

The road to 2020 targets and the learnings from the emblematic South American plant genus *Nassauvia* (Asteraceae)

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Received: 1 July 2016/Revised: 18 September 2016/Accepted: 21 October 2016/
Published online: 1 November 2016
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Abstract The elaboration of a comprehensive database about the distribution of the South American genus *Nassauvia* has allowed investigate its conservation biogeography. The combined use of historical (Dispersal Vicariance Analysis) and ecological (UPGMA) biogeographical approaches has led to detecting past, present and future critical areas in the evolution and persistence of the genus. According to the size of distribution areas, number of locations, environmental niche models, and predicted shifts of these spatial characteristics following the Intergovernmental Panel on Climate Change forecasts for the next decade, it has been possible to award the level of global and national risk for all species of the genus and assign their corresponding IUCN categories. Severe gaps in legal and in situ conservation policies have been detected within the region, making it urgent the adoption of measures aimed at preventing the extinction of the most endangered species. We identify a future dramatic loss of *Nassauvia* species in the Andes and conversely a species increase in Patagonia. Patagonia has emerged as the cradle of the genus and could be its refuge in the future according the predictions targeted by climate change.

Communicated by Daniel Sanchez Mata.

This article belongs to the Topical Collection: Biodiversity Conservation and Reserves.

Electronic supplementary material The online version of this article (doi:10.1007/s10531-016-1245-0) contains supplementary material, which is available to authorized users.

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Keywords Dispersal Vicariance Analysis · UPGMA · Environmental Niche Models · Red listing · Gap Analysis

Introduction

Biodiversity loss has accelerated in recent decades. This crisis of biodiversity has been recognized by the Convention on Biological Diversity (CBD), whose members have set targets to promote actions towards conserving biodiversity and arrest falls under way in the state of biodiversity for the year 2020 (O'Connor et al. 2015). Likewise, biodiversity conservation involves a biogeographic question since one of the main tasks in conservation is to select the most appropriate areas for conservation (Posadas et al. 2006). Although some authors have attempted to make connections between biogeographical patterns and processes that occur in vastly different spatial and temporal scales (e.g., Hengeveld and Haeck 1982; Bock and Ricklefs 1983; Brown 1995) a few of them have concerned on how integrate them to be fully utilized in fields such as conservation (e.g., Crisci et al. 2006; Kraft et al. 2010; Menini Neto and Campostrini Forzza 2013). The historical biogeography involves several approaches, among them the Dispersal-Vicariance Analysis or DIVA (Ronquist 1997; Crisci et al. 2003), which provides historical explanations about the processes (dispersal, vicariance, extinction and duplication) that led to species distributional patterns. On the other hand, ecological biogeography encompasses, among other subjects, present and future biogeographic regionalizations for example through multivariate analysis (like UPGMA, Unweighted Pair Group Method with Arithmetic mean) or Environmental Niche Models (ENMs, cf. Araújo and Peterson 2003). ENMs predict the geographic range of species associating environmental variables and known species' presence records to identify environmental conditions within which populations can occur now or under predicted future scenarios (Peterson 2003; Bellard et al. 2012; Araujo and Peterson 2012). In conservation terms, these methods have been used for detecting species richness patterns (Fajardo et al. 2014) or for awarding threat status using the popular IUCN categories of risk (Keith et al. 2014; Syfert et al. 2014).

Whilst theories and analyses in biodiversity conservation have increased in the last years, the shortage of high-quality data is one of the biggest challenges facing conservation studies (Richardson and Whittaker 2010; Hortal et al. 2015), the so called Linnean and Wallacean shortfalls. Thus, we selected the Andean-Patagonian plant genus *Nassauvia* (Asteraceae) for our study, in which these impediments are minimized, because it has a series of taxonomic treatments (Cabrera 1982; Katinas 1995; Katinas et al. 2008a) and morphological (Tortosa et al. 2004), evolutionary (Katinas et al. 2008b) and ecological (Nicola et al. 2014) studies. Moreover, a nearly entire morphological (Freire et al. 1993) and partial molecular-based (Maraner et al. 2012) generic phylogenies have been published.

