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RESEARCH

Population genetics and lineage structure of the endangered Bolivian chinchilla rat *Abrocoma boliviensis*

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Abstract
Studies on conservation genetics of endangered species can identify which populations should be the focus of management plans. The endangered Bolivian chinchilla rat, *Abrocoma boliviensis*, is currently threatened by its rarity and anthropogenically driven transformation of the landscape it inhabits. Given its conservation status, restricted geographic range and limited information about its natural history, understanding how its genetic diversity is apportioned is crucial to inform any potential conservation efforts for *A. boliviensis*. In this study, we assessed the genetic diversity and population structure of *A. boliviensis* as a first approximation to a comprehensive evaluation of the species. Mitochondrial data from 12 individuals revealed high levels of genetic distance, nucleotide diversity and polymorphisms, all of which indicate the existence of three separate clades. This was further supported by reduced-representation genomic data, which showed little to no admixture between these clades. This lack of gene flow suggests that the lineages have followed separate evolutionary trajectories and should be recognized, at minimum, as distinct evolutionarily significant units. Our contribution highlights the urgency with which survey efforts must become the first order of action. The generation of new population-level data will be essential to refine our understanding of the species, clarify the evolutionary trajectories of its lineages, and inform effective conservation strategies.

Keywords Abrocomidae · South America · Andes · EDGE species · Population structure

Introduction

Molecular approaches and population genetic analyses have become common practice in conservation studies. The field of conservation genetics identifies threats related to low density and small population sizes and provides tools to better understand demographically driven processes (Willi et al. 2022). It can also contribute to the management and conservation of species by identifying which populations should be the focus of these efforts. This can be achieved

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through the recognition of evolutionarily significant units (ESUs) (Ryder 1986; Casacci et al. 2014). These units are attributed when populations are highly differentiated in their genetics and ecology, presumably because each unit is on a different evolutionary, and potentially adaptative, path (Funk et al. 2012; Willi et al. 2022). For example, population genetic studies of endangered or otherwise threatened taxa have found evidence for separate ESUs in mammals (Degner et al. 2007; Cossíos et al. 2012; Teixeira et al. 2023), birds (Quintela et al. 2010; Murphy et al. 2011), reptiles and amphibians (Borges et al. 2018; Muniz et al. 2018; Castillo-Morales et al. 2023). Understanding the genetic status of species is essential because small populations are especially vulnerable when genetic depletion occurs, potentially compromising their survival in the face of environmental change(O'Brien 1994). This phenomenon is particularly relevant for species inhabiting naturally fragmented habitats, where the effects of genetic drift may be amplified (Willi et al. 2022).

Since the 1950's, Bolivian landscapes have been transformed by a variety of players (e.g., indigenous groups, colonists, and corporations) and practices (e.g., traditional agriculture, mechanized agriculture, cattle ranching or forest use), with most of the settlement and deforestation occurring around the city of Santa Cruz and the Yungas region near the city of La Paz (Killeen et al. 2008). The land cover on the eastern cordillera of Bolivia has been converted to agricultural or bare land at the expense of the forests and pastures that covered this region in the past. This trend is particularly evident in fertile valleys and on moderate slopes below 2000 m, which have been extensively converted for agricultural use (Brandt and Townsend 2006). A local inhabitant of this region, the Bolivian chinchilla rat (*Abrocoma boliviensis*) is only found in mid-to-high elevation forests of the eastern Andes in Bolivia and is considered a rare species, as data exists on less than 20 individuals since its description in 1990 (Tarifa et al. 2009; Quinteros-Muñoz 2015; Hidalgo-Cossio et al. 2016; Quiroga Pacheco et al. 2020).

Rarity in a species can be determined based on abundance or restricted geography, and while not all rare species are necessarily at risk of extinction, their low abundance and/or constrained distributions make them more vulnerable to stochastic events (Drever et al. 2012). In the latest assessment of *A. boliviensis* for the International Union for Conservation of Nature (IUCN) Red List of Threatened Species, the species is classified as critically endangered under criteria B1ab(i, ii, ii) (Bernal 2016). This means that the species' range extent is smaller than 100 km^2, severely fragmented or known to exist at a single location (the distribution of *A. boliviensis* was limited to its type locality in the department of Santa Cruz), and its habitat presents a continuing decline in area, extent and/or quality. Moreover, the species is listed among the 100 EDGE (Evolutionarily Distinct and Globally Endangered) mammal species worldwide, a designation reserved for taxa that are both highly evolutionarily distinct and threatened with extinction (Gumbs et al. 2023).

