens. Material is described in Appendix A. Besides the material directly analyzed by us, data for *E. wilsoni* and *E. chiribaya* were gathered from Baker et al. (2009) and Medina et al. (2014), respectively.

Morphological dataset

We chose thirty-two morphological characters most based on the ones described by Medina et al. (2014). We also replaced *Molossus* for *Nyctinomops* as outgroup. The morphological characters we used are as follows: Character 1—Internarial ribs: covered by warts (0); covered by small hairs (1). Character 2—Small and pointed warts on upper border of the ears: present (0); absent (1). Character 3—Size of ears: large (0); very large (1). Character 4—Long and semicircular antitragus: absent (0); present (1). Character 5—Shape of the tragus: squarish (0); slightly squared with the upper edge directed in a posterior position (1); pointed (2). Character 6—Upper lips: deeply wrinkled (0); slightly wrinkled (1); smooth (2). Character 7—Size of the body: small (0); medium (1); large (2). Character 8—Ratio between second phalanx of fourth finger and total length of the body: large (>0.1; 0.13–0.2) (0); small (<0.1; 0.05–0.08) (1). Character 9 – Dorsal pelage coloration: light brown to slightly grayish (0); dark brown to blackish (1). Character 10—Frequency of fungiform papillae on the dorsal and lateral regions of the tongue: abundant (0); reduced (1). Character 11—Relative position of upper incisors: parallel (0); divergent (1). Character 12—Shape of incisors: flattened (0); conical (1). Character13—Protofossa on the upper incisors: absent (0); present (1). Character 14—Position of first upper premolar: lined with toothrow (0); labially placed (1). Character 15—relative size of first upper premolar: small (0), large (1). Character 16—Hypocone on M1 and M2: present (0); absent (1). Character 17—Length of third commissure on M3: very long (0); medially developed (1); reduced (2); vestigial or absent (3). Character 18—Length of rostrum: medium (0); long (1). Character 19—Outline of mid-dorsal region of skull: curved (0); flattened (1). Character 20—Angle between rostrum and braincase: straight (0); concave (1). Character 21—Width of rostrum: medium (0); narrow (1); large (2). Character 22—Width of post-orbital region: enlarged (0); narrowed (1). Character 23—Shape of basisphenoid pits: slightly squarish (0); oval (1). Character 24—Depth of basisphenoid pits: deep (0); shallow (1); very deep (2). Character 25—Rib between basisphenoid pits: wide (0); narrowed (1). Character 26—Lateral wall of braincase in dorsal view: curved (0); enlarged posteriorward (1). Character 27—Opisthocranium in lateral view: straight (0); curved dorsally and anteriorly (1); extended posteriorly (2). Character 28—Development of mandible: gracile (0); massive (1). Character 29—Glans penis: covered with spines (0); spineless (1). Character 30—Shape of glans penis: oval with three basal lobes (0); oval but without three-lobed structure (1). Character 31—Length of glans penis: long (0); short (1). Character 32—*Os penis*: present (0); absent (1).

Molecular dataset

We obtained the entire mitochondrial Cytochrome *b* (cyt *b*) gene sequence of the new species of one specimen from Brazil (CMUFLA 1889); Bolivian specimens of the new species, *Eumops trumbulli* and *E. delticus* had no tissue available for sequencing. DNA extraction from a small portion of the liver was performed with a standard phenol–chloroform–isoamyl alcohol protocol (Sambrook et al., 2001). The protocols for PCR amplifications and sequencing reactions follow those described in Redondo et al. (2008). The sequence of the new species was assembled and checked for quality using DNA Baser Sequence Assembler v3.x 2011. Additionally, we gathered 33 sequences of *Eumops* from GenBank representing 13 of the 16 recognized species for the genus, one of *Tadarida brasiliensis* and one of *Nyctinomops macrotis* (outgroups). As the sequences downloaded from GenBank were partial cyt *b* data, we used a smaller segment (688 bp) of the new species to compare all taxa. The sequence of the new species was deposited in GenBank under accession number: KT324614.

Sequences were aligned using the Muscle algorithm (Edgar 2004) implemented in MEGA 5.05 (Tamura et al., 2011) and the alignment is available on demand from the authors. MEGA 5.05 was also used to check if the new species sequence was not a pseudogene and to calculate the genetic distance as intraspecific and interspecific sequence divergence with a Kimura 2-parameter (K2P) model (Kimura 1980).

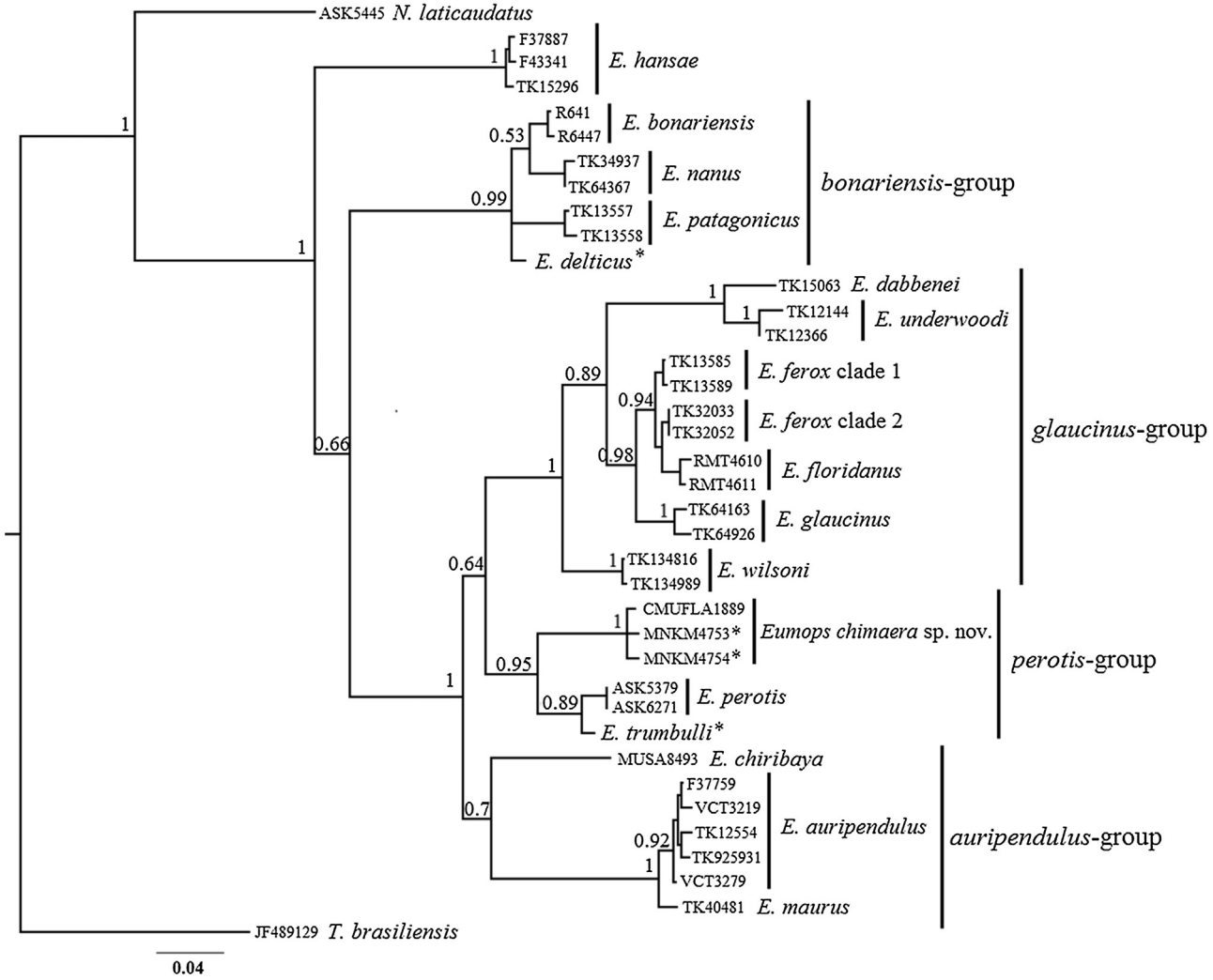

Fig. 1. Bayesian tree of *Eumops* species generated with 688 base pairs of the Cytochrome *b* gene and 32 morphological characters. Values represent Bayesian posterior probabilities (PP). Note the detached position of the new taxon with respect to the other *Eumops* species. See Appendix A for museum acronyms and collection sites. Asterisks indicate taxa presenting only morphological data.