The genus *Nassauvia* (39 species) is an emblematic South American genus of perennial plants (geophytes, hemicryptophytes or chamaephytes), distributed from Bolivia to the Malvinas/Falkland Islands. It belongs to the tribe Nassauvieae, an early-branching lineage in the phylogenetic tree of the family Asteraceae (Ortiz et al. 2009). It is endemic to a relatively narrow area of South America, with most species concentrated in the Andes and Patagonia and three species confined to the Malvinas/Falkland archipelago. Despite its relatively high number of species, it is a morphologically well-defined genus with some

particularities such as the tendency of clustering the flowering heads into capitula of capitula (Katinas et al. 2008a), and the deciduous pappus in most species which barely can aid in the plants dispersion. Species of *Nassauvia* also play an important role constituting communities that define phytogeographical districts, like western and central Patagonic districts, corresponding to the Patagonian Province (e.g., *N. axillaris*, *N. glomerulosa*, *N. ulicina*) (Cabrera 1971).

A well-built and comprehensive database combined with biogeographical analyses would provide the opportunity to assess the level of risk and the degree of in situ conservation of *Nassauvia* species. This assessment allows using *Nassauvia* as a surrogate in the diagnosis of the degree of compliance with the Global Strategy of Plant Conservation (GSPC) and their goals for the year 2020 in the Andean-Patagonian region. The GSPC, emanating from the Convention on Biological Diversity, includes different goals for that deadline, among which are the Target 2 requiring an assessment of the conservation status of all known plant species, and Target 7 demanding at least 75% of known threatened plant species conserved in situ (Sharrock 2012). In this paper, we examine the progress to these targets in the Andean-Patagonian scope and provide elements for GSPC implementation and debate on the recommendations to successfully reach that deadline.

We present an analysis of the genus *Nassauvia* through the integration of different approaches of biogeography and conservation methods. Our main goals are to: (1) characterize the richness and distribution patterns of *Nassauvia*; (2) determine important plant areas based on biogeographical analyses; (3) evaluate the threat status of the *Nassauvia* species by means of the IUCN risk categories scheme at global and regional scales and check their degree of in situ conservation; (4) conduct an assessment on the compliance of the Andean-Patagonian network of national parks in effectively conserving the most threatened species. A concept map showing our framework, that includes approaches and methodologies, is depicted in Fig. 1.

Materials and methods

Area and study group

The study area comprises the whole range of the genus, which is South America south of 20°S latitude from southern Bolivia to Tierra de Fuego at the southern extreme of Argentina and Chile. The Malvinas/Falkland archipelago is also included since it harbors three species of *Nassauvia*. Following the recent Morrone's (2015) proposal of biogeographical regionalization, the study area should correspond to the Andean Region and includes the South American transition zone, and Central Chilean, Subantarctic and Patagonian sub-regions (Fig. 2).

The whole study area encompasses different ecosystems or biomes: (1) the Andean highlands with a typical dry and cold high-mountain climate, and grassy and chamaephyte steppes as predominant vegetation; (2) the Andean temperate mixed deciduous and evergreen forest covering from 35 to 55°S latitude, whose climate is cold temperate, with abundant snow in the winter and frosts during almost the entire year; (3) the extra-Andean semidesert known as Patagonia (from 37°S in Argentina and 43°S for Chile to Cape Horn at 56°S), that includes mainly the Atlantic lowlands and coasts, the southern archipelagos, and the valleys, table lands, and high plains extending between the Andes and the Atlantic Ocean, with a semiarid shrubby steppe vegetation; and (4) the Malvinas/Falkland Islands, a

