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Resolving the taxonomic status of *Abrothrix andina* (Rodentia, Cricetidae): evidence from topotypic specimens

Mauro N. Tammone[1], Erika Cuellar Soto[2], Carola Cañón[3], Jonathan A. Guzmán[4], and Ulyses F.J. Pardiñas[5*].

[1]Instituto de Investigaciones en Biodiversidad y Medioambiente, CONICET-UN Comahue, Bariloche, Argentina. E-mail: mtammone@comahue-conicet.gob.ar (MNT).
[2]Department of Biology, College of Science, Sultan Qaboos University, Muscat, Oman. E-mail: e.soto@squ.edu.om (ECS).
[3]Cape Horn International Center for Global Change Studies and Biocultural Conservation (CHIC), Puerto Williams; Pontificia Universidad Católica de Chile, Facultad de Ciencias Biológicas, Departamento de Ecología; and Instituto Milenio Centro de Regulación del Genoma (CRG), Santiago, Chile. E-mail: carolacanonv@gmail.com (CC).
[4]Laboratorio de Historia Natural (LAHN), Universidad de Concepción, Campus Los Ángeles, Chile. E-mail: jguzman@udec.cl (JAG).
[5]Instituto de Diversidad y Evolución Austral (IDEAus-CONICET), Puerto Madryn, Argentina; and Instituto Nacional de Biodiversidad (INABIO), Quito, Ecuador.
[*]Corresponding author: ulyses@cenpat-conicet.gob.ar

Recent studies have demonstrated that the Andean sigmodontine rodent *Abrothrix andina* (Sigmodontinae, Abrotrichini) is neither widespread nor a senior synonym of several nominal taxa (i.e., *dolichonyx*, *cinnamomea*, *jucundus*, *gossei*, and *polius*) described from Argentina, Chile, and Peru since the 19th century. However, a comprehensive taxonomic and nomenclatural reassessment requires the examination of type material. Here, we address this by analyzing topotypic specimens collected from three Andean localities near Santiago de Chile (Chile), the type locality of *A. andina*. *Cytochrome b* sequences from these specimens cluster within *Abrothrix olivacea*. These results support treating *Abrothrix andina* (Philippi in Philippi & Landbeck, 1858) as a junior synonym of *Abrothrix olivacea* (Waterhouse, 1837). Additionally, the nominal form *Abrothrix gossei* (Thomas, 1920) warrants recognition as a distinct species of *Abrothrix*, sister to *A. olivacea*. Although this study appears to complete the taxonomic reassessment of *A. andina*, a remote possibility remains that its holotype, currently lost, represents a still-unsampled Andean highland population, now extinct or extremely rare due to climate change.

Keywords: *Abrothrix gossei; Abrothrix olivacea*; Argentina; Chile; *cytochrome b*; topotype.

Estudios recientes han demostrado que el roedor sigmodontino andino *Abrothrix andina* (Sigmodontinae, Abrotrichini) no es ni una especie de amplia distribución, ni un sinónimo principal de varios taxones nominales (i.e., *dolichonyx*, *cinnamomea*, *jucundus*, *gossei* y *polius*) descritos desde el siglo XIX en Argentina, Chile y Perú. Sin embargo, una reevaluación taxonómica y nomenclatural integral requiere el examen del material tipo. Aquí abordamos esta cuestión mediante el análisis de especímenes topotípicos recolectados en tres localidades andinas cercanas a Santiago de Chile (Chile), la localidad tipo de *A. andina*. Las secuencias del *citocromo b* de estos especímenes se agrupan dentro de *Abrothrix olivacea*. Estos resultados respaldan tratar a *Abrothrix andina* (Philippi in Philippi & Landbeck, 1858) como sinónimo junior de *Abrothrix olivacea* (Waterhouse, 1837). Además, la forma nominal *Abrothrix gossei* (Thomas, 1920) merece ser reconocida como una especie distinta de *Abrothrix*, hermana de *A. olivacea*. Aunque este estudio parece completar la reevaluación taxonómica de *A. andina*, persiste la posibilidad remota de que su holotipo, actualmente perdido, represente una población altoandina aún no muestreada, hoy extinta o extremadamente rara debido al cambio climático.

Palabras clave: *Abrothrix gossei; Abrothrix olivacea*; Argentina; Chile; *citocromo b*; topotipo.

Since the late 20th century, sigmodontine rodents have received renewed taxonomic attention, leading not only to the description of new taxa but also to the revision of well-established species. In many cases, such revisions have resulted in the resurrection of nominal forms previously regarded as synonyms, thereby expanding the recognized diversity of the group (e.g., Myers *et al.* 1990; Jayat *et al.* 2016; Rocha *et al.* 2018) and demonstrating that some supposedly widespread species are, in fact, composite taxa. Less frequently, recent taxonomic reassessments have shown that supposedly widespread species, long maintained under taxonomic stasis, are actually composites of erroneously synonymized nominal forms.

