

Detecting areas of endemism with a taxonomically diverse data set: plants, mammals, reptiles, amphibians, birds, and insects from Argentina

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Abstract

The idea of an area of endemism implies that different groups of plants and animals should have largely coincident distributions. This paper analyses an area of 1152 000 km², between parallels 21 and 32°S and meridians 70 and 53°W to examine whether a large and taxonomically diverse data set actually displays areas supported by different groups. The data set includes the distribution of 805 species of plants (45 families), mammals (25 families), reptiles (six families), amphibians (five families), birds (18 families), and insects (30 families), and is analysed with the optimality criterion (based on the notion of endemism) implemented in the program NDM/VNDM. Almost 50% of the areas obtained are supported by three or more major groups; areas supported by fewer major groups generally contain species from different genera, families, or orders.

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The present study aims to evaluate the distributional concordance among a diverse group of taxa, by using an optimality criterion specifically designed for detecting areas of endemism. In other words, this is one of the first approximations to analyse total evidence in a biogeographical context. Studies of endemism for taxonomically wide samples are difficult because specialists in a given group seldom have access to first-hand information on the distribution of other groups; the only way to

cover a wide array of diverse taxa is to have studies in which numerous authors, with different specialties, collaborate.

In the past two decades, a considerable number of empirical studies to define and quantify areas of endemism have been published. Part of that production can be related to the development of different methods of analysis, starting with parsimony analysis of endemism (PAE; Morrone, 1994), which highlighted the need to formalize and assess the identification of areas of endemism with clear and accessible protocols. Several alternative methods followed PAE (e.g. Geraads, 1998;

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Linder, 2001; García-Barros et al., 2002; Hausdorf and Hennig, 2003), trying to improve on the original idea. Szumik et al. (2002) and Szumik and Goloboff (2004) proposed a method that takes into account the spatial component of endemism (ignored by the other methods) and allows for non-hierarchical results (required by most other methods). It is clear that the notion of endemism includes a spatial concept by definition but Szumik et al. (2002, p. 806) are the first to point out that the spatial component has been previously ignored:

“A method used to identify areas of endemism must consider the taxa occurring in a given area and their position in space. This spatial component has not been included in pre-existing clustering methods, and thus those methods (designed only to recover hierarchy) cannot be adopted for identification of areas of endemism.”

Method of analysis aside, most of these local and global empirical studies were focused on a particular group of taxa (genus, family, order, or class), analysed with a single cell size (e.g. $1 \times 1^\circ$, $2 \times 2^\circ$). Nevertheless, the concept of an area of endemism implies distributional concordance among different groups, not within a single group:

“An endemic taxon is restricted to a region and is found nowhere else. The range of distribution of a taxon is determined by both historical and current factors. Whatever the factors are, if they affect (or have affected) in a similar way different taxonomic groups, there will be congruence in the patterns of endemism in different groups. Thus, areas that have many different groups found there and nowhere else can be defined as areas of endemism.” (Szumik et al., 2002, p. 806)

This paper represents the first attempt to bring together a set of high-quality data provided by a large number of specialists for diverse groups of plants, mammals, reptiles, amphibians, birds, and insects. Additionally, a comparison between the results and some of the previous hypotheses, focusing in particular on Cabrera and Willink’s biogeographical division, is presented (Fig. 1).

Materials and methods

The 805 species analysed represent 53 orders, 129 families and 463 genera (Table 1; see also Appendix 1 for a list of number of species per order and family). The species were chosen because either (i) they were previously used as typical of some biogeographical area, or (ii) they have narrow distributions in the study region. Almost all the records used are connected to actual specimens in one of the major collections in Argentina (the only exception being birds, for which sighting is widely considered as acceptable for identification). Many of these vouchers are the result of years of collection and taxonomic study by the authors. The data

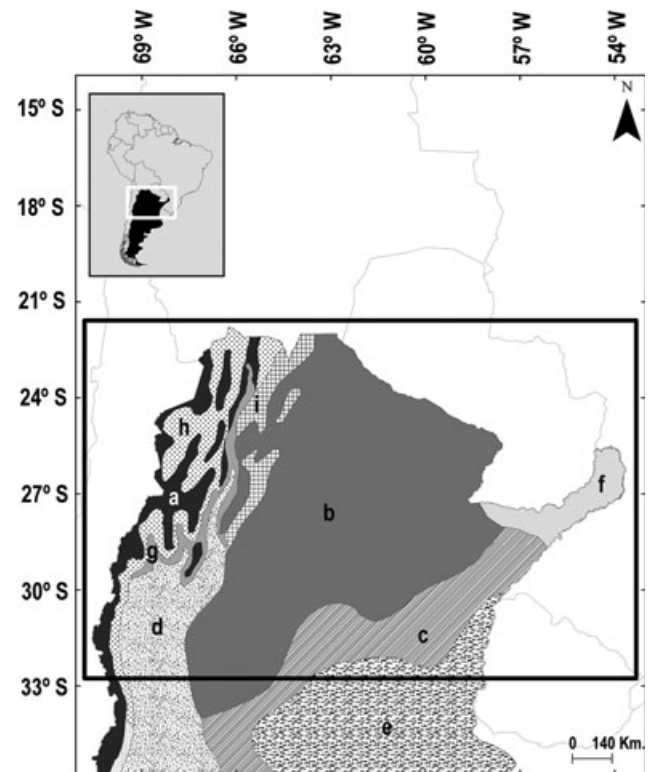


Fig. 1. Biogeographical divisions for the study region according to Cabrera and Willink (1973).

set contains almost 14 500 records. In many cases (especially birds and mammals) the records were insufficient to assess the real distribution of the taxa; in those cases, the presumed distribution was estimated by the respective specialist (see Fig. 2 for a map of species diversity).

The present data set is unique among biogeographical studies not only for the number and diversity of plant and animal taxa, but also because it was compiled, edited, and corroborated by 25 practising taxonomists, whose work specializes in the study region. Thus, it differs substantially from data sets constructed by downloading data from biodiversity websites.

