Conservation biogeography and diversity of tarantulas in Argentina

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Abstract

Introduction:

There is significant concern regarding the impact of many human activities and the subsequent biodiversity loss. Protected areas stand as crucial global conservation tools, their correct selection and design play a key role. The biology characteristics of tarantulas make them vulnerable to fragmentation in time and space, yet they remain underrepresented in ongoing conservation initiatives.

Aims/Methods:

This study seeks an integrative biogeographic approach to conservation by assessing multi-specific distribution patterns, specific richness, and tarantula endemism in Argentina. To achieve this, we performed an endemicity analysis using the optimality criterion and a panbiogeographical approach. Finally, we evaluated the protection degree of the areas obtained with the known protected areas.

Results

The most supported areas of endemism and the richest were found in Southern Andean Yungas and the Atlantic Forest of Alto Paraná. Also, the Valdivian Temperate Forest was recovered as an area of endemism. From panbiogeographic analysis, biogeographic nodes were located in La Rioja, Formosa and Salta provinces. Many of the obtained areas exhibit low or no degree of protection.

Discussion/Conclusion:

There is partial agreement among the different results obtained (species richness, areas of endemism, biogeographic nodes) with previous studies in relation to relevant conservation areas. Some new areas identified are also relevant for tarantula conservation.

Implications for insect conservation:

We propose priority conservation areas of Argentinean tarantulas and emphasize their significance for the persistence of their populations.

Introduction

Conservation biogeography is a recent discipline that applies biogeographical principles, theories, and analyses related to the distribution dynamics of taxa to solve many problems related to biodiversity conservation (Escalante and Morales 2015; Whittaker et al. 2005). The primary objective of this discipline is to identify areas that can serve as reservoirs for species, populations, biological assemblages, and ecosystems. This selection is based on the concepts of complementarity, irreplaceability, and vulnerability, following the guidelines of systematic conservation planning (Torres Miranda et al. 2011). The discipline's focus on identifying suitable areas is directly related to the current challenges in designing protected areas, which could be a problem in terms of conservation, as it requires the active participation from governmental entities. In Argentina, there are 437 protected areas, which cover 11.9% of the country's continental surface (Ferrero 2018). However, the regional distribution of these protected areas is concentrated in specific regions, neglecting other important environment across Argentina. Protected areas are considered one of the primary global conservation tools, mitigating various anthropogenic impacts, including deforestation, grazing, agriculture, and biodiversity loss (Portelli and Díaz Gomez 2017).

In recent decades, systematic conservation planning involves the identification of priority conservation areas (PCAs) by considering not only the highest number of endemic species, representativeness, and complementarity, but also the isolation of these areas from pressures that could threaten their persistence (Margules and Sarkar 2009). The PCAs play a crucial role in preserve species habitat and the associated environmental processes. While there is no unified criterion for selecting PCAs, recent studies advocate for the inclusion of "marginal" species, such as arthropods and spiders, which have traditionally been overlooked in PCAs proposal (Wilson et al. 2012).

The geographic distribution of endemic species represents a historical and ecological footprint of all biological entities, making these endemic areas significant for biodiversity conservation plans (Zhao et al. 2021). Although there are various definitions of areas of endemism, usually they are described as regions delimited by the congruent distribution of at least two endemic taxa, indicating spatial homology (Morrone 2001; Platnick 1991). Searching areas where taxa with diverse characteristics and evolutionary histories coincide enhances the reliability of biogeographic relationship hypotheses, as a shared distribution among different groups suggest common evolutionary processes (Estrada Sánchez et al. 2019). Common approaches in conservation biogeography for identifying areas of endemism include panbiogeography (Arzamendia and Giraudo 2012; Craw et al. 1999; Croizat 1958) and the optimality criterion (Szumik et al. 2002; Szumik and Goloboff 2004).

Regarding to the optimality criterion, is one of the most recent methods employed to identify areas of endemism. This criterion incorporates an optimization approach based on Platnick's (1991) definition of areas of endemism, which assess the number of taxa present and their contribution to the area, detecting congruencies in the distribution of the different taxa to establish areas of endemism.

Panbiogeography is a theory within historical biogeography that recognizes the coevolution of geographical barriers and biotas, summarized in the concept that "earth and life evolve together" (Croizat 1964). This approach assumes that the coincident distribution of different taxa means the presence of ancestral biotas, whose geographic ranges have become fragmented through vicariant events (Grehan 2011). Panbiogeography consists in constructing individual tracks based on point distribution and generalized tracks (overlapping of individual tracks). When two or more generalized tracks overlap in a particular area, a biogeographic node could be identified. Nodes are highly significant from a conservation perspective as they harbor biotic elements from many origins, thus could be considered as "hot spots" (Ferretti 2013). Biogeographic nodes are characterized as biological areas of endemism or centers of high diversity (Heads 2004). In this context, nodes can aid in identifying PCAs that possess the highest biogeographic diversity, taking into account the species richness, and the distinctiveness of the biota present within those nodes.

Tarantulas (Theraphosidae) are considered within the group of “marginal species”. This group exhibit several life-history traits that are relevant when considering the establishment of PCAs (Wilson et al. 2012). These traits include limited dispersal capacity, long life cycles, habitat specificity, and site fidelity (Newton et al. 2020). Such characteristics model species population structures and contribute to geographic fragmentation over space and time. Consequently, many taxa within this family have restricted geographic distributions, making them highly vulnerable and relevant to focus conservation efforts. Moreover, tarantulas are not only impacted by anthropogenic activities that modify their habitats but also by the effects of global climate change. Unfortunately, particular aspects of spider conservation have been overlooked in many studies, possibly due to negative cultural perception based mainly on a lack of knowledge. Effective management of tarantula populations relies on understanding their main threats, ecological significance, and the development of public policies that engage society in management, protection, and conservation actions (Mendoza 2020).

Despite an increase in taxonomic and biological knowledge of Argentinean tarantulas, information regarding their distribution patterns and conservation status remains scarce (Copperi et al. 2011; Ferretti 2015; Schwerdt et al. 2019). This study aims to i) develop an integrative biogeographic approach to tarantula conservation by evaluating multispecies distribution patterns studying species richness, and identifying areas of endemism; ii) evaluate these patterns in relation to existing protected areas and proposing potential PCAs for tarantulas.

Materials and methods

Distribution data and map preparation

The geographic distribution of all species belonging to the family Theraphosidae in Argentina has been determined, including species that are reliable identified and taxonomically valid. Distribution points were compiled from published geographic coordinates found in taxonomic works available in the World Spider Catalog (2023) (https://wsc.nmbe.ch/) and GBIF (www.gbif.org/es/). In addition, geographic coordinates of species found during our field campaigns in recent years were also included. For localities without precise geographic coordinates, georeferencing was achieved using Google Maps (www.google.com.ar/maps) or Geody (www.geody.com).

All distribution points were exported to DIVA GIS v7.5 (Hijmans et al. 2001) and converted into shape format to be projected on Argentina shapes using QGIS v3.24 (www.qgis.org/es/site/).

