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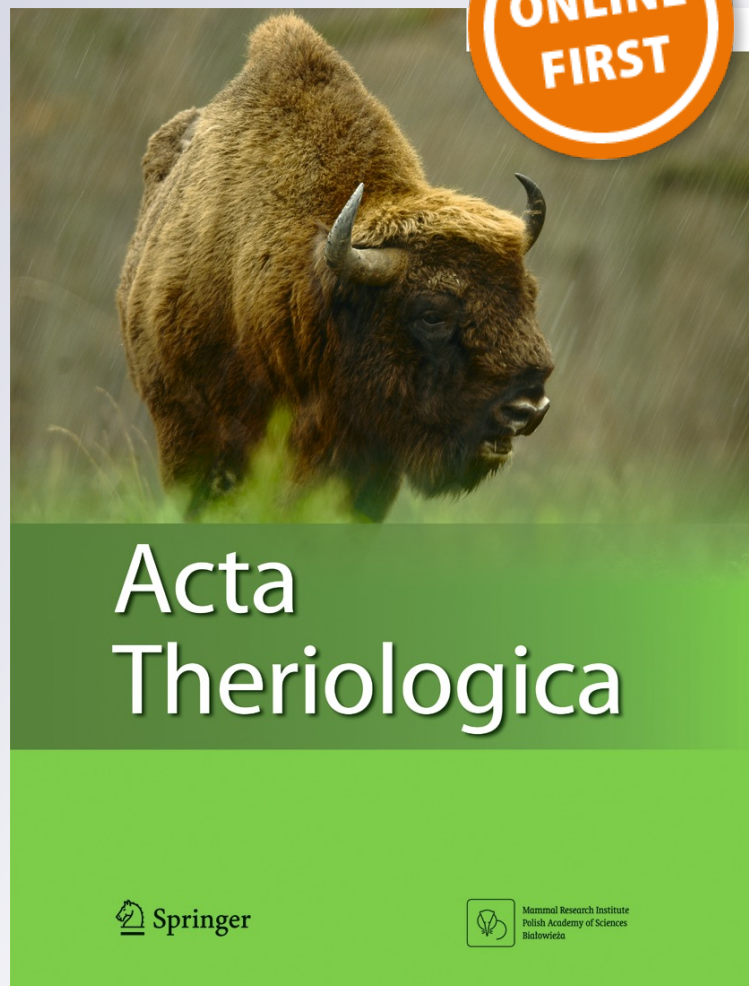
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A cytogenetic, molecular genetic and morphological study of Patagonian chinchilla mice *Euneomys* (Rodentia, Cricetidae) in the Southern Central Andes

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Abstract *Euneomys* is a genus of sigmodontine rodent endemic to South America, distributed along the Andes of Argentina and Chile and in adjoining Patagonian steppe. Here, we studied specimens of *Euneomys* from different localities in the Central Andes, Mendoza Province, Argentina. Karyotypic analyses confirm the presence of a new karyomorph of *Euneomys chinchilloides*, the form $2n=34$, $FN=62-64$. This new karyomorph differs from the form *E. chinchilloides* with $2n=36$, $FN=64-66$. The chromosome complement with $2n=36$ has an extra pair of small acro-telocentric chromosomes that is not present in individuals with $2n=34$. We also found small differences in molecular analyses with the mitochondrial COI gene. We recovered two monophyletic clades, one with

specimens with $2n=34$ and the other one with specimens with $2n=36$, which are separated by a range of 0.7 to 1.2 % sequence divergence. Individuals from the two clades also show some morphological differences. Significant difference in the length of ear was found between the specimens with $2n=34$ and 36 , and qualitative differences in the shape of the incisive foramen, the palate, and the palatine fossa were observed. The modification on fundamental and diploid number that we found between the two karyomorphs of *E. chinchilloides* can be the result of tandem chromosome fusion; such rearrangements are strongly negatively heterotic and lead to reproductive isolation between differentiated populations. Thus, the integrated cytogenetic, molecular, and morphologic analyses show concordant differentiation between the two karyomorph types of the uncommon *E. chinchilloides* from the Southern Central Andes of Argentina. The evidence presented here might reflect a recent and/or incipient allopatric speciation event. Further investigations are needed to elucidate the taxonomic and distributional status of species of *Euneomys*.