The study region is a rectangular area between 21° and 32° S and 70° and 53° W in Argentina, comprising more than $1152\,000\text{ km}^2$ of the Neotropical region, equivalent to the area of South Africa (as analysed by Linder, 2001), or twice that of Spain and Portugal (as analysed by García-Barros et al., 2002). The high biogeographical diversity of this zone is well known (e.g. Cabrera and Willink, 1973; Fig. 1). Other studies by Vervoort (1979), Dinerstein et al. (1995), and Morrone (2001, 2006) are also important. Some of these studies (Cabrera and Willink, 1973; Vervoort, 1979) did not use the term “endemic” or “endemism” but simply listed plants and a few animals characterizing each of the biogeographical “divisions” proposed. Because of

the complexity of the region, there is substantial disagreement among the proposals. It is also clear that many of these biogeographical divisions continue outside the study region (e.g. extending into Bolivia); moreover, some of the taxa included here are absent outside of the study region, while others are present. It should therefore be noted that whenever we report an area of endemism defined by species that are distributed outside the study region as well, what we present may be only a patch of the area. It remains to be seen whether such areas persist in future studies as an area of endemism defined by the same species. However, a compilation of distributions such as the present one offers an opportunity to provide first-step testable hypotheses of areas of endemism for future analyses of neighbouring regions or analyses at more inclusive scales. One could be tempted to criticize the present study by claiming that the study region is inadequate or not natural, or that the taxa present outside of this region must be ignored or eliminated from the analysis. However, this would be equivalent to using the same

arguments that were misdirected against phylogenetic analyses in the past, when criticizing it for dealing with possibly incomplete monophyletic groups (Sokal, 1975, p. 258; see rebuttal by Farris, 1979, p. 486). The tree resulting from a cladistic analysis for a specific set of taxa makes a statement only about the relationships of the included taxa; those taxa not included in the analysis could land—in future analyses—on any branch of the tree. The present analysis, likewise, specifies—for each cell in the grid—the membership, or lack thereof, to a given area; nothing is stated or implied about cells that would occupy an extended grid.

The data set was analysed with the heuristic algorithms of NDM-VNDM ver. 2.7 (Goloboff, 2007), which apply the methodology of Szumik and Goloboff (2004). The method, which is grid-dependent, basically evaluates spatial concordance among two or more taxa for a given set of cells (area of endemism): assigning a score of endemicity for a given taxon, according to how well the taxon distribution matches a given set of cells (area). Then, the total endemicity score for a given set of cells (area) is the summation of the individual taxon scores (for details see the methodological explanation of Szumik and Goloboff, 2004; and the empirical case of Navarro et al., 2009). Beyond the formula and/or the criteria, the programs NDM/VNDM were developed with the idea that:

“An explicit method to identify areas of endemism should relate relevant evidence and conclusions... Acceptance of those conclusions (i.e., boundaries of areas) that are best supported by available evidence requires (in principle, at least) evaluation of all possible conclusions, selecting the ones judged as optimal based on the established criterion.” (Szumik et al., 2002, p. 806)

Table 1
Number of orders, families, genera, and species for each major taxonomic group analysed

	Orders	Families	Genera	Species
Plants	27	45	115	187
Insects	5	30	177	300
Reptiles	1	6	21	89
Amphibians	1	5	20	41
Birds	9	18	46	49
Mammals	10	25	84	140
Total	53	129	463	805

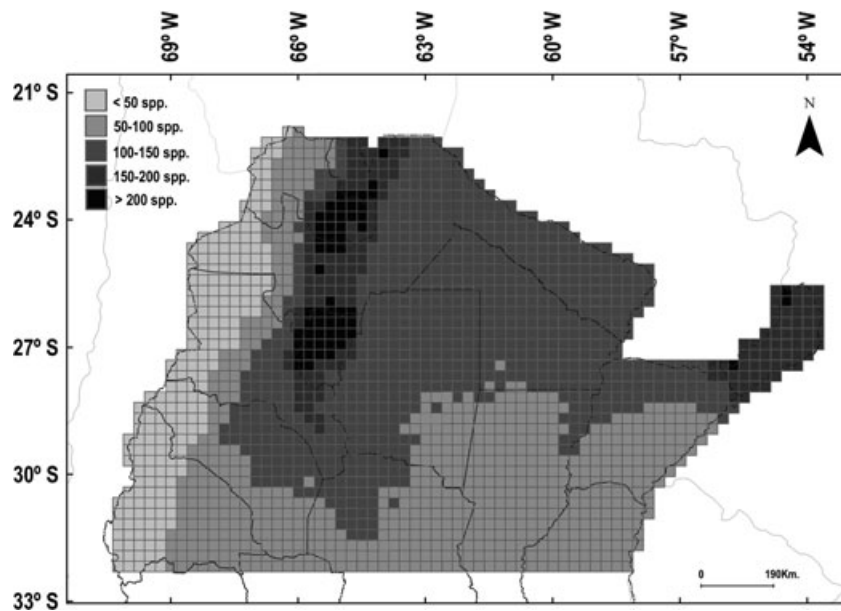


Fig. 2. Species diversity in the study region on cells of $0.25 \times 0.25^\circ$.

With few exceptions, previous analyses provide no justification for the cell size selected. It has been proposed (Aagesen et al., 2009; Casagrande et al., 2009) that using several grid sizes provides a kind of measure of support for a particular area of endemism. More importantly, the shape and size of some areas of endemism may make them hard to identify if only a single grid size is used—using several grid sizes increases the probability of finding all areas (especially in cases such as the Andes, where steep and rugged terrain leads to very small areas, detectable only with small grid sizes). Thus, three grid sizes (0.25°, 0.50° and 1°, where 1° is equivalent to almost 100 km) were used.

Given that some sets of cells (areas of endemism) differ little in both the composition of cells and their endemic taxa, the results were grouped with the consensus option of VNDM (see Aagesen et al., 2009; Navarro et al., 2009, for additional discussion of search protocols). The consensus option used here combines all the areas of endemism that share a (user-defined) percentage of endemic taxa with at least some other area in the consensus.

Results

In total, 126 consensus areas (Table 2) were obtained, 24 (19%) of which were defined by a single taxonomic group (mostly plants or insects, and rarely by mammals or amphibians). In all these areas with a unique taxonomic group, however, the endemic taxa belonged to different genera, families, and orders. Overall, 47.6% of the consensus areas were supported by three or more taxonomic groups when comparing the total of 126 consensus areas under the three different grid sizes (Table 2). Instead of discussing each of the resulting areas found by the present analysis (beyond the scope of the present paper), it is our aim to discuss those areas

well supported by all or most of the different taxonomic groups used, illustrating cases where endemism can indeed be supported by widely different groups of taxa. Two such areas (supported by the six taxonomic groups) are the Atlantic Forest (Selva Paranaense—Neotropical, Fig. 3) and the north Yungas sector (tropical Bermejo-Toldo-Calilegua, Fig. 4). Both of these areas are recovered in all grid sizes and in every case were supported by the six major taxonomic groups included in the data set (see Appendices 2 and 3).

Topographically, the study region consists of lowland plains that rise from approximately 70 m in the east to approximately 300 m in the west, and the Andes in the west with deep valleys and peaks reaching above 6000 m. The complexity of the western part of the region is directly reflected in the higher number of consensus areas found west of 64°W, compared with the number found east of the same longitude (see Table 3). Consensus areas that extend both east and west of 64°W appear more clearly when the cell size is increased, which helps detect wide-ranging distribution patterns such as the Chaco scrubland (Fig. 5a).