Table 1
Average Kimura 2-parameter distances between species of *Eumops* bats based on 688 base pairs of the Cytochrome *b* gene. Intraspecific divergence is on the diagonal. Outgroups were not included.

		n	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	*E. auripendulus*	5	0.9														
2	*E. bonariensis*	2	16.8	0.5													
3	*E. dabbenei*	1	14.0	18.0	–												
4	*E. ferox*	4	14.6	15.6	11.1	0.7											
5	*E. floridanus*	2	16.7	17.6	12.9	1.9	0.9										
6	*E. glaucinus*	2	15.2	17.5	11.7	4.6	5.7	1.9									
7	*E. hansae*	3	20.3	19.3	22.2	20.9	22.1	20.6	0.9								
8	*E. maurus*	1	2.7	16.9	14.8	14.5	16.7	15.7	19.6	–							
9	*E. nanus*	2	18.3	6.0	18.2	17.3	19.0	17.2	20.9	19.1	1.1						
10	*E. patagonicus*	2	18.0	3.9	17.9	7.0	15.9	17.7	19.6	17.9	7.0	0.6					
11	*E. perotis*	2	13.9	17.0	12.8	12.8	14.0	14.6	18.6	13.5	17.6	17.3	0.2				
12	*E. chiribaya*	1	13.6	18.6	14.6	14.6	16.7	16.1	19.2	13.2	18.1	18.6	12.3	–			
13	*E. underwoodi*	2	16.5	18.8	6.4	11.2	13.2	13.0	23.1	15.3	20.0	18.8	12.4	16.3	1.5		
14	*E. wilsoni*	2	14.3	14.3	14.4	7.3	8.3	9.0	19.3	14.3	16.6	15.8	10.5	13.5	12.3	0.2	
15	*E. chimaera* sp. nov.	1	13.7	16.0	12.8	11.8	13	13.2	17.8	13.3	16.3	16.2	7.9	12.4	14.0	11.1	–

Phylogenetic analysis

Partition Finder 1.0.1 (Lanfear et al., 2012) was used to select the best partitions and models of sequence evolution using the Akaike Information Criterion (AIC; Akaike, 1974). We defined separate data blocks for the three codon positions. The best scheme selected was performing the three codon positions separately under the following models: SYM+I+G for the first codon position, GTR+G for the second codon position and GTR for the third codon position. For morphological partition we used the standard stochastic model (Mkv) (Lewis, 2001). The Mk model assumes equal state fre-

quencies. This model could be combined with equal or gamma distributed rates across "sites" (i.e., characters) but not with a proportion of invariable "sites" because constant morphological characters were absent in the data matrix, making it impossible to estimate the proportion of invariable sites/character (Nylander et al., 2004).

A Bayesian Inference analysis was conducted in MrBayes 3.1.2 on the Cipres portal (https://www.phylo.org/). The best-fit partitioning schemes and models for each dataset were specified as determined by Partition Finder. The number of generations necessary to be run and the "burn-in" were determined by examining the log likelihood (lnL) plots with Tracer 1.6 (Rambaut and Drummond, 2003). Convergence was evaluated through *standard deviation of split frequencies* for topology (less than 0.001) and *potential scale reduction factor* (PSRF, it must approach 1) for continuous parameters. Four (one cold and three heated) simultaneous Markov chains were run for 20 million generations, trees were sampled every 200 generations, with the first 10% of the generations discarded as "burn-in".

Morphometric analysis

Principal Component Analysis (PCA) was used to explore the variance-covariance of 10 cranial measurements of 128 specimens and 10 species of *Eumops*. The following cranial measurements were taken following Medina et al. (2012): greatest length of skull (GLS), condyle-incisive length (CIL), palatal length (PAL), zygomatic breadth (ZIB), post-orbital breadth (POB), braincase breadth (BCB), length of upper canine-last molar (C-M), upper molar breadth (M-M), mandible length (MAL), and length of lower canine-last molar (c-m). These included the new specimens, plus others of the small, medium, and large-sized taxa of the genus. All the measurements were log-transformed to achieve normalization for the analyses. The first two components of the PCA were selected to represent the most important variables defining species groups, and then the difference between groups was assessed by discriminant function analysis (DFA, Brown & Wicker 2000). We performed two PCA analyses, one including 10 species and the other with only three medium-sized species (*Eumops chimaera* sp. nov., *E. glaucinus*, and *E. auripendulus*). The PCA and DFA analyses were performed with the software PAST 3.06 for Windows (Hammer et al., 2001).

Results and discussion

Phylogenetic analysis

The new species described in this report was recovered sister to the clade containing *E. perotis* + *E. trumbulli*, and was supported with high posterior probability (PP = 0.95) (Fig. 1). The average cyt *b* pairwise distance between the new species and *E. perotis* is 7.9% (Table 1). Unfortunately, cyt *b* sequences are not available for *E. trumbulli*. The specimen we sequenced representing the new species (CMUFLA 1889—Brazil) can be distinguished by 50 fixed nucleotides differences when compared from its sister group *E. perotis*, nine of which representing autapomorphies for the new species (Table 2). The genetic relationship between the new species and *E. perotis* + *E. trumbulli* (Fig. 1) agrees with some shared morphological traits, in particular the large body, including forearm, and size and shape of ears. We further highlight the high level of morphological and molecular divergence of the new species (Tables 1 and 2; Appendix C) as compared with its sister species (*E. perotis* and *E. trumbulli*, Fig. 1), supporting its recognition as a new species. Our analysis also recovered paraphyly of *E. ferox* as in Bartlett et al. (2013) probably due its recent age resulting in incomplete lineage sorting.

Table 2
Fixed nucleotide changes in cyt *b* between *Eumops chimaera* sp. nov. and *E. perotis* (*N* = 2). A = adenine, C = cytosine, G = guanine, and T = thymine. Position refers to the nucleotide position in the cyt *b* gene from the complete mitochondrial genome of *Artibeus jamaicensis* (see Pumo et al., 1998). Asterisks indicate the autapomorphies for *E. chimaera sp. nov*.