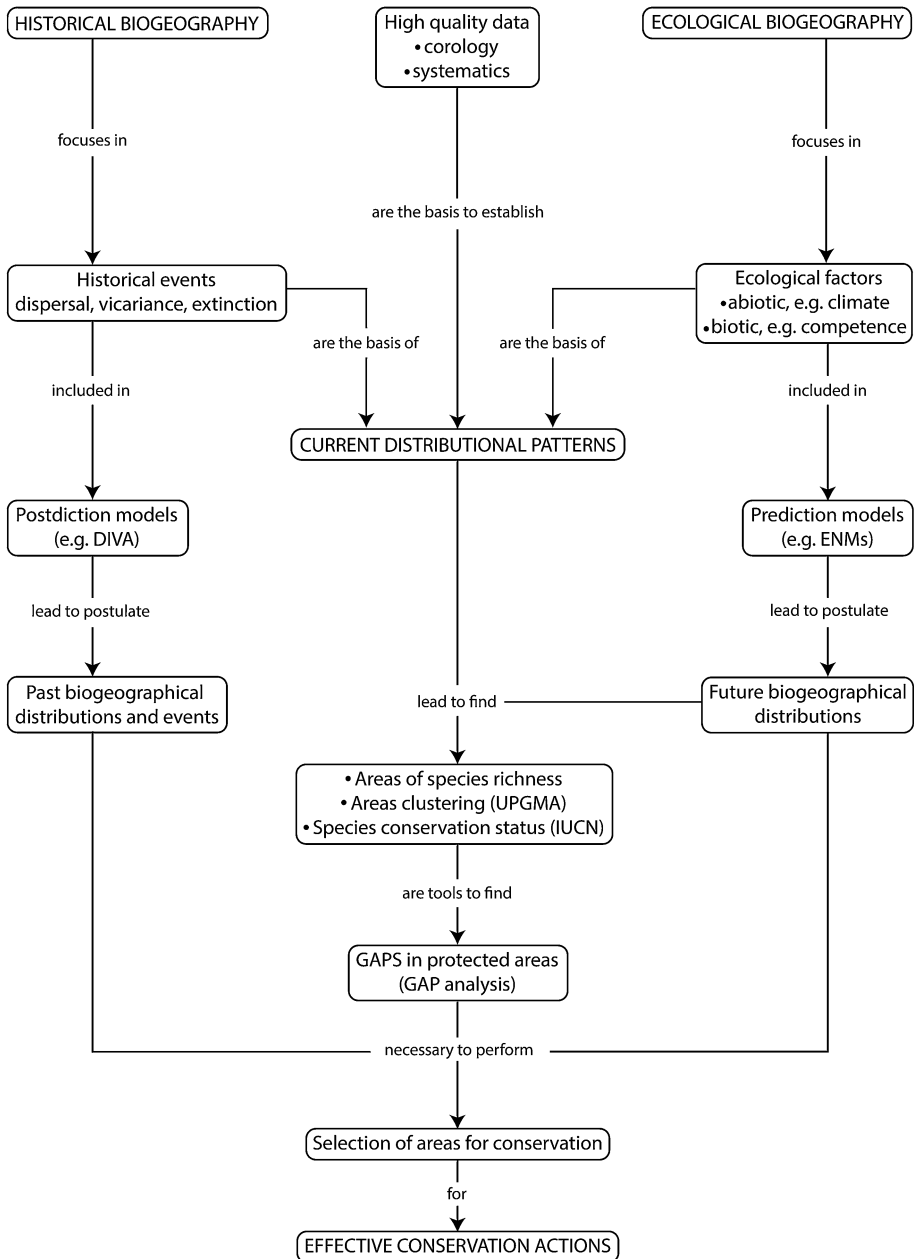


Fig. 1 Concept map showing the framework of this paper; the methodologies are in parentheses

tundra or a steppe where the climate is cold and humid, with snow most of the year (Cabrera and Willink 1973). The species of *Nassauvia* commonly inhabit the arid extra-Andean semidesert and the Andean highlands.