Given that in a region such as this it is quite impossible to have records uniformly sampled, a small grid size applied to all the records would render almost

Table 2

Relationship between number of major taxonomic groups (6 to 1) supporting any of 126 consensus areas obtained for the three grid sizes

No. of taxonomic groups	Grid size			No. (%) of consensus areas
	0.25°	0.5°	1.0°	
6	2	4	3	9 (7.1)
5	1	1	6	8 (6.4)
4	2	5	10	17 (13.5)
3	2	8	16	26 (20.6)
2	13	17	12	42 (33.3)
1	9	8	7	24 (19.0)
Total	29	43	54	126

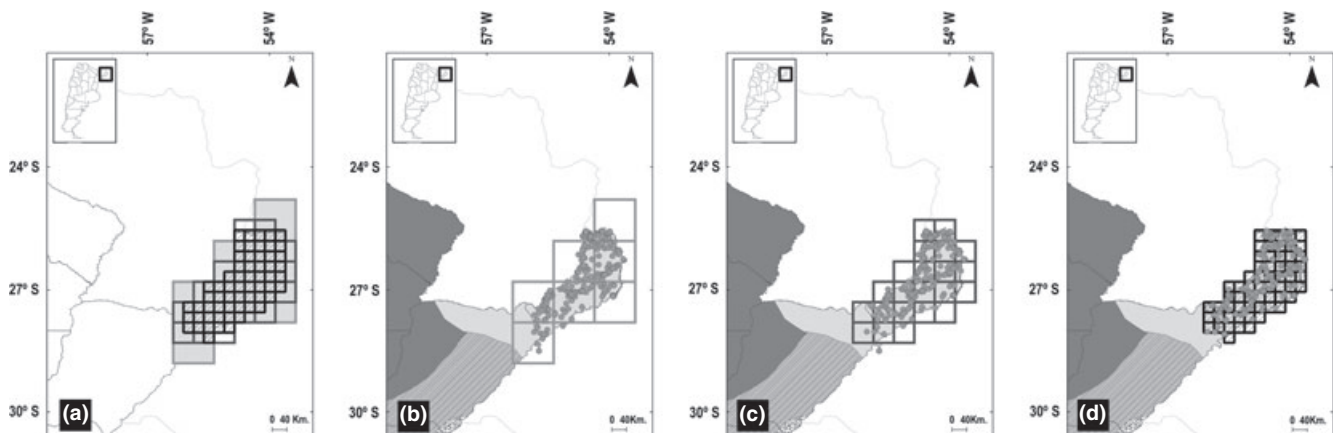


Fig. 3. Atlantic Forest. (a) Concordance between the consensus areas of the three grid sizes; (b) consensus area under 1° grid size; (c) consensus area under 0.50° grid size; (d) consensus area under 0.25° grid size.

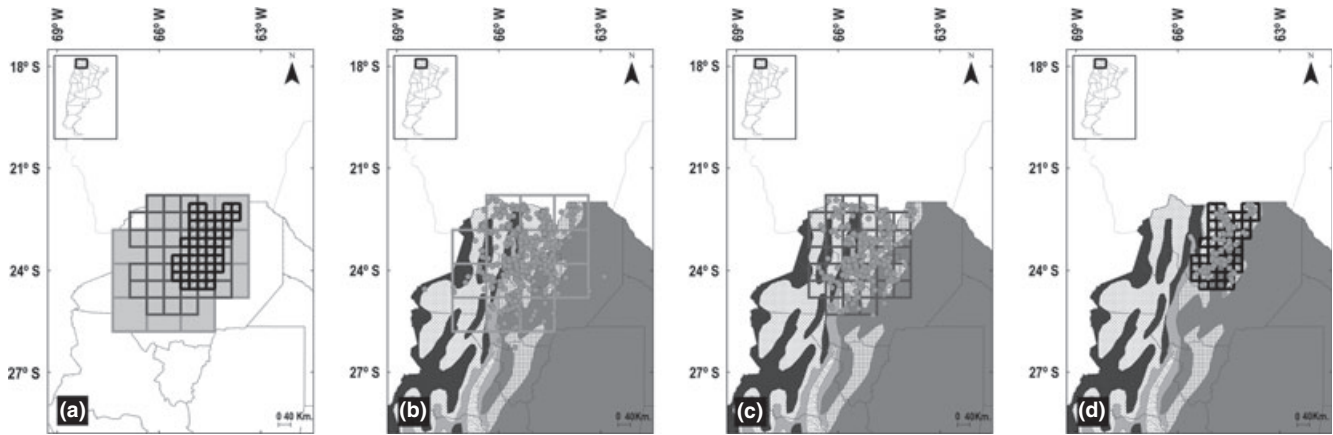


Fig. 4. Northern Yungas. (a) Concordance between the consensus areas of the three grid sizes; (b) consensus area under 1° grid size; (c) consensus area under 0.50° grid size; (d) consensus area under 0.25° grid size.

Table 3
Number of consensus areas in Northwestern Argentina (NWA), Northeastern Argentina (NEA), or in both regions (NA), for the three grid sizes

Region	Grid size		
	0.25°	0.5°	1.0°
NWA > 64°	20	25	24
NEA < 64°	8	10	10
NA	1	8	20

any distribution entirely discontinuous and make large areas of endemism unrecognizable.

One objection against using 1° cell size is that it could lead to overlapping different distribution patterns in the

same area. As an example, Fig. 5b (grid size 1°) depicts a consensus of areas that lumps distribution patterns running north–south of organisms found at different altitudes. The grass species of *Deyeuxia* are found in Puna and High Andean environments above 3000 m, as is the case of the Llama and Vicuña. However, species from lower altitudes such as the bush *Bulnesia schickendantzii* (Zygophyllaceae) and the grass *Panicum chloroleurum* also appear as endemic to this area under grid size 1°, confusing the preconceived limits of the biogeographical strata found in the Andes (Fig. 6), as the altitudinal range of the species in the area shows.