Position	*Eumops chimaera* sp. nov.	*Eumops perotis*
14257	T	C
14266	C	A
14270	C	T
14276	G	A
14293	A	G
14311	T	C
14314	C	T
14320*	T	C
14347	T	C
14356	T	C
14359	T	C
14365	T	C
14368	C	T
14377	C	T
14380*	G	A
14389*	A	T
14398	C	T
14401	C	T
14434	T	C
14461	T	C
14464	G	A
14498	G	A
14506	T	C
14563*	G	A
14566	A	C
14594*	T	C
14596	A	T
14608	T	C
14668*	T	C
14686	C	T
14719	C	T
14722	T	C
14773	C	T
14788	C	T
14797	T	C
14806*	G	A
14815	C	T
14833	C	T
14837	C	T
14845	T	C
14849	T	C
14851	A	C
14859	C	T
14861	A	G
14878*	T	A
14879	C	T
14887	C	T
14890	T	C
14897	T	C
14932*	T	C

Within *Eumops* we can recognize four species groups (Fig. 1) herein referred to as *bonariensis*-group (*E. bonariensis*, *E. nanus*, *E. delticus*, and *E. patagonicus*), *glaucinus*-group (*E. floridanus*, *E. glaucinus*, *E. wilsoni*, *E. ferox*, *E. dabbenei*, and *E. underwoodi*), *perotis*-group (*E. perotis*, *E. trumbulli*, and new species), *auripendulus*-group (*E. auripendulus*, *E. maurus*, and *E. chiribaya*), and a basal lineage composed only by *E. hansae* (Fig. 1).

Morphometric analyses

The PCA analysis for the 10 *Eumops* species showed that two of the principal components explained 98.85% of the total variation (Table 3, Fig. 2). PC1 explained most of the variation (95.44%), with all positive scores, being the highest for PAL, c-m, MAL, and CM. PC2 contributed with 3.41% of the variation, where the highest positive values were for BCB and POB, and negative values for

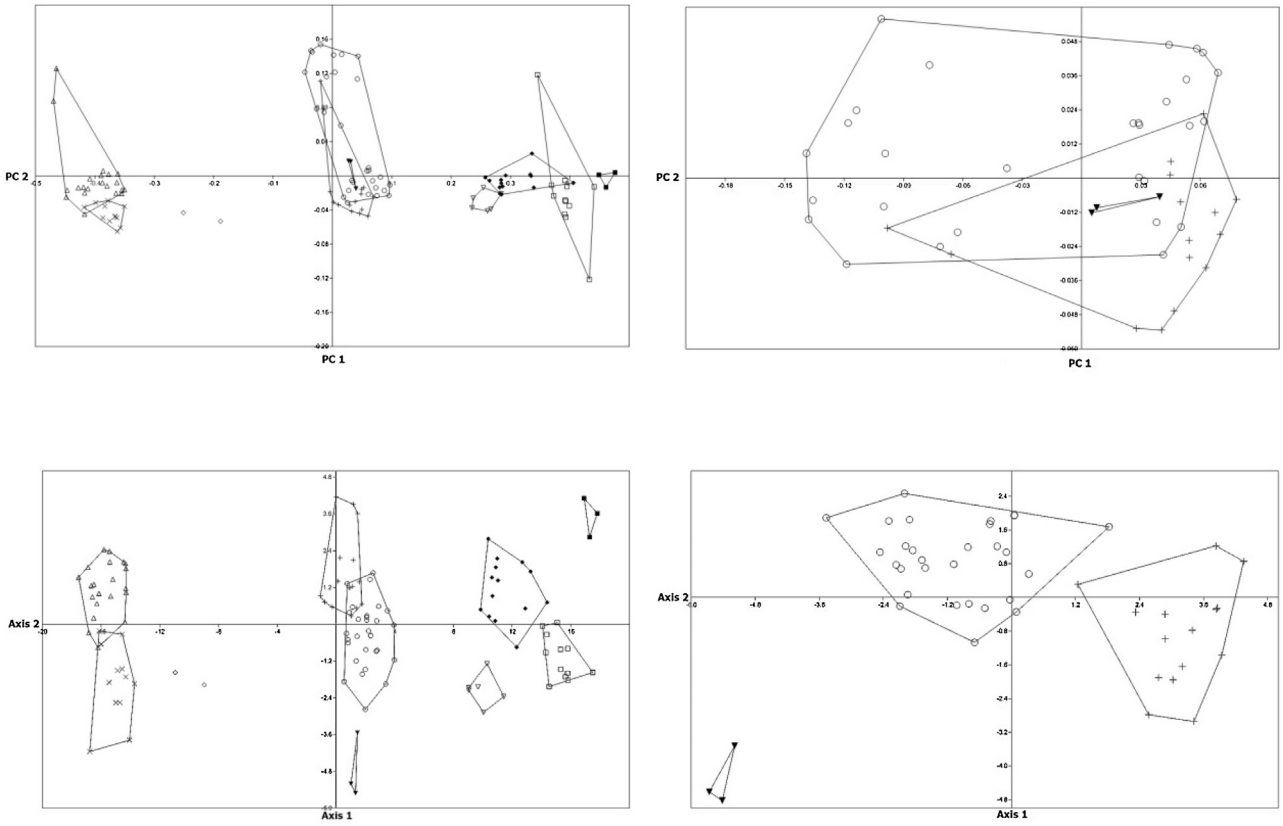

Fig. 2. Plots of PCA (above left) and DFA (below left) of 10 cranial measurements of 118 specimens belonging to 10 species of *Eumops*: *E. chimaera* sp. nov. (filled triangles inverted), *E. patagonicus* (empty triangles), *E. hansae* (empty diamonds), *E. delticus* (cross ×), *E. glaucinus* (empty circles), *E. auripendulus* (cross +), *E. underwoodi* (filled diamonds), *E. trumbulli* (empty triangles inverted), *E. perotis* (empty squares), and *E. dabbenei* (filled squares); PCA (above right) and DFA (below right) of 10 cranial measurements of 37 specimens belonging to three species of *Eumops*: *E. chimaera* sp. nov., *E. glaucinus* (empty circles), and *E. auripendulus* (cross +).

Table 3
PCA and DFA scores of the character variance and covariance matrix for ten cranial measurements of 118 bat specimens belonging to 10 *Eumops* species (*E. chimaera* sp. nov., *E. patagonicus*, *E. hansae*, *E. glaucinus*, *E. auripendulus*, *E. delticus*, *E. dabbenei*, *E. underwoodi*, *E. trumbulli*, and *E. perotis*).

Charactes	Principal component		Discriminant function	
	PC 1	PC 2	DF 1	DF 2
GLS	0.32	−0.09	3.99	74.32
CIL	0.32	−0.05	38.81	−156.46
PAL	0.37	−0.83	−1.55	18.35
ZIB	0.31	0.12	−21.32	−21.70
POB	0.19	0.21	11.67	20.43
BCB	0.26	0.41	20.44	10.03
C-M	0.35	0.09	32.75	−15.99
M-M	0.29	0.16	8.01	63.62
MAL	0.35	0.09	4.94	8.80
c-m	0.36	0.16	25.53	13.50
Eigenvalue	0.08	0.00	134.20	2.69
Variance (%)	95.44	3.41	95.25	1.91

PAL and CIL. The small-sized species (*E. patagonicus*, *E. delticus*, and *E. hansae*) showed the lowest scores along the axes, while the medium-sized species (*E. glaucinus*, *E. auripendulus*, and *E. chimaera* sp. nov.) showed intermediate values. The large-sized species (*E. trumbulli*, *E. underwoodi*, *E. perotis*, and *E. dabbenei*) presented the highest scores along the axes.

PCA for three medium-sized species only (*E. chimaera* sp. nov., *E. auripendulus*, and *E. glaucinus*) showed that two first principal components explained 88.15% of the total variation (Table 4, Fig. 2), where PC1 explained most of it (77.24%). The highest positive values were for PAL, GLS, CIL, and MAL, while negative values were for

Table 4
PCA and DFA scores of the character variance and covariance matrix for ten cranial measurements of 47 bat specimens belonging to three medium-sized *Eumops* species (*E. chimaera* sp. nov., *E. glaucinus*, and *E. auripendulus*).