The Andean cricetid *Abrothrix andina* (Philippi in Philippi & Landbeck 1858) has recently emerged as a paradigmatic example of the latter case. Historically, this member of the subgenus *Angelomys* was considered a widespread species ranging from central-western Argentina and Chile to southern Peru (e.g., Patterson *et al.* 2015; Pardiñas 2017; Teta *et al.* 2017; Tammone *et al.* 2025a; 2025b). This taxon was notable not only for its broad latitudinal distribution, spanning approximately 10 degrees, but also for its historically inclusive concept, which subsumed five nominal forms described between the late 19th and early 20th centuries. These are, in chronological order: *Hesperomys dolichonyx* Philippi, 1896, *Hesperomys dolichonyx cinnamomea* Philippi, 1896, *Akodon jucundus* Thomas, 1913, *Akodon gossei* Thomas, 1920, and *Akodon andinus polius* Osgood, 1944 (Philippi 1896; Thomas 1913; 1920; Osgood 1943; 1944). Within this general taxonomic framework, *A. andina* has also been studied in other contexts, such as physiology, ecology, and natural history (e.g., Bozinovic 1993; Bozinovic *et al.* 1988; 1990; 1999; Rosenmann and Ruiz 1993; López-Cortés *et al.* 2007).

From a taxonomic perspective, Mann (1978) suggested that *A. andina* might be conspecific with *Abrothrix olivacea* (Waterhouse 1837). However, it was not until recently that two studies employing *cytochrome b* sequences provided key insights into the taxonomy of *A. andina* and *A. olivacea*. Tammone *et al.* (2025a) showed that topotypes of *A. gossei* from Mendoza (Argentina) form the sister group to *A. olivacea*, whereas individuals assigned to *A. polius* from southern Peru were nested within *A. olivacea*. Subsequently, Tammone *et al.* (2025b) confirmed that *A. jucundus* and *A. dolichonyx*, two other nominal taxa included under *A. andina*, also clustered within *A. olivacea*. However, a crucial piece of this taxonomic puzzle is to determine the status of the populations of *A. andina* inhabiting the Andes near Santiago de Chile, as this region corresponds to the type locality of the species (Philippi and Landbeck 1858; Philippi 1900).

Here, we focus on the status of these high-Andean populations of *A. andina* from localities near Santiago de Chile in order to assess Mann's (1978) hypothesis. Sequencing of topotypic specimens provides further evidence supporting the synonymy of *A. andina* with *A. olivacea*. The main taxonomic and nomenclatural implications of these findings are discussed.

Materials and methods

Sampled localities correspond to Andean ranges in central and northern Chile, in the Region Metropolitana and Tarapacá, respectively (Table 1; Figure 1 and Figure 2). Specimens were secured following the guidelines established by the American Society of Mammalogists (Sikes *et al.* 2016). Collections were authorized by the Servicio Agrícola y Ganadero de Chile (SAG) RESOLUCIÓN EXENTA Nº: 6230/2024 to JG. Primary taxonomic identification was based on geographic distribution and external morphology. Vouchers were deposited in the Laboratorio de Estudios de Mamíferos, Universidad Nacional de Concepción (LEM-UCLA, Los Ángeles, Chile). Currently, they are cataloged under the field number JG (= collector number of Jonathan Guzman), which will be updated to LEM once the numbering process is completed.

Genomic DNA was extracted using the DNeasy Blood and Tissue kit (Qiagen, Valencia, California), following the manufacturer's instructions. PCR amplification of the entire *cytochrome b* (*cyt b*) locus (1,140bp) was achieved using two pairs of primers: MVZ05-16, MVZ23-14. Mastermix, and thermocycling conditions were the same as detailed previously (Smith and Patton 1999; Tammone *et al.* 2016). Sequencing was performed at Macrogen Inc (Seoul, South Korea). The obtained sequences (GenBank accession numbers PX116190-PX116201) were used to perform a phylogenetic analysis in combination with 53 sequences retrieved from GenBank, representing all known populations of *Abrothrix* from central and northern Andean ranges from Chile and Argentina. The complete dataset includes our newly sampled topotypes of *A. andina*, plus samples from all nominal forms recognized within *A. olivacea* (Quiroga-Carmona *et al.* 2022; Tammone *et al.* 2025a), *A. gossei* (Tammone *et al.* 2025a), as well as other five species of *Abrothrix* (i.e., *hirta*, *illutea*, *lanosa*, *longipilis*, and *sanborni*; Supplementary Data SD1). Sequences of *Geoxus valdivianus* and *Paynomys macronyx* were used as outgroup.

Phylogenetic trees were generated by maximum likelihood algorithms (ML; RAxML v.8, Stamatakis 2014) and Bayesian inference (BI; MrBayes 3.2.7a; Ronquist *et al.* 2012), using the CIPRES Getaway portal (Miller *et al.* 2010). ML analysis was run 1,000 times using the rapid Bootstrap protocol, followed by identification of the tree with the best ML score. BI analysis was run for 2 million generations

Table 1. Basic data of the specimens of *Abrothrix andina* analyzed in this paper. References: **JG** = collector number of Jonathan Guzman. Numbers (#) correspond to those in Figure 1.