Besides finding areas similar to those proposed previously, the present analysis also yielded two strongly supported distribution patterns which were found in all

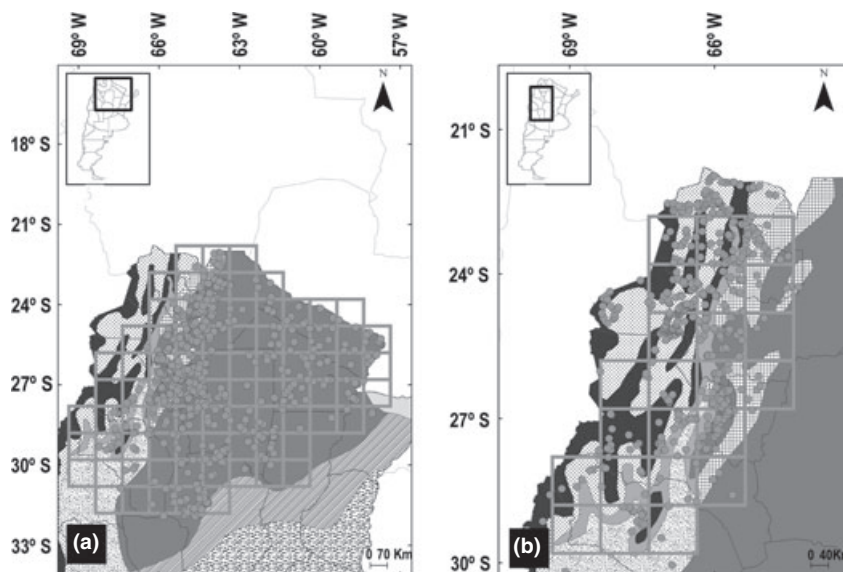


Fig. 5. (a) Consensus area of the Chaco Scrubland under 1° grid size; (b) consensus area of Puna–High Andean under 1° grid size.

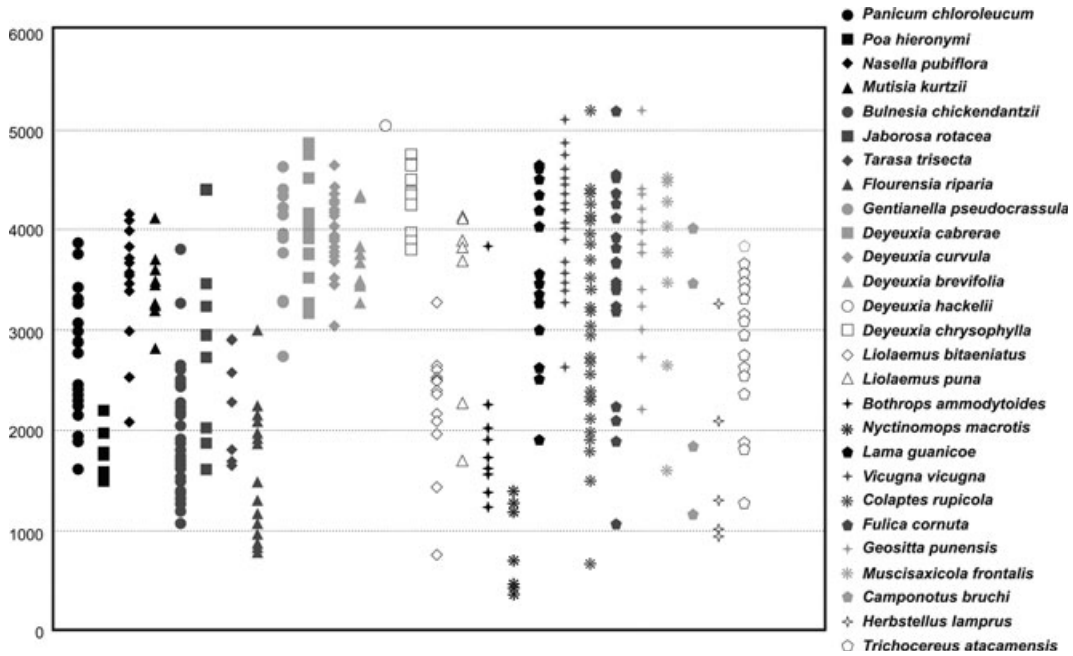


Fig. 6. Altitude range of the species which give score to the consensus area of Puna–High Andean sector under 1° grid size (see Fig. 5b).

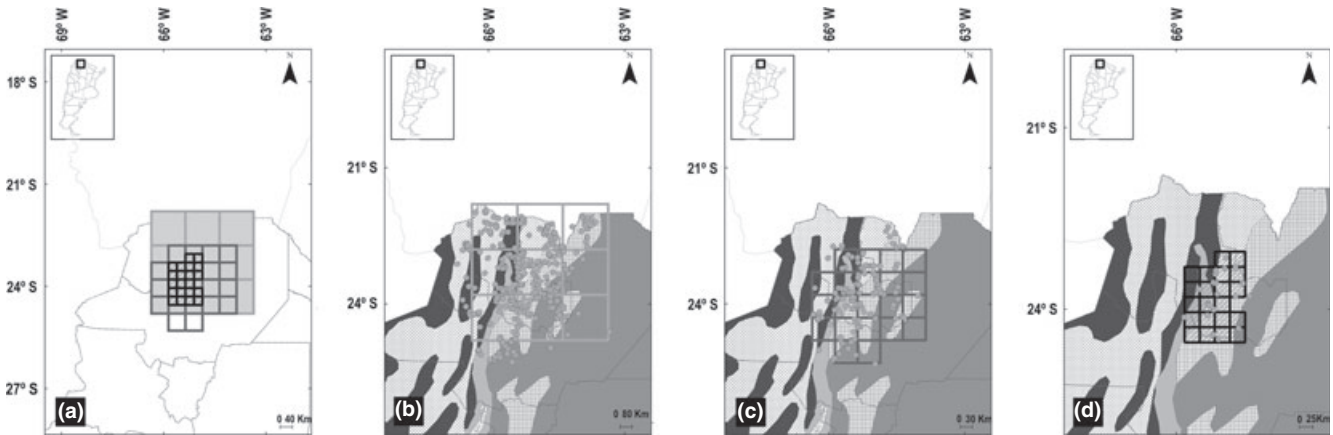


Fig. 7. Cordillera Real. (a) Concordance between the consensus areas of the three grid sizes; (b) consensus area under 1° grid size; (c) consensus area under 0.50° grid size; (d) consensus area under 0.25° grid size.

grid sizes (Figs 7 and 8). Both areas are found in topographically variable parts of the Andes and both include strong gradients in altitude, temperature, and rainfall. These areas appear as major centres of endemism in northern Argentina, resistant to change in analytical parameters (here, changes in grid sizes), and with high taxonomic diversity (with a wide array of endemic species and families).

The northernmost area (Fig. 7) lies in the southern part of the Cordillera Real, occupying ca. 23 000 km², from 22°50' to 24°50'S and from 64°50' to 66°W. This area had also been identified in earlier studies (Aagesen

et al., 2009) of the distribution of grasses within a portion of the current study region. Using a grid size of 0.5° (Fig. 7c), the area is supported by 33 species, including 21 plant species from 11 families. Ongoing studies of plant distribution have identified 47 plant species from 18 different families as strictly endemic to this area. Here, the area is also supported by 11 species and seven families of animals (see Appendix 4).

