

The enigma of the Yepes' armadillo: *Dasyopus mazzai*, *D. novemcinctus* or *D. yepesi*?

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Abstract: The long-nosed armadillos of the *Dasyopus* genus are the richest and more widespread extant xenarthra. In 1933, the prominent Argentinean mammalogist José Yepes studied specimens collected by Salvador Mazza and named a new species: *D. mazzai*. Several authors interpreted that the holotype of the species was a juvenile of *D. novemcinctus*. In 1995, Vizcaíno support the synonymy with *D. novemcinctus* but accepted the existence of an endemic species of northwestern Argentina that dedicated to Yepes (*D. yepesi*). Morphological studies have questioned the synonymy of the species with *D. novemcinctus*. In this contribution we reviewed the identity of the type material by sequencing a DNA fragment of 212 bp, product of the 16S ribosomal unit of Dasypodidae. Both samples of the holotype (bone and muscle) and of a specimen from the north of Santa Fe province have a 100% similarity with the *D. yepesi* / *D. sabanicola* sequences available in the GenBank. These results indicate that the type specimen of *D. mazzai* is neither a *D. novemcinctus* nor another species of the *Dasyopus* genus previously named. *Dasyopus mazzai* is revalidated and the eastern boundary in the Chaco region is confirmed. Field work is required to confirm the conservation status and current distribution of this endemic mulita.

Key words: Argentina, Chaco region, long nosed armadillo, Salta, Santa Fe, Yungas region.

Resumen: El enigma de la mulita de Yepes: *Dasyopus mazzai*, *D. novemcinctus* o *D. yepesi*? Las mulitas del género *Dasyopus* representan el género más rico y ampliamente distribuido de los xenartros actuales. En 1933 el destacado mastozoólogo José Yepes estudió los especímenes colectados por Salvador Mazza y nominó una nueva especie: *D. mazzai*. Varios autores interpretaron que el holotipo era un ejemplar juvenil de *D. novemcinctus*. En 1995, Vizcaíno aceptó la sinonimia con *D. novemcinctus*, pero reconoció la existencia de una especie endémica del noroeste de Argentina que dedicó a Yepes (*D. yepesi*). Estudios morfológicos han cuestionado la sinonimia de esta especie con *D. novemcinctus*. En esta contribución se revisó la identidad del material tipo secuenciando un fragmento de ADN de 212 bp, que codifica parte de la unidad ribosomal 16S de Dasypodidae. Ambas muestras del holotipo (hueso y músculo) y de un espécimen del norte de la provincia de Santa Fe presentan 100% de similitud con secuencias de *D. yepesi*/*D. sabanicola* disponibles en el GenBank. Los resultados indican que el ejemplar tipo de *D. mazzai* no pertenece a *D. novemcinctus* ni a otra de las especies del género *Dasyopus* previamente nominadas. Se revalida *D. mazzai* y se confirma el límite oriental de su distribución en la región chaqueña. Se requieren trabajos de campo para confirmar el estado de conservación y el rango de distribución actual de la especie.

Palabras clave: Argentina, Chaco, mulita, Salta, Santa Fe, Yungas.

INTRODUCTION

The long-nosed armadillos or “mulitas” belong to the Dasypodidae family, the earliest diverging clade inside the Cingulata by the middle Eocene (Gibb *et al.*, 2016; Delsuc *et al.*, 2016).

With seven species (see below), *Dasyopus* is the extant xenarthra genera most diverse and more widespread (Wetzel *et al.*, 2007; Hautier *et al.*, 2017). The earliest record for the genus comes from the Late Pleistocene (Lujanian) of South America (Vizcaíno *et al.*, 1995; Castro, 2015), but

based on molecular evidence, Gibb *et al.* (2016) suggest that it must have radiated by the middle Miocene.