#	Field no.	Locality	Region	Lat	Long	Alt (m)
4	JG 001	Quebrada de Choja	Tarapacá	-21.085278°	-68.867222°	3400
15	JG 459	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
15	JG 465	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
15	JG 466	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
15	JG 467	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
15	JG 468	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
15	JG 471	El Colorado, Farellones	Metropolitana	-33.343293°	-70.294183°	2780
16	JG 473	Lomas del Viento, Farellones	Metropolitana	-33.358908°	-70.326116°	2436
16	JG 474	Lomas del Viento, Farellones	Metropolitana	-33.358908°	-70.326116°	2436
16	JG 475	Lomas del Viento, Farellones	Metropolitana	-33.358908°	-70.326116°	2436
16	JG 476	Lomas del Viento, Farellones	Metropolitana	-33.358908°	-70.326116°	2436
18	JG 479	2 km E El Volcán, Cajón del Maipo	Metropolitana	-33.828802°	-70.046349°	1850

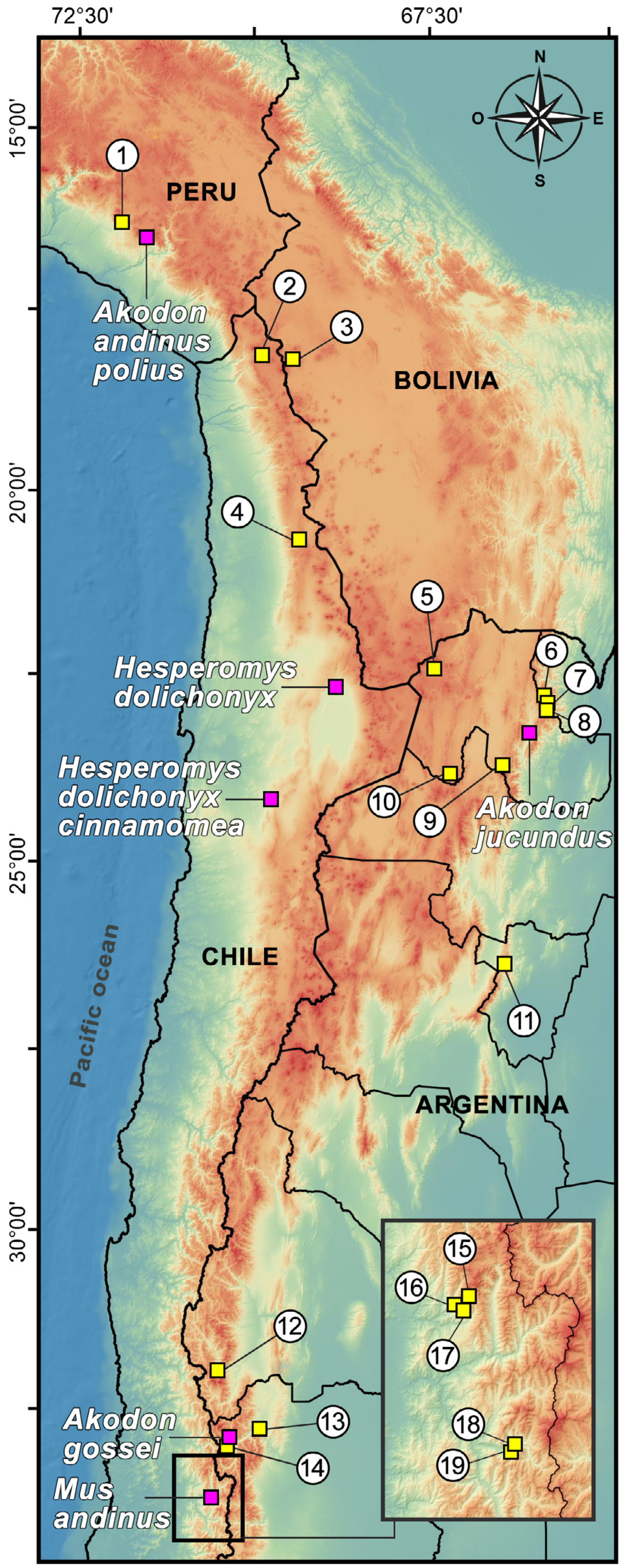


Figure 1. Map of the central Andes depicting type localities of the nominal forms (purple squares) traditionally associated to *Abrothrix andina* and the localities represented by sequences in the phylogenetic analyses (yellow squares). From north to south, type localities are: Salinas, Peru (*polius*); San Pedro de Atacama, Chile (*dolichonyx*); Campo Laguna, Argentina (*jucundus*); Leoncitos, Chile (*cinnamomea*); Puente del Inca, Argentina (*gossei*); and the Andes near Santiago, Chile (*andinus*). Localities represented by sequences are: (1) Arequipa; (2) Putre; (3) PN Sajama; (4) Quebrada de Choja; (5) Laguna de Vilama; (6) Abra de Zenta; (7) Abra Colorada; (8) Laguna Verde; (9) Nevado del Chañi; (10) Volcán Tuzgle; (11) Lagunas de Huaca Huasi; (12) Cerro Mercedario; (13) Uspallata; (14) Cristo Redentor; (15) El Colorado; (16) Lomas del Viento; (17) Valle Nevado; (18) Cajón del Maipo; and (19) Lo Valdés.

with sampling every 1,000 generations using one cold and three hot chains. Twenty-five percent of sampled trees were removed as a conservative measure of burn-in, which was assessed using Tracer 1.7 (Rambaut *et al.* 2018). This analysis was repeated four times using different numbers of initial seeds, after which the convergence of the resulting trees was assessed. We use the GTR+F+I+G4 substitution model as estimated by Corrected Akaike Information Criterion using ModelFinder (Kalyaanamoorthy *et al.* 2017). Strongly supported clades are considered those with posterior probabilities (PP) ≥ 0.95 for BI and bootstrap values (MLB) ≥ 75% for ML. Following identification of well-supported nodes, percent sequence divergence (p-distance; Nei and Kumar 2000) was calculated among and within clades using a pairwise deletion mode for missing data in MEGA 11 (Tamura *et al.* 2021).