In recent years, sampling efforts from various research projects added eight new localities in the departments of Potosí, Cochabamba, Tarija, and Santa Cruz (Tarifa et al. 2009; Quinteros-Muñoz 2015; Hidalgo-Cossio et al. 2016; Quiroga Pacheco et al. 2020), noticeably expanding the species' distribution along the Bolivian eastern cordillera encompassing two main phytogeographic regions: the Yungas and the Boliviano-Tucumano forest (Josse et al. 2011). Coming from Peru into central Bolivia, Yungas forests can be found in Cochabamba and part of Santa Cruz across an extensive altitudinal gradient (500-4,000 m), after which the southern portion of the eastern cordillera is dominated by Boliviano-Tucumano forests interspersed with Dry Interandean forests in the departments of Santa Cruz and Tarija. This transition occurs at about 18°S. With these new localities, *A. boliviensis* is now distributed across a mixed landscape of montane, dry, and subtropical forests (i.e., Yungas, Dry Interandean, and Tucumano forests) broken up by deep valleys and steep slopes (Rex and Hanratty 1989; Graham et al. 2001) (Fig. 1).

Unfortunately, even as new localities for *A. boliviensis* are found, the threats to its habitat remain the same (i.e., ecosystem conversion and degradation by human action) and new questions about population connectivity and genetic status of its lineages arise. Here, we use molecular data from samples collected in all these new localities to evaluate the status (i.e., genetic diversity) of *A. boliviensis* and describe, if present, the structure of its populations. Given the fragmented landscape in which the species is found, we expect a pattern consistent with isolation by distance and low gene flow. While this study represents a first approximation to a comprehensive evaluation of the species, the scarcity of information available makes our contribution a valuable resource to inform future research, monitoring and, ultimately, conservation efforts.

Materials and methods

Specimens examined

Twelve specimens from ten localities spanning the known distribution of *Abrocoma boliviensis* were used, including a topotypic specimen (Fig. 1; Table S1). Specimens were all procured via institutional loans from natural history collections. All tissue samples included in our analysis are accompanied by voucher specimens (Table S1).