Morphologically, the genus is characterized by a long and slender rostrum, long ears, long tail and a smooth and a relatively bare carapace (except in *D. pilosus* which has a dense coat of hair that hides the carapace). Nowadays, *Dasypus* species occur from the southern United States to center of Argentina (Wetzel *et al.*, 2007; Abba *et al.*, 2012; Loughry & McDonough, 2013). Six species are clearly recognized (but see Feijó *et al.*, 2018): the seven-banded armadillo (*D. septemcinctus* Linnaeus, 1758), the nine-banded armadillo (*D. novemcinctus* Linnaeus, 1758), the southern long-nosed armadillo (*D. hybridus* Desmarest, 1804), the northern long-nosed armadillo (*D. sabanicola* Mondolfi, 1968), all belonging to the subgenus *Dasypus* (Wetzel & Mondolfi, 1979); the greater long-nosed armadillo (*D. kappleri* Krauss, 1862), assigned to its own subgenus *Hyperoambon* (Wetzel & Mondolfi, 1979); and the hairy long-nosed armadillo (*D. pilosus* Fitzinger, 1856), assigned to the subgenus *Cryptophractus*, which has been recently proposed to raise to genus level (Castro *et al.*, 2015). The identity of a seventh taxon has been the subject of discussion over more than seventy years.

In 1933, the prominent Argentinean mammalogist José Yepes (1897–1976) named and described *Dasypus mazzai* Yepes, 1933. The specimens that Yepes used for the original description of this armadillo were donated by the physician and epidemiologist Salvador Mazza (1886–1946), well-known for his studies in several endemic diseases of South American. During the Regional pathologies study mission, carried on in 1926 in the north of Argentina, Mazza, who had installed his laboratory in a railway car, focused on different potential vectors of trypanosomiasis (Chagas-Mazza disease). In doing so, he gathered a notable collection of mammals currently housed in the Mammalogy Section of the Museo Argentino de Ciencias Naturales “Bernardino Rivadavia” of Buenos Aires (MACN-Ma). Among them the armadillos are particularly conspicuous (see Abba & Vizcaíno, 2008).

Hamlett (1939) interpreted that part of the material referred to *D. mazzai* by Yepes actually belonged to a new species that had to be named and based on the scarce specimens available, added a few more distinctive features. According to Hamlett (1939), Yepes was aware of the issue and reexamined the material. This work was never published but, *D. mazzai* continued to be accept-

ed in general systematic compilations (Cabrera, 1957; Olrog, 1976, 1979)

In their exhaustive revision of the long nosed armadillos, Wetzel & Mondolfi (1979) tried to reconstruct the history of the collections numbers of the specimens assigned to *D. mazzai* by Yepes. They concluded that “*D. mazzai* is a composite, a junior synonym of *D. novemcinctus* and *D. hybridus* and that use of *D. mazzai* may also infringe upon *D. septemcinctus*” Wetzel & Mondolfi (1979: 55). It should be clarified here, that the specimen MACN-Ma 31.213 that Yepes (1933) quote in the page 229 is not the Holotype of *D. mazzai*, but the holotype of *Chlamyphorus truncatus patquiensis* described by Yepes (1939), so this was a simple mistake in Yepes (1933).

In 1995 Vizcaíno revised the holotype and paratype of *D. mazzai* and compared with new specimens collected by him using numerical techniques to analyze the variation observed (Vizcaíno, 1995). In each analysis performed the specimens studied appeared well differentiated from other species of the genus. As a consequence, Vizcaíno named a new species, *Dasypus yepesi*, dedicating the species to Dr. J. Yepes, to whom he considered corresponded the merit of having noticed the morphological separation of this taxon with respect to those previously recognized. The type specimen was housed in the Museo de La Plata (MLP).

Recently, based on the evidence available in the literature Feijó & Cordeiro-Estrela (2014) claimed that the holotype *D. mazzai* is not a juvenile of *D. novemcinctus* and, hence, that *D. mazzai* is a valid species, with *D. yepesi* as a junior synonym. Gibb *et al.* (2016) described a DNA sequence of a specimen of the type series *D. yepesi* as possessing very similar mitogenomes to *D. sabanicola*. A recent morphometric analysis of long-nosed armadillos by Hautier *et al.* (2017) did not include *D. mazzai*-*D. yepesi*. Finally, the most recent morphometric analyses of *Dasypus* genus by Feijó *et al.* (2018) support the validity of *D. mazzai*.