Taxonomic inference in this study follows an integrative, lineage-based approach, in which species are interpreted as independently evolving evolutionary lineages identifiable through multiple lines of evidence (de Queiroz 2007; Fujita *et al.* 2012). Given the scope of the present work, focused on resolving the identity of a nominal taxon based on topotypic material, we do not implement algorithmic species delimitation methods. Instead, taxonomic decisions are based on the concordance of: (i) phylogenetic placement of topotypic or near-topotypic populations; (ii) relative levels of genetic divergence in comparison with recognized species and clades within *Abrothrix*, and (iii) consistency with available phenotypic and historical taxonomic evidence. Under this framework, the absence of genealogical exclusivity, combined with low genetic divergence and lack of consistent phenotypic differentiation, is interpreted as evidence against species-level distinction.

Results

Topotypes of *Abrothrix andina* from Andean localities near Santiago de Chile (Farellones and Cajón del Maipo; Table 1, Figure 1) are phylogenetically nested within *Abrothrix olivacea*, forming a well-supported clade (PP = 0.98; MLB = 89%; Figure 3). This clade also includes typical *A. olivacea* from Valparaíso and populations extending from La Serena to Parinacota in northern Chile (Figure 3: "central-north" *A. olivacea* clade). This "central-north" clade is sister to a group comprising *A. olivacea* from central to southern Patagonia in Argentina and Chile (PP = 0.98; MLB = 77%; Figure 3: "central-south" clade).

A third well-supported clade of *A. olivacea* (PP = 0.98; MLB = 77%) includes two distinct groups: one from Mendoza Province, Argentina (Las Leñas, Las Loicas, and La Valenciana; Figure 3: "Mendoza" clade), and another from Tierra del Fuego (Argentina and Chile; Figure 3: "south" clade). Two additional *A. olivacea* clades were identified in the Altiplano. One (PP = 1; MLB = 99%) comprises the new sequence from Tarapacá (Quebrada de Choja) together with samples from southern Peru, Bolivia, and Argentina (Figure 3: "dolichonyx-polius" clade). The other (PP = 1; MLB

Figure 2. Sampled localities of typical *Abrothrix andina* and external appearance of selected specimens. (A) Landscape view of Farellones, Chile; (B) Lo Valdés, Chile; (C–F) topotype of *A. andina* (JG 479), photographed fresh-dead: (C) dorsal view, (D) lateral view, (E) ventral view, and (F) detail of tail and hind foot. Photographs by Jonathan A. Guzmán Sandoval.

= 100%) consists exclusively of samples from Salta and Jujuy, Argentina (Figure 3: "jucundus" clade).

Percent sequence divergence within the clade including topotypes of *A. andina* (Farellones and Cajón del Maipo) and typical *A. olivacea* (Valparaíso) was 1.5% (Figure 4). Comparable values were observed within other *A. olivacea* clades and among other species of *Abrothrix* (e.g., *A. hirta* = 1.4%; Figure 4). Divergence between clades of *A. olivacea* ranged from 4.4% to 6.5%, whereas divergence among recognized species of *Abrothrix* varied from 10% to 13% (Figure 4). These patterns support the conspecificity of topotypic *A. andina* with *A. olivacea*.

Phenotypically, topotypes of *A. andina* from the high Andes near Santiago de Chile are indistinguishable from *A. olivacea* (e.g., Osgood 1943; Mann 1978; Pine *et al.* 1979; Rodríguez-Serrano *et al.* 2006, 2008; Figure 2). These rodents are small (total length = 167 mm; tail = 67 mm; hind foot with claw = 23 mm; ear = 16 mm; weight = 33 g; Supplementary Data SD2), with grayish-brown dorsal pelage tinged with olive, grayish ventral fur, moderate countershading, and an inconspicuous lateral line.

The eyes are small, surrounded posteriorly by a subtle ring of lighter, very short hairs, producing a soft contrast with the dark eye. The ears are rounded and moderately haired, lacking distinct pre-auricular whitish patches but occasionally showing subtle lighter hairs. The tail is sharply bicolored. The manus and pes are sparsely haired, with acute claws slightly longer than those of typical *A. olivacea* (cf. Osgood 1943). Overall, both molecular and morphological evidence indicate that the type-locality populations of *A. andina* are fully nested within *A. olivacea*.