The layers for the different maps used were obtained from www.diva-gis.org (political provinces of Argentina), from the biogeographic provinces of Arana et al. (2017) (www.exa.unrc.edu.ar/page/?elEspinal), and ecoregions from Olson et al. (2001) (www.sciencebase.gov).

Species richness

We calculate specific richness for political provinces, biogeographic provinces, and ecoregions by overlaying the distribution maps on spatial layers using QGIS v3.24. Those points located on the boundaries of the evaluated regions were considered as presence points for both regions.

Endemicity analysis

Optimality criterion

To identify areas of endemism (AE), we applied the optimality criterion proposed by Szumik et al. (2002) and Szumik and Goloboff (2004), which was implemented in the software NDM/VNDM v3.1. Grid sizes of 2°, 1.5°, and 1° were used. To evaluate the performance of the approach, we implemented an analysis without applying cell fills and also proved the fill options for 100, 50, and 25 of observed presences. Those areas with an endemicity index (EI) higher than 2 were retained. A flexible consensus of 100 was used to summarize the areas obtained.

Panbiogeography

Species distributions were analyzed using the software Croizat (Cavalcanti 2009). This method generates individual tracks of each species and then overlap them resulting in generalized tracks. The parameters used in Croizat were: cut value = 1.5, lmax = 0.5, lmin = 0.5, maxline = 1, ci = 0.8, strategy = croizat0. The individual and generalized tracks were then exported in shape format and overlapped using QGIS v3.24 program to identify biogeographic nodes.

Priority areas for conservation

The areas of endemism obtained, along with the distribution points of the species that contributed to them, were overlapped with the layer containing the information of protected areas in Argentina (https://www.argentina.gob.ar/ambiente/areas-protegida/mapa). Based on the extent of these areas, the degree of protection for the endemic areas was evaluated, as well as the distribution patterns of the species that contribute to these areas.

Results

Distribution records and species richness

We obtained 580 georeferenced records for the 42 tarantula species distributed in Argentina (Table 1).

Table 1
List of tarantula’s species analyzed with their respective record numbers.

Species	**Number of records**
Acanthoscurria chacoana Bréthes 1909	10
Acanthoscurria cordubensis Thorell 1894	36
Acanthoscurria musculosa Simon 1892	48
Catumiri argentinense (Mello-Leitão 1941)	59
Catumiri parvum (Keyserling 1878)	2
Cyriocosmus versicolor (Simon 1897)	5
Euathlus diamante Ferretti 2015	7
Euathlus grismadoi Ríos-Tamayo 2020	1
Euathlus mauryi Ríos-Tamayo 2020	3
Euathlus pampa Ríos-Tamayo 2020	1
Euathlus sagei Ferretti 2015	4
Euathlus tenebrarum Ferretti 2015	4
Euathlus truculentus L. Koch 1875	6
Eupalaestrus campestratus (Simon 1891)	9
Eupalaestrus crassimetatarsis Borges, Paladini and Bertani 2021	2
Eupalaestrus larae Ferretti and Barneche 2012	3
Eupalaestrus weijenberghi (Thorell 1894)	26
Grammostola anthracina (C. L. Koch 1842)	6
Grammostola burzaquensis Ibarra 1946	14
Grammostola chalcothrix Chamberlin 1917	21
Grammostola diminuta Ferretti, Pompozzi, González and Pérez-Miles 2013	7
Grammostola doeringi (Holmberg 1881)	61
Grammostola inermis Mello-Leitão 1941	36
Grammostola pulchripes (Simon 1891)	25
Grammostola quirogai Montes de Oca, D'Elía and Pérez-Miles 2016	8
Grammostola vachoni Schiapelli and Gerschman 1961	54

Species	Number of records
Hapalotremus chasqui Ferretti, Cavalllo, Chaparro, Ríos-Tamayo, Seimon and West 2018	4
Hapalotremus martinorum Cavallo and Ferretti 2015	4
Homoeomma elegans (Gerschman and Schiapelli 1958)	2
Homoeomma uruguayense (Mello-Leitão 1946)	22
Phrixotrichus pucara Ferretti 2015	1
Phrixotrichus vulpinus (Karsch 1880)	9
Plesiopelma aspidosperma Ferretti and Barneche 2013	2
Plesiopelma longisternale (Schiapelli and Gerschman 1942)	56
Plesiopelma paganoi Ferretti and Barneche 2013	2
Tmesiphantes crassifemur (Gerschman and Schiapelli 1960)	2
Tmesiphantes mutquina (Perafán and Pérez-Miles 2014)	2
Tmesiphantes uru (Perafán and Pérez-Miles 2014)	5
Tmesiphantes yupanqui (Perafán and Pérez-Miles 2014)	1
Pterinopelma longisternalis (Bertani 2001)	2
Pterinopelma roseus (Mello-Leitão 1923)	2
Vitalius paranaensis Bertani 2001	6

The resulting overlap of all distribution records in Argentina are shown in Fig. 1. We found that 22 species were exclusively distributed in Argentina, accounting for 52% of the total. These species include *Euathlus diamante* Ferretti 2015, E. *grismadoi* Ríos-Tamayo 2020, *E. mauryi* Ríos-Tamayo 2020, *E. pampa* Ríos-Tamayo 2020, *E. sagei* Ferretti 2015, E. *tenebrarum* Ferretti 2015, *Euapalestrus larae* Ferretti and Barneche 2012, *Grammostola chalcothrix* Chamberlin 1917, *G. diminuta* Ferretti, Pompozzi, González and Pérez-Miles 2013, *G. doeringi* (Holmberg 1881), *G. inermis* Mello-Leitão 1941, *G. vachoni* Schiapelli and Gerschman 1961, *Hapalotremus chasqui* Ferretti, Cavalllo, Chaparro, Ríos-Tamayo, Seimon and West 2018, *H. martinorum* Cavallo and Ferretti 2015, *Homoeomma elegans* (Gerschman and Schiapelli 1958), *Phrixotrichus pucara* Ferretti 2015, *Plesiopelma aspidosperma* Ferretti and Barneche 2013, *P. paganoi* Ferretti and Barneche 2013, *Tmesiphantes crassifemur* (Gerschman and Schiapelli 1960), *T. mutquina* (Perafán and Pérez-Miles 2014), *T. uru* (Perafán and Pérez-Miles 2014), and *T. yupanqui* (Perafán and Pérez-Miles 2014).

Most species showed between one and six georeferenced records, and also between six and 11 records. However, many species had more than 50 records.

Table 2

List of the provinces, biogeographic provinces and ecoregions of Argentina with their respective specific richness of the family Theraphosidae.