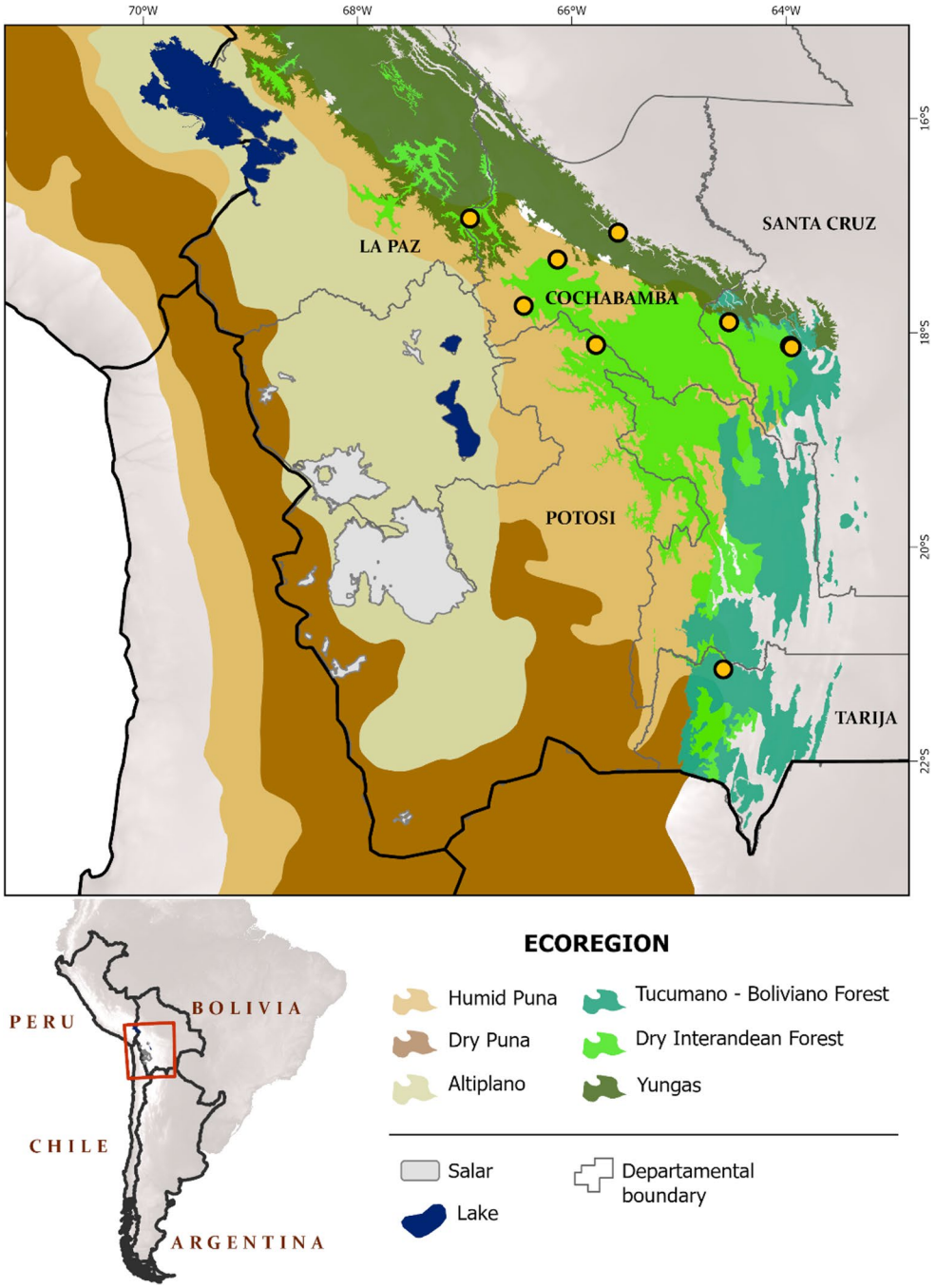

Fig. 1 Geographic distribution of the samples included in this study (yellow circles in the map). Ecoregions in the area are depicted to show that the Bolivian chinchilla rat is found in different habitat types. While the southernmost record of *A. boliviensis* in the state of Tarija appears to be from Tucumano-Boliviano forests, so far in the area, the species has been recorded in patches of Dry Interandean forest

DNA extraction, PCR amplification, and sequencing of the cytochrome b gene

Relationships among individuals of *A. boliviensis* were first evaluated using a mitochondrial marker (cytochrome b or *Cyt-b* gene). Genomic DNA was extracted from muscle or liver tissue using the DNEasy® Blood and Tissue Kit from Qiagen following manufacture's protocol and PCR amplifications followed Salazar-Bravo et al. (2023). One sample of *A. boliviensis* was a skin snippet that was first washed and hydrated following the protocol of de Moraes-Barros and Morgante (2007). The sample was subdivided so that one was processed with the Qiagen kit and the other with the *Quick*-DNA Fecal/Soil kit from Zymo Research following manufacture's protocol. Skin extractions were then combined for subsequent PCR procedures. This extraction took place in a laboratory that had not processed mammals before. PCR amplifications were viewed in 1% agarose

gel, and successful amplifications were sent to Psomagen USA (Maryland) for standard Sanger-sequencing. Single sequences were assembled into a contiguous sequence in DNASTAR v 5.52 and aligned and edited in the software Mesquite v3.61 (Maddison and Madisson 2019) using the MUSCLE option (Edgar 2004). The final matrix included 810 bp of *Cyt-b* for twelve individuals of *A. boliviensis*. Detailed information about the primers used and PCR cycling conditions is available as supplementary material.

Analyses of cytochrome b

A *Cyt-b* gene tree was built with maximum likelihood (ML) searches implemented through the IQ-TREE web server (Trifinopoulos et al. 2016). Partition by codon was specified but allowing IQ-TREE to determine the best-fit substitution model for the data. Clade support was assessed via rapid bootstrapping with 1000 iterations. Trees were rooted at mid-point. Using data available for other species in the family Abrocomidae, inter- and intraspecific genetic variation was assessed via genetic distances calculated with the Kimura 2-parameter model as implemented in Mega 10 (Kumar et al. 2018), including distances between clades of *A. boliviensis* assigned based on the results the ML tree (see results section and Fig. 2).

To further explore the genetic diversity of *A. boliviensis*, nucleotide diversity (π), haplotype number (h) and diversity (*Hd*), and polymorphic sites were calculated using DnaSP v6 (Rozas et al. 2017). In addition, Fu's *Fs* and Tajima's *D* tests of neutrality were calculated in DnaSP to infer the species' historical demography.

Reduced-representation genome-level variation

To determine whether the genetic distances and levels of nucleotide diversity obtained from *Cyt-b* were indeed representative of the evolutionary history of the species and not biased by the unique characteristics of the mitochondrial genome (i.e., maternal inheritance), we explored the population structure of *A. boliviensis* using a genome-wide reduced representation approach. A subset ($n=9$) of the samples processed in this study were sequenced following the Genotyping-by-sequencing (GBS) methods described in Elshire et al. (2011) at the University of Wisconsin Biotechnology Center. The samples were digested with enzymes nsiI and bfaI and sequenced using an Illumina NovaSeq 6000 to produce paired end reads (2×150 bp). GBS methods produce non-barcoded R2s, which can bias analyses in Stacks 2 (Rochette et al. 2019). Therefore, all downstream analyses were performed with the single-end dataset using the High Performance Computing Center at Texas Tech University.

Loci filtering and SNP calling

After demultiplexing, size-selection (130 bp), and performing quality control checks on the reads, we ran several iterations of the *denovo_map* program in STACKS 2 (Rochette et al. 2019), modifying the parameters **-m** (which determines coverage depth in the ustacks module), **-M** (which determines the number of mismatches allowed to form a stack in the ustacks module) and **-n** (which controls the number of mismatches allowed between individuals when building the catalog in cstacks) to find the most appropriate combination to use in downstream analyses given our data. A detailed description of the process is given in the supplementary material.