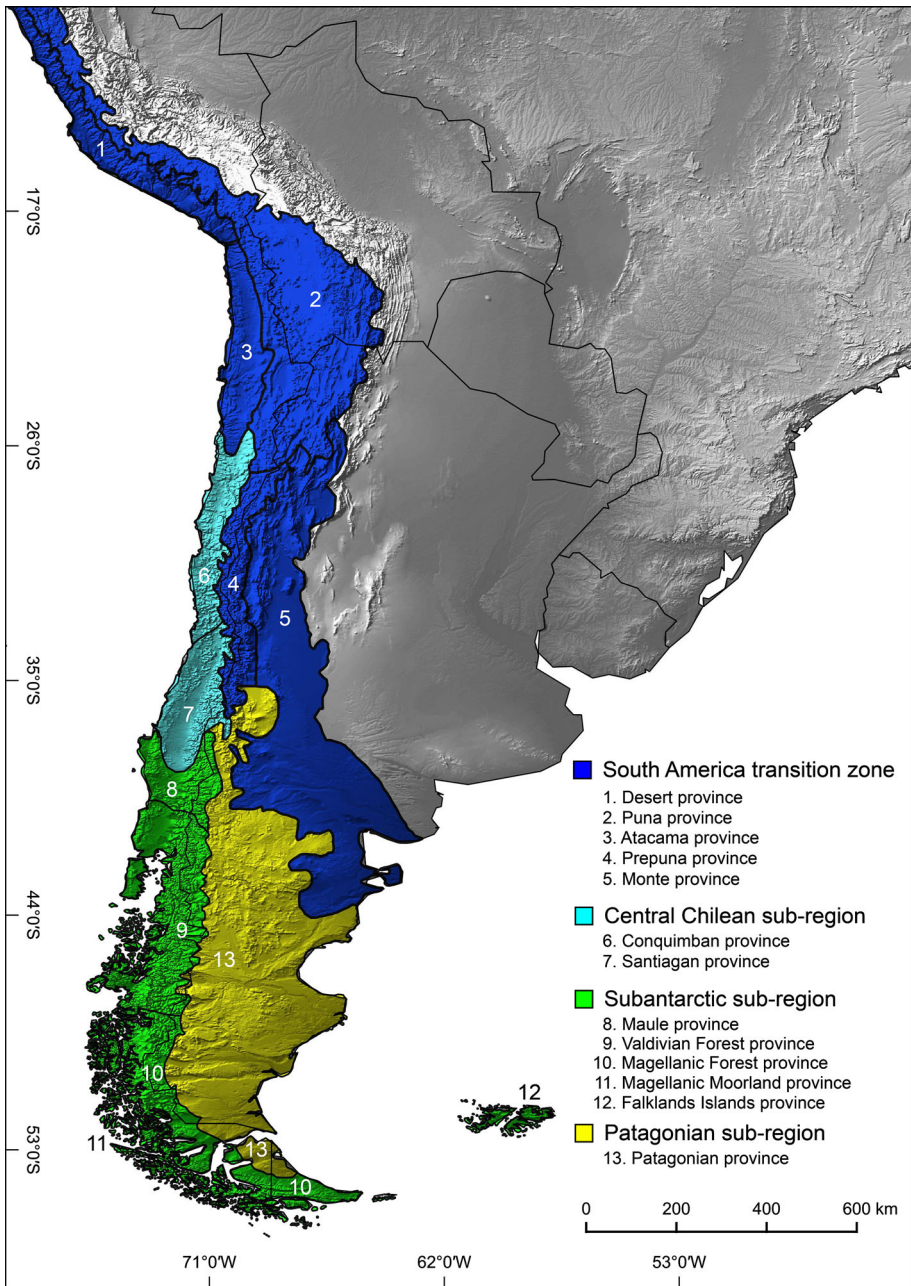


Fig. 2 Biogeographic regionalization of the Andean region (modified from Morrone 2015). (Color figure online)

The information on the distribution of specimens of *Nassauvia* is based on the literature (Cabrera 1971, 1982; Kalin Arroyo and Marticorena 1988; Upson et al. 2013; Katinas 2015), on the investigation of herbarium materials, and on databases. Our team has

conducted fieldwork for decades in the natural habitats of the genus, and besides this we have revised and compiled a large database for *Nassauvia*. More than 1500 specimens deposited at the main Argentinian herbaria (LP, BAB, SI, BA) have been critically reviewed and checked as well as those data hosted on the Global Biodiversity International Facility (7% of total records, see Online Resource 1). This allowed us to determinate unrecognized specimens and to correct many misidentifications which otherwise would have produced cascade errors in our work.

All those records that were not originally georeferenced by their authors were referred, when possible, to their corresponding coordinates using cartographic maps, atlases and topographical electronic databases. We obtained a total of 1.056 records of locations for all species of the genus (see Supplementary Information, Online resource 1 for a list of all records) with an average accuracy of georeferencing lower than 10 km². For the biogeographical analyses, the raw distribution data were later summarized according to their presence along the UTM (Universal Transverse Mercator) grid of c. 100 km side using the R package *letsR* (Vilela and Villalobos 2015). Thus, a data matrix of 141 observations, all those squares with the presence of at least one taxon, by 39 variables (species) was obtained.