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Introduction

Cricetids of the subfamily Sigmodontinae (Reig 1981) are the most speciose group of rodents in the New World, with 74 genera and 380 species arranged into nine tribes (Musser and Carleton 2005; D'Elia et al. 2007); however, the taxonomic affinities of several genera are under debate. This is true for the genus *Euneomys* Coues (1874), placed in the tribe Reithrodontini by Musser and Carleton (2005), but treated

as Sigmodontinae *incertae sedis* by others (Smith and Patton 1999; D'Elía 2003; D'Elía et al. 2007; Salazar-Bravo et al. 2013). *Euneomys* is endemic to South America and is distributed along the Andes of Argentina and Chile and in adjoining Patagonian steppe areas, at elevations ranging from 1800–3000 m above sea level. Although authors have reviewed the taxonomy and systematics of the genus, “relatively few specimens exist to substantiate the specific taxonomy and distribution of the genus” (Musser and Carleton 2005:1114). Six additional named forms have been described [*fossor* Thomas (1899); *petersoni* Allen (1903); *mordax* Thomas (1912); *ultimus* Thomas (1916); *dabbeni* Thomas (1919); *noei* Mann (1944)], and their nomenclatural status has varied over time. Of the four currently recognized species (*Euneomys chinchilloides*, *Euneomys fossor*, *Euneomys mordax*, *Euneomys petersoni*; Musser and Carleton 2005), *E. mordax* and *Euneomys noei* (this last included as synonym of *E. mordax*) were described from the Central Andes of Argentina and Chile.

Thomas (1901) first validated the generic status of *Euneomys* and later described *E. mordax* (1912) from “Fort San Rafael, Province of Mendoza” based on a specimen collected by T. Bridges. The location of the type locality was clarified by Pearson and Lagiglia (1992), who made a historical reconstruction of the trips by T. Bridges between Fort San Rafael and Talca, Chile, and restricted the type locality to the region near the Volcán Peteroa, Malargüe Department, Mendoza Province, Argentina. Mann (1944) described *E. noei*, from “Valle de la Junta, Cajón del Río Volcán, a 2.400 m. de altura” in Chile, based on body size and cranial differences from *E. chinchilloides* and five other named forms.

Hershkovitz (1962) reviewed the genus and questioned the validity of *E. mordax* suggesting that it “may prove to be no more than a subspecies of *E. chinchilloides*.” Pine et al. (1978, 1979) demonstrated that there were at least two species or species groups in the genus based on dental characterization. Yañez et al. (1987) synonymized all named forms of *Euneomys* into *E. chinchilloides* based on morphological characters. Subsequently, Reise and Gallardo (1990) described the karyotype of *E. mordax* ($2n=42$, FN=66; Paso Pino Hachado, Chile) and *E. chinchilloides* ($2n=36$, FN=66; Bariloche, Argentina and Coihaique, Chile) from Argentina and southern mainland Chile, concluding that both species are valid and proposed that *E. chinchilloides* is a polytypic species composed of three subspecies (*chinchilloides*, *noei*, and *petersoni*), which have qualitative, quantitative, and ecological differences. The karyotype of *E. chinchilloides* from the type locality in Tierra del Fuego, Argentina, was later found to differ in fundamental number ($2n=36$, FN=68) from the specimens studied by Reise and Gallardo (1990) (Lizarralde et al. 1994).

Over the last two decades, new records from the Central Andes in Argentina have expanded the known distributional

ranges of some species of *Euneomys* (Ojeda et al. 2005; Pardiñas et al. 2010; Lessa et al. 2010). Additional specimens of *E. mordax* were reported from Malargüe, Mendoza Province, Argentina, and a new karyomorph ($2n=34$, FN=62) was reported in three specimens from Valle Hermoso, Malargüe, Mendoza Province, Argentina (Ojeda et al. 2005). Although *E. chinchilloides* originally was known from Tierra del Fuego, Chile, additional distributional records have reported the species from Paso Pino Hachado, Neuquén, Argentina (Reise and Gallardo 1990) and Copahué, Argentina (70 km N Paso Pino Hachado, Neuquén, between 1600 and 2100 m; Pearson and Christie 1991; Lessa et al. 2010). The distribution of *E. chinchilloides* is currently known to extend northward to Laguna de la Niña Encantada ($35^{\circ} 10' S$, Mendoza Province) (Massoia et al. 1994; Pardiñas et al. 2008) and to Parque Provincial Aconcagua, Mendoza ($32^{\circ} 48' 55.92'' S$, $69^{\circ} 56' 28.60'' W$, 2922 m) (Pardiñas et al. 2010). Recently, phylogeographic studies of several individuals of *E. chinchilloides* from Patagonia found genetic differentiation between samples from Tierra del Fuego and southern Patagonia and samples from central-northern Patagonia and Mendoza (Lessa et al. 2010).

Recent collecting efforts in Mendoza Province in the year 2000, as well as earlier survey work on the mammals of Argentina by international research teams from 1990–1995, have yielded a new material that has permitted us to update the cytogenetic, taxonomic, and distributional status of species of *Euneomys* in this general region and perform brief molecular and morphological comparisons with other representatives of *Euneomys* in this area.

Material and methods

Specimens examined and study sites

We studied specimens of the genus *Euneomys* from different localities in the Central Andes, Mendoza Province, Argentina (Fig. 1) and included measurements from topotypic animals from Tierra del Fuego, Argentina. Some specimens were snap-trapped with museum special traps; others were live-trapped using Sherman traps. Animals were prepared following standard procedures, and tissues were preserved in 96 % ethanol or frozen. All voucher specimens, tissue samples, and cell suspensions are housed in the Mammal Collection of the Instituto Argentino de Zonas Áridas (CMI)-(IADIZA), CCT Mendoza-CONICET, Argentina; the Mammal Collection of the Sam Noble Oklahoma Museum of Natural History (OMNH); and the Oklahoma Collection of Genomic Resources (OCGR) (Appendix Supplementary Material). Animals collected during this study were handled following the procedures recommended by the American Society of Mammalogists (Sikes et al. 2011).