The southernmost area (Fig. 8) occupies valleys, slopes, and peaks of the Sierras Calchaquies, between 25°50' and 28°S and 64°50' and 66°10'W, with an area of 31 000 km². Under a grid size of 0.25° (Fig. 8b) the area

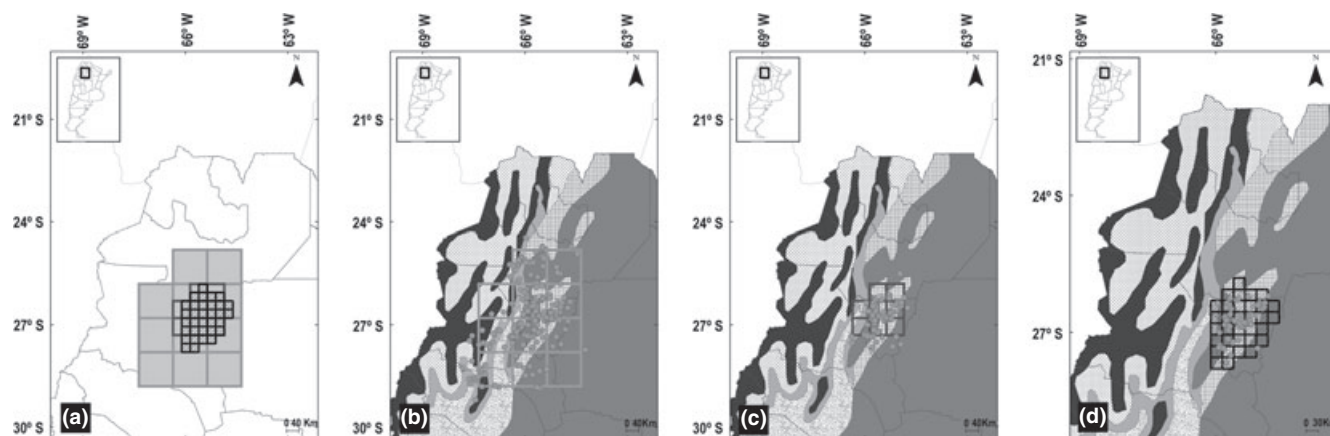


Fig. 8. Valles Calchaquies. (a) Concordance between the consensus areas of the three grid sizes; (b) consensus area under 1° grid size; (c) consensus area under 0.50° grid size; (d) consensus area under 0.25° grid size.

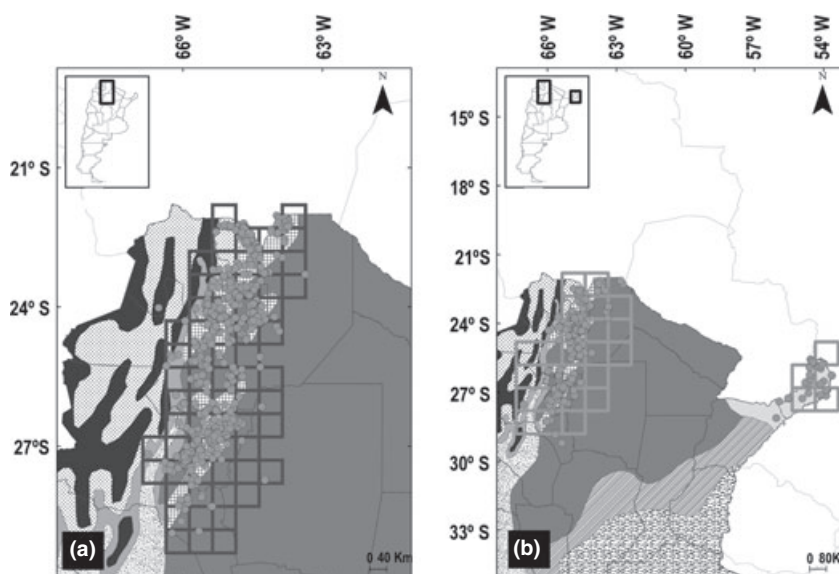


Fig. 9. (a) The deciduous tropical forest (Yungas and Atlantic Forest) under 0.5° grid size; (b) the tropical tails entering Argentina in two disjoint patches under 1.0° grid size.

is supported by two grass species (see Appendix 5), but 64 plant species from 21 families are known to be endemic to this area (Zuloaga et al., 2008). In addition to plants, the area is supported by 28 species of animals from eight families.

Discussion

The main aims of the present study were to explore to what extent different taxonomic groups can co-occur and support similar areas of endemism. The general idea of such areas is not associated with a specific causal factor; if a single factor affects the distribution of diverse groups of organisms, they will be expected to show

similar spatial patterns. Regardless of whether the causal factor is historical or ecological, our results indicate that when all the evidence is analysed for a given region it is possible to obtain areas supported by diverse taxonomic groups (Navarro et al., 2009).

Besides, a causal factor need not have affected the entirety of the biota, so that different groups (with different ecological requirements, for example) may have different, or even overlapping, distributional patterns. Yet, and regardless of overlaps, all the repetitive patterns are (possible sampling artefacts aside) equally real, in the sense that each of them is the result of some common factor (Szumik and Goloboff, 2004). It is also important to note that the present method allows partial

overlapping between areas of endemism, but does not require it; cases of overlap in the results are a consequence of the data, not of the method.

Almost all the main biogeographical units proposed in previous studies (Cabrera and Willink, 1973; Cabrera, 1976; Stange et al., 1976; Cracraft, 1985; Willink, 1991; Morrone, 2001, 2006) were recovered in the analysis: the Atlantic Forest (Fig. 3), the Campos (Grasslands) District, the Chaco shrubland (Fig. 5a), the deciduous tropical Yungas forest (Fig. 9a), the Puna highland, and the tropical tails entering Argentina in two disjoint patches (Fig. 9b). Each of these tropical tails represents part of a broader area that extends towards the north of the South American continent. Besides the general spatial concordance with previously suggested biogeographical units, the species that support the various areas also agree in general with previous biogeographical studies based on individual groups (plants: Aagesen et al., 2009; reptiles: Giraudo et al., 2008; Arzamendia and Giraudo, 2009; mammals: Barquez and Diaz, 2001; insects: Navarro et al., 2009; birds: Straube and Di Giacomo, 2007). It is beyond the scope of the present paper either to discuss the biogeographical units in detail or to provide extensive species lists of the supporting species for each area; these aspects will be treated in a separate publication. However, it should be noted that several of the species appearing as endemic to certain areas are currently on red-lists of threatened species at national or global level (Collar et al., 1992; Diaz and Ojeda, 2000; Lavilla et al., 2000; Barquez et al., 2006; Lopez-Lanus et al., 2008; BirdLife International, 2011).