Most parameter combinations provided qualitatively similar results (i.e., the distribution and grouping of samples, as well as the amount of variance explained in the PCAs) when reads were shared by at least 80% of the individuals (*-r*=0.8). In VCFtools, these r80 files were further filtered using the options --max-meanDP 50 (to remove loci with high depth values), --minDP 7 (to ensure all genotypes were determined with at least 7 reads) and --thin 150 (to select only one SNP per locus). While it is common to perform allele filtering based on minimum allele frequency (in part to remove sequencing errors), we decided against it because this dataset has a low number of individuals, in some cases with only one individual representing a genetic cluster, and therefore any filtering based on MAF could potentially remove alleles that are biological relevant. Finally, for downstream analyses, the files generated with the Stacks settings **M=4** and **n = 5** were used because they provided the better balance between a high number of variants and avoiding combining paralogous or repetitive loci (Paris et al. 2017).

Population analyses

With the filtered dataset described above, we performed PCAs with PLINK v1.9. We then used the same dataset as input to run the *populations* module of STACKS once more and generate a structure file. Population structure was assessed using the software STRUCTURE v2.3.4 (Pritchard et al. 2000). Following the developer's recommendations, the analysis was run assuming admixture is present (NOADMIX=0), providing sampling location to assist the clustering (LOCPRIOR=1), and specifying either an independent or a correlated allele frequency model (FREQSCORR=0 and 1, respectively). Sampling location was provided as a prior because our dataset has both a low number of individuals and a relatively small number of SNPs, which hinders the software's capability to detect genuine population structure. Moreover, the model developed by Hubisz et al.

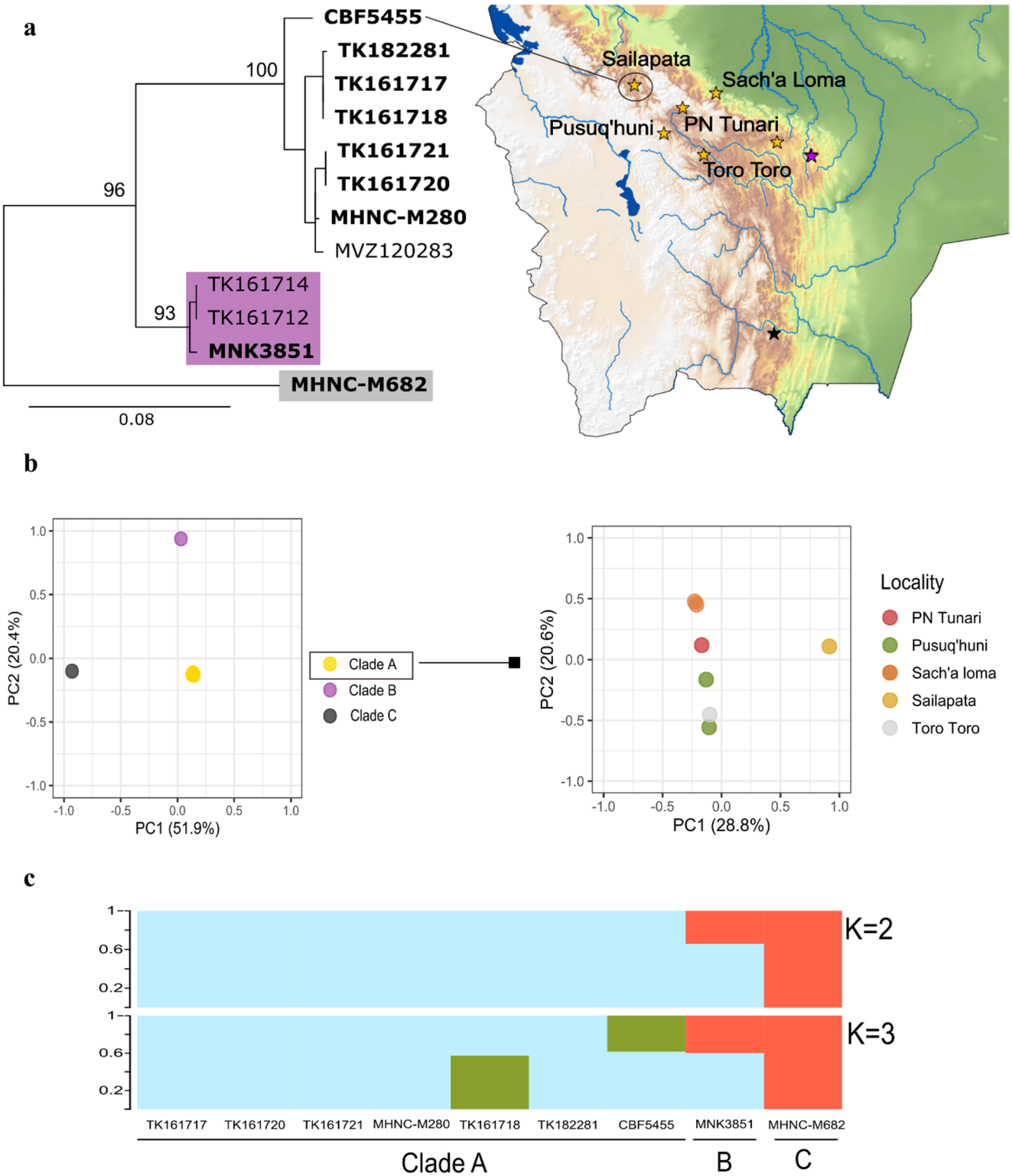

Fig. 2 Population structure of *A. boliviensis*. **a**: *Cyt-b* tree with corresponding localities on the map to the right (bolded catalog numbers represent individuals for which GBS was performed); **b**: PCA plots built from GBS data, the panel on the right only includes members of clade A. **c**: STRUCTURE bar plot

