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New records of *Oryzomys couesi* (Alston, 1877) (Cricetidae, Rodentia) in Colombia, with remarks on its taxonomy, morphology, and geographic distribution

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Abstract. *Oryzomys couesi* (Alston, 1877) has a restricted geographic distribution in South America. Until now, it was only known from Montería, Córdoba, in the Caribbean region of Colombia. Here, we add three geographic records; a recent individual was recorded in Urabá, Antioquia, and during the identification process, we found six specimens from two localities around Isla de Salamanca National Park, Magdalena, whose identity have remained unpublished so far. These specimens represent additional geographic records of *O. couesi* in Colombia and South America. A cytochrome b sequence from the Urabá specimen increases the taxonomic and biogeographic relevance of these records.

Key words. Biogeography, Caribbean, cytochrome b, Oryzomyini, systematics

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Introduction

Within the Neotropical rodents (order Rodentia), the family Cricetidae is the most diverse in terms of its taxonomic content, with at least 520 species distributed in almost 97 genera and four subfamilies: Arvicolinae, Neotominae, Tylomyinae, and Sigmodontinae (Pardiñas et al. 2021; Brito and Pardiñas 2025). The Sigmodontinae comprise the vast majority of the Cricetidae in South America, representing a large radiation (90 genera, over 500 species), with representatives in virtually all habitats, from sea level to the high Andes, and from the tropical forests of the Amazon to some of the most arid biomes of the Pacific coast between Peru and Chile (Hershkovitz 1962; D'Elía and Pardiñas 2015; Brito and Pardiñas 2025). These genera and species are distributed in 13 living tribes, although the phylogenetic relationships between these tribes are rather uncertain (Salazar-Bravo et al. 2016; Pardiñas et al. 2021, 2022; Salazar-Bravo et al. 2023; Brito and Pardiñas 2025).

The distribution patterns of the major groups of Sigmodontine are reasonably well known. The Oryzomyini, one of the most diverse tribes (31 living genera), extend from North America to Central and South America, with a distribution almost equivalent to that of the entire Sigmodontinae (Reig 1986; Weksler 2006, 2015), but its greatest diversity is reached in northern South America (D'Elía and Pardiñas 2015; Prado et al. 2015). Species of the genus *Oryzomys* Baird, 1857, called rice rats (Goldman 1918), are very close in morphology to other related genera and are difficult to distinguish by their external characters, so the most prominent characters for taxonomic assignment are mostly cranial and dental (Percequillo 2015). The current recognized diversity of the genus includes eight species with widely varied distribution ranges: *O. palustris* (Harlan, 1837) (southeastern United States), *O. texensis* Allen, 1894 (southeastern United States and northeastern Mexico), *O. couesi* (Alston, 1877) (North, Central and northern South America), *O. mexicanus* Allen, 1897 (Mexico and Central America), *O. fulgens* Thomas, 1893 (Mexico), *O. albiventer* Merriam, 1901 (Mexico), *O. dimidiatus* (Thomas, 1905) (Nicaragua), and *O. gorgasi* Hershkovitz, 1971 (Colombia and Venezuela), in addition to three extinct species (*O. antillarum* Thomas, 1898, *O. nelsoni* Merriam, 1898, and *O. peninsulae* Thomas, 1897) (Carleton and Arroyo-Cabrales 2009; Hanson et al. 2010; Percequillo 2015; Pardiñas et al. 2017; MDD 2025).