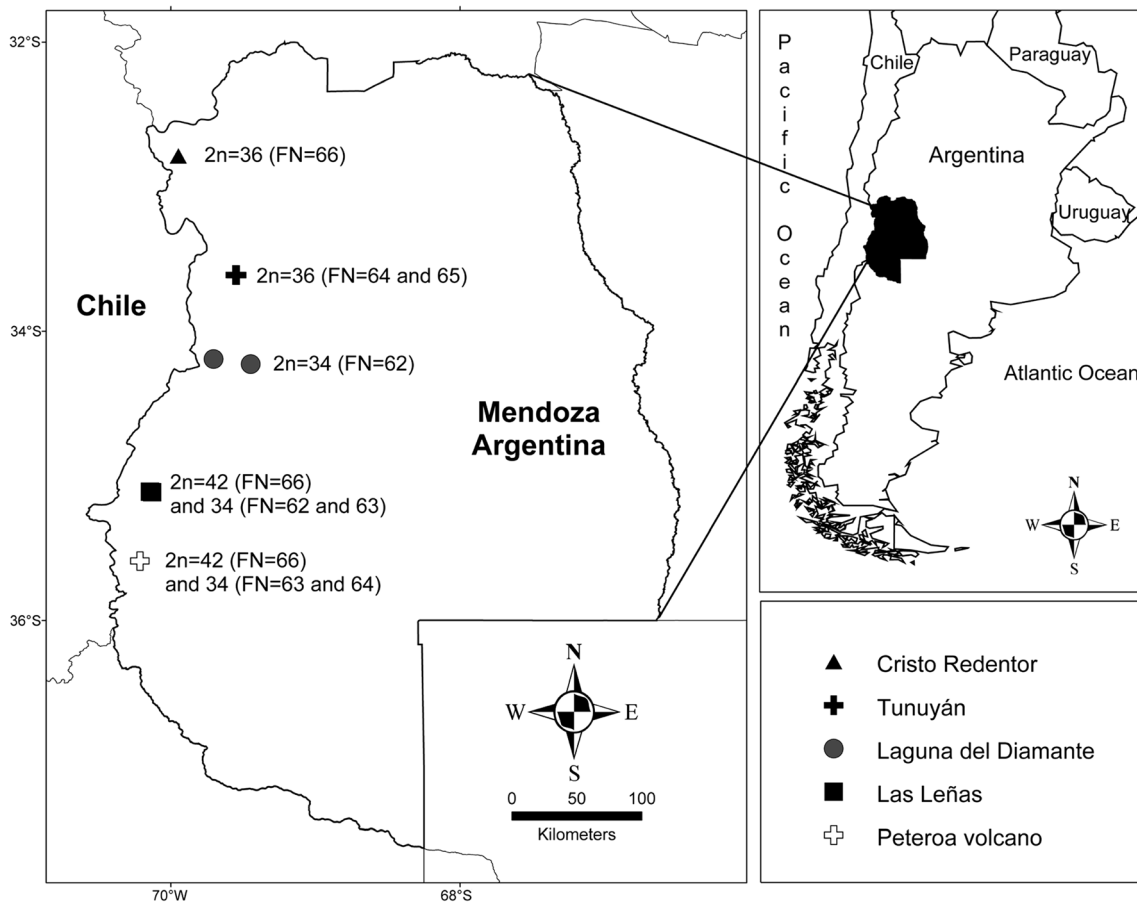


Fig. 1 Map of the sample localities and geographic occurrence of the different karyomorphs of *Euneomys* species in Mendoza Province, Argentina

Karyotypic analysis

Sixteen individuals of *Euneomys* were karyotyped using standard chromosome techniques (Verma and Babu 1995). C-bands for 6 *E. chinchilloides* were induced according to Sumner (1972). Ten metaphase spreads were counted for each specimen.

Molecular analysis

A partial segment of the mtDNA cytochrome oxidase subunit I (CO I) gene (DNA barcode region) was recovered from 15 individuals of *Euneomys*, using standard high-throughput barcoding protocols (Ivanova et al. 2006, 2007). PCR amplification using M13-tailed primer cocktails C_FishF1t1/C_FishR1t1 was done as described in Borisenko et al. (2008). Products were sequenced bidirectionally as described in Hajibabaei et al. (2005). Sequences were assembled and manually edited in CodonCode Aligner software version 3.5.2. DNA barcode data are stored in the Barcode of Life Data System (Ratnasingham and Hebert 2007) and have been submitted to GenBank data base (HM418381–HM418394).