Provinces	**Richness**
Salta	16
Chaco	12
Misiones	12
Mendoza	10
Santiago del Estero	9
Córdoba	9
Tucumán	8
La Rioja	8
Entre Ríos	8
Buenos Aires	8
Formosa	7
Catamarca	7
Jujuy	6
Santa Fe	6
Neuquén	6
Corrientes	5
San Juan	4
San Luis	4
La Pampa	4
Rio Negro	4
Chubut	2
Santa Cruz	0
Tierra del Fuego	0
Biogeographic provinces	
Chaco	22
Yungas	15

Provinces	**Richness**
Pampeana	14
Monte	13
Paraná Forest	11
Araucaria Forest	6
Cuyana High Andean	5
Comechingones	4
Patagonia	3
Maule	3
Puna	1
Valdivian Forest	1
Magellanic Forest	0
Ecoregions	
Dry Chaco	21
Southern Andean Yungas	15
Humid Pampas	13
Atlantic Forest of Alto Paraná	11
Espinal	10
Humid Chaco	8
Paraná Flooded Savannah	8
Low Monte	8
Southern Andean Steppe	7
High Monte	7
Southern Cone Mesopotamian Savanna	5
Patagonian Steppe	4
Valdivian Temperate Forest	3
Araucaria Moist Forest	3
Central Andean Puna	1
Central Dry Andean Puna	0

Provinces	Richness
Magellanic Subpolar Forest	0

Regarding the species richness in provinces, biogeographic provinces and ecoregions of Argentina (Table 2), the highest values were observed in Salta, Chaco, Misiones, and Mendoza provinces. Santa Cruz and Tierra del Fuego were the only provinces without distribution records. Based on biogeographic provinces, the richest regions were Chaco, Yungas, Pampeana and Monte, while Magellanic Forest had no records. Among the ecoregions, the Dry Chaco had the highest number of species, followed by the Southern Andean Yungas, Humid Pampas, Atlantic Forest of Alto Paraná, and Espinal, which exhibited similar levels of richness. The Central Dry Andean Puna and Magellanic Subpolar Forest ecoregions showed no tarantula records.

Optimality criterion

The NDM/VNDM analysis identified 65 areas of endemism.

The analysis of endemicity without cell fills found one area of endemism using 2° and 1.5°grids, while no endemism area was found using 1° grid (Table 3) (Fig. 2; Figs. 1 and 3 in Online Resourse).

Table 3
Areas of endemism obtained for the different unfilled grid sizes, together with the species supporting these areas and their endemicity value expressed in parentheses. GZ = grid size, Ae = areas of endemism, EI = endemicity index.

GZ	Ae	Number of cells	EI	Species
2°	Ae_0	5	2.04–2.30	*Eupalaestrus campestratus* (0.643), *Pterinopelma roseus* (0.700), *Homoeomma elegans* (0.700)
1.5°	Ae_0	4	2–2.25	*Euathlus sagei* (0.750), *Phrixotrichus vulpinus* (0.500), *Euathlus tenebrarum* (0.750)
1°	—	—	—	—

When applying cell fills of 100 under whit different grid sizes, a total of 17 areas of endemism were found (Table 1 in Online Resourse). Using a 2° grid size, five AE were identified (EI = 3–6). The analysis with a 1.5° grid size found eight AE (EI = 2.2–4.5), and a 1° grid size resulted in four AE (EI = 2-3.2).

Implementing a cell fill of 50, under different grid sizes, resulted in a total of 24 areas of endemism (Table S2 in Online Resource). Analysis for 2° identified 12 AE (EI = 2.2–4.3). Analysis for 1.5° revealed six AE (EI = 2.5–3.9), and for 1° six AE were obtained (EI = 2-2.8).

The analysis with cell fill of 25 using different grid sizes resulted in a total of 22 areas of endemism (Table 4). At a grid size of 2°, 13 AE were identified (EI = 2-4.5). Using a 1.5° grid size, five AE were found (EI = 2-3.3), and using a 1° grid size, four AE were obtained (EI = 2-2.8) (Fig. 3; Figs. 2 and 4 in Online Resource).

Table 4

Areas of endemism obtained for the different grid sizes with fill 25, together with the species supporting these areas and their endemicity value expressed in parentheses. GZ = grid size, Ae = areas of endemism, EI = endemicity index.

GZ	Ae	Number of cells	EI	Species
2°	Ae$_0$	5	2.04–2.29	*Euathlus pampa* (0.7), *Tmesiphantes mutquina* (0.9), *Hapalotremus chasqui* (0.444)
	Ae$_1$	5	3.83–4.08	*Cyriocosmus versicolor* (0.409), *Hapalotremus martinorum* (0.7), *Tmesiphantes crassifemur* (0.8), *Tmesiphantes yupanqui* (0.7), *Hapalotremus chasqui* (0.444), *Plesiopelma paganoi* (0.389), *Tmesiphantes uru* (0.389)
	Ae$_2$	6	4.28–4.53	*Cyriocosmus versicolor* (0.417), *Plesiopelma aspidosperma* (0.333), *Tmesiphantes crassifemur* (0.750), *Tmesiphantes yupanqui* (0.667), *Hapalotremus chasqui* (0.450), *Plesiopelma paganoi* (0.833), *Tmesiphantes uru* (0.833)
	Ae$_3$	5	3.95–4.20	*Eupalaestrus campestratus* (0.556), *Homoeomma elegans* (0.9), *Pterinopelma roseus* (0.9), *Eupalaestrus crassimetatarsis* (0.7), *Pterinopelma longisternalis* (0.9)
	Ae$_4$	7	3.92–4.17	*Cyriocosmus versicolor* (0.423), *Hapalotremus chasqui* (0.857), *Tmesiphantes crassifemur* (0.714), *Euathlus pampa* (0.643), *Hapalotremus martinorum* (0.643), *Tmesiphantes yupanqui* (0.643)
	Ae$_5$	8	2.18–2.43	*Eupalaestrus campestratus* (0.938-1), *Vitalius paranaensis* (0.545-0.7), *Eupalaestrus crassimetatarsis* (0.626–0.643)
	Ae$_6$	4	3.12–3.37	*Euathlus sagei* (0.750), *Phrixotrichus pucara* (0.750), *Euathlus tenebrarum* (0.875), *Phrixotrichus vulpinus* (0.750)
	Ae$_7$	3	2.97–3.22	*Hapalotremus chasqui* (0.429), *Tmesiphantes crassifemur* (1), *Tmesiphantes yupanqui* (0.833), *Plesiopelma paganoi* (0.357), *Tmesiphantes uru* (0.357)
	Ae$_8$	4	2.5–2.75	*Plesiopelma paganoi* (1), *Tmesiphantes uru* (1), *Tmesipantes crassifemur* (0.5)
	Ae$_9$	5	2.12–2.37	*Cyriocosmus versicolor* (0.556), *Plesiopelma aspidosperma* (1), *Eupalaestrus larae* (0.571)
	Ae$_{10}$	4	3–3.25	*Homoeomma elegans* (1), *Pterinopelma roseus* (1), *Pterinopelma longisternalis* (1)
	Ae$_{11}$	5	3.2–3.45	*Euathlus pampa* (0.7), *Tmesiphantes crassifemur* (0.8), *Hapalotremus chasqui* (1), *Tmesiphantes yupanqui* (0.7)