Discussion

Abrothrix andina was originally described as *Mus andinus* from a single specimen (Philippi and Landbeck 1858). It was characterized as a small rodent with dark-gray dorsal

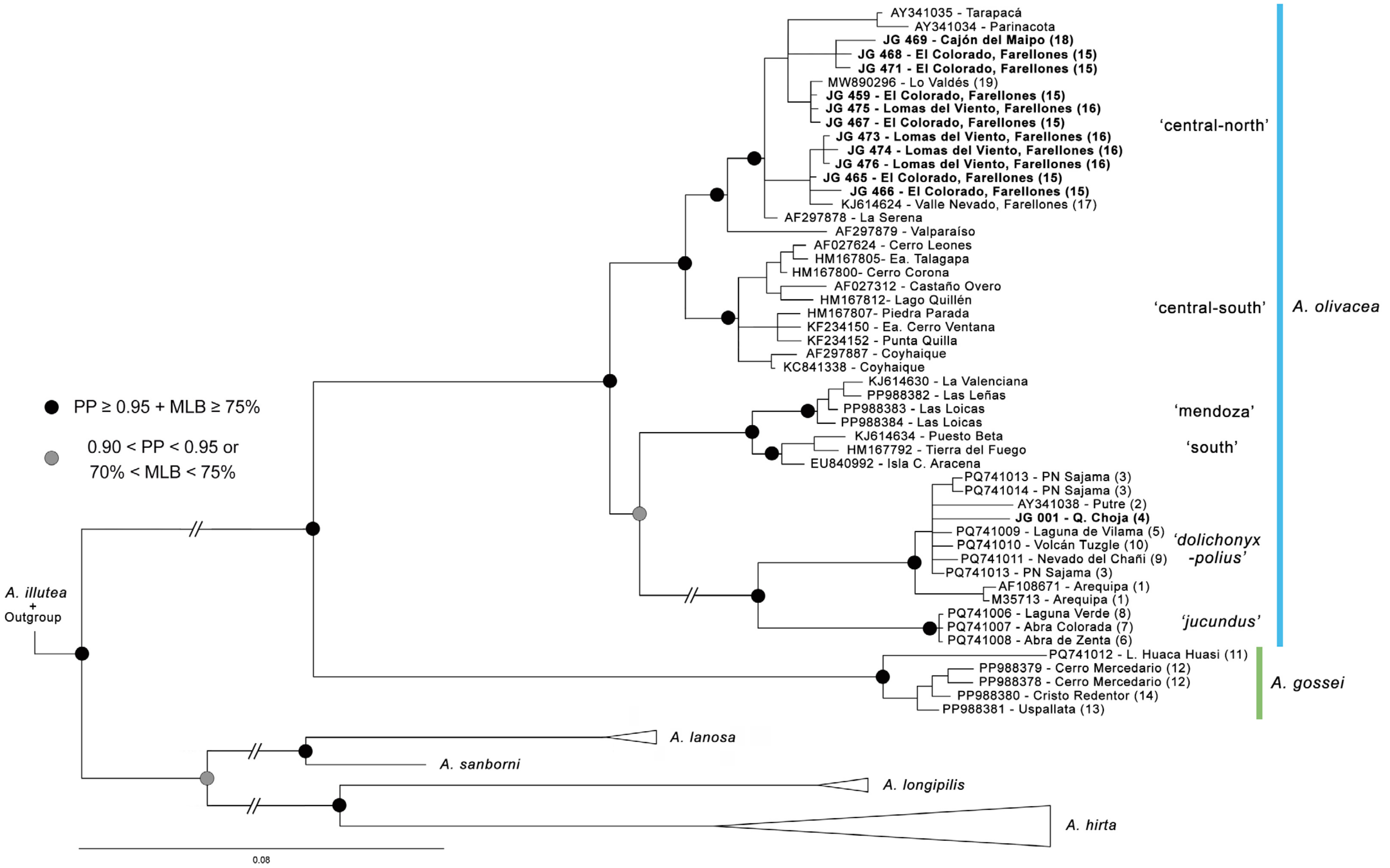


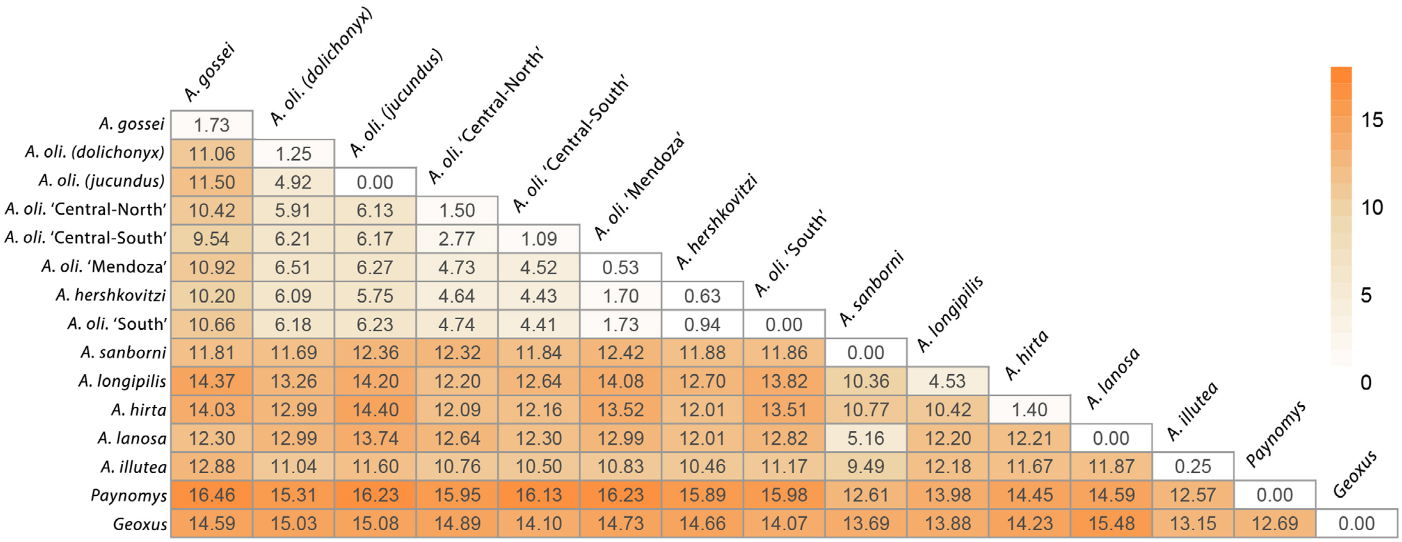
Figure 3. Phylogenetic reconstruction derived from new and available *cyt b* sequences of *Abrothrix*, represented by the final Bayesian 50% majority-rule consensus tree.

fur, similar to *Mus musculus*, and a bluish-white ventral surface. Ears were well-haired but short, barely reaching the distance between the eye and the ear; the tail was approximately half the head-body length, blackish above and white below, densely haired; and the feet were covered with white fur, with elongated, compressed claws on both manus and pes. Original measurements reported were: head and body length ~100 mm; tail length ~50 mm; ear length ~10 mm; hind foot with claws ~20 mm; and claws ~4 mm (Philippi and Landbeck 1858). The description emphasized the soft and lax nature of the fur, the much longer claws compared to *M. musculus*, and the overall resemblance to *Abrothrix longipilis* (cited as *Mus longipilis*) and *A. olivacea* (cited as *Mus rengeri* [sic]). This account was later translated into Spanish and supplemented with a color illustration of the living animal (Philippi 1900).

Thomas (1920), describing *Akodon gossei* from the Andes of Mendoza Province, emphasized differences from *M. andinus*, including larger size, gray (not rufous) dorsal coloration, elongated claws, and the absence of light ear patches. He concluded that *M. andinus* was "evidently quite a different animal" (Thomas 1920). However, Osgood (1943) was the first to examine the original material directly and synonymized *A. gossei* under *A. andina*, rejecting color and metric differences proposed by Thomas (1920). Osgood (1943) also redescribed *dolichonyx*, from northern Chile, and later *A. andinus polius* from Salinas, Arequipa, Peru (Osgood 1944). These studies laid the foundation for the concept of *Abrothrix andina* as a widespread, polytypic high-Andean sigmodontine, a view maintained by subsequent authors (e.g., Mann 1978; Patterson *et al.* 2015; Pardiñas 2017; Teta *et al.* 2017).

Despite its historical and nomenclatural significance, typical *A. andina* remained largely unexamined. The holotype has not been subject to modern taxonomic reassessment since its redescription by Osgood (1943). This omission is notable given that the type locality, "Andibus elevatis prov. Santiago" (Philippi and Landbeck 1858) falls within a region of intense research on *Abrothrix* and other sigmodontines. Consequently, *A. andina* has been overlooked or misinterpreted in several studies, including Pine *et al.* (1979), Reise and Venegas (1987), Gallardo *et al.* (1988), Barrantes *et al.* (1993), Smith and Patton (1999), and more recent systematic studies (Cañón *et al.* 2014; D'Elía *et al.* 2015).

The topotypes sampled in this study from Farellones and Cajón del Maipo (Andes near Santiago de Chile) correspond morphologically and metrically to both the original holotype description (Philippi and Landbeck 1858) and Osgood (1943) redescription. These specimens are small *Abrothrix* (total length ≈ 167 mm; tail ≈ 67 mm; hind foot with claw ≈ 23 mm; ear ≈ 16 mm). Dorsally, the pelage is gray to gray-olivaceous, ventrally washed whitish, and countershading is moderate. Ears are rounded, well-haired, and lack post-auricular whitish patches. The tail is sharply bicolored, and manus and pes are sparsely haired with