(2009) evaluates whether the sampling locations are informative; only if they are, does the software use them. Using the command-line version of the program, the analysis ran for values of K from 1 to 9. Each Kvalue ran 20 times with BURNIN = 200 000 and NUMREPS = 500 000. To determine the most appropriate Kvalue, we followed the Evanno method (Evanno et al. 2005) implemented through the STRUCTURE HARVESTER software (Earl and vonHoldt 2012). We used the program Structure Plot v2.0 to generate the bar plots (Ramasamy et al. 2014). Finally, isolation by distance (IBD) was tested and plotted with the package adegenet using Nei's distance metric (Jombart and Ahmed 2011) in R v4.0.5.

Results

Cyt-b dataset

Analysis of mitochondrial data from 12 individuals of *A. boliviensis* revealed substantial genetic distances, high nucleotide diversity, and a high level of polymorphism, collectively indicating the presence of three distinct clades. Genetic distances among *Cyt-b* sequences in *A. boliviensis* were considerable, ranging from 0.3% to 13.9% (Table 1). But the highest distance within *A. boliviensis* (i.e., 13.9%) was smaller than the distance found between *A. boliviensis* and its sister species *A. cinerea* (17.4% on average). These levels of divergence support the classification of samples of *A. boliviensis* into three separate clades. Clade A includes all samples from Cochabamba, a sample from Potosi, and one sample from Santa Cruz (this represents the northern part of the distribution of the species in La Paz and the mesothermic valleys of central Cochabamba), clade B includes samples TK161712 + TK161714 + MNK3851 from the edge of the mountain rainforest in westernmost Santa Cruz Department, and clade C is represented by sample MHNC-M682 in the southern edge of the known distribution of the species in the Department of Tarija (in Fig. 2a: yellow, purple and black stars, respectively).

Values of nucleotide diversity and polymorphic sites were highly dependent on whether samples of *A. boliviensis* were grouped or not (Table 2). When all samples (regardless of clade) were pooled, nucleotide diversity was 0.045 and 121 polymorphisms were present. Once samples of *boliviensis* were grouped into clades, it became clear that the sample from clade C inflated the values found for the whole species. When this clade was removed (i.e., clades A and B were combined), nucleotide diversity was 0.033 while polymorphisms were 68. Given that all samples of *A. boliviensis* came from separate localities, every individual (except for the two samples from Pusuq'huni) had a unique haplotype in clades A and B which was reflected in their high haplotype diversity. *Fs* values were positive for *A. boliviensis* but only significant when clades A and B were combined. A similar trend was found for Tajima's *D* values (Table 2).

Table 1 Average genetic distances (%) between clades of *Abrocoma boliviensis* calculated from cytochrome b sequences using Kimura 2-parameter. Values of genetic distance to its sister species *Abrocoma cinerea* are included for comparison. Bold values on the diagonal represent distances within clades

		1	2	3	4
1	*A. boliviensis* (clade A)	**1.3**			
2	*A. boliviensis* (clade B)	7.2	**0.3**		
3	*A. boliviensis* (clade C)	13.9	12.1	-	
4	*A. cinerea*	18.8	16.2	17.3	**3.1**

Reduced-representation genome-level variation

After demultiplexing, the number of retained reads was 253 725 812. After running *denovo_map* the number of loci and polymorphic loci was 1 322 883 and 1 002 230, respectively. Finally, the number of variants retained after applying all filters in VCFtools was 2192 with an average depth per read of 17x.

The PCA plot built from GBS data supported the groups formed in the *Cyt-b* tree (Fig. 2b), with the PC1 explaining 51.9% of the variance between the specimen from clade C (Tarija) and the rest of the samples, and the PC2 explaining 20.4% of the variance found in the specimen from clade B (Santa Cruz). Because their distance in multivariate space was so marked, we could not assess any structure within clade A unless the other two clades were removed. By doing so, it became apparent that, as described by the *Cyt-b* tree, the sample from Sailapata was distanced from the rest and

Table 2 Genetic diversity of *A. boliviensis* based on cytochrome b sequences. Values for each clade and different groupings are also included. n: number of individuals, *h*: number of haplotypes, *Hd*: haplotype diversity, *Fs*: Fu's *Fs* statistic, and *D*: Tajima's *D* statistic. * indicates statistically significant results. na = neutrality tests were not performed for clades with less than 8 individuals