In the 90th anniversary of the incorporation of José Yepes to the Mammalogy Section of the Museo Nacional (today Museo Argentino de Ciencias Naturales “Bernardino Rivadavia”) (see Garcia, 2018), and like other colleagues (Galliari, 2018; Ojeda *et al.*, 2018; Gonzalez *et al.*, 2018), we aimed to honored to J. Yepes. The goal of our work is to test the identity of the holotype of *D. mazzai* (MACN-Ma 31.273) using molecular tools.

MATERIALS AND METHODS

Specimens

Dasypus mazzai: MACN-Ma 31.273 (Holotype, Fig. 1. A-B); Supp. Material 1) a cephalic shield, carapace and tail, body (without head) conserved in fluid, skull figured in Yepes (1933) lost. Locality: Argentina, Salta, Dto. Orán, Tabacal (Fig. 2), collected by Salvador Mazza on October 1931. Sample for DNA analyses includes a muscular tissue on fluid and a bone sample from caudal vertebrae dried on the tail. MACN-Ma 13222 (Paratype, Fig. 1. C-D; Supp. Material 2) a mounted skin, figured by Yepes (1933), the skull number JYV 32 actually lost (Figure 2B). Locality: According to Yepes (1933) Argentina, Salta, Dto. Orán, Tabacal (Fig. 2). Collected by Salvador Mazza. Vizcaíno (1995) considered it unknown, because that was the town where Mazza labeled the specimens collected by the inhabitants of the area, so that it cannot accurately determine where the specimen came from. Sample for DNA analyses includes dry tissue in the tail from the mounted skin.

Dasypus hybridus: MACN-Ma 30.17 and 30.18, carapace and skull. Locality: Argentina, Chaco, Pampa del Indio (Fig. 2). Collected by Jorge G. Dennler on January 1930. MACN-Ma 33.176, carapace and skull. Locality: Argentina, Santa Fe, Dto. General Obligado, Villa Guillermina (Fig. 2), Collected by Cecilio Romaña. MACN-Ma 36.980, carapace without locality data collected by Salvador Mazza (field number 45775). All samples for DNA analyses include dry muscular tissue attached on the inner carapace.

Dasypus novemcinctus: MACN-Ma 27796 (DanoFPLM), Female. Locality: Argentina, Formosa, Pirane, La Marcela. Collected by A. M. Abba on June 3, 2016. DanoCLI Adult female. Locality: Argentina, Corrientes, Laguna Iberá (GPS: 28.546945 S; 59.19597 O). Collected by A. M. Abba on December 1, 2008. DanoCMC. Locality: Argentina, Corrientes, Monte Caseros, Ruta 14. Collected by A. M. Abba on December 4, 2008. DanoFTM. Locality: Argentina, Formosa, Tres Mojonas, Est. Ñupira. Collected by A.M. Abba on December 30, 2012 (Fig. 2). With the exception of MACN-Ma 27796 specimen (muscular tissue), all samples for DNA analyses include ear biopsy of captured and released living animals.

DNA sequence

We choose a 16s rRNA of 212 bp length in which *D. novemcinctus*, *D. hybridus* and *D. yepesi* have three different haplotypes determined by