GZ	Ae	Number of cells	EI	Species
	Ae_{12}	3	2.66–2.91	*Euathlus tenebrarum* (1), *Phrixotrichus vulpinus* (0.833), *Phrixotrichus pucara* (0.833)
1.5°	Ae_0	6	2.97–3.22	*Cyriocosmus versicolor* (0.550), *Plesiopelma aspidosperma* (0.563), *Tmesiphantes uru* (0.667), *Hapalotremus chasqui* (0.450), *Tmesiphantes crassifemur* (0.750)
	Ae_1	4	2.56–2.81	*Hapalotremus chasqui* (0.438), *Tmesiphantes crassifemur* (0.875), *Hapalotremus martinorum* (0.5), *Tmesiphantes uru* (0.750)
	Ae_2	6	2.04–2.29	*Euathlus pampa* (0.667), *Hapalotremus martinorum* (0.750), *Hapalotremus chasqui* (0.625)
	Ae_3	4	2.12–2.37	*Euathlus sagei* (0.750), *Phrixotrichus vulpinus* (0.5), *Euathlus tenebrarum* (0.875)
	Ae_4	5	3.08–3.33	*Eupalaestrus crassimetatarsis* (0.389), *Pterinopelma longisternalis* (0.9), *Homoeomma elegans* (0.8), *Pterinopelma roseus* (1)
1°	Ae_0	5	2.74–2.99	*Plesiopelma paganoi* (0.7), *Tmesiphantes uru* (0.643), *Tmesiphantes crassifemur* (0.7), *Tmesiphantes yupanqui* (0.7)
	Ae_1	9	2.14–2.39	*Euathlus sagei* (0.722), *Phrixotrichus vulpinus* (0.591), *Euathlus tenebrarum* (0.833)
	Ae_2	6	2.58–2.83	*Homoeomma elegans* (0.750), *Pterinopelma roseus* (1), *Pterinopelma longisternalis* (0.833)
	Ae_3	5	2.2–2.45	*Euathlus tenebrarum* (0.5), *Phrixotrichus vulpinus* (1), *Phrixotrichus pucara* (0.7)

The regions where these areas of endemism were found remained consistent across different grid sizes and fill options. In this way, we present the regions based in the most detailed hypothesis, using a 1° grid size and cell fills of 25. Thus, we identified AE in the Atlantic Forest of Alto Paraná, Araucaria Moist Forest, Dry Chaco, Southern Andean Yungas, Valdivian Temperate Forest, Patagonian Steppe, and Low Monte ecoregions.

Panbiogeography

Panbiogeographic analysis produced 38 individual tracks (Fig. 4a). Individual tracks could not be constructed for the following species due to having a single distribution record: *Euathlus grismadoi, E. pampa, Phrixotrichus pucara*, and *Tmesiphantes yupanqui*. By overlapping the individual tracks, we identified 17 generalized tracks with support from at least two individual tracks (Table 3 in Online Resourse) (Fig. 4b). The overlapping of the generalized tracks revealed four biogeographic nodes. The biogeographic node N1 it is located in La Rioja province, supported by the generalized traces T8, T15 and T17. The N2 it is located in Tucumán province supported by T6, T13, T16 and T17. The N3 it is located in

Salta province supported by T7, T16 and T17, finally, N4 it is located in Formosa province supported by T10, T15 and T16 (Fig. 4c).

Areas of endemism and their relation to protected areas

In relation to the evaluation of protection for the identified areas of endemism from previous analyses, approximately 20% of the AE obtained for the Atlantic Forest of Alto Paraná and the Araucaria Moist Forest are currently protected by inclusion in natural reserves (Fig. 5a). The AE identified in the Southern Andean Yungas, Dry Chaco, and Central Andean Puna regions are protected in a high degree, with approximately 70% of coverage (Fig. 5b). For the Valdivian Temperate Forest, Patagonian Steppe, and Low Monte, around 40% of the region is protected by some natural reserves, predominantly along the Andes Mountains region (Fig. 5c). When considering the distribution patterns of the endemic species contributing to each AE, the highest percentages of protection covering by natural reserves is evidenced in Misiones and Neuquén provinces (Fig. 5a, c). Contrary, in Salta province, most of the protected areas do not include the distributional ranges of the species contributing to the specific AE (Fig. 5b).

Discussion

The distribution records for tarantulas in Argentina usually were low for most species. This could be not only to the lack of sampling effort in many regions but also to the restricted geographic ranges exhibited by some species due to the specificity of their occupied environments (Ferretti et al. 2012). However, some particular species displayed a higher number of records, which could correspond to species with wide distributions (e.g., *Plesiopelma longisternale* (Schiapelli and Gerschman 1942)), synanthropic species (e.g., *Catumiri argentinense* (Mello-Leitão 1941)) or large species that are easy to found (e.g., the genera *Acanthoscurria* and *Grammostola*).

In Argentina, Theraphosidae is widely distributed, ranging from the central Chubut province in the south to the most northern provinces. The highest species richness was observed in the provinces of Chaco, Misiones, Mendoza, and Salta, as well as in the biogeographic provinces of Chaco, Monte, Pampeana, and Yungas. Among the ecoregions, Dry Chaco, Southern Andean Yungas, Humid Pampas, and Atlantic Forest of Alto Paraná exhibit the highest richness. The high richness observed in Salta province (Yungas region) has been previously documented for spiders (Rubio 2015), indicating that this region is characterized by high biodiversity due to variations in altitude variation of vegetation, which generate the coexistence of species from different biogeographic origins along a gradient. A high diversity of plants has also been observed in the dry region of Chaco, being the richest in terms of endemic taxa, which is related to its unique climatic characteristics (Morales et al. 2019). Chaco also has a significant biodiversity, with approximately 145 mammal species (10% endemic), 409 bird species, 54 reptile species, and 34 amphibian species recorded in the region (Bucher and Huszar 1999). In northeastern Argentina, numerous studies have been conducted on the high diversity of spiders, particularly jumping spiders (Rubio 2014), where it is postulated that the Paranaense forest of Misiones possess high biodiversity and endemism level similar to the Yungas. In addition, the high richness of tarantulas found in Mendoza province, as revealed in this study, has not been reported for other taxa. Therefore, we strongly suggest that new biodiversity studies at this region should be conducted in order to unveil its significance in relation to areas of endemism.

The areas of endemism obtained, which remained consistent under different fill options and grid sizes, include the ecoregions of Atlantic Forest of Alto Paraná, Araucaria Moist Forest, Dry Chaco, Southern Andean Yungas, Valdivian Temperate Forest, Patagonian Steppe, and Low Monte. These areas of endemism were also identified within the biogeographic provinces of Parana Forest, Araucaria Forest, Pampeana, Chaco, Yungas, Puna, Monte, Patagonia, Maule, and Valdivian Forest. The analysis without fill option revealed areas of endemism for the ecoregions of Atlantic Forest of Alto Paraná, Araucaria Moist Forest, Southern Cone Mesopotamian Savanna, Humid Chaco, and Paraná Flooded Savanna using a 2° grid. The 1.5° grid resulted in areas of endemism in the ecoregions of Valdivian Temperate Forest, Patagonian Steppe, and Low Monte. Consequently, these areas of endemism without fill option were located within the biogeographic provinces of Paraná Forest, Araucaria Forest, Pampeana, and Chaco (2° grid) and within the biogeographic provinces of Monte, Patagonia, Maule, and Valdivian Forest (1.5° grid). The use of different grid sizes often leads to the identification of distinct patterns, which are influence by specific characteristics of the data, such as the spatial distribution. Furthermore, by using different grid sizes in the analyses allowed us for the recognition of areas of endemism with different attributes, including size and species composition. As proposed, the identification of these areas using different grid sizes provides strong support (Casagranda et al. 2009). Although the analysis without cell fill does not enable us to estimates potential species presence, filling the cell with different parameters provides valuable information as it may reflect the dispersal characteristics specific to the taxa studied. In this study, employing different filling options resulted in the identification of areas of endemism within the same regions, but with a higher number of supporting cells, potentially due to the implementation based solely on observed distribution records (Casagranda et al. 2009).