Species (*n*)	Group	Nucleotide diversity	Polymorphic sites	h	Hd	Fs	D
A. boliviensis (12)	All individuals	0.045	121	10	0.917	1.57	0.23
A. boliviensis (11)	clade A + B	0.033	68	9	0.905	2.0*	0.23
A. boliviensis (8)	clade A	0.012	28	7	0.875	1.48	0.23
A. boliviensis (3)	clade B	0.003	4	2	0.533	na	na
A. boliviensis (4)	clade B + C	0.045	83	3	0.71	na	na

explained 28.8% of the variation (Fig. 2b). The remaining samples showed virtually no separation on the horizontal axis, but there was differentiation seen on the y-axis that explained 20.6% of the variation. The distribution of these samples appears to follow an east to west gradient, from the easternmost sample in Sach'a Loma across the Rocha–Caine–Grande River system to the western samples in Pusuq'huni and Torotoro (Fig. 2a).

Following the Evanno method, population structure in *A. boliviensis* was better explained at K = 2 and when independent allele frequencies are used (Mean LnP = -10,202, SD = 14.1, and ΔK = 342.5). In this case, one population consisted of all samples from clade A (with inferred ancestry of 1) and another population represented the sample from clade C (with inferred ancestry of 1). The sample from clade B showed admixture with most ancestry shared with clade A (0.658) and less with clade C (0.342) (Fig. 2c). At higher values of K, values of LnP plateau, SD increased and ΔK were significantly smaller than for K = 2. In addition, assignment of samples to other populations became harder to explain given our knowledge of the species and the system. For example, at K = 3 a third cluster was assigned to samples CBF5455 (ancestry of 0.382) and TK161718 (ancestry of 0.572) (Fig. 2c). Plots of the results generated by STRUCTURE HARVESTER are available as supplementary material.

Tests of isolation by distance suggested that the structure seen in *A. boliviensis* follows a pattern of IBD, but that other biological scenarios might explain some of it as well. Despite the scatter plots showing a positive correlation between genetic and geographic distance, the original value of the correlation between distance matrices (the black dot) fell inside the reference distribution (the histogram itself) indicating that isolation by distance was not significant (Fig. 3).

Discussion

Analyses of mitochondrial and nuclear regions of the genome show that samples of *Abrocoma boliviensis* evaluated in this study represent three separate clades. This is evidenced by the high values of genetic distance (Table 1), little to no admixture (Fig. 2), and long divergence times between lineages (i.e., clade C diverged ~ 5.4 Ma and clades A and B diverged ~ 2.8 Ma) (Arenas-Viveros 2024). The genetic structure found within *A. boliviensis*, namely clades A, B and C, is evident in both the Cyt-b gene tree and the PCA and STRUCTURE analyses performed with GBS data (Fig. 2). In addition, we found that these genetic clusters occupy regions of the country that differ in ecological and phytogeographical characteristics: clades A and B occur in regions dominated by Yungas or Dry Interandean forests, while clade C occurs in a mosaic of Boliviano-Tucumano and Dry Interandean forests. Altogether, this suggests that these lineages have been on separate evolutionary pathways and should therefore be identified, at minimum, as separate ESUs.

A case could also be made to elevate each clade to the hierarchy of subspecies or, alternatively, to elevate clades A and B to subspecies level and assign the individual from southern Bolivia (i.e., Clade C) to a new species. However, we prefer to take a much more conservative position with the understanding that genetic divergences by themselves are not taxonomic characters. Moreover, comparative studies on the morphology and ecology of members of each clade are lacking, and until these pieces of the puzzle are included, it would be difficult to draw well-supported conclusions on the taxonomy of the species. For instance, another Andean highland specialist, the vicuna (*Vicugna vicugna*), is divided, based on mitochondrial studies, into subspecies from the Wet and Dry Puna respectively, but this taxonomic arrangement is also supported by morphological and genetic traits (Marín et al. 2007). In addition, it is necessary to incorporate additional data from clades B and C, and to determine whether the absence of samples from the department of Chuquisaca (i.e., the region between clades B and C along the eastern Andes) is biologically meaningful or the result of sampling bias. This consideration is important because other species of conservation concern in the region, such as the Andean cat (*Leopardus jacobita*) have a naturally fragmented distribution, and it is recommended that this is taken into account for future conservation actions (Cossíos et al. 2012).

While our results are supported by both mitochondrial and nuclear data, the small number of samples in our study must be considered when interpreting results, especially from demographic analyses. Levels of nucleotide diversity (π) and number of polymorphic sites in the Bolivian chinchilla rat are undoubtedly affected by whether ESUs are grouped or evaluated individually. Just including the specimen from Tarija (i.e., clade C) doubles the number of polymorphisms (121 vs. 68) and adds 36% more nucleotide diversity (0.045 vs. 0.033) than when not included (Table 2). Compared to the mitochondrial diversity of two highland specialists, the mountain degu -a rodent- (*Octodontomys gliroides*) ($\pi = 0.0059$ and 24 polymorphisms) and the Andean cat ($\pi = 0.0011–0.0027$ and 15 polymorphisms), *A. boliviensis* has higher nucleotide diversity and number of polymorphisms regardless of clade grouping. This is interesting because the distribution of both species covers a large geographic area through the Altiplano from central Peru (in the case of the Andean Cat) or northern Bolivia (for the mountain degu) to Chile and Argentina (Cossíos et al.