Characters	Principal component		Discriminant function	
	PC 1	PC 2	DF 1	DF 2
GLS	0.205	0.138	117.430	−15.452
CIL	0.144	0.289	−107.870	45.665
PAL	0.909	0.062	−14.232	5.729
ZIB	0.021	0.361	−64.056	−115.420
POB	−0.122	0.549	−39.113	58.897
BCB	−0.295	0.316	−42.415	14.976
C-M	0.041	0.331	−28.077	−20.848

M-M, POB, and BCB. The PC2 contributed with 10.91% of the variation, with all positive scores, with the highest for POB, ZIB, C-M, MAL, BCB, and M-M. *E. chimaera* sp. nov. presented an intermediate values between the species *E. auripendulus* and *E. glaucinus* along the axes.

The DFA scores for the 10 *Eumops* species showed 95.25% of the variation for the first and 1.91% for the second canonical axes (Table 3). The multivariate space of these functions showed a separation among all species except for *E. auripendulus* and *E. glaucinus*, which overlap with each other (Fig. 2). The scores of the first axes showed a high positive correlation in the discriminant function for CIL, C-M, c-m, and BCB, while the second axes had a positive correlation for GLS, M-M, and POB and a negative correlation for CIL (Table 3).

For the second analysis including only medium-sized species (*E. chimaera* sp. nov., *E. auripendulus*, and *E. glaucinus*), the DFA showed 74.89% of the variation for the first and 25.11% for the second

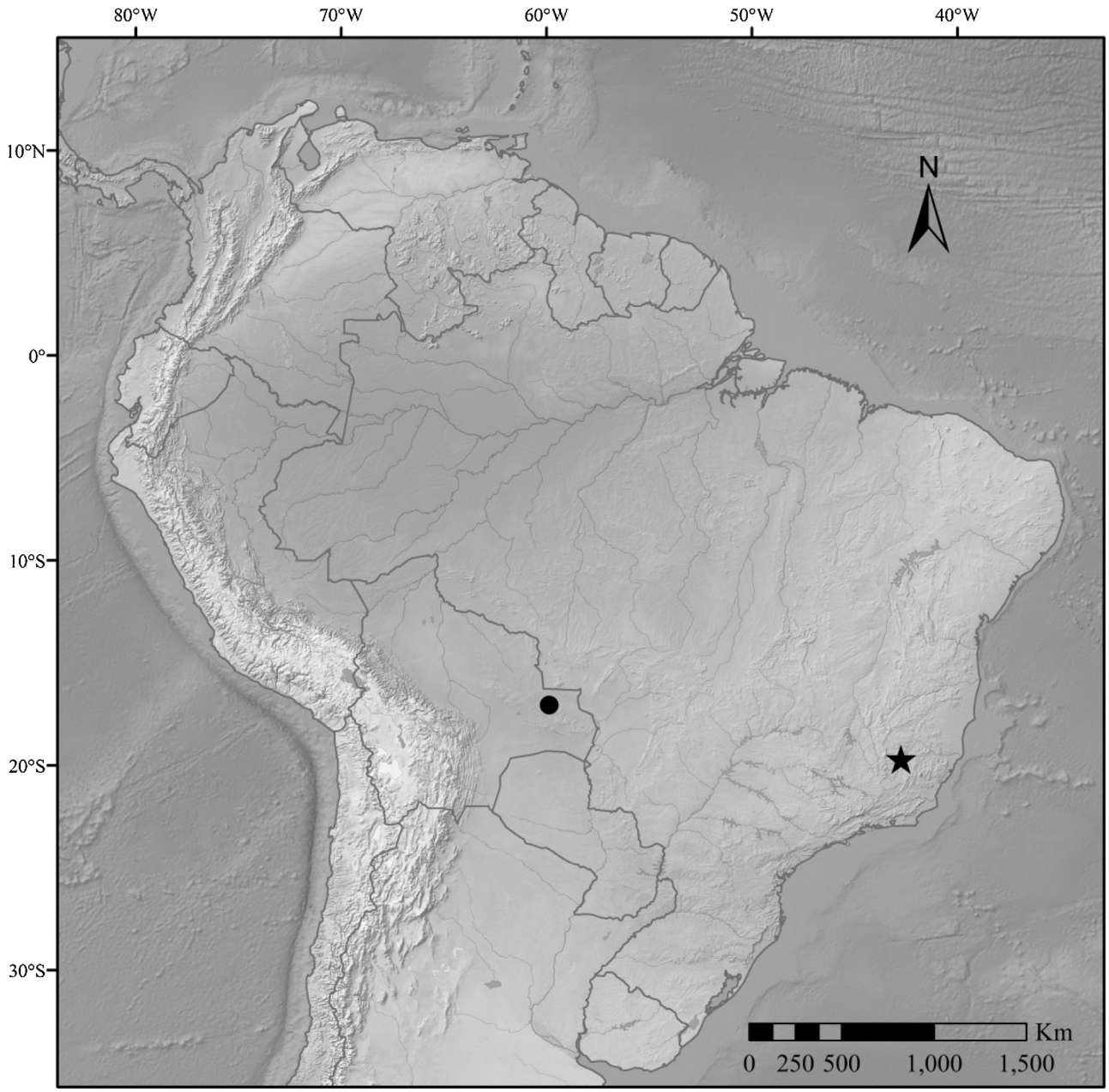

Fig. 3. Collection sites of specimens of *Eumops chimaera* sp. nov., where (⋆) is type-locality type and (●) paratypes locality.

canonical axes (Table 4). The plots multivariate space of these functions showed a separation among three species without overlap among these species (Fig. 2b).

Taxonomy

Family Molossidae Gervais, 1856
Genus *Eumops* Miller, 1906
Eumops chimaera new species
Chimeraís Bonneted Bat

Holotype—CMUFLA 1889, adult male, preserved in alcohol with skull and tissue (liver) removed. The specimen is in good condition of preservation, with the exception of the left forearm that is broken. The specimen was observed flying roughly 20 m high over a lagoon in Parque Estadual do Rio Doce (PERD), southeastern Brazil, and it was probably attracted by insects flying next to the light from our flashlight. The individual was collected by K.V. Lobão on 24 October 2013 with permission from the Instituto Chico Mendes (ICMBio, process 18528-3).

Paratypes—The two paratypes were collected by R.C. Paca, at Tierra Comunitaria de Origen Turubó-Este, in the chaparral forest, a semi-deciduous Chiquitano forest, Santa Cruz, Bolivia (17°3′34.7″S–59°51′30.1″W, 382 m a.s.l). Paratypes include two adult males: MNKM 4753 (skin and skull) and MNKM 4754 (fluid preserved), both collected on 11 July 2009.

Type-locality—Parque Estadual do Rio Doce (PERD), municipality of Marliéria, state of Minas Gerais, Brazil (19°29′S–19°48′W) (Fig. 3). PERD is largest semi-decidual forest remnant in Minas Gerais and it presents roughly plane relief with elevation varying from 300 to 500 m a.s.l. The area is covered by semi-deciduos forest with tall trees (30 m) (Tavares et al., 2007). Bosque Chiquitano, Chaparal de Abayoy, Bolivia, is composed by dense and shrubby vegetation (Paca et al., 2012).