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The delimitation of *Oryzomys couesi* has undergone several taxonomic modifications throughout its history, being originally described as *Hesperomys couesi* by Alston (1877), and later included in *Oryzomys* by Thomas (1983). In his landmark revision of the genus, Goldman (1918) maintained it as a valid species, but Hall (1960) included it as a subspecies of the more widely distributed *O. palustris* (Harlan, 1837); however, from morphological and genetic revisions, Benson and Gehlbach (1979) and Schmidt and Engstrom (1994), respectively, its specific status was revalidated and has remained as such ever since. Subsequently, new systematic reviews have clarified some relationships, and with them, the taxonomy of the *O. couesi* complex, said to include 25 names associated as synonyms or subspecies (Musser and Carleton 2005). Carleton and Arroyo-Cabrales (2009) morphologically distinguished some populations of western Mexico, such as *O. couesi mexicanus* from the Pacific coast, valleys and mountain slopes, *O. albiventer* (extinct), and *O. nelsoni* (extinct). Then, Hanson et al. (2010) using molecular evidence validated the distinction of *O. couesi* and *O. mexicanus*, at the species level, and similarly with *O. palustris* and *O. texensis* (see Rose 2023, 2024). Recently, González-Ruiz et al. (2024) assessed the morphological distinction of *O. fulgens* with respect to *O. couesi* and *O. mexicanus,* recognizing it as another valid species. Hanson et al. (2010) also distinguish at least two other genetic lineages in Central America and northern South America, but without definitively associating them with any of the names available in the region (*gatunensis*, *azuerensis*, *dimidiatus*) due to the lack of comparative material for that decision. Thus, *O. couesi* currently includes 13 synonyms or subspecies (MDD 2025).

In South America, *Oryzomys couesi* was first reported from a specimen from a rice crop near Montería, department of Córdoba, in the Caribbean region of Colombia (Hershkovitz 1987; Figure 1). So far, reports for Colombia are restricted to six specimens from this same region, collected between 1983–1986, and assigned to *O. couesi gatunensis* by researchers from the Field Museum of Natural History (Zoology), in Chicago (Solari et al. 2013). A series of specimens associated with this species was obtained in the Isla de Salamanca National Park, department of Magdalena, between 1969–1978, but did not have precise taxonomic identification until 2007, and have not been reported as such in the literature. In this report we present a new geographic record for Colombia, in the department of Antioquia, verify the diagnostic characteristics of the available specimens, and discuss some taxonomic and ecological aspects of these records for the country.

Methods

One of the records reported here derives from a fieldwork conducted in rural areas of the Urabá region of Antioquia, between 2022 and 2023. Animals were captured in primary and secondary forest areas, in fields dedicated to agriculture, and in peri-domestic areas, averaging five nights per sampling site. All captured animals were immediately processed for collecting data and samples, which were deposited in the Colección Teriológica de la Universidad de Antioquia (CTUA), Medellín,

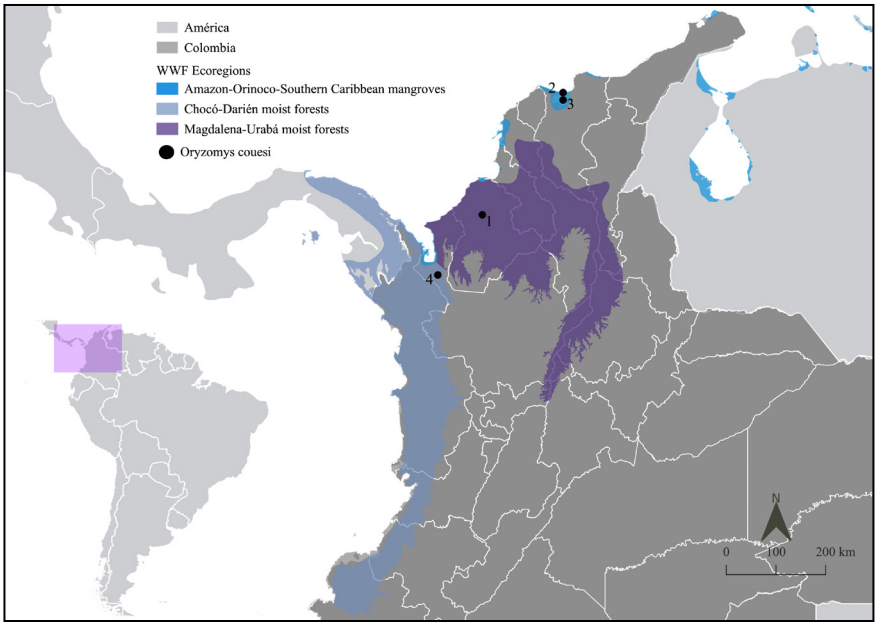

Figure 1. Records of *Oryzomys couesi* in northern Colombia, showing the ecoregions of Olson et al. (2001) associated with these records. Localities: 1 = Montería, Córdoba (Hershkovitz 1987); 2 = PNN Isla de Salamanca (this report); 3 = SFF Ciénaga Grande, Magdalena (this report); 4 = Chigorodó, Antioquia (this report).