	A. gossei	*A. oli. (dolichonyx)*	*A. oli. (jucundus)*	*A. oli.* 'Central-North'	*A. oli.* 'Central-South'	*A. oli.* 'Mendoza'	*A. hershkovitzi*	*A. oli.* 'South'	*A. sanborni*	*A. longipilis*	*A. hirta*	*A. lanosa*	*A. illutea*	*Paynomys*	*Geoxus*
A. gossei	1.73														
A. oli. (dolichonyx)	11.06	1.25													
A. oli. (jucundus)	11.50	4.92	0.00												
A. oli. 'Central-North'	10.42	5.91	6.13	1.50											
A. oli. 'Central-South'	9.54	6.21	6.17	2.77	1.09										
A. oli. 'Mendoza'	10.92	6.51	6.27	4.73	4.52	0.53									
A. hershkovitzi	10.20	6.09	5.75	4.64	4.43	1.70	0.63								
A. oli. 'South'	10.66	6.18	6.23	4.74	4.41	1.73	0.94	0.00							
A. sanborni	11.81	11.69	12.36	12.32	11.84	12.42	11.88	11.86	0.00						
A. longipilis	14.37	13.26	14.20	12.20	12.64	14.08	12.70	13.82	10.36	4.53					
A. hirta	14.03	12.99	14.40	12.09	12.16	13.52	12.01	13.51	10.77	10.42	1.40				
A. lanosa	12.30	12.99	13.74	12.64	12.30	12.99	12.01	12.82	5.16	12.20	12.21	0.00			
A. illutea	12.88	11.04	11.60	10.76	10.50	10.83	10.46	11.17	9.49	12.18	11.67	11.87	0.25		
Paynomys	16.46	15.31	16.23	15.95	16.13	16.23	15.89	15.98	12.61	13.98	14.45	14.59	12.57	0.00	
Geoxus	14.59	15.03	15.08	14.89	14.10	14.73	14.66	14.07	13.69	13.88	14.23	15.48	13.15	12.69	0.00

Figure 4. Heatmap showing percent sequence divergence at the *cyt b* locus between clades of *Abrothrix* identified in the phylogenetic analysis, generated using the pheatmap R package.

slightly elongated claws. These traits clearly distinguish them from *A. gossei*, which has conspicuous white ear patches (Thomas 1920; Contreras and Rosi 1981; Tammone *et al.* 2025a; Figure 5).

The conducted phylogenetic analyses recover topotypes of *A. andina* within a well-supported clade that also includes typical *A. olivacea* from Valparaíso and populations extending from La Serena to Parinacota in northern Chile. Percent sequence divergence within the topotype-inclusive clade is 1.5%, similar to within-species divergence in other *Abrothrix* (e.g., Cañón *et al.* 2014; D'Elía *et al.* 2015; Quiroga-Carmona *et al.* 2022).

Taken together, molecular and morphological data indicate that the studied topotypes belong to the same taxon as the *M. andinus* holotype, supporting synonymy with *A. olivacea*. Recognizing *A. andina* as junior synonym of *A. olivacea* reveals the remarkable complexity of this species. *A. olivacea* spans ~40° latitude from southern Peru to Tierra del Fuego, making it one of the most geographically widespread sigmodontines (Patterson *et al.* 2015; Cañón *et al.* 2024; Cairampoma *et al.* 2024; Tammone *et al.* 2025a; 2025b). Historically, over 30 nominal taxa, have been subsumed under *A. olivacea* (Philippi and Landbeck 1858; Thomas 1913; 1920; Osgood 1944; Rodríguez-Serrano *et al.* 2006; Teta *et al.* 2017; Tammone *et al.* 2025a; 2025b). This extensive synonymy is unparalleled among widespread abrotrichines, such as *A. jelskii* or *A. hirta* (e.g., Patterson *et al.* 2015).

An alternative to considering *Abrothrix olivacea* as a polytypic species is to recognize it as a complex of cryptic or still poorly known species. Similar cases have been documented in sigmodontine rodents, where species once thought to be widespread and singular were later found to comprise multiple distinct units. In such instances,

Figure 5. External appearance of two *Abrothrix* from high Andean ranges. (A) individual attributed to *A. andina* photographed in wild at Embalse del Yeso, 50 km southeast of Santiago de Chile. (B) individual of *A. gossei* photographed in wild at Refugio Andino Cerro Mercedario, San Juan, Argentina. Photographs by T. Aronson and M. Tammone.

molecular markers have played a central role in shaping new taxonomic hypotheses. For example, following Hershkovitz's (1962) influential revision of *Calomys*, several large-bodied populations previously assigned to different nominal forms within this phyllotine genus were grouped under a single species, *Calomys callosus*. Today, *C. callosus* is understood as a species complex comprising at least seven distinct taxa (e.g., González-Ittig *et al.* 2022). The history of sigmodontine taxonomy reflects shifts between expansive and restrictive classifications. Over the past two centuries, taxonomic schools have alternatively expanded species concepts—subsuming nominal forms as synonyms—or refined them, reinstating previously synonymized taxa as valid species. This pattern is exemplified by taxa such as *Akodon boliviensis* and *Oligoryzomys flavescens* (see Myers *et al.* 1990; González-Ittig *et al.* 2010). Recent studies, including the present contribution, suggest that *A. olivacea* exhibits a geographically structured genealogy composed of monophyletic clades, with inter-clade genetic divergences ranging from 1% to 7% (e.g., Lessa *et al.* 2010; Giorello *et al.* 2021; Quiroga-Carmona *et al.* 2022; 2023; Tammone *et al.* 2025b: Figure 4). Additionally, phenotypic differences among populations are evident, as past researchers have distinguished *A. andina* from *A. olivacea* in northern Chile (e.g., Palma *et al.* 2005), or *A. xanthorhina* from *A. olivacea* in Argentine Patagonia (e.g., Lozada *et al.* 1996; Smith *et al.* 2001). However, despite being a moderately well-studied sigmodontine, *A. olivacea* inhabits an extensive and environmentally heterogeneous range, leaving substantial gaps in its known distribution. Some monophyletic groups identified in the current *cyt b* phylogeny may simply reflect inadequate sampling rather than true evolutionary lineages. For instance, north of Santiago, a ~1,000 km region remains unsampled (Figure 1). At the other end of the species' range, haplotypes from the southernmost Chilean populations have only recently been reported (Cañón *et al.* 2024) and await integrative analysis. In summary, whether *A. olivacea* will ultimately be divided into multiple species remains uncertain. If taxonomic partitioning occurs, numerous available names could be used to designate new binomial or trinomial combinations (e.g., Smith *et al.* 2001; Rodríguez-Serrano *et al.* 2006).