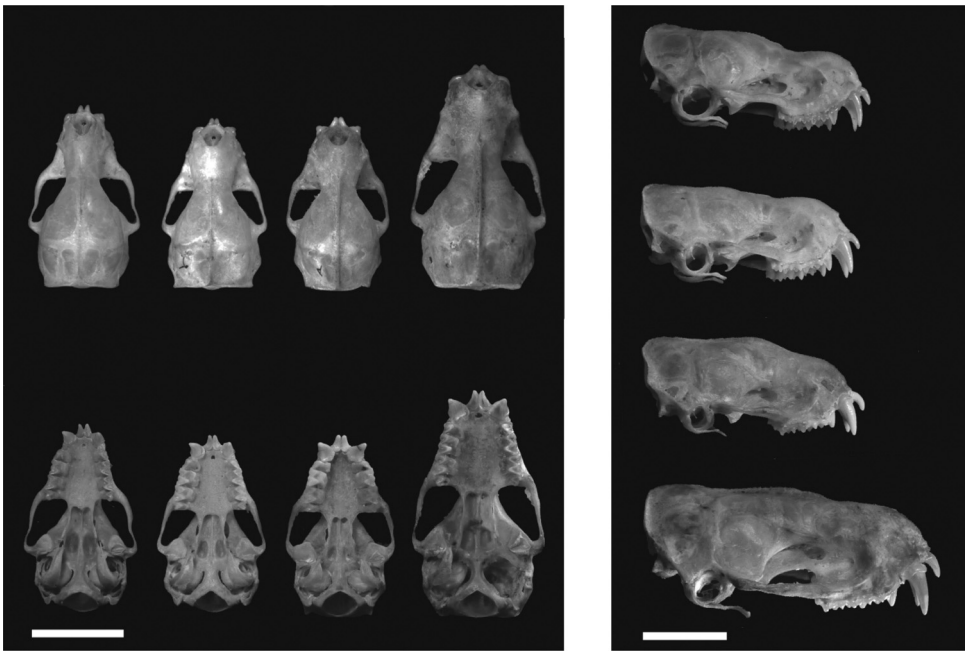

Fig. 4. Left side: dorsal (top) and ventral (bottom) views of adult skulls of *Eumops chimaera*, *E. glaucinus*, *E. auripendulus* (two similar medium-sized species) and *E. perotis* (syster-group of *E. chimaera*). Right side: lateral view of the skulls from top to bottom in the same order. (Scale bar 10 mm).

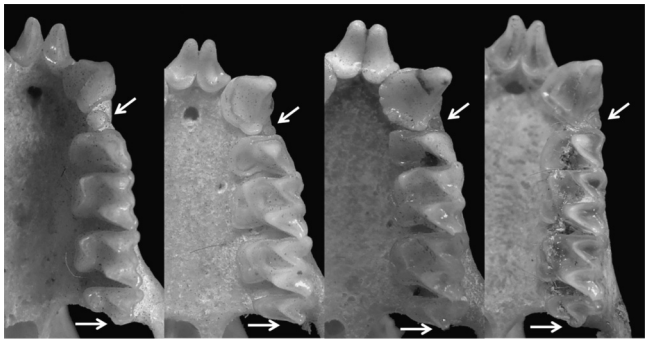

Fig. 5. Upper toothrow indicating position and size of first upper premolar (top arrows) and the relative length of the third commissure of M3 (bottom arrow). Left to right: *Eumops chimaera*, *E. glaucinus*, *E. auripendulus*, and *E. perotis.*

Etymology—From latinized Greek *chimaera*, in reference to the mythical entity composed of parts of several creatures (Brown 1956). In this case the name refers to the different morphological characteristics that define *E. chimaera* and are shared with distinct groups of species within *Eumops*. Noun treated here in apposition.

Diagnosis—Three characters of *E. chimaera* are autapomorphic: concavity between the rostrum and braincase (Fig. 4), and first upper premolar wide and lined with toothrow (Fig. 5). Other characters facilitate diagnosis of *E. chimaera*: Large ears (> 28.00 mm); inner fold in the ear roughly developed not covering part of antitragus; relatively short skull (24.50–24.90 mm) and long forearm (66.00–68.50 mm) (Table 5); opistocranium not extended posteriorly and braincase is wide in dorsal view (Fig. 4); basisphenoid pits roughly deep; third commissure on M^3 developed as long as second commissure (Fig. 5).

Description—Face blackish, weakly haired. Rounded, large (27.5–31 mm), thin and blackish ears; ears connected with each other on top of the head with upper border of the ears without pointed warts; inner fold in the ears weakly developed not covering the anti-tragus even partially. Anti-tragus longer (8.8 mm) than high (4.35); tragus squarish, 3.6 mm high. Line of rigid, pointed and blackish warts covering the upper border of nostrils; internarial region with a skinny crest covered by small and spoon-like hairs. Dorsal pelage is dark brown and the venter slightly lighter; long dorsal hairs at scapula level ~7–8 mm with basal third light brown colored and dark brown tip; monochromatic ventral hairs. Interfemoral membrane is grayish and lighter than the wing membrane. Gular gland presents. External dimensions (in millimeters): Total length of body 78–91; length of tail 58.00–61.00; length of ear 27.50–31.00; height of tragus 3.60–3.80; calcar 21.00–23.42; length of forearm 66.60–68.34; length of metacarpal III 68.30–71.5; phalanx I 28.40–29.77; phalanx II 24.3–24.8; length of metacarpal IV 68.20–69.18; phalanx I 22.65–23.22; phalanx II 6.00–6.61; length of metacarpal V 40.90–41.54; phalanx I 21.90–23.06.

Medium-sized and robust skull with a wide braincase and a short with not extended opistocranium (Fig. 4); shortened rostrum, slightly domed at the nostril region, resulting in concavity at limit region between the braincase and rostrum (Fig. 4). Basisphenoid pits are large, more rectangular than oval, roughly deep and separated from each other by a thin bone crest (0.75 mm) (Fig. 4). Dental formula 1/1, 1/1, 2/2, 3/3. Overall morphology of teeth as for the genus but first upper premolar is larger and lined with the toothrow (Fig. 5). Third commissure on M^3 is as long as the second one (Fig. 5).

Comparisons—*E. chimaera* presents a unique set of characters, including three morphological autapomorphies (size and position of first upper premolar and angle between braincase and rostrum – Fig. 4, 5) unique in *Eumops*; but most traits are shared with some species groups within *Eumops* (Bartlett et al., 2013; Medina et al., 2014). The body, forearm and ear dimensions are similar to large-sized *E. perotis*, *E. trumbulli*, and *E. underwoodi*. Overall skull shape in *E. chimaera* resembles *E. perotis* and *E. trumbulli* due to the slender rostrum, but similar to *E. glaucinus* due the short braincase. Shape and depth of basisphenoid pits resemble *E. chiribaya* and *E. glaucinus*, and relatives. Third commissure of M^3 is long and intermediary between *E. trumbulli* plus *E. chiribaya* (shorter) and *bonariensis*-group plus *E. hansae* (longest). Dark brown pelage coloration is shared only with *E. maurus* and some *E. perotis*. Squarish anti-tragus and roughly developed skinny fold in ears are present in most of species of *Eumops.*

Table 5
Comparative measurements (mm) of type series and the others of *Eumops* species ($N = 117$). Numbers include mean ± SD and ranges. Cranial and forearm measurements of new type specimens and those of other *Eumops* species used in the analyses ($N = 117$). Description of acronyms is in Methods section.