Antioquia, Colombia. Subsequently, mammal specimens, their ectoparasites, and tissues were stored in 75% or 96% isopropyl alcohol.

Studying additional collections, we detected other six specimens from the lower Magdalena valley, primarily assigned to *O. couesi* and deposited at the Mammal Collection of the Instituto de Investigación Alexander von Humboldt (IAvH-M), in Villa de Leyva, Boyacá, which were examined by one of the authors (SCA).

The taxonomic identification of these specimens was performed using taxonomic keys and reviews (Goldman 1918; Hershkovitz 1987; Sánchez et al. 2001; Weksler 2006; Carleton and Arroyo-Cabrales 2009; Weksler and Percequillo 2011; Percequillo 2015) and comparative material in the aforementioned mammal collection. In addition, selected cranio-dental measurements were taken with electronic calipers (Mitutoyo, accuracy: 0.01 mm), as proposed by these references.

In the case of the Antioquia specimen, DNA was extracted from liver tissue stored in 96% isopropyl alcohol using the DNeasy® Tissue Qiagen® kit, and DNA purification was performed using the Gene-Jet Genomic DNA purification kit (Thermo Fisher Scientific). The mitochondrial cytochrome b gene (1143 bp) was amplified using the polymerase chain reaction (PCR) method and the primers Mus14095 for the forward and Mus15398 for the reverse (Percequillo et al. 2011). PCR amplifications were performed with reaction volumes of 20 µL (2 mM $MgCl_2$, 2 µM dNTP, 0,5 µM primers, buffer 1×, 0.05 units of Taq Polymerase (Thermo Scientific), ~30 ng DNA) and modifying the protocol proposed in this same publication: initial denaturation at 94 °C for 2 min, followed by 35 denaturalization cycles of 94 °C for 30 s each, annealing of 52 °C for 40 s, and a final extension of 72 °C for 1 min; finally, it closed with a final extension cycle of 7 min at 72 °C. Successful product of the reactions were enzymatically purified with Exonuclease I (20U/µL) (New England Biolabs) and Calf Intestine Alkaline Phosphatase (CIP, 10 U/µL) (New England Biolabs), following the manufacturer's instructions. PCR products were sequenced in both directions (forward/reverse) at Macrogen Inc. (South Korea), using the Sanger sequencing method. This new sequence was processed using Geneious v. 11.0.4 (Kearse et al. 2012) and then edited visually and manually. The nucleotide identity of the sequence was evaluated using the BLAST tool of NBCI (GenBank).

Results

(Rodentia: Cricetidae: Sigmodontinae: Oryzomyini)

***Oryzomys couesi* (Alston, 1877)**

Figures 2, 3

New records. COLOMBIA — **Antioquia** • Chigorodó, Finca La Pradera; 07.5519°N, 076.6072°W; 145 m a.s.l.; 14 Apr. 2023; Laura Aramendiz Macías leg.; field number LAM 024; in peri-domiciliary area of a rural house; Sherman trap set in ground, right behind house; 1 ♂, fluid-preserved specimen in 75% isopropyl with skull removed; CTUA 6407 — **Magdalena** • Parque Natural Nacional Isla de Salamanca, 0.5 km al W de Los Cocos; 10.9666°N, 074.4166°W; June 1969; J. Hernández-Camacho, C. León, and H. Chiriví lg.; 5 ♂, skins and skulls, IAvH-M-85, IAvH-M-86, IAvH-M-90, IAvH-M-91, and IAvH-M-92 • SFF [Santuario de Flora y Fauna] Ciénaga Grande, Caño El Cojo; 10.8333°N, 074.4166°W; 1978; L.M. Moreno leg.; 1 ♀, skin and skull, IAvH-M-3768.