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Appendix 1

Names of orders and families used in the study (with number of species per family)

Order	Family	<i>n</i>	Order	Family	<i>n</i>
Plants			Cingulata	Dasypodidae	10
Aquifoliales	Aquifoliaceae	1	Didelphimorphia	Caluromyidae	1
Asparagales	Amaryllidaceae	3		Didelphidae	22
	Anthericaceae	1	Lagomorpha	Leporidae	1
Asterales	Asteraceae	32	Perissodactyla	Tapiridae	1
	Campanulaceae	1	Pilosa	Bradypodidae	1
Brassicales	Brassicaceae	2		Myrmecophagidae	2
	Bromeliaceae	12	Primates	Atelidae	1
Caryophyllales	Amaranthaceae	1		Cebidae	2
	Cactaceae	4	Rodentia	Chinchillidae	3
	Caryophyllaceae	1		Erethizontidae	2
	Portulacaceae	1		Hydrochoeridae	1
	Podocarpaceae	1		Myocastoridae	1
Cucurbitales	Begoniaceae	2	Birds		
Cyatheales	Cyatheaceae	1	Charadriiformes	Charadriidae	1
Dipsacales	Valerianaceae	1		Recurvirostridae	1
Fabales	Fabaceae	7	Columbiformes	Columbidae	1
	Betulaceae	1	Galliformes	Cracidae	2
Gentianales	Apocynaceae	6	Gruiformes	Rallidae	2
	Gentianaceae	2	Passeriformes	Cinclidae	1
	Rubiaceae	3		Formicariidae	2
Incertae sedis	Boraginaceae	1		Fringillidae	9
Lamiales	Acanthaceae	1		Furnariidae	8
	Calceolariaceae	2		Mimidae	1
	Gesneriaceae	1		Rhinocryptidae	1
	Lamiaceae	3		Thamnophilidae	2
	Lauraceae	1		Tyrannidae	5
	Orobanchaceae	1	Piciformes	Picidae	4
	Plantaginaceae	1		Ramphastidae	1
	Scrophulariaceae	1	Psittaciformes	Psittacidae	3
	Verbenaceae	6	Tinamiformes	Tinamidae	1
Liliales	Alstroemeriaceae	3	Trochiliformes	Trochilidae	3
Malpighiales	Euphorbiaceae	5	Amphibians		
Malvales	Malvaceae	5	Anura	Bufonidae	8
Myrtales	Myrtaceae	1		Hylidae	16
	Onagraceae	1		Leptodactylidae	15
Oxalidales	Oxalidaceae	2		Microhylidae	1
Pandanales	Velloziaceae	1		Strabomantidae	1
Piperales	Aristolochiaceae	2	Insects		
	Piperaceae	3	Lepidoptera	Geometridae	21
Poales	Cyperaceae	2		Noctuidae	64
	Poaceae	38	Diptera	Asilidae	2
Polypodiales	Aspleniaceae	2		Asteiidae	1
Ranunculales	Papaveraceae	1		Bibionidae	3
Sapindales	Anacardiaceae	1		Chloropidae	5
Solanales	Convolvulaceae	4		Clusiidae	1
	Solanaceae	11		Ephydriidae	24
	Zygophyllaceae	1		Micropezidae	5
Reptiles				Mycetophilidae	2
Squamata	Boidae	2		Pipunculidae	7
	Dipsadidae	21		Platypezidae	3
	Elapidae	4		Sciomycidae	1
	Leptotyphlopidae	7		Stratiomyidae	3
	Liolaemidae	47		Syrphidae	5
	Viperidae	8		Tabanidae	4
Mammals				Tachinidae	5
Artiodactyla	Camelidae	2	Hemiptera	Dactylopidae	5
	Cervidae	6		Diaspididae	23
	Tayassuidae	3	Hymenoptera	Apidae	14

Appendix 1

(Continued)

Order	Family	<i>n</i>	Order	Family	<i>n</i>	
Carnivora	Canidae	5	Crabronidae	26		
	Felidae	9		Eumenidae	7	
	Mephitidae	1		Formicidae	11	
	Mustelidae	5		Ichneumonidae	1	
	Procyonidae	2		Pompilidae	4	
Chiroptera	Molossidae	18	Vespidae	38		
	Noctilionidae	2	Embioptera	Anisembiidae	3	
	Phyllostomidae	17		Archembiidae	9	
	Vespertilionidae	24		Teratembiidae	7	

Appendix 2

Endemic species of the consensus area “Atlantic Forest” (Fig. 3)