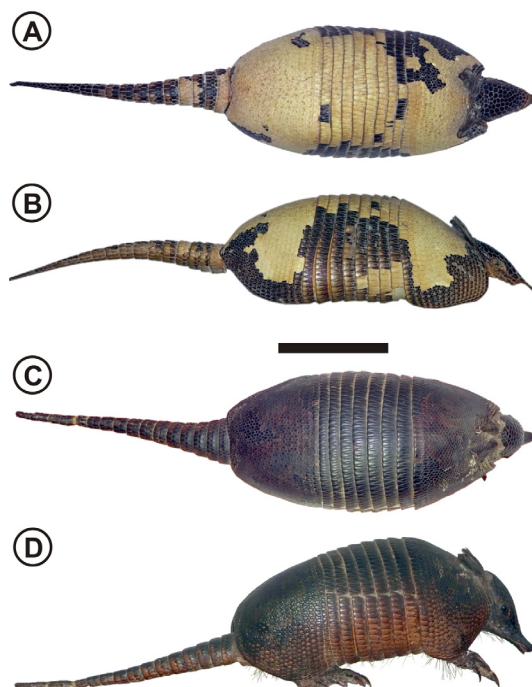


Fig. 1. Cephalic shield, carapace and tail of specimen MACN-Ma 31.273, Holotype of *D. mazzai* Yepes, 1933 in dorsal norm (A) and right lateral norm (B). Mounted skin of specimen MACN-Ma 13222 Paratype of *D. mazzai* in dorsal norm (C) and right lateral norm (D). Scale bar = 10 cm.

15 variable sites. The two sequences of *D. novemcinctus* available in the GenBank (KT818542.1 from French Guiana and Y11832 from USA) present a percentage of differentiation of 2% for the Dasypodidae 16S ribosomal RNA (16S rRNA). This differentiation is less than that presented by most of the sequences belonging to the different species studied. However, this high differentiation inside *D. novemcinctus* could be reflecting the differentiation of two geographical lineages, of perhaps two different species (see Gibb et al., 2016). In order to evaluate the variability in the selected fragment we included four specimens of *D. novemcinctus* from Argentina in the analysis (see above). In addition, the sequences of *D. hybridus* (GenBank KT818540) and *D. septemcinctus* (GenBank KT818546) show a similarity of 100% for the chosen fragment. Gibb et al. (2016) found that this two mitogenome sequences have a 99.3% identity and referred as probably misidentification. Indeed, the *D. septemcinctus* sequence belongs to an animal collected in north Argentina and up to date there as a wide amount of evidence that this species is absent from this