Finca La Pradera is immersed in a heterogeneous matrix of vegetation cover and land use, which includes pastures for cattle ranching, secondary and riparian forests typical of the Very Humid Tropical Forest (bmh-T) life zone (Holdridge 1967). Although characterized as the predominant habitat of the species (Benson and Gehlbach 1979; Wolfe 1985; Hershkovitz 1987), no flooding areas were recorded near this site. However, the region includes several particularly humid areas and numerous creeks and streams. As the original labels for specimens from PNN Isla de Salamanca and SFF Ciénaga Grande have no precise data, coordinates were assigned using the Ornithological Gazetteer of Colombia (Paynter 1997), resulting in two close points around the PNN Isla de Salamanca (Table 1). These specimens were identified as *Oryzomys couesi* by M. Gómez-Laverde (as a handwritten note), in 2007, and subsequently re-examined by S. Cifuentes during our study. Despite the original method of preservation of the specimens, it was only possible to fully compare and describe the skull of one of them (IAvH-M-90; Figure 2) because the others were broken. However, we had access to these specimens and confirmed their identification based on selected key characteristics, mainly of the skull and dentition.

Identification. The CTUA 6407 is a comparatively small rodent; measurements taken in the field are total length, 220 mm; tail length, 117 mm; hindfoot length, 30 mm; ear length, 15 mm, and mass, 30

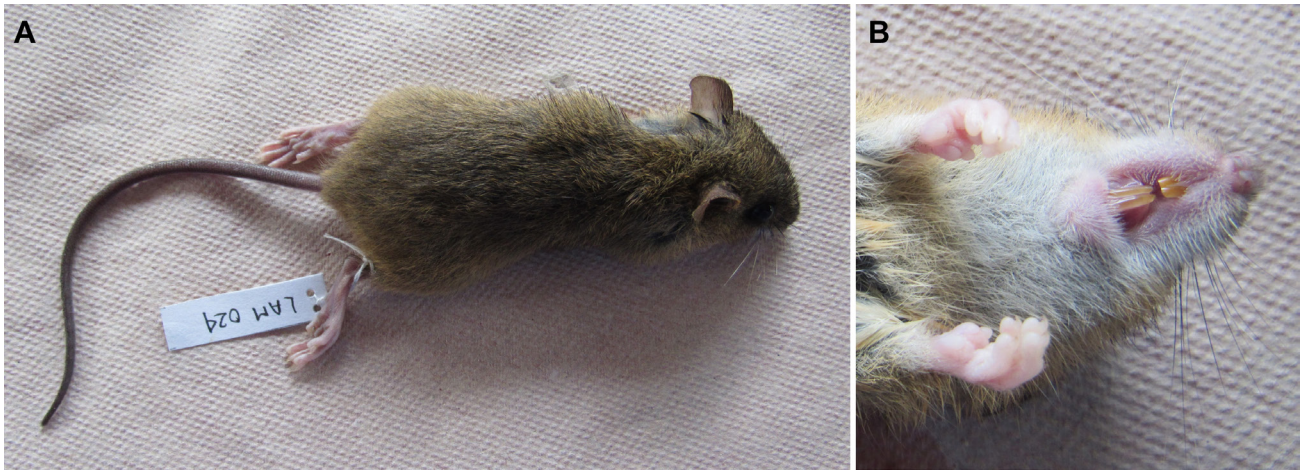

Figure 2. *Oryzomys couesi*, CTUA 6407, from Chigorodó, Antioquia, showing some of its diagnostic external traits. **A.** Dorsal fur. **B.** Oral region.