Most of the areas of endemism identified for tarantulas in Argentina are congruent with previous findings for other taxonomic groups. Thus, the Atlantic Forest of Alto Paraná and Araucaria Moist Forest region, has been proposed as area of endemism for plants (Szumik et al. 2012), fish (Araya et al. 2021), reptiles (Giraudo and Arzamendia 2018; Szumik et al. 2012), mammals, birds, insects (Szumik et al. 2012), and other mygalomorph spiders (Ferretti et al. 2014). Also, the Yungas region is considered an hyper diverse area, with proposed endemicity in plants (Aagesen et al. 2012; Szumik et al. 2012), reptiles, mammals (Sandoval et al. 2010; Sandoval et al. 2021; Szumik et al. 2012), birds, insects (Cuezzo et al. 2007; Navarro et al. 2009; Szumik et al. 2012) and other mygalomorph spiders (Ferretti et al. 2014). The Valdivian Forest and Patagonian Steppe also exhibit areas of endemism in insect species (Domínguez et al., 2006) and other mygalomorph spiders (Ferretti et al. 2014). The identification of areas of endemism through the overlapping distribution of diverse endemic taxa suggest the presence of different speciation processes by common factors (Szumik et al. 2002).

Some particular theraphosid species contributed significantly to endemicity in the same areas, and this was consistent across different grid sizes. Notably, the species *H. elegans*, *Pterinopelma roseus* (Mello-

Leitão 1923), *P. longisternalis* (Bertani 2001), and *Eupalaestrus crassimetatarsis* Borges, Paladini and Bertani 2021 are exclusively associated with the Atlantic Forest of Alto Paraná and the Araucaria Moist Forest, supporting this area of endemism. It should be emphasized that although *P. roseus* and *P. longisternalis* are also distributed in Brazil, their geographic records are restricted to the same ecoregions (Bertani 2001). In the Yungas region, species such as *H. martinorum, H. chasqui, Euathlus pampa, T. crassifemur, T. yupanqui*, and *T. mutquina* are strictly associated with the Southern Andean Yungas, Dry Chaco, and to the Central Andean Puna in a more restricted range. The genus *Hapalotremus*, recently discovered in Argentina, comprises species restricted to high-altitude cloud forest environments (Cavallo and Ferretti 2015; Ferretti et al. 2018), while *Tmesiphantes* exhibits a disjunct distribution in the Argentinean Yungas and the Brazilian Cerrado (Fabiano da Silva et al. 2019). Similarly, *Euathlus sagei*, *E. tenebrarum*, *Phrixotrichus pucara*, and *P. vulpinus* (Karsch 1880) show strong support for the endemicity of the areas in the Valdivian Temperate Forest, Patagonian Steppe, and the Low Monte. These species are characteristics representatives of the Andean Patagonian Forests in southwestern Argentina, but both genera have their highest diversity in Chile (Ferretti 2015). Using a grid size of 2° with fill of 25, we identified an area of endemism in the Dry Chaco region that was not recovered with other parameters. This area is supported by the species *Cyriocosmus versicolor* (Simon 1897), *Plesiopelma aspidosperma*, and *Eupalaestrus larae*. In a previous study on mygalomorph spiders, the Dry Chaco was not recovered as an area of endemism (Ferretti et al. 2014), indicating that by increasing the sampling effort and improve our knowledge about the distribution of tarantula species, new areas can be identified.

Regarding the panbiogeographic analysis under a conservation framework, we identified biogeographic nodes, usually considered relevant for the conservation because could represent areas of biotic convergence that can also comprise centers of endemism or centers of high diversity (Heads 2004). Thus, we propose four biogeographic nodes in Argentina. The first node is located in La Rioja province, where no areas of endemism were recovered using the optimality criterion. However, this node is associated with the Dry Chaco, which exhibit the highest tarantula richness, thus could be considered as a potential area of endemism to be considered for future conservation actions. Two additional nodes were associated with the Southern Andean Yungas, a high richness ecoregion also characterized by previously identified areas of endemism, emphasizing its conservation significance. Finally, another node was located in the Humid Chaco, which also displayed high richness, and where an area of endemism for mygalomorph spiders had been proposed previously (Ferretti et al. 2014).

Both the optimality criterion and panbiogeography showed similar results for the Southern Andean Yungas region in northwestern Argentina. Therefore, this area should be considered as prioritary for future conservation actions. Despite its relatively high degree of protection compare to the extent of existing protected areas, unfortunately, most tarantula's distributional records fall outside these areas because they are primarily located in the transition zone to the Dry Chaco. It is important to note that the Yungas environment is highly fragmented and significantly impacted by the anthropogenic activities, thus preventing even the continuity of species dispersal within the phytogeographic unit (Barquez and Diaz 2001).

In the Atlantic Forest of Alto Paraná region in northeastern Argentina, high species richness was observed, and areas of endemism were identified using the optimality criterion. However, this region has a low degree of protection relative to the identified areas. Nonetheless, the existing protected areas cover most of the distribution points of the endemic species that contributed to the area of endemism. Thus, two possible scenarios could be suitable: the species have been collected only inside the protected areas, indicating a bias in the sampling effort; or these species cannot persist outside the protected areas due to habitat modification and disturbances, thereby emphasizing the importance of protected areas for the conservation of relictual populations. Consequently, the Atlantic Forest is one of the most devastated and threatened ecosystems, where conservation is a key issue to maintaining species with large habitat requirements and preserving complete species assemblages, where ecological and evolutionary processes are constantly advancing (Giraudo et al. 2008).

Regarding the areas of endemism identified through the optimality criterion in the Valdivian Temperate Forests, a high degree of protection is observed with the extension of the existing protected areas, which cover almost all the distribution points of the endemic species that contributed to the area. The temperate forests of southern South America are globally significant ecosystems due to their high level of endemism (Smith Ramírez 2004), which should lead to them being protected in terms of conservation.

The areas of endemism identified through a panbiogeographic approach in La Rioja and Formosa provinces are not covered by any protected area. Therefore, these regions are crucial areas to prioritize for future conservation actions. This is not only because they are considered priority areas for conservation based on the present study, but also because they belong to the regions of Dry and Humid Chaco, both of which exhibit higher levels of tarantula’s diversity.