Richness

Species richness was obtained by two different but complementary ways according to the grain size. On one hand, the total number of species per cell along the UTM grid of 100 × 100 km of side was computed with the package *letsR* and later mapped by means of QGIS (QGIS 2012). The grid size was chosen after finding that narrower lattices not allowed adequately represent the diversity patterns due to sampling bias.

On the other hand the number of different species present in each location (cf. Whittaker 1972) was based on the predictive results of the Environmental Niche Models (ENMs) when reclassified by the Minimal Predicted Area (MPA) threshold (Engler et al. 2004; Guisan et al. 2006; Pearson et al. 2007; Jiménez-Alfaro et al. 2012) to transform the potential area occupied by the species into estimates of presence and absence and stacked to generate the richness model (de la Estrella et al. 2012). ENMs were generated using the Maxent algorithm (Phillips et al. 2006). This algorithm is appropriate for presence-only data and has been considered to generate the best output out of many different models (Elith et al. 2006; Ortega-Huerta and Peterson 2008). Species background areas were selected by using a 250 km buffer from the MCP (Minimum Convex Polygon) generated from presence data to maximize the AUC (Area Under the Curve) (Van Der Wal et al. 2009). Default settings were maintained except when species presence localities were greater than 5, so 75% of the occurrence locations were used for building the model and the remaining 25% were used for testing the accuracy of the model; ten replicates were always used. The future climate predictors were derived from the general circulation model (CCCMA: CGCM2) for 2020, under the IPCC (Intergovernmental Panel on Climate Change) emission scenario (A2a) for predicting future distributions (Ramirez and Jarvis 2008). Scenario A2a assumes a more intense change in temperature and precipitation.

Changes on Extent of Occurrence (EOO) and Area of Occupancy (AOO) (see Conservation status of the species according to IUCN categories) between 2010 and 2020 were based on MPA threshold due to the appropriate identification of all plant specimens were confirmed by Katinas, Grossi, Apodaca and Vitali. This second approach provides an idea of species richness not only considering where every species is recorded but also where is expected to be found. Furthermore, this last approach allows additionally considering future scenarios and project prospective changes in species richness. Data preparation,

ENMs and statistics were carried out in Idrisi Selva v.17.02 environment (Clark Labs, Clark University). In the absence of more precise studies on dispersal capacity and because most species of *Nassauvia* have its main dispersal element (the pappus) deciduous and hence non-functional, a conservative distance of at least 50 km was taken to rule out the rescue effect between populations on both sides of national borders (cf. IUCN 2012).

Cluster analysis (UPGMA)