A 594 bp fragment of COI was analyzed. Electropherograms were scored using PROSEQ version 2.91

(Filatov 2002) and aligned using the default parameters of CLUSTAL X (Thompson et al. 1997). Genetic distances between groups (i.e., species) were examined using MEGA version 4 (Tamura et al. 2007). The K2P distance (Kimura 1980) was used because it is a good metric when distances are low (Nei and Kumar 2000) and is the most frequently used for mammals. Phylogenetic relationships were reconstructed using neighbor-joining (NJ) and maximum parsimony (MP). The NJ tree using K2P distances was inferred with MEGA4 (Tamura et al. 2007). MP analyses were executed in PAUP 4.0b10 (Swofford 2002), and all characters were treated as unordered and equally weighted. MP trees were inferred from 200 replicates of heuristic search with random addition sequences and tree-bisection-reconnection branch swapping. In both analyses, node stability was tested using 1000 bootstrap replicates (Felsenstein 1985). Trees were rooted with the outgroup criterion using sequences obtained from GenBank for *Abrothrix xanthorhinus* (HM418451) and *Phyllotis xanthopygus* (HM418535). Relationships between haplotypes were examined in a network, obtained using the median-joining approach implemented in Network 4.6.1.2 software (<http://www.fluxus-technology.com>).

Morphological analysis

Measurements of 6 external and 14 cranial and dental characters were recorded from specimens of *E. chinchilloides* ($2n=36$) from Mendoza and *E. chinchilloides* from the type locality in Tierra del Fuego, *E. mordax* ($2n=42$), and *E. chinchilloides* ($2n=34$). Only adult specimens were used in the analyses (3rd molar erupted). Means, standard deviation (SD), and range were calculated. Comparisons between males and females of *E. chinchilloides* were performed with a Mann–Whitney *U* test. For this last analysis, individuals with both karyomorphs were grouped because of low sample size. No significant differences between males and females were detected, and individuals of both sexes were pooled for the morphometric analyses. The following external measurements (in mm, except weight, in g) were taken with a ruler: total length, length of tail, length of head and body, length of hind foot, length of ear, and weight. Cranial and dental measurements were recorded with digital calipers to the nearest 0.1 mm following (Hershkovitz 1962). Statistical analyses (including univariate descriptive values for all measurements and the evaluation of mean differences of the *T* test for homogeneous or heterogeneous variances, depending on each case) were performed on all measurements using INFostat 2008 (Di Rienzo et al. 2008).

Results

Chromosomal analyses

Ten individuals of *E. chinchilloides* had $2n=34$, FN=62–64 (Figs. 1 and 2a). The only individual with FN=64 had a karyotype with 16 pairs of banded autosomes (15 metacentric or submetacentric, and pair 5 subtelocentric). Six individuals had FN=62 with one pair of medium-sized acro-telocentric autosomes (pair 13 when arranged by size), instead of a banded pair. The three individuals with FN=63 presented a heteromorphic pair 13 with one acro-telocentric and one banded chromosome (Fig. 2a).

Four individuals of *E. chinchilloides* had $2n=36$, FN=64–66 and exhibited an extra pair of small acro-telocentric chromosomes that was not present in individuals with $2n=34$ (Fig. 2b). Two individuals exhibiting FN=66, with 16 pairs of banded autosomes (metacentric or submetacentric and pair 5 subtelocentric), and one small pair of acro-telocentric autosomes (pair 17). One individual with FN=64 had one pair of medium-sized acro-telocentric chromosomes (pair 13 when arranged by size), instead of a banded pair; one specimen with FN=65 had a heteromorphic pair 13 composed of one acro-telocentric and one banded autosome (Fig. 2b).

Two specimens of *E. mordax* had identical karyotypes with $2n=42$, FN=66. The autosome complement included 9 pairs of metacentric, 4 pairs of subtelocentric, and 7 pairs of small acro-telocentric chromosomes.

Irrespective of the diploid number, the X-chromosome was a medium-sized acro-telocentric and the Y was a small subtelocentric. The X-chromosome was the largest acro-telocentric pair and contained a large pericentromeric block of constitutive heterochromatin (CH). Pair one of the autosomes was banded and had a large block of pericentromeric CH, expanding toward the chromosome arms. Most chromosomes possessed small CH in centromeric regions. Additionally, small telomeric and interstitial blocks of CH and faint C-bands were present in some chromosome plates. No additional arms of CH were detected with C-banding that could explain the observed variation in FN (Fig. 2c).