Politically, recognizing *A. andina* as a junior synonym of *A. olivacea* reduces by one the number of species recorded in Chile, lowering the count from eight to seven (D'Elía *et al.* 2020). Despite this reduction, *Abrothrix* remains the most diverse sigmodontine genus in Chile, nearly doubling the species richness of its closest competitor, the phyllotine *Eligmodontia* (D'Elía *et al.* 2020). However, this issue is not settled, as an additional *Abrothrix* species, *A. gossei*, is likely present in west-central Chile. Its known distribution extends to Las Cuevas and Cristo Redentor, being both localities in Mendoza Province, very near the Chilean border (Da Rosa *et al.* 2020; Tammone *et al.* 2025a). The continuous Andean habitat along the Mendoza River strongly suggests its occurrence in Chile. Notably, Thomas (1920) reported *A. gossei* in "Chili," based on a specimen labeled as *Mus andinus*, received from R. Philippi.

Abrothrix gossei, previously considered a synonym of *A. andina*, is now confirmed as a valid species and the sister taxon to *A. olivacea*. Its distribution extends from northern Mendoza to Tucumán, with specimens characterized by small size (total length ~140 mm; weight ~18 g), dense pelage, small rounded ears with prominent post-auricular white patches, large claws, and short bicolored tails (Thomas 1920; Osgood 1943; Contreras and Rosi 1981; Ferro and Barquez 2008; Tammone *et al.* 2025a; 2025b). According to Thomas (1920), the species is also entering in Chile. The karyotype of *A. gossei* has been described from Mendoza and San Juan populations (Da Rosa *et al.* 2020).

A remote possibility remains that the holotype of *M. andinus* represents a taxon distinct from here studied topotypes. Collected in 1857 during the Little Ice Age (Villalba 1994), environmental conditions may have supported populations now extirpated. Glacial retreat in the Andes has accelerated over the past century (Masiokas *et al.* 2008; Lopez *et al.* 2010), and altitudinal shifts in small mammal assemblages have been documented (Mann 1944; Mella 2006), including also regional extinctions (Cuellar Soto *et al.* 2026). Whether *A. andina* sensu stricto (i.e., restricted to its holotype) persists or has been replaced by *A. olivacea* remains unknown. The loss of the holotype (J. Canto, pers. comm.) prevents direct testing, but museomic approaches could clarify this historical uncertainty.

Conclusions

Based on the evidence presented herein, we consider *Mus andinus*, currently referred to as *Abrothrix andina*, to be a junior synonym of *Abrothrix olivacea*.

This conclusion is supported by: (1) Topotypic specimens of *A. andina* are nested within *A. olivacea* and do not form a distinct lineage; (2) Low divergence (~1.5%) between topotypic *A. andina* and *A. olivacea* falls within intraspecific variation and is far below interspecific levels; (3) No consistent phenotypic differences distinguish topotypic *A. andina* from *A. olivacea*; and (4) Sampled populations correspond to the type region and agree with historical descriptions.

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Declaration of Artificial Intelligence use

Artificial intelligence was used exclusively to assist with language editing and stylistic refinement of the manuscript. Specifically, the authors used ChatGPT (OpenAI; model version GPT-5.2) to improve clarity, grammar, coherence, and consistency of academic English. ChatGPT is accessible via: https://openai.com/chatgpt. AI tools were not used for data generation, data analysis, figure preparation, image manipulation, statistical analyses, or interpretation of results. All scientific content, analyses, conclusions, and final editorial decisions are entirely the responsibility of the authors.

Author contributions

The authors accepted responsibility for the entire content of this manuscript and approved its submission. Mauro N. Tammone: laboratory analysis, investigation, writing–original draft. Erika Cuellar Soto: investigation. Carola Cañón: laboratory analysis. Jonathan Alexi Guzman Sandoval: data collection. Ulyses F.J. Pardiñas: conceptualization, investigation, supervision, writing–original draft. All the authors: Writing–review and editing.

Supplementary data

SD1. List of sequences downloaded from GenBank that were used to construct the phylogeny.

SD2. External measurements of the specimens sequenced as part of this study. Collector: Jonathan A. Guzman Sandoval.

Data availability

The studied material is available in public collections. Genetic data can be accessed in the public database GenBank (accession numbers PX116190-PX116201). Additional raw data can be found in the supplementary material files or obtained upon request from the corresponding author.

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