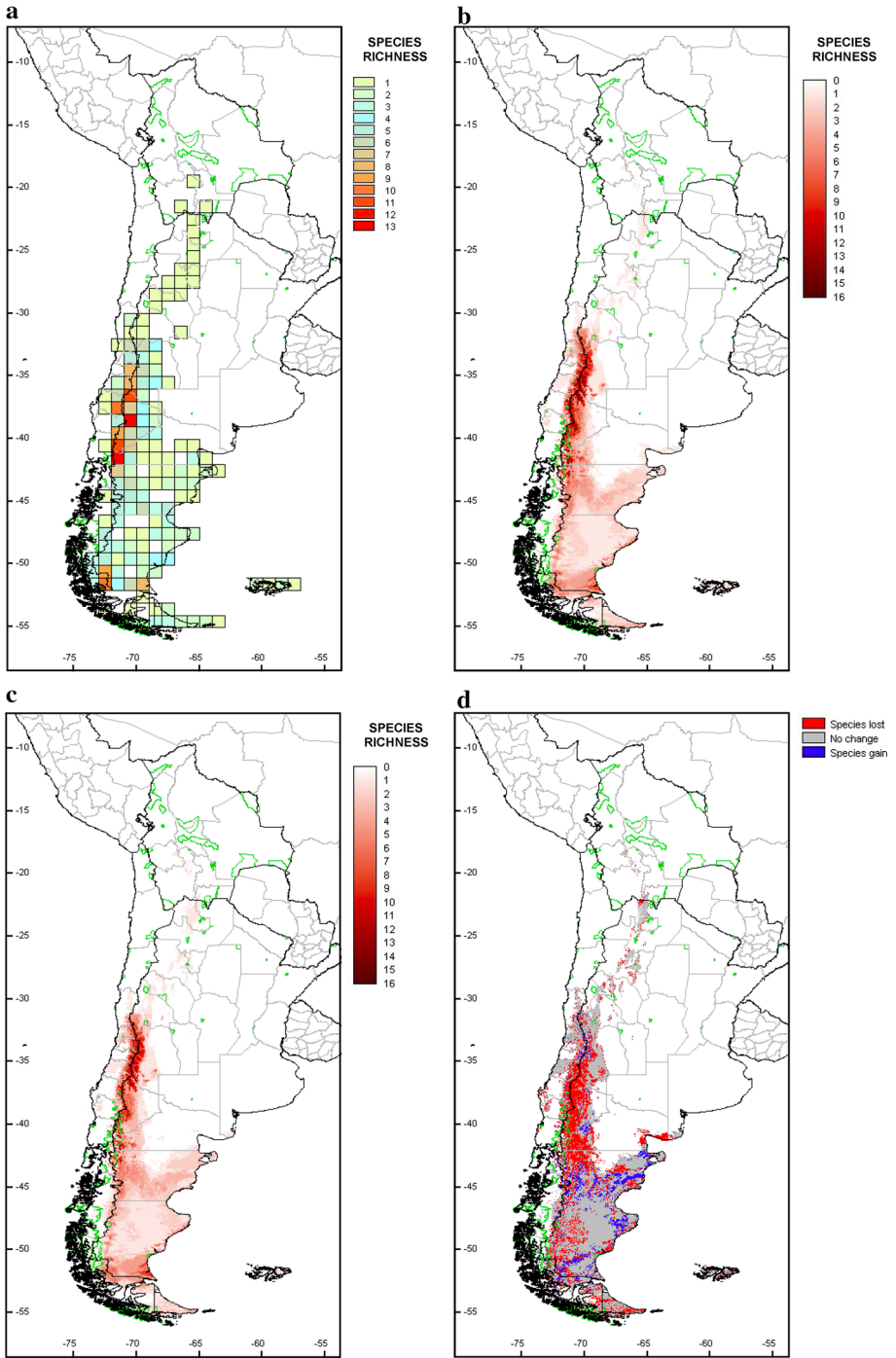
We generated a matrix of pairwise distance of beta diversity between grid cells using β_{sim} index, which is a robust estimate of the ‘true’ species turnover and it is not affected by differences in species richness (Kreft and Jetz 2010). β_{sim} values ranges from 0 (grid cells share same species composition or the species composition of one grid cell is a subset of the other) to 1 (no shared species). We then performed a cluster analysis using the UPGMA clustering method (Sneath and Sokal 1973), an efficient algorithm repeatedly employed in regionalization (Kreft and Jetz 2010; Daru et al. 2016). All these analyses were performed in R (R Core Team 2011), using the packages *betapart* (Baselga and Orme 2012) and *cluster* (Maechler et al. 2013). The optimum number of clusters (regions) was selected using the function ‘elbow’ in the package *GMD* (Zhao et al. 2011).

Dispersal-vicariance analysis (DIVA)

The dispersal-vicariance analysis was implemented in the software Reconstruct Ancestral States in Phylogenies ver. 3.2 (RASP; Yu et al. 2015) on the basis of the phylogenetic tree of *Nassauvia* obtained by Freire et al. (1993) where nearly all species were sampled. The DIVA algorithm implemented in RASP requires the tree to be fully resolved, and the phylogenetic tree of Freire et al. (1993) is resolved only at the level of subgenera and sections, but has many polytomies at the infrageneric levels. We thus performed four cladistic analyses using *Triptilion* as outgroup (Freire et al. 1993; Katinas et al. 2008a) to solve these polytomies in *Nassauvia*. In all cases, one tree was obtained for each and assembled in the backbone tree (see Supplementary Information, Online resource 2 to see the table of characters, data matrix, tree resolution, tree length, consistency index, and retention index for each analysis). Areas of endemism for *Nassauvia* species were determined following the biogeographical scheme for the Andean Region proposed by Morrone (2015) (Fig. 2): A. Malvinas/Falklands Islands Province; B. Valdivian Forest Province; C. Puna and Monte Provinces; D. Prepuna Province; E. Patagonian Province; F. Magellanic Forest Province; G. Coquimban Province; H. Santiagan Province. Also, we included the I. Atlantic Province (Morrone 2014) in the analysis for the genus *Cephalopappus*, used as one of the outgroups (Freire et al. 1993).