Phylogenetic and distance analyses

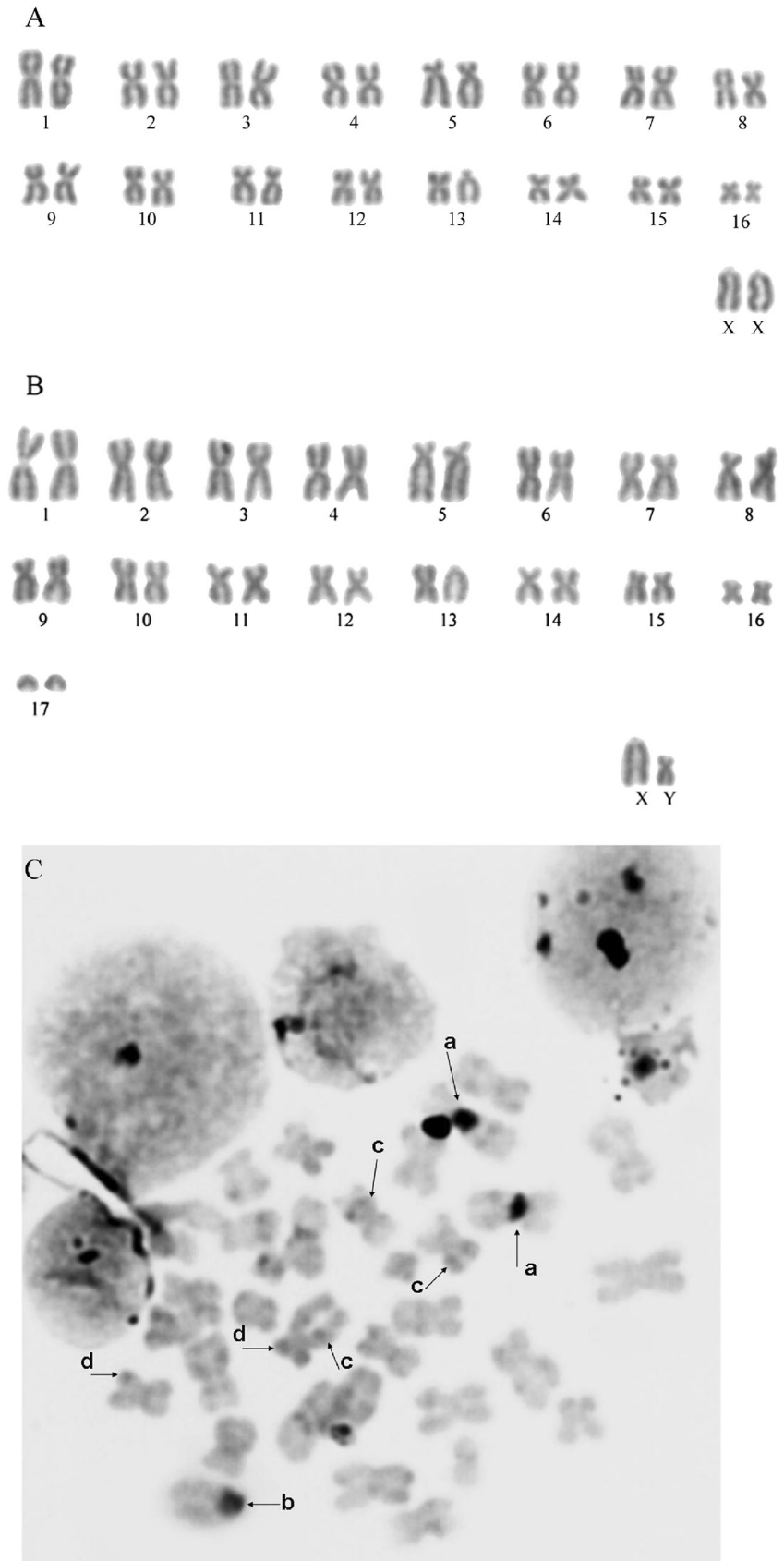
Alignment of the sequences showed 75 variable sites, including 69 singletons and 6 parsimony informative sites. No gaps (insertions–deletions) were detected in the alignment. Comparisons between individuals of *E. chinchilloides* ($2n=36$), *E. chinchilloides* ($2n=34$), and *E. mordax* ($2n=42$) exhibiting the three karyomorphs were calculated using Kimura 2-parameter corrected distances (Table 1 Supplementary Material). Sequence variation between individuals with the same diploid number was low: 0 % within *E. chinchilloides* ($2n=36$) and 0.3 % within *E. chinchilloides* ($2n=34$). In contrast, molecular distances ranged from 0.7 to 1.2 % ($X=0.9$ %) between *E. chinchilloides* ($2n=36$) and *E. chinchilloides* ($2n=34$). Moreover, the mean percent sequence divergence values between *E. chinchilloides* ($2n=36$) and *E. chinchilloides* ($2n=34$) in relation with *E. mordax* were 12.6 % and 13.1 %, respectively.

The topologies of trees constructed using NJ (Fig. 1 Supplementary Material) and MP (Fig. 2 Supplementary Material) were congruent and supported the grouping of specimens with identical $2n$. The clade containing *E. mordax* was sister to all other individuals of *Euneomys* examined, which formed two haplogroups. One group was composed exclusively of specimens of *E. chinchilloides* with $2n=36$ and the second with specimens with $2n=34$. Their consistent separation on the phylogenetic tree was supported by bootstrap values in the range of 77 to 59 % (Fig. 2 Supplementary Material). The haplotype network (Fig. 3) showed a similar topology, with few mutational steps between *E. chinchilloides* ($2n=36$) and *E. chinchilloides* ($2n=34$).