Biogeographic studies can make significant contribution to conservation policies. For instance, areas of endemism and biogeographic nodes may represent complex biotic regions, which deserve to be conserved. This contribution serves as a starting point for systematically planning of the protected areas. Recognizing endemic areas, along with endemic taxa and areas of high richness, is the initial step for more detailed studies (threat categories, socioeconomic value, political, and cultural aspects). The ultimate goal is to identify and propose the inclusion of these areas in a protected areas system. In the future, by combining this approach with diverse phylogenetic, geographic, and ecological studies of each species in the region, we can generate effective tools and valuable information to assist organizations and people making decisions on conservation policies.

Considering the biological characteristics and habitat requirements of the species under study (Fukushima et al. 2019; Guerra-Serrudo et al. 2023), the persistence of populations that currently lack any degree of protection could be mainly affected by the continuous degradation and modification of their natural environments (Aguilera et al. 2019; Guerra-Serrudo et al. 2023). Therefore, it is imperative to consider the areas identified through this contribution for future conservation actions, as this region could play a key role in preserving the diversity of Theraphosidae spiders in South America.

Conclusions

The restricted geographic distribution and habitat specificity of tarantulas can be viewed from both positive and negative perspectives. From a positive standpoint, these characteristics contribute to preserving the historical biogeographic signal, enabling the study of species' evolutionary history and their relationship with the environment. This study, through the identification of areas of endemism and the observation of numerous endemic taxa, further support tarantulas as an excellent model for biogeographic research. On the other hand, the negative aspect arises from the limited dispersal capacity of tarantulas, which result in a high level of local endemicity due to their restricted geographic distribution. Coupled with the specific habitat requirement, tarantulas become a vulnerable group. Additionally, they are under threats such as the increasing popularity of illegal pet trade, which enhances their vulnerability.

Considering these factors, along with their intrinsic value and the ecosystem services they provide, it is evident that tarantulas deserve protection.

In recent years, there has been an increasing destruction and degradation of natural environments, leading to habitat fragmentation and population isolation in patches; these factors further increase the risk of extinction. Therefore, the importance of protected areas in Argentina and their connection to the tarantula endemism areas identified in this study is emphasized to mitigate the threats affecting those populations.

Declarations

AUTHOR CONTRIBUTIONS: Conceptualization: [Maite Allegue], [Nelson Ferretti]; Methodology: [Maite Allegue], [Leonela Schwerdt], [Nelson Ferretti]; Formal analysis: [Maite Allegue], [Leonela Schwerdt], [Nelson Ferretti]; Investigation: [Maite Allegue], [Leonela Schwerdt], [Nelson Ferretti]; Writing- original draft preparation: [Maite Allegue]; Writing-review and editing: [Leonela Schwerdt], [Nelson Ferretti]; Funding acquisition: [Nelson Ferretti].

Competing interest. The authors declare no competing interest

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Figures

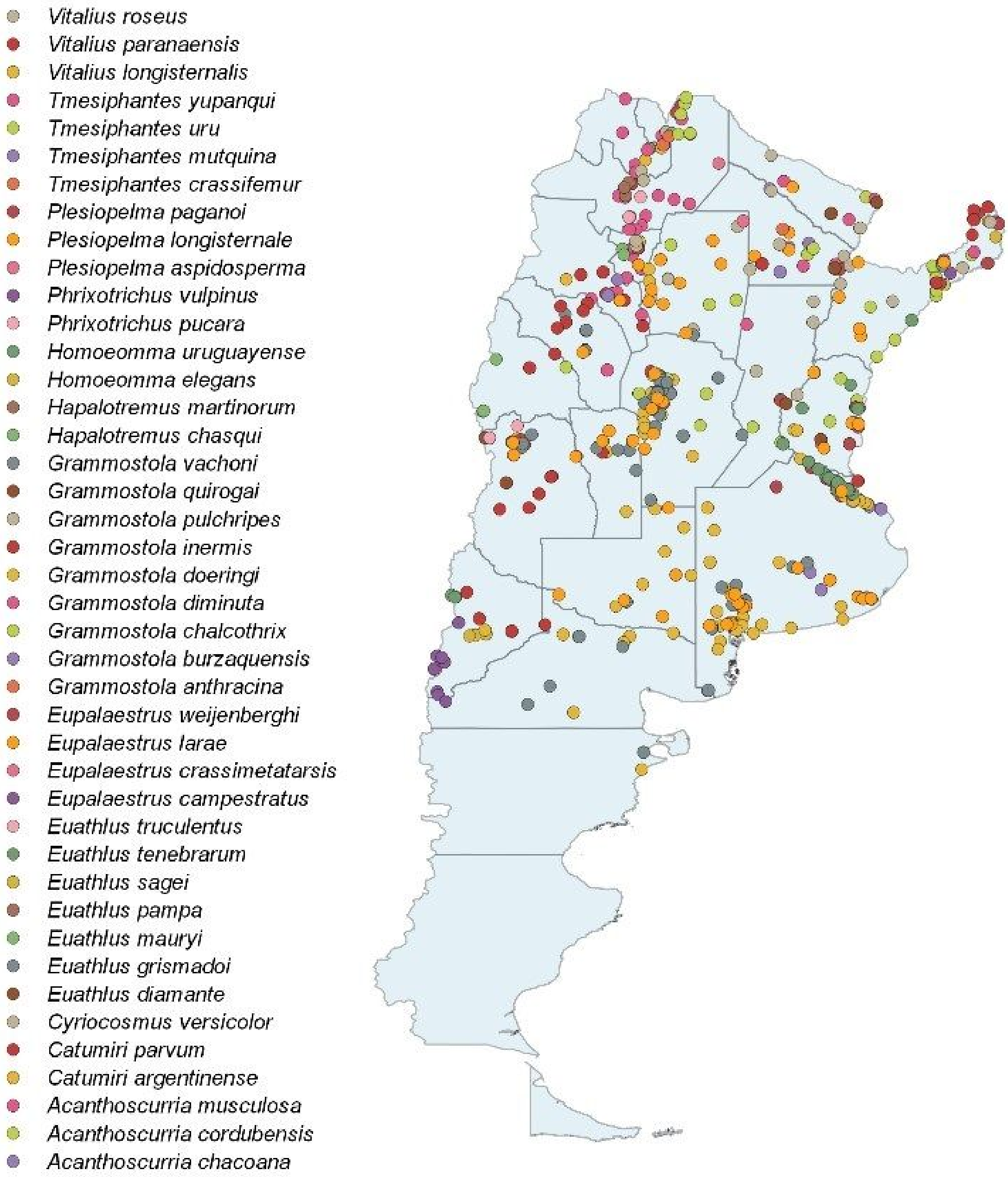

Figure 1

Distribution of species of the family Theraphosidae projected over provinces of Argentina