	Eumops chimaera (Holotype) CMUFLA 1889	*Eumops chimaera* (Paratype) MNKM 4754	*Eumops chimaera* (Paratype) MNKM 4753	*E. auripendulus* ($N = 15$)	*E. delticus* ($N = 12$)	*E. dabbenei* ($N = 3$)	*E. glaucinus* ($N = 29$)	*E. hansae* ($N = 2$)	*E. patagonicus* ($N = 21$)	*E. perotis* ($N = 12$)	*E. trumbulli* ($N = 6$)	*E. underwoodi* ($N = 14$)
GLS	24.9	24.52	24.43	24.93 ± 0.75 (23.25–25.72)	21.6 ± 6.22 (18.10–33.90)	21.65 ± 6.22 (18.12–33.88)	24.31 ± 0.94 (22.62–26.02)	20.96 ± 0.77 (20.41–21.5)	17.94 ± 0.49 (16.92–18.84)	32.49 ± 0.80 (30.85–34.00)	29.78 ± 0.47 (29.09–30.28)	29.61 ± 1.23 (28.07–32.82)
CIL	24.11	24.43	24.49	23.01 ± 0.74 (21.32–23.78)	20.40 ± 5.56 (17.20–31.60)	20.38 ± 5.56 (17.19–31.55)	23.41 ± 0.81 (21.98–24.87)	20.00 ± 0.79 (19.44–20.56)	16.79 ± 0.45 (15.84–17.59)	31.26 ± 0.65 (30.07–32.68)	28.41 ± 0.52 (27.85–29.06)	28.29 ± 0.97 (27.18–30.63)
PAL	10.99	10.04	10.05	10.76 ± 1.00 (8.05–11.68)	9.50 ± 3.10 (7.50–15.70)	9.50 ± 3.10 (7.54–15.72)	9.71 ± 1.54 (7.44–11.66)	9.16 ± 0.43 (8.85–9.46)	7.39 ± 0.67 (5.33–7.93)	14.84 ± 1.84 (10.93–19.37)	13.34 ± 0.38 (12.90–13.78)	13.68 ± 0.43 (13.02–14.75)
ZIB	15.15	15.6	15.45	14.56 ± 0.27 (14.14–15.06)	12.60 ± 3.78 (10.60–20.20)	12.59 ± 3.78 (10.57–20.24)	14.82 ± 0.48 (13.71–15.46)	12.39 ± 0.52 (12.02-12.75)	10.75 ± 0.47 (9.41–11.3)	18.77 ± 0.41 (17.69–19.36)	16.96 ± 0.27 (16.7–17.29)	17.81 ± 0.81 (16.69–19.96)
POB	4.74	4.59	4.59	4.67 ± 0.19 (4.46–5.10)	4.40 ± 0.99 (3.60–6.50)	4.40 ± 0.99 (3.60–6.52)	5.04 ± 0.16 (4.78–5.37)	4.26 ± 0.09 (4.19–4.32)	4.09 ± 0.16 (3.83–4.35)	5.46 ± 0.20 (5.22–5.89)	5.10 ± 0.09 (4.99–5.22)	5.65 ± 0.15 (5.33–5.90)
BCB	11.70	11.63	11.51	10.88 ± 0.35 (10.52–11.81)	9.50 ± 2.40 (8.10–14.20)	9.47 ± 2.40 (8.08–14.24)	11.58 ± 0.71 (10.20–12.85)	8.98 ± 0.21 (8.83–9.13)	8.71 ± 0.23 (8.20-9.29)	13.43 ± 0.77 (12.56–15.45)	12.56 ± 0.45 (11.92–13.26)	13.3 ± 0.41 (12.68–14.12)
C-M	9.78	9.32	9.32	9.46 ± 0.24 (8.84–9.82)	8.10 ± 2.69 (6.60–13.40)	8.11 ± 2.698 (6.59–13.44)	9.61 ± 0.25 (9.18–10.12)	7.72 ± 0.22 (7.56–7.87)	6.72 ± 0.17 (6.38–7.06)	12.87 ± 0.25 (12.50-13.44)	11.44 ± 0.24 (11.19–11.85)	11.77 ± 0.31 (11.38–12.40)
M-M	9.60	9.76	9.65	10.16 ± 0.23 (9.78–10.50)	8.70 ± 2.56 (6.80-13.90)	8.65 ± 2.56 (6.83–13.88)	10.22 ± 0.32 (9.41–10.72)	8.54 ± 0.37 (8.27–8.80)	7.71 ± 0.25 (7.35–8.19)	12.89 ± 0.29 (12.54–13.40)	11.26 ± 0.14 (11.04–11.45)	12.14 ± 0.27 (11.80–12.66)
MAL	17.8	17.93	18.41	18.53 ± 0.45 (17.54–19.32)	15.90 ± 5.28 (12.90–26.40)	15.85 ± 5.28 (12.91–26.40)	18.59 ± 0.59 (17.45–19.54)	15.51 ± 0.49 (15.16–15.85)	12.83 ± 0.32 (12.18–13.54)	24.28 ± 0.61 (23.33–25.72)	21.99 ± 0.44 (21.42–22.54)	22.84 ± 1.21 (21.15–25.35)
c-m	10.08	10.45	10.70	10.58 ± 0.25 (10.17–10.97)	8.90 ± 3.12 (7.10–15.00)	8.87 ± 3.12 (7.13–15.00)	10.63 ± 0.26 (10.06–11.13)	7.71 ± 0.25 (7.53–7.88)	7.2 ± 0.20 (6.92–7.56)	14.02 ± 0.30 (13.61–14.56)	12.44 ± 0.14 (12.25–12.60)	12.88 ± 0.51 (12.29–13.81)

Eumops chimaera is easily distinguished from smallest species of the *bonariensis*-group and *E. hansae* by larger size of external characters (Table 5), shape of skull (dorsally flattened in outline and shorten opistocranium), and third commissure on M^3 roughly developed in *E. chimaera* (it is slightly longer than the second commissure, N-inverted, in *bonariensis*-group and *E. hansae*).

Among medium-sized species (Fig. 1), *E. chimaera* can be distinguished from *E. auripendulus*, *E. chiribaya*, and *E. maurus* (*auripendulus*-group) by its larger size in external, ear and forearm dimensions, squarish anti-tragus (pointed in *E. auripendulus* and *E. maurus* but squarish in *E. chiribaya*), basisphenoid roughly deep (shallow in *auripendulus*-group but deep in *E. chiribaya*), wide and short opistocranium (posteriorly extended in *E. auripendulus* and *E. maurus* – Fig. 4), and third commissure of M^3 relatively developed (very reduced, V-shaped in *auripendulus* – group excluding *E. chiribaya*— Fig. 5). *E. chimaera* differs from *E. glaucinus* and relatives (*E. wilsoni*, *E. floridanus*, *E. underwoodi*, and *E. ferox–glaucinus*-group) in presenting a longer third commissure on M^3, roughly deep basisphenoid pits and very close each other, darker pelage coloration (light brownish or grayish pelage in *E. glaucinus* and relatives but there is variation), and wider and rounded ears.

E. chimaera can be distinguished from large-bodied species such as *E. underwoodi* and *E. dabbenei*, by its dark brown pelage, shorter forearm and skull, and longer third commissure on M^3 instead V-shape. *E. perotis* and *E. trumbulli* can be distinguished from *E. chimaera*, their sister-group (Fig. 1), by the larger size of ears, forearm and skull (Table 5), usually light brown or grayish pelage (dark brown in *E. chimaera*), developed inner skinny fold in ears hiding part of antitragus (antitragus is completely apparent, not partially covered in *E. chimaera*), haired and brownish face (blackish and weakly haired in *E. chimaera*), long rostrum (shorter in *E. chimaera*), and very deep and wide basisphenoid pits (basisphenoid pits roughly deep in *E. chimaera*) (Fig. 4).