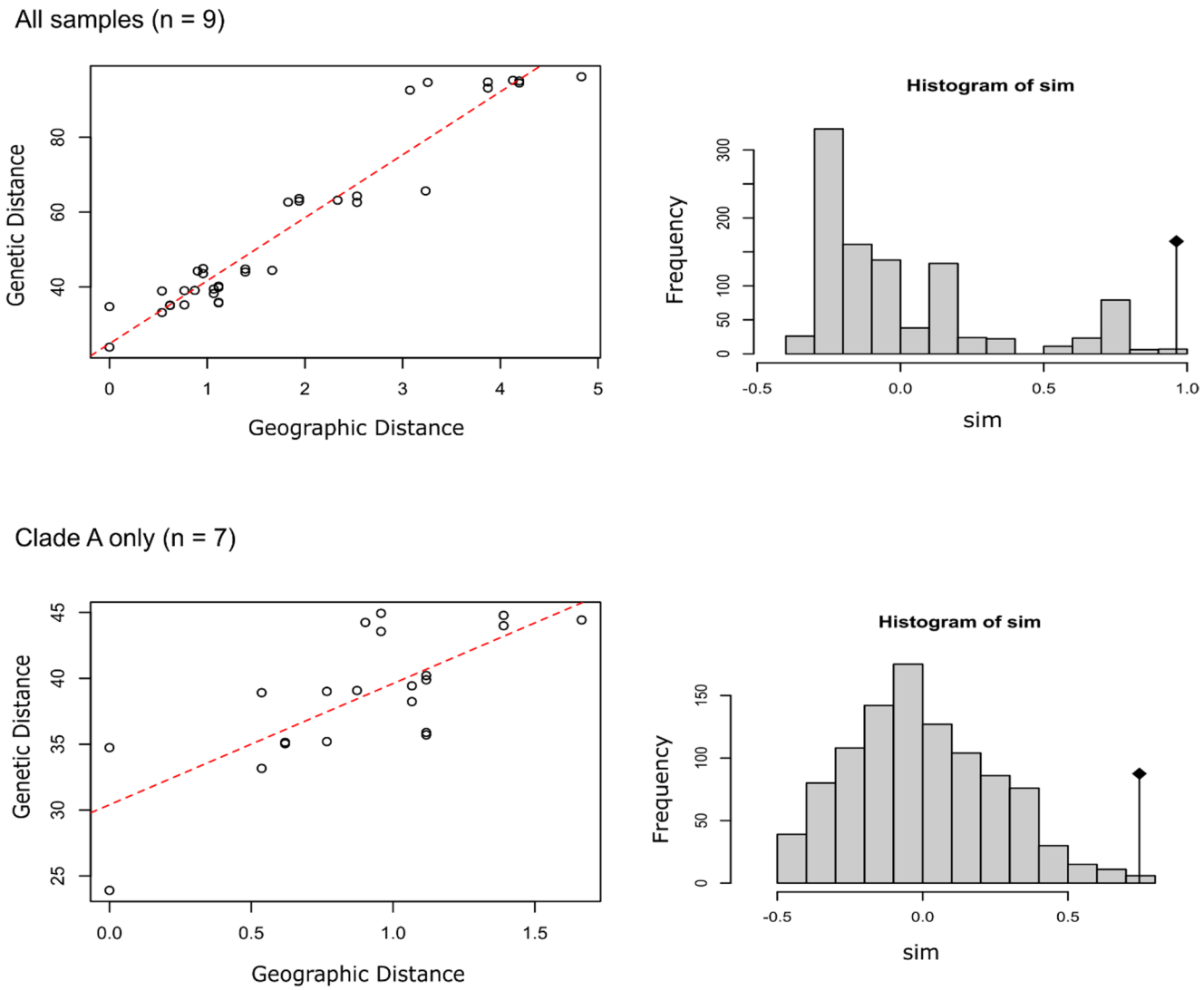

Fig. 3 Plots of isolation by distance for *A. boliviensis*. In the histograms, the original value of the correlation between distance matrices is shown by the black dot and compared to the reference distribution

2012; Rivera et al. 2016). Meanwhile, the known distribution of *A. boliviensis* is restricted to eastern Bolivia. This highlights that a species restricted to a single slope of the Andes within one country can harbor greater genetic diversity and polymorphism than species distributed across a much larger area of the continent. In contrast, when values were calculated for clades A and B separately, both nucleotide diversity (π=0.012 and 0.003, respectively) and polymorphisms (28 and 4, respectively) dropped significantly. This demonstrates how each ESU carries unique diversity that is not found in other populations, and reinforces the hypothesis that any impact on one of these lineages might result in drastic genetic loss for the species; furthering the case for separate efforts in their monitoring, research, and conservation (Borges et al. 2018).