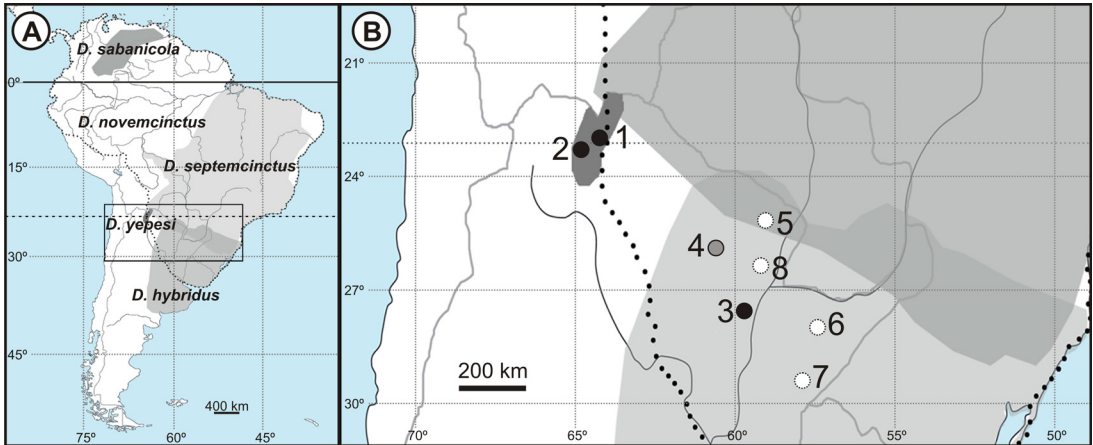


Fig. 2. (A) Map showing the distribution of the *Dasypus* species cited in this paper. In different grays shows the distribution of *D. sabanicola*, *D. septemcinctus*, *D. yepesi* and *D. hybridus*, and with line point shows the limit of *D. novemcinctus* distribution. (B) Detail of the area that comprise this study and localities of principal specimens. 1- Holotype and Paratype of *D. mazzai* (black dot, Argentina, Salta, Dto. Orán, Tabacal, MACN-Ma 31.273 and 13222 respectively), 2- Type locality *D. yepesi* (black dot, Argentina, Salta, Dto. Orán, San Andrés, MLP 30.III.90.8), 3- *D. mazzai* (black dot, Argentina, Santa Fe, Dto. General Obligado, Villa Guillermina, MACN-Ma 33.176), 4- *D. hybridus* (grey dot, Argentina, Chaco, Pampa del Indio, MACN-Ma 30.17 and 30.18), and four specimens of *D. novemcinctus* from Argentina (white dots), 5- MACN-Ma 27796 (Formosa, Pirane, La Marcela), 6- DanoCLI (Corrientes, Laguna Iberá), 7- DanoCMC (Corrientes, Monte Caseros, Ruta 14), 8 - DanoFTM (Formosa, Tres Mojonés, Est. Nupira).

country (Abba & Vizcaíno, 2008; Abba *et al.*, 2012). Based on morphologic and morphometric analysis, Feijó *et al.* (2018) proposed that *D. hybridus* and *D. septemcinctus* are synonyms but this assignation is uncertain until have been a support by a robust molecular analysis.

Mitochondrial DNA extraction and PCR amplification

The first steps of DNA extraction protocols differed depending on the sample source. Dried tissue samples were incubated overnight at 37° C in extraction buffer containing 10 µl of proteinase K, 10 mg/ml; 5 µl of RNase, 20 mg/ml and 10% SDS. For bone samples, approximately 50 mg of bone powder was incubated with stirring for 24 hours in 1 ml of EDTA 0.5 M, pH = 8. The mix was then centrifuged for 10 min at 14,000 rpm and the precipitate was stored for the posterior extraction and purification of DNA. The sample stored in formaldehyde was first washed in 70% ethanol for 30 min and then incubated with stirring for 24 hs in TE buffer at 37° C, replacing the buffer every 8 hours. After these first steps, DNA was isolated from all samples by phenol-chloroform extraction and alcohol precipitation.

Aliquots of total DNA were used as templates in Polymerase Chain Reaction (PCR) in order to amplify a 212 bp double-stranded DNA product

from the Dasypodidae 16S rRNA mitochondrial gene. Each PCR had a reaction volume of 20 µl and contained 1X Easy Taq buffer (20 mM Tris-HCl, pH = 8.3, 20 mM KCl, 10 mM NH₄SO₄, 2 mM MgSO₄), 0.4 mM of each deoxynucleotide triphosphate, 0.5 µM of forward and reverse primers, 0.5U of Easy Taq DNA polymerase (TransGen Biotech), 3.5 mM MgCl₂, 2 µg/µl BSA (New England Biolabs), 4 µl of DNA extract and water to reach the final volume reaction. The primer pair used was, arm16SF (5'-TAAG-TAGAGGTGAAAG ACCAAC -3') and arm16SR (5'-TGCTTTAGGCCAACTATGT-3'). It was developed using Primer3 online software using the complete sequences of the mitochondrial genome of *D. hybridus*, *D. novemcinctus* and *D. yepesi* as reference (GenBank: KT818540, KT818542, and KT818547, respectively). We chose this short DNA fragment due to the difficulty to amplify longer fragments from old bone and tissue sample and because it contains several variable sites that allow the distinction of the species to which the studied samples could belong (see above). Amplification protocol consisted in a single denaturation step at 94° C for 4 min, followed by 20 cycles of denaturation at 94° C for 30 s, annealing at 43° C (annealing temperature - 5° C) for 30 s, and extension at 72° C for 30 s; 20 cycles of denaturation at 94° C for 30 s, annealing at 48° C