Morphological analysis

No significant differences between sexes of *E. chinchilloides* were obtained in the univariate analyses (Table 2

Fig. 2 **a** Standard Giemsa-stained karyotype of *Euneomys chinchilloides* (laterally grooved) ($2n=34$, FN=63; CMI 07389 from Las Leñas locality). **b** Standard Giemsa-stained karyotype of *Euneomys chinchilloides* (laterally grooved) ($2n=36$, FN=65; CMI07434 from Tunuyán). Sex chromosomes (XY) are also indicated. **c** C-banding pattern of *Euneomys* (laterally grooved) ($2n=34$, FN=64; CMI 07410 from Volcán Peteroa locality). The arrows indicate (a) centromeric heterochromatic block, (b) X-chromosome with a heterochromatic block, (c) interstitial heterochromatic block, and (d) telomeric heterochromatic block



Supplementary Material). Standard external and cranial measurements for all specimens analyzed are presented in Table 3 Supplementary Material. The only statistically significant morphometric difference found between the specimens with $2n=34$ and 36 was the average value of ear length, with that of *E. chinchilloides* $2n=34$ form being shorter (21.43 mm) than that of *E. chinchilloides* $2n=36$ (23.33 mm) ($t=-3.73$; $p=0.0058$). Interestingly, average ear lengths of the specimens from Tierra del Fuego were smaller than the other samples studied here (Table 3 Supplementary Material) and those from other populations (Reise and Gallardo 1990). Maxillary tooth row length tended to be greater in *E. chinchilloides* from Mendoza with $2n=36$, than in the form with $2n=34$ (Table 3 Supplementary Material). *E. mordax* was larger in body size than *E. chinchilloides* and the form with $2n=34$ (Table 3 Supplementary Material), which is consistent with previous reports (Pearson and Christie 1991; Reise and Gallardo 1990). Qualitative comparisons showed cranial differences between specimens with $2n=34$ and those having $2n=36$ (Fig. 4). The 7 specimens with $2n=34$ had a curved incisive foramen (4a), parallel palate with deep and wide grooves (4b), and elongated and shallow palatine fossa (4c). Three of the 4 examined specimens with $2n=36$ possessed a straight incisive foramen (4a).

Discussion

The results of the chromosome analyses confirm the presence of a new karyomorph of *E. chinchilloides* with $2n=34$ (Ojeda

et al. 2005), which also display moderate differences in molecular and morphological characters with respect to other forms of *Euneomys* from Mendoza Province [*E. chinchilloides* ($2n=36$) and *E. mordax* ($2n=42$)]. *Euneomys* with the new karyomorph are distributed in west-central Argentina. No heterozygous individuals with $2n=35$ were detected. This suggests that natural hybrids between $2n=36$ and $2n=34$ karyomorphs may not exist. Additionally, both lineages show reciprocal monophyly for the studied gene. While introgressions could be difficult to identify, the congruence between both sets of data (chromosomes and COI sequences) in the same individuals strongly suggests the absence of hybridization.

Cytogenetic analyses suggest that the observed modifications of both fundamental and diploid number between the two karyomorphs assigned to *E. chinchilloides* can be the result of tandem chromosome fusion. This mechanism has been described in other sigmodontine rodents (Elder 1980; Spotorno et al. 2001 and literature cited therein). The effects of such rearrangements are profound and lead to reproductive isolation between differentiated populations even without significant differences in gene sequences (King 1993; Taylor 2000). Aside from differentiation in diploid number, the $2n=36$ and $2n=34$ forms have a polymorphism that modifies the number of autosome arms. The chromosome modifications that may explain this variation could be an inversion, centromeric shift, or addition of heterochromatic arms (King 1993; Engelbrecht et al. 2011). C-banding did not reveal conspicuous heterochromatic arms in the $2n=34$ (nor in FN=63 or 64) nor the $2n=36$ (FN=65) karyomorphs, suggesting that inversions or centromeric shifts are the most likely explanations for this polymorphism. Inversions are very common among

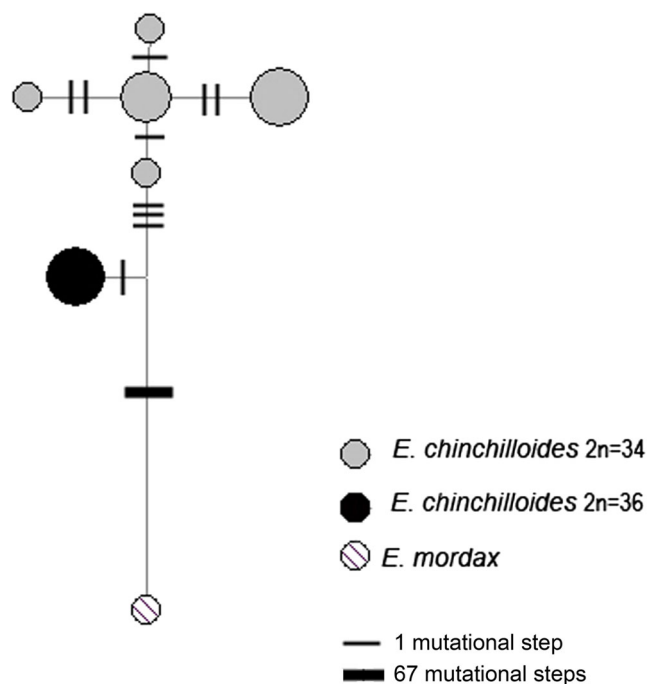


Fig. 3 *Euneomys* haplotype network. The sizes of circles are related to haplotype frequency