Values of Fu's *Fs* and Tajima's *D* were all positive regardless of grouping arrangement and only significant for *Fs* when clades A and B were pooled, suggesting a scenario of population bottleneck or the effect of balancing selection. Taken at face value, our results suggest that populations of *A. boliviensis* may have undergone genetic bottlenecks which, combined with the species' restricted distribution range, underscore the need for further conservation efforts. Unfortunately, there are no long-term estimates of population trends in any species of abrocomid to compare to, and while our results are limited by sample size, they provide an approximation to the status of these populations.

The evolutionary history of extant abrocomids traces its origins to about 10 Ma, when the Andes and its surrounding lowlands where still experiencing orogenic changes that in turn transformed the landscape and promoted divergence

(Gregory-Wodzicki 2000; Garzione et al. 2008; Graham 2009). The ancestor of *A. boliviensis* was on its own evolutionary pathway shortly before 6 Ma (Arenas-Viveros 2024) when the eastern cordillera experienced a second uplift (Garzione et al. 2008). At this point, the eastern slope of the Andes has had its characteristic corrugated topology since it first uplifted about 10 Ma, and as the mountain chain kept elevating, this jagged landscape created barriers for the movement of taxa at mid, and now also, high elevations (Graham 2009). Moreover, seasonally Dry Tropical Forests which had a continuous distribution from the Andean foothills to the Caatingas in Brazil during the upper Pleistocene, became disjunct and fragmented by other habitat types (e.g., Tucumano-Boliviano forests in the southern distribution of *A. boliviensis*) (Mogni et al. 2015). These historical barriers to migration along with adaptations to different environments (i.e., the different ecoregions inhabited by northern and southern samples) could explain the levels of divergence and the little to no admixture found between lineages of *A. boliviensis*. In addition to historical processes, the extensive transformation and exploitation of the landscape inhabited by the Bolivian chinchilla rat (Brandt and Townsend 2006; Killeen et al. 2008), could be a potential source of discontinuity for the species, and even if some of its populations are currently doing well this might not be the case as the environment changes in the future.

The ESUs described in this study (i.e., clades A, B and C) could have been isolated from one another by past processes and might continue to be by modern transformation and degradation of the landscape. One of the main purposes of identifying and conserving ESUs is to maintain genetic diversity that will maximize the evolutionary and adaptive potential of a species in the face of environmental change (Funk et al. 2012). This is of special importance in the eastern Andes because, in addition to human-driven transformation, studies have shown that vegetation shifts in the past (mostly of *Polylepis* woodlands within the Andean grasslands) have been mediated by variations in temperature, precipitation and burning regime (Williams et al. 2011), all of which are amplified by climate change. *Abrocoma boliviensis* is known to be associated with forested areas, unlike other abrocomids in the Altiplano that inhabit more open environments (Patton and Emmons 2015), and changes to the landscape threaten the future of its populations unless intervention for the management and conservation of the native landscape takes place.

In addition to being endangered and endemic, the Bolivian chinchilla rat is also rare, but this might present an advantage in at least one aspect of its conservation. When the aim is to preserve diversity, rare species are one of the best indicators to select sites for management and conservation (Lawler et al. 2003). In fact, protected areas that have been delineated to conserve rare species have been shown to protect biodiversity more generally (Drever et al. 2012). Moreover, the presence and maintenance of rare species contributes to and supports the functional structure of assemblages and ecosystems (Mouillot et al. 2013; Leitão et al. 2016). All of this, along with the potential to assign an economic value to the conservation of *A. boliviensis* (e.g., from ecotourism and conservation donations for a charismatic species), might help persuade the appropriate authorities and agencies to launch systematic monitoring and research programs (Drever et al. 2012).

In conclusion, based on the results presented herein and how little is known about *Abrocoma boliviensis*, our study highlights the urgency with which survey efforts must become the first order of action. Once more population-level data becomes available, demographic, ecological, and genetic studies should provide a better understanding of the species and the evolutionary trajectory of its lineages, including whether a taxonomic rearrangement is needed. This, in turn, will better inform any management and conservation actions, including areas for monitoring, creation of protected areas and corridors, and mitigation plans to reduce the effects of anthropogenic transformation of the landscape.

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Author contributions Daniela Arenas-Viveros and Jorge Salazar-Bravo contributed to the study conception and design. Material preparation and data collection were performed by all authors. Analyses were performed by Daniela Arenas-Viveros. The first draft of the manuscript was written by Daniela Arenas-Viveros. All authors read and approved the final manuscript.

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Data availability Data is provided within the manuscript or supplementary information files. Sequence data will be deposited in GenBank.

Declarations

Competing interests The authors declare no competing interests.

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