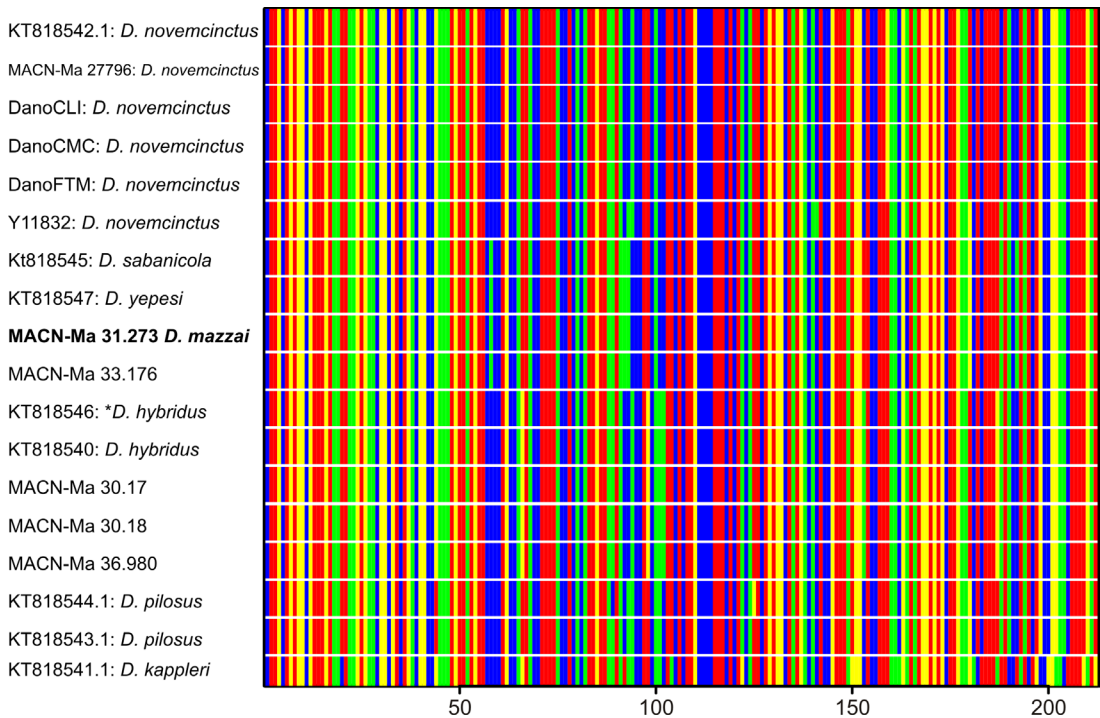


Fig. 3. Alignment of the 212 bp fragment of the 16S ribosomalRNA mitochondrial gene amplified from museum specimens and GenBank sequences. First base of museum specimen sequences corresponds to position 1421 in the *Dasypus yepesi* mtDNA complete genome (GenBank: KT818547). Color key: red A, yellow G, green C and blue T. Asterisk indicates the sequence here referred as *D. hybridus*. Holotype of *D. mazzai* in bold.

for 30 s, and extension at 72° C for 30 s and a final extension at 72° C for 5 min. PCR products were resolved in 1% agarose gel electrophoresis and visualized under UV light. A 10 µl aliquot of the amplification products were purified using the EXO/SAP enzymatic method and sent to an external laboratory (Biotechnology Institute of INTA Castelar, Argentina) where sequencing was performed with the same primers used in PCR reactions in an ABI 377 Automated DNA Prism™ Sequencer (Applied Biosystems Inc).

Data analyses

Sequences were checked and manually edited using Chromas v.2.6.5 free software (www.technelysium.com.au/chromas.htm), aligned in MEGA 7 (Kumar et al., 2016) and compared with those sequences previously published for the Dasypodidae family (Genbank: KT818540-47 and Y11832) using the nucleotide BLAST online tool (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) and registering their identity percentages.