Figure 3. Dorsal, ventral, and lateral views of the skull, and lateral view of the mandible, of the specimens IAvH-M 90 (left) and CTUA 6407 (right), representing the new records of *Oryzomys couesi* for Colombia. Scale bar: 10 mm.

g. The dorsal fur is slightly coarse, showing a cinnamon-brown color, predominantly ochraceous, with blackish tips (Figure 2); the sides are slightly lighter, without the darkening look; ventrally, the fur is noticeably paler, with an overall dirty white or slightly grayish appearance; the whitish fur extends proximally from the upper lip through the entire mystacial area, and both sides of the nose (Figure 2). Short ears, not protruding much from the fur, and covered with short, orange hair; the eyes are

Table 1. Summarized records of *Oryzomys couesi* in Colombia. The record from Montería, Córdoba, correspond to the original report by Hershkovitz (1987). Specimens deposited at the Field Museum of Natural History (FMNH), Chicago; Colección de Mamíferos del Instituto Humboldt, (IAvH-M), Villa de Leyva; Colección Teriológica, Universidad de Antioquia (CTUA), Medellín.

Locality	Coordinates	Specimens
Córdoba: Montería	08.7576, −75.8769	FMNH 125408, 127250, 127251, 127252, 127253, 127254
Magdalena: PNN Isla de Salamanca, 0.5 km al W de Los Cocos	10.9666, −74.4166	IAvH-M-85, IAvH-M-86, IAvH-M-90, IAvH-M-91, IAvH-M-92
Magdalena: SFF Ciénaga Grande, Caño El Cojo	10.8333, −74.4166	IAvH-M-3768
Antioquia: Chigorodó, Finca La Pradera	7.55194, −76.6072	CTUA 6407

moderately large; the rostrum is short. The tail is longer than head-and-body length, and dorsally darker. Hindfoot relatively robust, dorsally covered by white hair; the sole is scaly, and with a pink appearance (not dark or black; Figure 2), interdigital pads on the hindfeet are small and separated, with hypothenar.

Cranially, the rostrum is short and broad; interorbital region has conspicuous and expanded supraorbital ridges; the parietal expands moderately to the lateral surface of skull (Figure 3); the interparietal is elongated but does not contact the parietals; posterior margin of the incisive foramina reaching M1's procingulum; a couple of well-developed posterolateral palatal pits, inside deep depressions of the palate (Figure 3); carotid circulation pattern showing the derived condition, with the sphenofrontal foramen being absent. These same traits were observed in the skull of the specimens FMNH 125408 and IAvH-M-90 (Figure 3). The cranio-dental measurements of the CTUA 6407 are: Greatest skull length: 27.58 mm, Condyle-incisive length; 25.29 mm; zygomatic width: 15.28 mm; breadth of braincase: 12.49 mm; nasal length: 10.90 mm; least interorbital breadth: 4.94 mm; M1–M3 length: 4.81 mm. These values are very similar to those reported by Hershkovitz (1987) for specimens from Montería, Colombia, but slightly smaller than those from Mexican populations (Carleton and Arroyo-Cabrales 2009).

The genetic analysis retrieved an 867-bp fragment of the cytochrome b gene (GenBank accession number PX240483), which BLAST identified as *Oryzomys couesi azuerensis*, with over 98.7% identity by comparison with two available sequences (NK 101623 and 101644). The latter came from specimens of Panama, Veraguas, Montijo, Cerro Hoya (Hanson et al. 2010).

Other species of sigmodontine rodents (tribe Oryzomyini) recorded during sampling at the Urabá region include *Casiomys alfaroi* (Allen, 1891), *Neacomys tenuipes* Thomas, 1900, *Oecomys trabeatus* Allen & Barbour, 1923, *Oligoryzomys delicatus* (Allen & Chapman, 1897), *Transandinomys talamancae* (Allen, 1891), and *Zygodontomys cherriei* (Allen, 1895). In addition, we recorded the Echimyids *Hoplomys gymnurus* (Thomas, 1897) and *Proechimys semispinosus* (Tomes, 1860), and the introduced murids *Mus musculus* Linnaeus, 1758, and *Rattus rattus* (Linnaeus, 1758) (the latter in peri-domiciliary areas). A single immature tick (*Amblyomma* sp., Ixodidae) was found on the *Oryzomys couesi* CTUA 6407 specimen; it could not be identified to species by morphology or 12S RNA sequencing. A real-time PCR assay detected a fragment of the rickettsial gltA gene, confirming the infection of the *Amblyomma* tick (L. López-Diez pers. comm.).