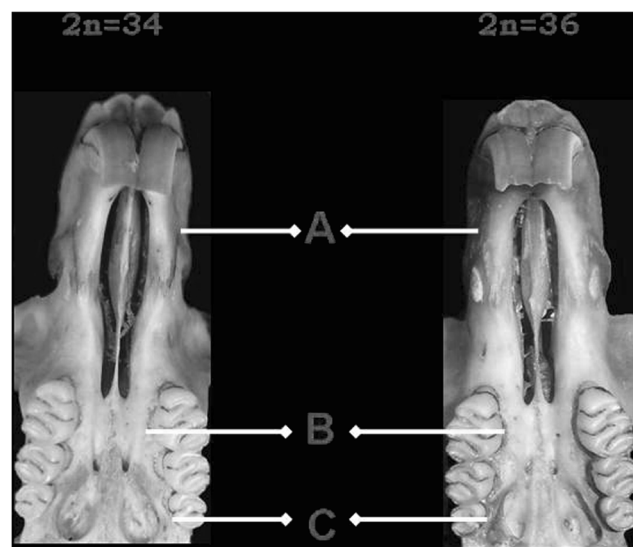


Fig. 4 Morphological comparisons between *E. chinchilloides* ($2n=36$) and *E. chinchilloides* ($2n=34$). **a** Incisive foramen. **b** Parallel grooves of palate. **c** Depression of the palate

rodents (Patton and Sherwood 1983) and have been observed as polymorphisms in other sigmodontine species. For example, two sister species in *Graomys* that show low to moderate molecular differentiation share a polymorphic inversion similar to the one detected here (Zambelli et al. 1994; Martínez et al. 2010).

The karyomorph of two *E. chinchilloides* with $2n=36$ and $FN=66$ was similar to those reported by Reise and Gallardo (1990) and Ojeda et al. (2005) under the name *E. chinchilloides*, but differs in FN from the one described by Lizarralde et al. (1994) from the type locality in Tierra del Fuego. Additionally, the morphology of sex chromosomes of *E. chinchilloides* observed here matches with that reported by Reise and Gallardo (1990), but differs from that described by Lizarralde et al. (1994). In all of our samples, as well as in those studied by Reise and Gallardo (1990), the X-chromosome was acro-telocentric. However, the only female described by Lizarralde et al. (1994) had a karyotype with all banded chromosomes. While differences in X-chromosome morphology have been observed among species of the same genus in sigmodontines (Bonvicino et al. 2003; Lanzone et al. 2007), no polymorphism for this chromosome was found. The chromosome data presented here deserve further investigation, because if this karyotypic differentiation is caused by an inversion, it may lead to sterility of female hybrids since pairing and recombination of the heteromorphic X-chromosome in females can produce duplications and deficiencies in the absence of mechanisms preventing chiasma formation (King 1993; Engelbrecht et al. 2011). The high chromosome variability observed in *Euneomys* and its apparent geographic correlation was not detected before. Additional studies with wider geographic sampling and banding techniques for identifying the chromosomal rearrangements are essential for understanding their evolutionary and taxonomic significance.

The topology of the COI trees suggests a lack of mitochondrial introgression between the two sister karyomorphs of *E. chinchilloides*. The level of divergence between these forms is low and comparable to the minimum interspecific COI distances observed in some other mammals (Lissovsky et al. 2007; Borisenko et al. 2008; Francis et al. 2010). Genetic distances alone, while offering an operational framework for assessing cryptic diversity, are insufficient to act as the sole arbiters of taxonomic distinctiveness (Baker and Bradley 2006). However, the result of COI sequences analysis was congruent with the differences observed in chromosome numbers and morphology between the two groups.

No significant differences between the sexes of *E. chinchilloides* were obtained in the univariate analyses; therefore, measurements from individuals with both karyotype were pooled due to low sample size. Sexual dimorphism has been found in several other sigmodontinae species, for example, *Graomys* and *Salinomys* (Rodríguez et al. 2012;

Lanzone et al. 2014), but has not yet been detected in *Euneomys*. Any morphological differences between the two karyomorphs of *E. chinchilloides* are subtle. Only one was significant here; however, a higher sample size may be needed to detect less pronounced differences. Additionally, three qualitative characters varied among the specimens here, suggesting morphological differentiation between the karyomorphs of *E. chinchilloides*.