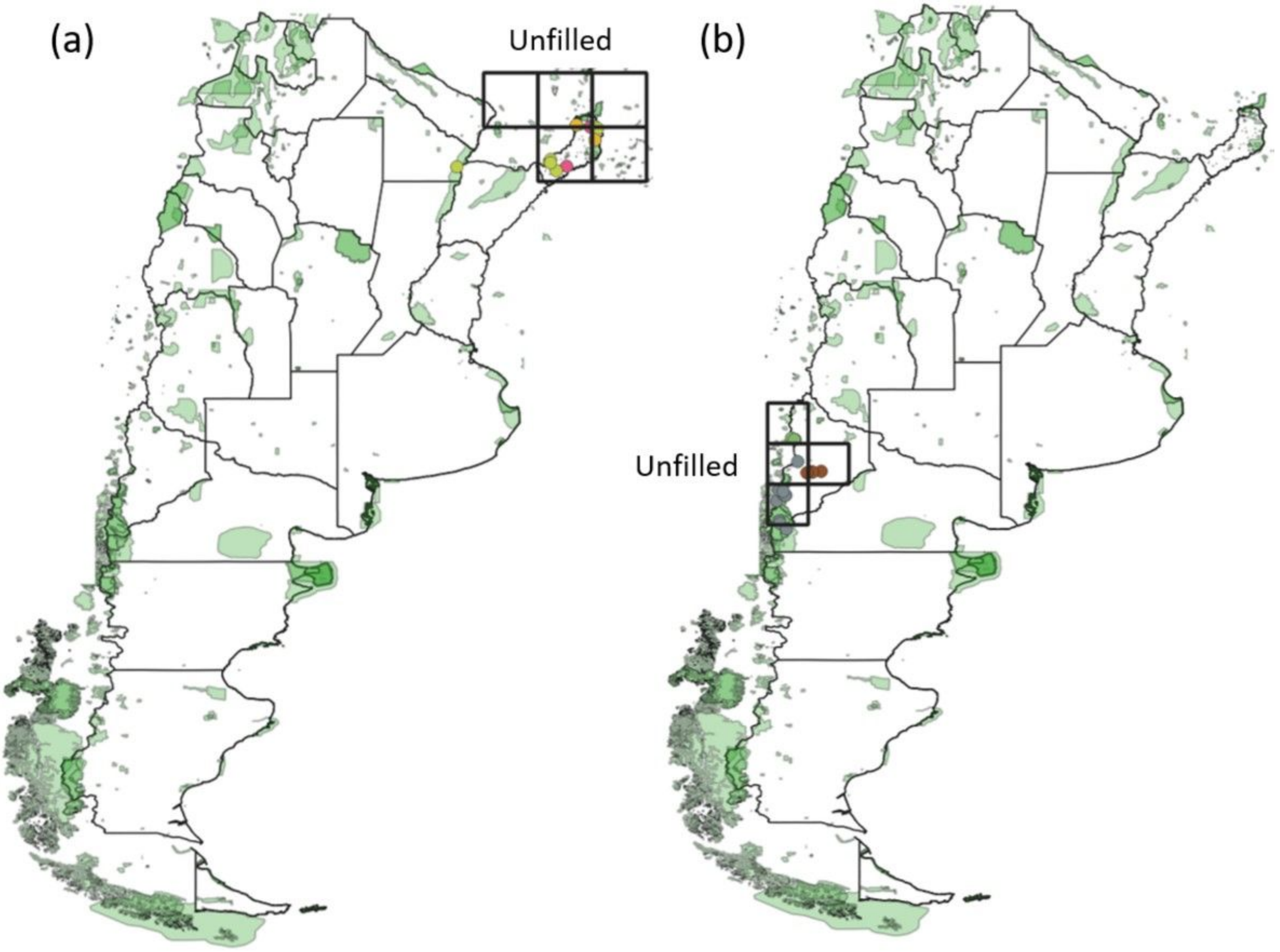

Figure 2

Areas of endemism obtained for Argentina without cell filling. a) 2° b) 1.5°. Protected areas are shown in green. The colored dots within the areas represent the distribution of the species that support them

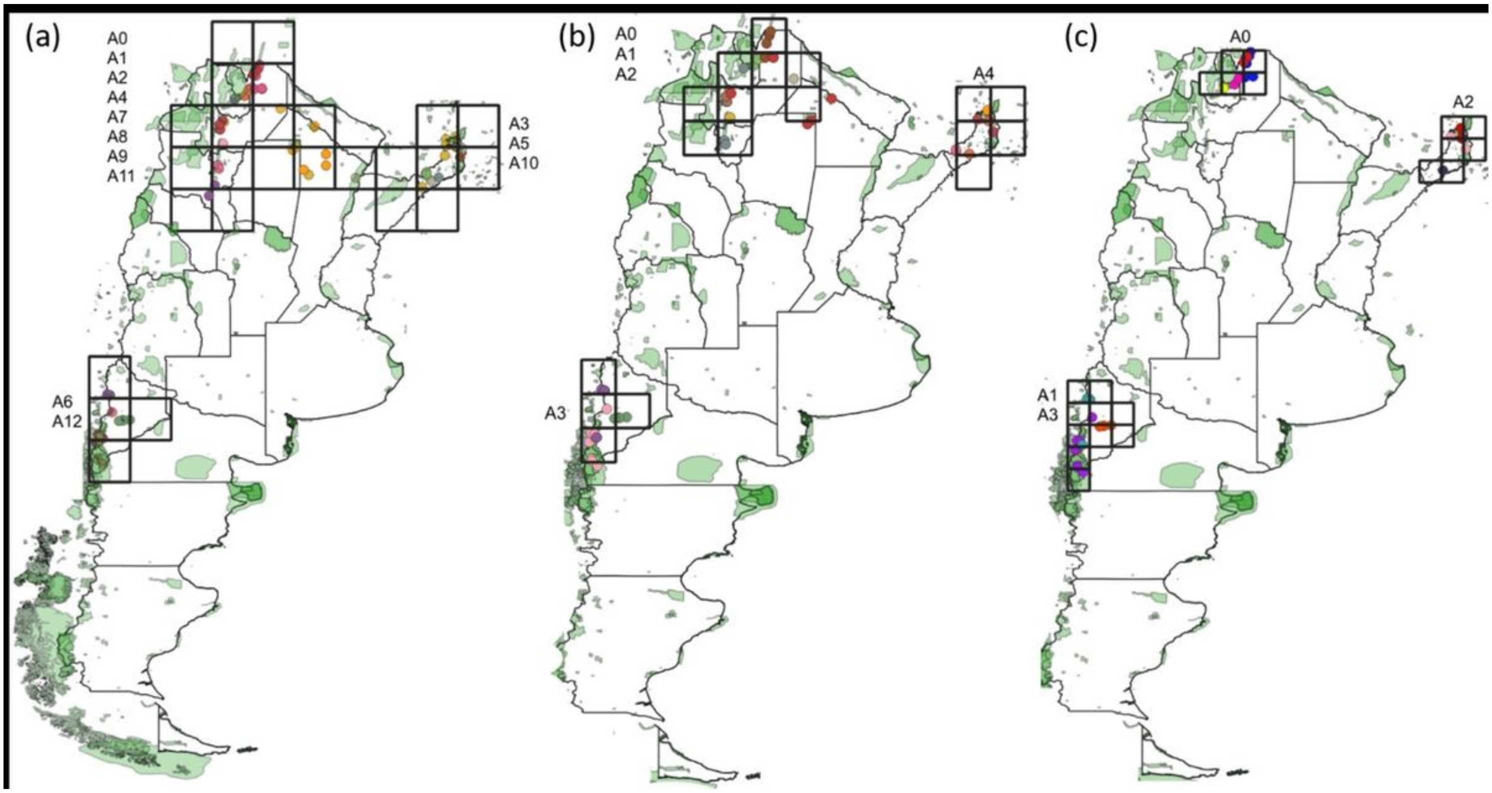

Figure 3

Areas of endemism obtained for Argentina with cell filling of 25. a) 2°. b) 1.5°. c) 1°. Protected areas are shown in green. The colored dots within the areas represent the distribution of the species that support them