Species	Grid size			Species	Grid size		
	0.25°	0.50°	1.00°		0.25°	0.50°	1.00°
BOT <i>Aristolochia burkartii</i>			0.63	AVE <i>Pionopsitta pileata</i>	1.00	0.95	1.00
BOT <i>Asplenium clausenii</i>	0.99	0.98	0.88	AVE <i>Stephanoxis lalandi</i>			0.50
BOT <i>Mikania summinima</i>			0.63	AVE <i>Thalurania glaucopsis</i>	0.93	0.50	0.70
BOT <i>Vernonia spicata</i>			0.79	AVE <i>Ramphastos dicolorus</i>			0.75
BOT <i>V. teyucuaensis</i>			0.79	AVE <i>Philydor lichtensteini</i>	0.96	1.00	1.00
BOT <i>Viguiera misionensis</i>			0.52	AVE <i>Sclerurus scansor</i>			0.63
BOT <i>Borreria loretiana</i>			0.80	AVE <i>Hypoedaleus guttatus</i>	0.96	1.00	1.00
BOT <i>Mecardonia grandiflora</i>			0.90	AVE <i>Mackenziaena leachii</i>			0.63
BOT <i>Eugenia lilloana</i>		0.56	0.96	AVE <i>Pyriglena leucoptera</i>	0.91	0.98	0.75
BOT <i>Hyptis australis</i>			0.79	AVE <i>Mionectes rufiventris</i>	0.92	0.95	0.95
BOT <i>Jacquemontia laxiflora</i>		0.81	0.92	AVE <i>Tangara seledon</i>	0.97	0.31	0.95
BOT <i>Melica hunzikeri</i>			0.63	ANF <i>Aplastodiscus perviridis</i>	0.99	0.90	0.88
BOT <i>Mesosetum comatum</i>			0.79	ANF <i>Hypsiboas curupi</i>	0.99	1.00	0.88
BOT <i>Peperomia misionense</i>			0.70	ANF <i>H. faber</i>	0.92	0.98	0.63
BOT <i>P. subpubistachya</i>	0.96	1.00	0.88	ANF <i>Scinax perereca</i>			0.80
BOT <i>Siphocampylus yerbalensis</i>			0.80	INS <i>Euclysia columbipennis</i>		0.78	0.80
BOT <i>Dyckia niederleinii</i>			0.83	INS <i>Oxydia gilva</i>		0.81	0.84
REP <i>Bothrops cotiara</i>			0.90	INS <i>Cliobata guttipennis</i>	1.00	0.93	0.84
REP <i>B. jararaca</i>	1.00	1.00		INS <i>Paralimna molosus</i>	0.89	1.00	
REP <i>B. jararacussu</i>	0.99	1.00	0.88	INS <i>Polistes melanosoma</i>		0.75	0.84
REP <i>B. moojeni</i>			0.70	INS <i>Parachartergus fraternus</i>	1.00	1.00	0.72
REP <i>Micrurus corallinus</i>	1.00	1.00		INS <i>Agelaia angulata</i>	1.00	1.00	0.95
MAM <i>Vampyressa pusilla</i>	0.93	1.00	0.80	INS <i>A. pallipes pallipes</i>	1.00	1.00	1.00
MAM <i>Histiopus velatus</i>	0.75	0.50		INS <i>Synoeca surinama</i>	1.00	1.00	1.00
MAM <i>Cynomops abrasus</i>		1.00		INS <i>Protonectarina sylveirae</i>	1.00	1.00	0.88
MAM <i>Molossops neglectus</i>	1.00	1.00	0.70	INS <i>Protopolybia sedula</i>			0.70
MAM <i>Micoureus demerarae</i>		0.50	0.52	INS <i>Myschocyttarus rotundicollis</i>		0.54	0.88
MAM <i>Monodelphis iheringii</i>	0.96	1.00		INS <i>Montezumia ferruginea</i>	1.00	1.00	0.96
MAM <i>M. scalops</i>	1.00	1.00	0.70	INS <i>M. aurata</i>		0.80	0.92
MAM <i>M. sorex</i>	0.99	1.00	0.95	INS <i>M. brethesi</i>		0.75	0.95
MAM <i>Caluromys lanatus</i>	0.99	1.00	0.90	INS <i>Monobia apicalipennis</i>			0.95
MAM <i>Chironectes minimus</i>		0.50	0.50	INS <i>Acromyrmex laticeps</i>	0.96	1.00	1.00
MAM <i>Didelphis aurita</i>	0.99	1.00	0.80	INS <i>Pseudomyrmex schuppi</i>	1.00	1.00	0.92
MAM <i>Gracilinanus microtarsus</i>	1.00	1.00	0.57	INS <i>Archembia dilate</i>			0.70
MAM <i>Metachirus nudicaudatus</i>	0.99	1.00	0.90	INS <i>Diradius plaumanni</i>			0.70
MAM <i>Pteronura brasiliensis</i>	1.00	1.00		INS <i>D. unicolor</i>			0.90
AVE <i>Aramides saracura</i>	1.00	0.98	0.75	INS <i>Oligembia mini</i>			0.70

The numbers are the maximum endemicity scores for the species (among all areas included in the consensus) for the three grid sizes (37 species in 0.25°, 48 species in 0.50°, and 67 species in 1.00°). Blanks indicate that the species is not endemic for the area.

Appendix 3

Endemic species of the consensus area “Northern Yungas” (Fig. 4)

Species	Grid size			Species	Grid size		
	0.25°	0.50°	1.00°		0.25°	0.50°	1.00°
BOT * <i>Anatherostipa brevis</i>		0.80	0.92	BOT* <i>Solanum zuloagae</i>		0.67	0.82
BOT * <i>Elymus tilcarensis</i>		0.83	0.78	BOT <i>Parapiptadenia excelsa</i>			0.6
BOT <i>Nassella punensis</i>			0.78	BOT <i>Bocconia integrifolia</i>	0.90	0.64	0.78
BOT * <i>Dicliptera cabreræ</i>			0.51	BOT <i>Cinnamomum porphyrium</i>			0.53
BOT * <i>Eupatorium saltense</i>			0.59	REP <i>Liolaemus albiceps</i>		0.83	
BOT * <i>Nassella yaviensis</i>		0.83		REP <i>Liolaemus chaltin</i>		1.00	0.58
BOT * <i>Rebutia marsoneri</i>		0.83	0.72	REP <i>Liolaemus irregularis</i>		0.89	0.75
BOT * <i>Nototriche sleumeri</i>		0.83		REP <i>Liolaemus multicolor</i>			0.7
BOT * <i>Barbaceniopsis humahuaguensis</i>		0.83	0.72	REP <i>Liolaemus orientalis</i>		0.62	0.85
BOT * <i>Vernonia lipeoensis</i>	0.92	0.76	0.94	REP <i>Liolaemus ornatus</i>			0.79
BOT * <i>Silene haumanii</i>		0.61	0.87	REP <i>Liolaemus pulcherrimus</i>		0.83	0.83
BOT * <i>Adesmia friesii</i>		0.66	0.75	REP <i>Liolaemus yanalco</i>		0.89	
BOT * <i>Nototriche friesii</i>			0.86	REP <i>Leptotyphlops striatulus</i>	0.92	0.83	0.92
BOT <i>Salvia calolophos</i>		0.79	0.77	MAM <i>Anoura caudifer</i>	0.94	0.60	0.66
BOT * <i>Arachis monticola</i>		0.60	0.74	MAM <i>Cynomops planirostris</i>		0.56	0.53
BOT * <i>Psychotria argentinensis</i>	0.95	0.76	0.94	MAM <i>Cryptonanus ignitus</i>		0.68	0.72
BOT * <i>Solanum caesium</i>	0.92	0.84	0.93	MAM <i>Thylamys venustus</i>	0.94	0.51	0.78
BOT <i>Solanum toldense</i>		0.52	0.78	MAM <i>Cebus apella</i>			0.51
BOT <i>Alsophila odonelliana</i>	0.95	0.72	0.92	MAM <i>Chaetophractus nationi</i>			0.81
BOT* <i>Aristida pubescens</i>			0.84	MAM <i>Chinchilla brevicaudata</i>			0.66
BOT* <i>Muhlenbergia atacamensis</i>			0.80	MAM <i>Coendou bicolor</i>	0.86	0.86	0.97
BOT <i>Eragrostis andicola</i>		0.92	0.77	MAM <i>Dasypus yepesi</i>	0.96	0.55	0.75
BOT <i>Nassella novari</i>			0.77	MAM <i>Leopardus wiedii</i>			0.89
BOT* <i>Senecio punae</i>			0.82	MAM <i>Tapirus terrestris</i>			0.8
BOT <i>Mutisia hamata</i>			0.95	MAM <i>Tayassu pecari</i>			0.76
BOT <i>Chuquiraga atacamensis</i>			0.71	AVE <i>Atlapetes fulviceps</i>			0.62
BOT* <i>Metastelma microgynostegia</i>		0.63	0.76	AVE <i>Grallaria albigula</i>	0.91	0.64	0.63
BOT <i>Conyza coronopifolia</i>		0.72	0.86	AVE <i>Penelope dabbenei</i>		0.64	0.9
BOT* <i>Senecio jujuyensis</i>		0.69	0.85	ANF <i>Gastrotheca christiani</i>		0.78	0.92
BOT* <i>Senecio tilcarensis</i>		0.83	0.72	ANF <i>Gastrotheca chrysosticta</i>			0.54
BOT* <i>Stevia jujuyensis</i>		1.00	0.85	ANF <i>Melanophryniscus rubiventris</i>		0.57	1.00
BOT* <i>Stevia yalae</i>		0.83	0.75	ANF <i>Phyllomedusa boliviana</i>	0.91	0.69	0.73
BOT* <i>Solanum calileguae</i>		1.00	0.77	ANF <i>Pleurodema marmoratum</i>		0.68	0.90
BOT* <i>Ipomoea volcanensis</i>		0.75	0.74	ANF <i>Telmatobius atacamensis</i>		0.69	
BOT <i>Bomarea boliviensis</i>		0.70	0.70	ANF <i>Telmatobius platycephalus</i>		0.75	0.77
BOT <i>Begonia boliviensis</i>			0.73	INS <i>Bassania jocosa</i>	0.91	0.83	0.89
BOT <i>Muhlenbergia phalaroides</i>		0.83	0.83	INS <i>Oxydia optima</i>		0.89	0.90
BOT <i>Calceolaria elatior</i>			0.64	INS <i>Herminodes carbonelli</i>		0.81	0.66
BOT * <i>Gamochoaeta longipedicellata</i>		0.75	0.70	INS <i>Scatella balioptera</i>			0.70
BOT* <i>Laennecia altoandina</i>		0.75	0.77	INS <i>Scatella hirticrus</i>			0.80
BOT* <i>Macropharynx meyeri</i>			0.88	INS <i>Scatella semipolita</i>			0.88
BOT* <i>Valeriana altoandina</i>			0.82	INS <i>Scatella glabra</i>		0.69	0.79
BOT* <i>Bartsia jujuyensis</i>		0.66	0.85	INS <i>Pachodynerus jujuyensis</i>		0.93	0.77
BOT <i>Begonia micranthera</i>			0.79	INS <i>Montezumia fritzi</i>			0.57
BOT* <i>Macropharynx meyeri</i>	0.91	0.64		INS <i>Chelicerca tigre</i>			0.54
BOT* <i>Mikania jujuyensis</i>		0.71	0.82	INS <i>Oligembia arbol</i>		0.59	0.83