RESULTS

Ten of the eleven samples analyzed could be amplified and sequenced successfully (Table 1; Fig. 3; Suppl. Material 3). The amplified 16S rRNA fragments obtained had a length of 212 bp and consisted in three haplotypes determined by 15 variable sites (Table 1). These haplotypes were compared with those 16S rRNA sequences previously published for the Dasypodidae family (Figure 3). The four *D. novemcinctus* samples analyzed showed a 100% similarity with *D. novemcinctus* GenBank sequence KT818542.1 (Table 1), a 98% similarity with *D. novemcinctus* GenBank sequence Y11832.1 and 93-97% similarity with 16S rRNA sequences from other Dasypodidae species. Samples MACN-Ma 31.273 (b= bone), MACN-Ma 31.273 (t= tissue) and MACN-Ma 33.176 showed a 100% similarity with *D. yepesi* and *D. sabanicola* sequences (Genbank: KT818547 and KT818545, respectively; Table 1) and a 95-97% similarity with 16S rRNA sequences from other Dasypodidae species, suggesting that these individuals belong to the species *D. yepesi/sabanicola*. Instead, samples MACN-Ma 30.17, 30.18 and

Table 1. Haplotypes and relative position of variable nucleotides in the 212 bp fragment of the 16S ribosomal RNA mitochondrial gene amplified from museum specimens. Haplotype A: GenBank KT818545 (*D. sabanicola*) and KT818547 (*D. yepesi*). Haplotype B: GenBank KT818540 and KT818546 (*D. hybridus*). Haplotype C: GenBank KT818542 (*D. novemcinctus*). * First base of museum specimen sequences corresponds to position 1421 in the KT818547 mtDNA complete genome.

Hap.	Collection number	Relative position of variable nucleotides*												
		58	66	92	93	94	98	101	102	153	164	180	187	192
A	31.273(b)													
	31.273(t)	C	A	C	C	T	A	T	T	A	T	G	A	C
	33.176													
B	30.17													
	30.18	T	G	T	T	C	G	C	C	C	C	A	G	T
	36.980													
C	27796													
	DanoCLI	T	A	T	T	C	A	T	T	T	G	C	A	A
	DanoCMC													
	DanoFTM													

MACN-Ma 36.980 showed a 100% similarity with *D. hybridus* sequences (Genbank: KT818540 and KT818546, respectively; Table 1) and a 95-97% similarity with 16S rRNA sequences from other Dasypodidae species, suggesting that these three individuals belong to *D. hybridus*. Finally, the sample MACN-Ma 13222 presented sequences of very low quality that prevented to identify the species to which they belong.

DISCUSSION

The four specimens of *D. novemcinctus* from Argentina show no variation in the amplified 16s rRNA fragments and share the same sequence with the Gibb *et al.* (2016) specimen from French Guiana (GenBank KT818542). In addition, this sequence has a 98% of similarity with the Arnason *et al.* (1997) from USA (GenBank Y11832). The divergence between the French Guiana and USA lineages was already established since Huchon *et al.* (1999) study. Further studies are needed to confirm that the specimens from French Guiana and Argentina belong to the same lineage. If this is the case, as the type locality for *D. novemcinctus* corresponds to “*America Meridionali*” (i.e., South America) and restricted to Pernambuco, Brazil, by Cabrera (1957: p. 225; see also Feijó *et al.*, 2018), the USA lineage might represent a previously unrecognized taxon.

Our results indicate that the holotype of *D. mazzai* (MACN-Ma 31.273) is not a specimen of *D. novemcinctus* (neither the South American nor USA lineages) as proposed by Hamlett (1939), Wetzel & Mondolfi (1979) and Vizcaíno (1995), nor any other of the *Dasypus* species previously nominated. Consequently, *D. mazzai*

must be considered a valid species as originally described by Yepes (1933). Furthermore, the sequences of the holotype of *D. mazzai* are identical to that of one the specimens of the hypodigm of *D. yepesi*, housed in the Museo de La Plata (MLP 30.III.90.2). Thus, nowadays the specimens of *D. mazzai* are housed in the collections of the MACN and MLP.

The recognition of *D. mazzai* as a valid species has further taxonomic consequences for the systematics of the genus that remain to be tested. Following Gibb *et al.* (2016) the complete mitogenomic sequence of the specimen of *D. yepesi* Vizcaíno, 1995 (MLP 30.III.90.2), show 98.7% identity with that of *D. sabanicola* Mondolfi, 1968 housed at National Museum of Natural History, Washington, USA (USNM 372834). Therefore if *D. sabanicola* and *D. yepesi* were considered the same species, *D. sabanicola* would be a junior synonym of *D. mazzai* Yepes, 1933. This opens an interesting distributional issue, because the same species would be represented by populations restricted to very distinct localities of South America, with a separation at least of 3000 km: the llanos of Venezuela and Colombia and in Northern Argentina. Further studies are needed to understand this possibly disjunct distribution.