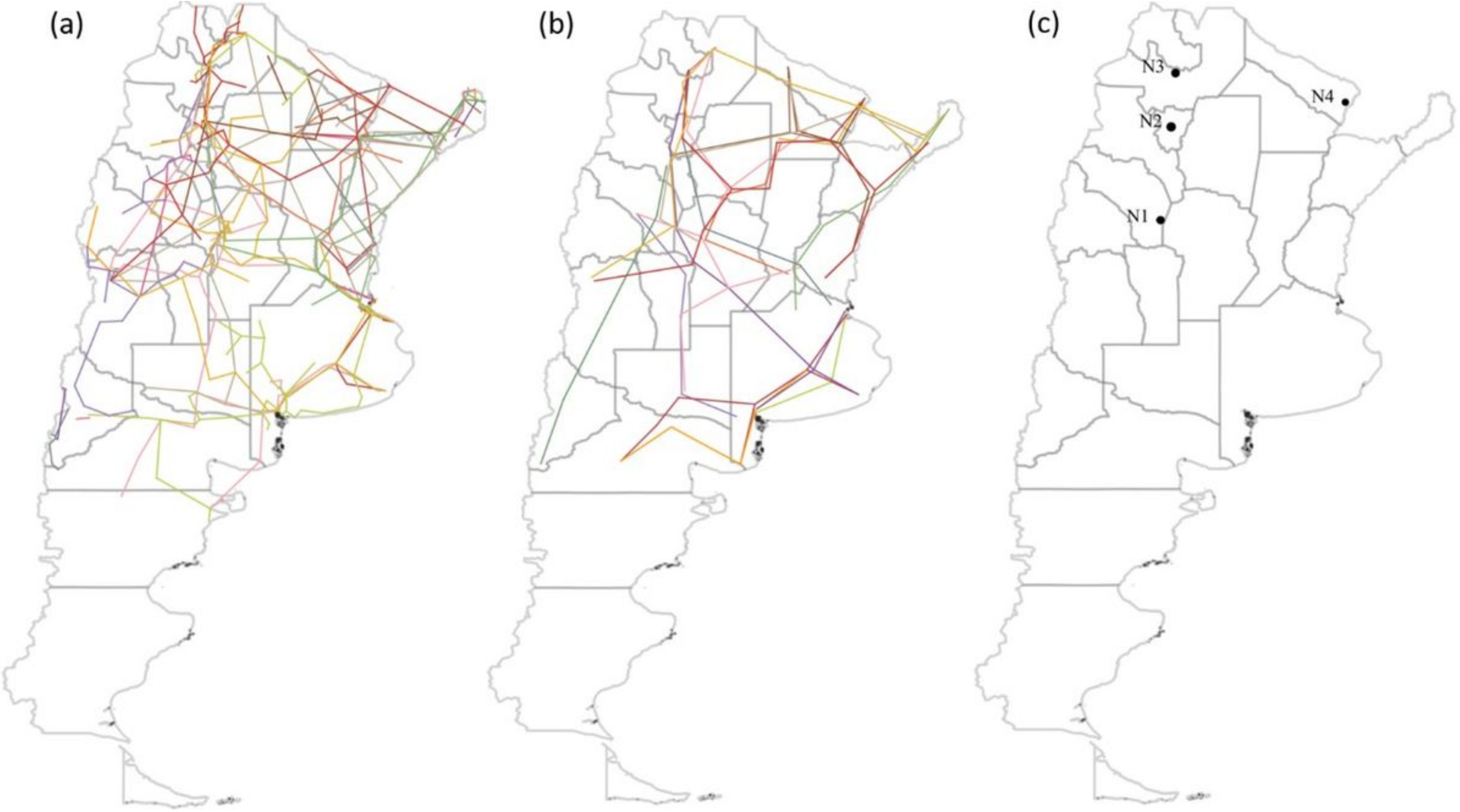

Figure 4

Maps of Argentina showing a) individual tracks b) generalized tracks c) biogeographic nodes obtained from the distribution points of the species of the family Theraphosidae

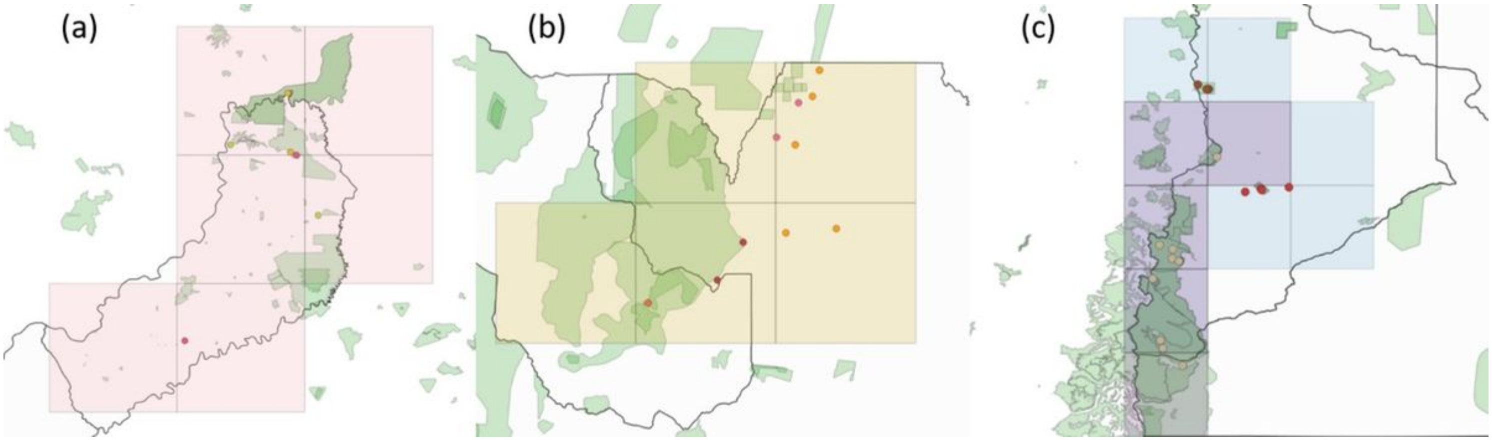

Figure 5

Areas of endemism obtained for Argentina for filling cells of 25 in 1° grids and the distribution points of the species that supported them. Protected areas are shown in green. a) Atlantic Forest of Alto Paraná and Araucaria Moist Forest. b) Southern Andean Yungas, Dry Chaco and Central Andean Puna. c) Valdivian Temperate Forest, Patagonian Steppe and Monte Bajo

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