The numbers are the maximum endemism scores for the species (among all areas included in the consensus) for the three grid sizes (14 species in 0.25°, 59 species in 0.50°, and 86 species in 1.00°). Blanks indicate that the species is not endemic for the area.

*Only present in the study region.

Appendix 4

Endemic species of the consensus area “Cordillera Real” under 0.5° grid size (Fig. 7c)

Species	0.50°	Species	0.50°
BOT * <i>Elymus tilcarensis</i>	0.83	BOT <i>Muhlenbergia phalaroides</i>	0.71
BOT * <i>Rebutia marsoneri</i>	0.83	BOT * <i>Gamochaeta longipedicellata</i>	0.43
BOT * <i>Barbaceniopsis humahuauensis</i>	0.83	BOT * <i>Laennecia altoandina</i>	0.71
BOT * <i>Silene haumanii</i>	0.55	BOT* <i>Mikania jujuyensis</i>	0.71
BOT * <i>Adesmia friesii</i>	0.40	BOT* <i>Solanum zuloagae</i>	0.67
BOT <i>Salvia calolophos</i>	0.76	REP <i>Liolaemus irregularis</i>	0.47
BOT * <i>Arachis monticola</i>	0.60	REP <i>Liolaemus pulcherrimus</i>	0.83
BOT * <i>Solanum caesium</i>	0.41	REP <i>Liolaemus yanalcu</i>	0.47
BOT <i>Eragrostis andicola</i>	0.75	REP <i>Leptotyphlops striatulus</i>	0.52
BOT* <i>Metastelma microgynostegia</i>	0.63	MAM <i>Cryptonanus ignitus</i>	0.68
BOT <i>Conyza coronopifolia</i>	0.72	ANF <i>Gastrotheca christiani</i>	0.78
BOT* <i>Senecio tilcarensis</i>	0.83	ANF <i>Melanophryniscus rubiventris</i>	0.49
BOT* <i>Stevia yalae</i>	0.83	ANF <i>Telmatobius platycephalus</i>	0.71
BOT* <i>Solanum calileguae</i>	1.00	LEP <i>Bassania jocosa</i>	0.52
BOT* <i>Ipomoea volcanensis</i>	0.75	LEP <i>Oxydia optima</i>	0.89
BOT <i>Bomarea boliviensis</i>	0.57	LEP <i>Herminodes carbonelli</i>	0.81

*Only present in the study region.

Appendix 5

Endemic species of the consensus area “Sierras Calchaquies” under 0.25° grid size (Fig. 8b)

Species	0.25°	Species	0.25°
BOT * <i>Nassella leptothera</i>	0.90	INS <i>Coxina turibia</i>	0.92
BOT * <i>Nassella fabrisii</i>	0.93	INS <i>Alypia australis</i>	0.89
REP <i>Liolaemus calchaqui</i>	0.85	INS <i>Aucula hilzingeri albirubra</i>	0.94
REP <i>Liolaemus heliodermis</i>	0.91	INS <i>Seirocastnia praefecta</i>	0.97
REP <i>Liolaemus pagaburoi</i>	0.85	INS <i>Galgula castra</i>	0.87
REP <i>Liolaemus griseus</i>	0.90	INS <i>Agrotis aspersula</i>	0.90
ANF <i>Gastrotheca gracilis</i>	0.87	INS <i>Platysenta glaucoptera</i>	0.83
ANF <i>Telmatobius laticeps</i>	0.88	INS <i>Jurinella tucumana</i>	0.92
INS <i>Pero olivacea</i>	0.96	INS <i>Mimapsilopa mathisi</i>	0.92
INS <i>Epimecis curvilnear</i>	0.96	INS <i>Nostima flavida</i>	0.93
INS <i>Bassania schreiteri</i>	0.90	INS <i>Dactylopius zimmermanni</i>	0.94
INS <i>Psaliodes prionograma</i>	0.93	INS <i>Anochetus altisquamis</i>	0.97
INS <i>Lissochlora sanguinipunctata</i>	0.96	INS <i>Pachycondyla striata</i>	0.96
INS <i>Synchlora suppomposa</i>	0.90	INS <i>Solenopsis angulata</i>	0.90
INS <i>Motya haematopis</i>	0.98	INS <i>Prionopelta punctulata</i>	0.91

*Only present in the study region.