Yepes (1933) stated that the type locality of *D. mazzai* in the Argentinean Yungas represents the western limit of its distribution, which extended eastwards to the North of Santiago del Estero and Santa Fe provinces, in the Chaco region. The identification of the sequence of the specimen MACN-Ma 33.176 (assigned to *D. hybridus* by Feijó & Cordeiro-Estrela 2014) from Villa Guillermina, Santa Fe (General Obligado

Department) as belonging to *D. mazzai* confirms the distributional range of *D. mazzai* in the Chaco region of Argentina (Fig. 2) proposed in the 1930's. As Yungas and the Chaco regions extended in the neighbor countries of Paraguay and Bolivia, the species could be present there too, which makes the distribution of *D. mazzai* needs to be updated.

Other *Dasypus* species reported in the distribution area of *D. mazzai* are *D. novemcinctus*, *D. hybridus* and probably *D. septemcinctus* (Wetzel & Mondolfi, 1979). Yepes (1933) used the MACN-Ma 30.17 and 30.18 specimens as *D. septemcinctus* in his cranial measurement comparison with those of the Holotype and Paratype of *D. mazzai* (both actually lost). Wetzel & Mondolfi (1979) assigned one of them to *D. septemcinctus* (MACN-Ma 30.18) and the other to *D. hybridus* (MACN-Ma 30.17) based on their canonical analyses of cranial measurements. Following Wetzel & Mondolfi (Page 54, 1979), the evidence of sympatry between both species in the Chaco region of Argentina was based in few specimens (including both before mentioned). In this work we follow the criteria of Gibb *et al.* (2016) and considered the sequence of *D. septemcinctus* ISEM T-3002 (Genbank: KT818546) from Argentina as misidentification, and considered it as belonging to *D. hybridus*. According the morphological characters and the DNA sequences of the specimens MACN-Ma 30.17, MACN-Ma 30.18 and MACN-Ma 36.980 we assign them to *D. hybridus*.

The DNA extraction using old samples (from 1930 decade) allowed us to evaluate the taxonomic assignation of *Dasypus* species from Yungas and Chaco of Argentina. These two forested regions are actually among the more degraded areas in the world (Malizia *et al.*, 2012, Kuemmerlet *et al.*, 2017). In addition, there are very poor data about conservation status, distribution, abundance and other biological parameters of the *Dasypus* armadillos inhabiting these regions. Their conservation status is quite preoccupant. *Dasypus hybridus* and *D. sabanicola* are catalogued as Near Threatened due to severe habitat loss and hunting throughout its range (Abba & Gonzales, 2014, Superina *et al.*, 2014) and "*D. yepesi*" is catalogued as Data Deficient (Abba & Vizcaíno, 2014). A reassessment of the conservation status of these species is highly needed, which encourages performing new field efforts to acquire new data of distribution and current population status of the *Dasypus* species in these regions.

As a closing remark, we regret that Yepes no

longer has an armadillo nominated after him. However, we understand that our impartial scientific results honor his work and his intention to pay homage to Dr. Salvador Mazza, by recognizing the correctness of his original identification of an endemic armadillo from northern Argentina.

CONCLUSIONS

The S16 rDNA sequences of the Holotype of *Dasypus mazzai* Yepes, 1933 MACN-Ma 31.273 are not compatible with the specimens of *Dasypus novemcinctus* from South America and USA and must be considered as corresponding to a different taxa.

The specimen MACN-Ma 33.176 from Villa Guillermina, Santa Fe province (General Obligado Department) belongs to *D. mazzai* and confirms the distributional range in the Chaco region of Argentina as was supposed by Yepes (1933).

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