In summary, this study described a new species of *Eumops* and presented a phylogenetic analysis including increased taxonomic sampling to recover relationships within the already well-studied genus (e.g., Eger, 1977, 2008; Dolan and Honneycutt, 1978; McDonough et al., 2008; Gregorin, 2009; Bartlett et al., 2013; Medina et al., 2014). We also confirmed some clades presented by other studies such as *E. maurus* + *E. auripendulus*, *E. glaucinus* + *E. underwoodi*, and *E. bonariensis* + *E. nanus* + *E. patagonicus* + *E. delticus*; the phylogenetic position of *E. hansae* is an open question at all (Dolan and Honneycutt, 1978; Freeman, 1979). However, the inclusion of additional morphological and genetic datasets (e.g., additional nuclear and mitochondrial loci) and sequencing of more key taxa (e.g., *E. trumbulli*, *E. auripendulus major*, and *E. delticus*) certainly will improve our perception of the *Eumops* phylogeny. Penial and tongue morphology, for example, has already been studied and proved be phylogenetically informative (Ryan, 1991a,b; Gregorin, 2003; Reardon et al., 2014; Gregorin and Cirranello, 2015).

Issues regarding species delimitation in mammals have recently been debated (Bradley and Baker, 2001; Gippoliti et al., 2013; Groves, 2013; Zachos et al., 2013; Zachos and Lovari, 2013; Heller et al., 2014), and include criteria to define species (e.g., monophyly, congruence of characters in combined analysis, and diagnosability), but little consensus has been reached. We agree with several authors regarding how species can be defined (evolving lineages) and regarding the difficulties in applying criteria to delimit species (Heller et al., 2014).

Certainly part of those disagreements is methodological and in many cases not immediately resolvable, as low sampling and absence of material for all analyses (e.g., tissue available for some key specimens), prohibit integrative taxonomy (study of variation, for example) as is desired (e.g., Padial et al., 2010; Heller et al., 2014). On the other hand, hypotheses of new species should be proposed even based on evidence from few or even one specimen, since an appropriate combined analysis can be carried-out (e.g., Medina et al., 2014) avoiding beta error (or false-negative, underestimating species diversity in not recovering, for example, cryptic species—Padial et al., 2010; Heller et al., 2014).

Those difficulties in delimiting species can be observed in the taxonomy of all mammals including recent Neotropical bats. Indeed, we can observe recent bat species described in a phenetic context without a phylogeny recovering monophyly and the authors using a combination of plesiomorphic and apomorphic characters to define species (e.g., González-Ruiz et al., 2011; Moratelli et al., 2011), species described based on holotype only without any variation having been studied (e.g., Medina et al., 2014), and species described in an integrative approach (Velazco et al., 2010). For *Eumops chimaera* we considered both monophyly and uniqueness of morphological traits, and cyt *b* gene divergences (7.9% from its syster-group *E. perotis*) as criteria to recognize the form here described at the species level. In fact, at least three morphological characters (size and position of first upper premolar and morphology of rostrum) are shared by specimens from Bolivia and Brazil and they were not found among *Eumops* species supporting our decision to consider all three specimens as the same new species (Fig. 1). Unfortunately we could not obtain cyt *b* gene sequences from the Bolivian specimens of *E. chimaera* or from *E. trumbulli*, but morphologically *E. chimaera* is quite distinct from *E. trumbulli*. Thus, even considering 7.9% of cyt *b* divergence as not conclusive *per se*, all data analyzed in conjunction makes the hypothesis presented here robust by congruence (Farias et al., 2001). Although 7.9% of divergence falls into the gray zone for the limit of mammal species (Baker and Bradley, 2006), the cyt *b* divergence for bats varied from 4 to 14.7%; however, authors considered 5% of divergence as a reference for the specific limit; the mean for bats, mostly phyllostomids, in Bradley and Baker (2001) was 6.3%. For *Eumops* cyt *b* divergence levels for the species recognition can be ever smaller. Within *Eumops glaucinus*-group species diverged from 3.6 to 8.4% (McDonough et al., 2008); *E. wilsoni* diverges from related species, *E. ferox*, *E. floridanus*, and *E. glaucinus*, in 6.8, 7.4, and 8.1%, respectively (Baker et al., 2009).

The morphological similarity and uniqueness of the Bolivian and Brazilian specimens, even with low sampling assumed, did not lead us to infer variation in their morphological autapomorphies thus avoiding a description of the different taxa in relation to geographical distance (alpha error or over-estimation of species diversity—Padial et al., 2010; Heller et al., 2014), though variation in size was observed in *E. chimaera* (Fig. 2). Although the distance (about 1500 km) between sites in Bolivia and Brazil is relatively great some medium and large-bodied species of *Eumops* (e.g., *E. dabbenei*, *E. auripendulus*, *E. glaucinus*, and *E. perotis*) are widespread throughout the neotropics, from the United States and Mexico to southern South America (Eger, 1977, 2008). Thus distance between Bolivia and Brazil is not considered an impediment to include all three specimens in *E. chimaera*. Also, many geographical gaps in Neotropical molossid bats clearly are artefacts of sampling bias; species are presently known only by holotype (*E. chiribaya*) or are by a few specimens (e.g., *E. dabbenei*, *E. hansae*, and *E. maurus*). These bats usually fly very high into the open space making their capture very rare in natural habitats and thus, their capture requires specific methodologies such as those used to net bats at the canopy level (Kalko and Handley, 2001), shot-gun, dust shot (Thomas and West, 1989), or we can use ultrasonic detectors to distinguish between aerial insectivore cryptic species (e.g., Jones and van Parijs, 1993). On the other hand, *Eumops* is a successful molossid bat living in cities where roosts (roofs, trees) and food (insects) are abundant, and studies focused to collect in those locals are a valuable source of information about variation and structure of colonies in common species as well as in discovering new taxa.

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Appendix A.

Specimens examined

Tadarida brasiliensis (total: 5)—Brasil: Minas Gerais: Lavras: CMUFLA 2061-2065.

Nyctinomops laticaudatus (Total: 6)—Mato Grosso, Cuiabá: MUZUSP 8515, 8529, 8531, 8538; São Paulo, São Sebastião: 15397–398.

Eumops auripendulus (total: 52)—Brasil: São Paulo: Bilac: DZSJRP 10979; Brotas: DZSJRP 13508-511; Capivari: MZUSP: 9044; Cravinhos: MZUSP 9046; Emas: MZUSP 7669; Furnas do Yporanga: MCZ 24822; Ilha de São Sebastião: MZUSP 2099; Ilha do Cardoso: MZUSP 27535, 27722; Itapetininga: MCZ 27313; Juquiá: MZUSP 7061; Mendonça: DZSJRP 2854-56; Mirassol: DZSJRP 2332, 3020; Onda Verde: DZSJRP 16718; Neves Paulista: DZSJRP 3339; Ribeirão Pires: DZSJRP 15607; Ribeirão Preto: 15382; Santa Fé do Sul: DZSJRP 3303; São Paulo: MZUSP 5818, 5825, 5977–81, 7062, 15388, 15409, 15643, 15658, 20418; São José do Rio Preto: DZSJRP 2480, 3287, 4849, 13523, 13530, 14503, 16314, 16429, 16718; Taquaritinga: DZSJRP 4134; Urupês: DZSJRP 2907, 2913–15. Bolivia: Santa Cruz, Angel Sandoval: MNKM 4750; Ñuflo de Chavez: MNKM 4515.

Eumops bonariensis (total: 19)—Brazil: Rio Grande do Sul: Bella União: AMNH 235959; Harmonia: AMNH 235960; Quinta: AMNH 235405-18; Uruguayana: AMNH 235961–63.

Eumops chiribaya (total: 1)—Peru: Moquegua: El Algarrobal: MUSA 8493 (holotype).

Eumops chimaera (total: 3)—Brazil: Minas Gerais: Parque Estadual do Rio Doce: CMUFLA 1889 (holotype). Bolivia: Santa Cruz, Tierra Comunitaria de Origen Turubo Este: MNKM 4753, 4754 (Paratypes).

Eumops dabbenei (total: 4)—Paraguay: Presidente Hayes, Villa Hayes: UMMZ 133763–64. Venezuela: FMNH 108310; Carabobo, Rio Uacauy: USNM 374169.