We suggested that the morphological, chromosomal, and molecular differences between specimens with $2n=36$ and $2n=34$ (referred to *E. chinchilloides*) are indicative of a recent and/or incipient allopatric speciation event. Another possibility could be that the karyomorphs correspond to differentiated populations which have not acquired reproductive isolation and could exchange genetic material in an unexplored part of their geographic range.

Our findings indicates that *E. chinchilloides* proper ($2n=36$) has an extensive latitudinal distribution ($32\text{--}68^\circ$ S) and extends further north than the other forms of *Euneomys*. *E. mordax* occupies an intermediate central distribution ($34\text{--}38^\circ$ S), and *E. chinchilloides* ($2n=34$) is confined to a restricted area within Mendoza Province ($34\text{--}35^\circ$ S). The habitat of *E. chinchilloides* ($2n=34$) is characterized by a high proportion of rocks mixed with sparse vegetation composed mainly of bunchgrasses, such as *Stipa* sp. (coirón [needlegrass]), *Poa* sp. (huecú [bluegrass]), and *Festuca* sp. (festuca [fescue]); ground cover plants such as *Azorella trifurcata* (yareta [nana]); and dwarf shrubs such as *Adesmia pinifolia* (leña amarilla [yellow brush]) and *Berberis empetrifolia* (calafate [crown barberry]). Here, we extend the distribution of *E. mordax* from Las Leñas 109 km to the north to Laguna del Diamante, Mendoza.

We expect that further collecting will extend the range of the $2n=34$ form into northern Mendoza Province given the contiguous nature of its habitat. Further investigations are necessary, including more genes and individuals covering localities from the Central Andes of Argentina to Patagonia, to elucidate the taxonomic and distributional status of *Euneomys* species.

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Appendix

Specimens examined: voucher specimens and tissue samples for the individuals sequenced in this study are deposited in the Mammal Collection of the Instituto Argentino de Zonas Áridas (IADIZA), Mendoza, Argentina (CMI); Sam Noble Oklahoma Museum of Natural History, Norman, Oklahoma (OMNH); Michigan State University Museum, East Lansing, Michigan (MSU); United States National Museum (USNM); and British Museum of Natural History, London (BM). Orthologous sequences from *Abrothrix xanthorhinus* and *Phyllotis xanthopygus* were obtained from GenBank. Locality information (from specimen tags), specimen catalog number, and GenBank number are given below for specimens used in this study. Specimens used in the karyotypic analysis are indicated with an asterisk (*).

Euneomys chinchilloides from Mendoza ($2n=36$) ($n=4$). Argentina: mendoza: Las Heras: Cristo Redentor: 32.8126° S, 70.0116° W (CMI 07405*, GenBank HM418381; CMI 07457*, GenBank HM418384). Argentina: mendoza: Tunuyán: Refugio Escarabelli: 33.6123° S, 69.5435° W (CMI 07353*, GenBank HM418382; CMI 07434*, GenBank HM418383).

Euneomys chinchilloides from Mendoza ($2n=34$) ($n=10$). Argentina: mendoza: Malargüe: Las Leñas: 35.0236° S, 70.0247° W (CMI 06802*, GenBank HM418385; CMI 06803*, GenBank HM418387; CMI 06806*, GenBank HM418386; CMI 07389*, GenBank HM418388; CMI 07435*, GenBank HM418394; CMI 07436*, GenBank HM418390; CMI 07437*, GenBank HM418392); Argentina: mendoza: Malargüe: near Volcán Peteroa: 35.2177° S, 70.5161° W (CMI 07419*, GenBank HM418393; CMI 07418*, GenBank HM418389). Argentina: mendoza: San Carlos: Laguna del Diamante: 34.1993° S, 69.7053° W (CMI 07328*, GenBank HM418391).

Euneomys chinchilloides from Tierra del Fuego ($n=4$). Argentina: Tierra del Fuego: Bahía Buen Suceso (USNM 482138, 482140). Chile: Straits of Magellan, near eastern entrance (BM 55.12.26.111); St. Martin's Cove, Hermite Island, Cape Horn Islands (BM 43.11.16.26).

Euneomys mordax ($n=8$). Argentina: mendoza: Malargüe: Las Leñas: 35.0236° S, 70.0247° W (CMI 06807*); Argentina: mendoza: Malargüe: near Volcán Peteroa: 35.2177° S, 70.5161° W (CMI 07448*, GenBank HQ860421). San Rafael: Fort San Rafael (BM 55.12.24.199). San Carlos: El

Cilindro Laguna Diamante, 3.138 m (OMNH 37096); Laguna Diamante, 3.261 m (OMNH 37104). Chile: Santiago: La Parva (USNM 399400, USNM 399401); La Junta, Lo Valdes 2500 (USNM 391817).

Abrothrix xanthorhinus ($n=1$). Argentina: mendoza: 34.244° S, 69.374° W (CMI AN33, GenBank HM418451).

Phyllotis xanthopygus ($n=1$). Argentina: mendoza: 32.775° S, 69.604° W (CMI AN69, GenBank HM418535).

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