Discussion

The specimen from Chigorodó, Antioquia (CTUA 6407), adjusts closely to the diagnosis of *Oryzomys couesi* (external, cranial, and dental morphology; Hershkovitz 1971; Carleton and Arroyo-Cabrales 2009; Weksler and Percequillo 2011; Percequillo 2015), with some measurements at the lower end of size variation. Also, it is morphologically distinguished from other oryzomyine rodents in the Caribbean of Colombia (Hershkovitz 1971, 1987). The most closely related species in northern South America would be *O. gorgasi*, which is described as having an evident pencil of terminal hairs at the tip of the tail (Sánchez et al. 2001), which is absent in our specimen (Figure 2); also, the skull of *O. gorgasi* is said to be distinctive by its short, blunt rostrum flanked by broad, deep zygomatic notches, and an interorbital region strongly convergent anteriorly with well-developed supraorbital beads that project as small shelves over the posterior part of the orbits, and continuing posteriorly as low temporal crests along the braincase (Hershkovitz 1971; Sánchez et al. 2001). The rostrum in our specimens (Figure 3) cannot be described as short or blunt, and the supraorbital margins being marked (beaded) do not extend posteriorly along the braincase. Also, in *O. gorgasi*, the hamular process of the squamosal is described as broad, reducing the subsquamosal fenestra to an inconspicuous notch that is almost completely occluded (Sánchez et al. 2001); but, in our specimens, the hamular process, being robust, does not occlude the subsquamosal fenestra, being always evident (Figure 3).

The geographic extension represented by these new records (Table 1) indicates that the distribution of *O. couesi* is far from being fully understood. Commenting on the record from the lower Sinú River, Caribbean lowlands of northern Colombia, Hershkovitz (1987) suggested that the species could also occur in the Pacific lowlands of the Colombian Chocó, which would connect with the record from Chigorodó. The latter extends the distribution of the species by 150 km to the southwest (Figure 1). Given the association of *Oryzomys* species with bodies of water and flooded microhabitats (Wolfe 1985), it could suggest the potential colonization of nearby regions (Chocó, Bolivar, Norte de Santander) sharing ecological characteristics with the known localities for the species. However, to our knowledge, there is no suggestion for a record in the lower basin of the Magdalena River (Ciénaga Grande and Isla de Salamanca), thus representing a geographic and ecological expansion for the species, from the original record at Monteria, by >280 km northeast (Figure 1). The updated distribution (Figure 1) indicates a great potential for dispersal between different ecoregions (humid forest of the Chocó–Darién and the Magdalena–Urabá; Olson et al. 2001) that contrast with those present throughout its distribution in North and Central America (Benson and Gehlbach 1979; Méndez 1993; Reid 2009). Available data are insufficient to make a complete description of its occupation in Colombia or to delimit its ecological associations. Within the distinctive set of abiotic conditions of these ecoregions, precipitation (as a proxy for humidity) stands out, which could be a key variable for niche modeling to assess the potential distribution of this species in the country.