Eumops delticus (total: 2)—Brazil: Amazonas, Humaitá: DZSJRP 12770; Itacoatiara: MZUSP 15221.

Eumops glaucinus (total: 76)—Rio de janeiro: Rio de Janeiro: MZUSP 8475. São Paulo: Barretos: DZSJRP 11663; Mirassol: DZSJRP 4534, 15615; Planalto: DZSJRP 16406; Rancharia: DZSJRP 11043-48; Regente Feijó: DZSJRP 10907-09; Ribeirão Preto: DZSJRP 10587; Rio Claro: DZSJRP 16488; São José do Rio Preto: DZSJRP 2404-05, 2574, 2714, 3070, 3110, 3284, 3709, 4517, 4531, 4558, 4567–68, 4570, 4759, 4777–78, 4780, 4791, 4829, 4848, 12530, 13568, 14476–77, 15672, 15674, 15681, 15691, 15997, 16313, 16424, 16433, 16529, 16531–32, 16536, 16554, 16575, 16584, 16594, 16608, 16610, 16676, 16722; São Paulo: MZUSP 15656–57. Bolivia: Santa Cruz: Entre Rios: MNKM 4751. Cordillera, Palmar de lãs Islas: MNKM 3484, 3470, 3468, 3476. Cordillera, Tucavaca: MNKM 3462. Andres Ibañez, Club de Tenis: MNKM 4749. Chiquitos, Charagua: MNKM 4019. Velazco, Parque Noel Kempff Mercado: MNKM 5201-02. Beni: Yacuma: CBF 6315, 6299, 275.

Eumops hansae (total: 14)—Brazil: Amazonas: Manaus: MZUSP 365, 17578; USNM 123827 (holotype of *E. amazonicus*). Santa Catarina: Colônia Hansa (presently, Corupá): USNM 20093 (holotype). São Paulo: São Paulo: MZUSP 15442. French Guiana: Paracou, Sinnamary: AMNH 267538. Guiana: Demerara: Arampa (3 km from Ituni): ROM 57304, 57330; Ituni: ROM 73014. Maruranau, Ishi Wau: ROM 3551; Rupununi, Machawira: ROM 35636. Panama: Darién: Tarcacuna: USNM 310278. Venezuela: Bolívar: 29 km El Dorado: USNM 387799. San Juan, 163 Km ESE Puerto. Ayacucho (Rio Manapiare): USNM 496750.

Eumops maurus (total: 2)—Ecuador: Napo, Pompeya Sur (ROM 106326). Guiana: Kanaku: BMNH 1.6.4.34 (holotype).

Eumops nanus (total: 13)—Colombia: Guajira, 32 km W. Maracaibo: USNM 441848–55. Panama: Boquerón, Chiriquí: USNM 104892, 331971–72. Venezuela, Falcón, Capatarida: USNM 441856, 495016.

Eumops patagonicus (total: 17)—Bolivia: Beni: San Joaquín: FMNH 116608-13. Yacuma, Reserva de La Paraba Barba Azul: MNKM 4770. Santa Cruz, Parque Noel Kempff Mercado: MNKM 5203. Paraguay: Fuerte Olimpo: AMNH 234710-18.

Eumops perotis (total: 56)—Brazil: Distrito Federal: Brasília: DZSJRP 10018. Maranhão: Barra do Corda: FMNH 23953–56. Minas Gerais: MZUSP 15660; Lagoa Santa: FMNH 20697-98, 20976, 20978, 20980, 20982, 20984, 20986; Lavras: CMUFLA 1048, 4039, 4080, 4091-92, 4100, 20046-48, 20052-54, 20201, 20203, 20205, 20207, 20209, 20221-23. São Paulo: Araraquara: DZSJRP 14912; Bonfim Paulista: DZSJRP 10585; Brotas (Fazenda São Francisco): DZSJRP 15711; Cedral: DZSJRP 16464-466; Montemor: MZUSP 15645; Ribeirão Preto: DZSJRP 14027, 16630, MZUSP 15644, 15661, 15664–66, 17571; Sales de Oliveira: DZSJRP 12595; São José do Rio Preto: DZSJRP 4828, 11673, 13588; São Pedro: DZSJRP 12585; Terra Roxa: DZSJRP 13548. Bolivia: Beni, Yacuma, Reserva de La Paraba Barba Azul: MNKM 4752.

Eumops trumbulli (total: 32)—Bolivia: Beni: Guayaramerin: AMNH 209899-902. Brazil: Amazonas: Humaitá: DZSJRP 13226, 15588; João Pessoa (presently, Eirunepé): FMNH 140796; Lago Tefé: AMNH 78861; Rio Amazonas: AMNH 78861. Pará: Cametá: MCZ 30607-08, MZUSP 5657; Ilha Taiuna: AMNH 97015; Mocajuba: AMNH 97016-18, 97020-22; Recreio, Rio Majary: AMNH 97341; Soure (Marajó Island): MCZ 49284-92; Villaringo do Monte: AMNH 96022, 97328. Rondônia: Guajará-Mirim: MZUSP 10673.

Eumops underwoodi (total: 7)—Honduras: La Paz: El Pedrero (6 km N Chinaela): AMNH 126862 (holotype), 129893–96. Mexico: Chiapas: 5 mi N Arriaga: TCWC 16372. Michoacán: Monte Tancitaro, Rancho Escondido, 3.2 km N Ape: UMMZ 89460.

Appendix B.

Morphological character matrix

Nyctinomops laticaudatus	00000000000000000000000000????
Tadarida brasiliensis	00000001000000000000011110000000
Eumops bonariensis	00111101011111010000001110101010
E. patagonicus	00111101011111010000001110101???
E. nanus	00111101011111010000001110101110
E. delticus	00111101011111010000001110101???
E. hansae	10111101011111010000000210101???
E. auripendulus	01112211111111013010001000201110
E. maurus	01112211111111013010001000202???
E. glaucinus	01010211011111012010011011111100
E. dabbenei	01012221011111012010211001101???
E. underwoodii	01012221011111012010211001101???
E. perotis	01110221011111012110100210001111
E. trumbulli	01110221011111011110100210001111
E. chiribaya	01110211011111011110021000????
E. chimaera sp. nov.	01110221111110111011011000????

Appendix C.

Optimization procedures of morphological characters

Optimization of characters is indicated by the arrows and synapomorphies for the main clades are based on the tree resulted from the combined analysis (cyt *b* + morphology) using unordered characters (Fig. 1). ^{H}—indicates convergence/parallelism and ^{R}—indicates a character state reversal.

Eumops: 3(0 → 1), 4(0 → 1), 5(0 → 1), 6(0 → 1), 10(0 → 1), 11(0 → 1), 12(0 → 1), 13(0 → 1), 14(0 → 1), 16(0 → 1), 27(0 → 1), 29(0 → 1), 31(0 → 1)

Eumops but inad covariance matrix for *E. hansae*: 1^{R}(1 → 0)

E. bonariensis-group: 24^{R}(0 → 1)

E. auripendulus-group + *E. glaucinus*-group + *E.perotis*-group: 2(0 → 1), 6(1 → 2), 7(0 → 1), 17(0 → 1),

E. auripendulus-group: 7^{H}(0 → 1)

E. perotis-group + *E. glaucinus*-group: 7 (0 → 2).

E. glaucinus-group: 3^{R}(1 → 0),

E. perotis-group: 21^{H} (0 → 1), 32 (0 → 1)

E. chimaera: 14^{R}(1 → 0), 15 (0 → 1), 20 (0 → 1), 24^{H} (0 → 1).

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