The cytochrome b sequence of the CTUA 6407 is the first available of *O. couesi* from South America, which allows us to comment on the results by Hanson et al. (2010). The geographic proximity and low divergence (1.2%) suggest that it probably represents the *Oryzomys* sp. 1 lineage of Hanson et al. (2010), being genetically distinct from both *couesi* and *mexicanus* (>10%). These authors did not assign a name to this lineage, but in GenBank it is listed as *O. c. azuerensis*. At the same time, its geographic distribution indicates potential identity with some taxa described for southern Central America: *O. gatunensis* Goldman, 1912 (Panama Canal zone) and *O. azuerensis* Bole, 1937 (Azuero Peninsula). However, their original descriptions provide little context to establish the taxonomic identity of the CTUA 6407 specimen; in fact, the most distinctive characteristic of *gatunensis* is its darker dorsal coloration, which made Goldman (1912, 1918) to associate it with *O. richmondi* from E Nicaragua, which is considered a synonym or subspecies of *O. couesi*. According to Bole (1937), Goldman suggested that he treat *azuerensis* as a subspecies of *O. couesi* whereas *gatunensis* would be just a geographic race. A key character seems to be the development of the supraorbital ridges, which are less conspicuous in *O. couesi* from the northern part of the range (Goldman 1918), and more evident in *gatunensus* and *azuerensis*, also evident in CTUA 6407 (Figure 3). Nevertheless, Handley (1966) treated both names as subspecies of *O. couesi*, suggesting that they were geographic (perhaps, morphological too) variants of that species. The chromosomal number (2N) of a female *O. couesi* (FMNH 127250) from Montería, is 56, which corresponds to what is known for *O. couesi*, *O. palustris*, and *O. texensis* (Hershkovitz 1987; Rose 2024). Hanson et al. (2010) found no detectable differences in karyotypes respective to geographic origin or taxonomic assignment for *O. couesi*, with some individuals from Mexico (eastern and western) and Honduras showing an FN of 56–58.

To establish the taxonomic identity of the genetic lineages identified by Hanson et al. (2021), *Oryzomys dimidiatus* (Thomas, 1905), endemic to Nicaragua and known from a few specimens (Genoways and Jones 1971), as well as *O. gorgasi* Hershkovitz, 1971, known from northwestern Colombia and northwestern Venezuela (Sánchez et al. 2001), should be included in these comparisons too. Whichever its definitive identity, the populations of *O. couesi* from southern Central America (Panama) to northern South America (Colombia) are genetically distinct from both *couesi* and *mexicanus* from their northern distributions (Hanson et al. 2010). Although this evidence suggests a potential relationship between the Colombian specimens and taxa such as the ones mentioned above, the lack of detailed descriptions or comprehensive taxonomic reviews for these groups makes it impossible, at present, to confidently determine whether the specimens correspond to any of these names (see Pardiñas et al. 2017). Without further taxonomic clarification, any precise assignment would remain uncertain, thus, validating our use of the name *O. couesi* for these records.

Finally, the record from Antioquia also highlights the importance of a correct diagnosis and identification of potential hosts, especially in groups with high diversity and complex taxonomy such as sigmodontine rodents. Taxonomic rigor is critical for studies considering the identification and surveillance of potential hosts for infectious agents with roles in public health, especially, for their role in natural cycles of vector-borne diseases (VBDs) such as rickettsiosis (Quintero et al. 2013; Serpa et al. 2021). Proper taxonomic assignment of these hosts is key to prevent, control, and understand the epidemiology of emerging and re-emerging zoonotic events, primarily in the dynamic scenario of

transformation of Neotropical landscapes that ultimately promotes changes in population patterns of small mammals, increasing the risk of spillover o pathogen jumping among species, as reported in other regions (Serpa et al. 2021). In addition, when genetic sequences are generated, available tools should facilitate accurate taxonomic and ecological characterization of hosts and pathogens, and a better understanding and management of these diseases' cycles.

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Additional information

Conflict of interest

The authors declare that no competing interests exist.

Ethical statement

No ethical statement is reported.

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Author contributions

Conceptualization: SS, LAM. Data curation: SS, LAM. Formal analysis: SS, SCA. Funding acquisition: SS. Investigation: SS, SCA, LAM. Methodology: SS, LAM, SCA. Resources: SS. Supervision: SS. Visualization: SCA, SS. Project administration: SS. Software: LAM, SCA. Validation: SCA, SS. Writing – original draft: SS. Writing – review and editing: SS, SCA, LAM.

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Data availability

All data that support the findings of this study are available in the main text.

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