Conservation status of the species according to IUCN categories

Global and national level threatened status of the 39 *Nassauvia* species were assessed mainly based on the application of the IUCN Red List Criterion B (IUCN 2001). Each species was modeled considering current distribution and climatic data set for 2010 and projected to 2020 climate (see Fig. 3b, c). Changes in predicted distribution were used to assess the conservation status. The criterion B focus on two spatial measures related to the distribution of the species: Area of Occupancy (AOO) and Extent of Occurrence (EOO). The AAO was assessed as the sum of the total number of cells of 2×2 km of side (IUCN



◀ **Fig. 3** **a** Current species richness of the genus *Nassauvia* obtained as the total number of species on each UTM cell of 100 km side. **b** Current species richness obtained as the total number of species found at each location using the predictive map of each one. **c** Projected species richness to 2020 based on the current species distribution. **d** Trend between current and 2020 predicted species richness pointing out places where it is expected to lose species (*in red*), places that may increase its richness (*in blue*) and places that will retain the same amount of species (*in grey*). National borders outlined in *black*; subnational administrative levels (provinces or regions) outlined in *pale grey*; National Parks are outlined in *green*. (Color figure online)

2016) after plotting the recorded location of the species. Modification of the future amount of localities and subpopulations for each species between 2010 and 2020 are solely based on reclassified maps by the MPA threshold. The EOO is recommended to be assessed by the minimum convex polygon (MCP) regarding IUCN (2001, 2016). We used the MPA threshold of each species with particular attention to the recommendations of IUCN (2016) when using ENMs instead of MCP.

To accommodate the time scale for the variation on EOO and AOO, bioclimatic variables were used for building the models for 2010 and projected for 2020 (see richness methodology). That way is fulfilled the time period proposed by IUCN (over a period of 10 years or 3 generations) and pointed out by Akçakaya et al. (2006). Environmental datasets used in the ENMs included 19 climate data variables from Worldclim (Hijmans et al. 2005, <http://www.worldclim.org/>) and the altitude obtained from SRMT (<http://srtm.csi.cgiar.org/>) and from the Climate Change Agriculture and Food Security (CCAFS 2013), all adjusted at the same spatial resolution (2×2 km). To avoid problems of co-linearity only uncorrelated variables were included to the model, correlation between variables was performed and was considered highly correlated if $R \geq 0.75$ (Pearson coefficient); we retained the variable considered to be the most biologically relevant for subsequent modeling when this occurred (see Supplementary Information, Online resource 3 for a list of variables used to build ENMs).

Gap analysis

A Gap analysis was performed to assess the protection degree of the genus *Nassauvia* within the different countries where the species occur. In the absence of a common framework of natural protected areas, with a large heterogeneity in their management and presumably in their effectiveness, we decided to limit the analysis to the figure of maximum protection, that is national parks (Category II of protected areas, cf. Dudley 2008). The respective layers of national protected areas were gathered from several sources: Bolivia (<http://www.sernap.gob.bo/>); Argentina (<http://www.sib.gov.ar/>); and Chile (<http://www.ide.cl/descarga/capas/item/parques-nacionales.html>). Malvinas/Falkland islands do not have any national park. Species records were superimposed over the network of national parks to identify which species were and were not included within them. The assessment was performed against the total regional network of national parks and against every national network to discuss deficits at different scales.

Results

Richness

The greatest richness of *Nassauvia* species, expressed as number of different taxa in each 100×100 km of side cell, occurred in the central-western area of Argentina and Chile, between the 35° and 41° S, ecotone zone between temperate forests, steppes and high

Andes (Fig. 3a). The richest square came to overcome a dozen of recorded species. A second smaller area of richness occurs at 51°S, in the ecotone of the high Andes and the temperate forests (Fig. 3a). The Patagonian Province has a relatively reduced richness when quantified by such grid. Current species richness obtained by the ENMs (Fig. 3b) coincided in emphasizing the maximum richness at the central-western area of Argentina and Chile, where several places reached up to values of 16 species expected per cell. A regional hotspot occurred around Río Gallegos (Santa Cruz province, Argentina).

Using the projected species distribution models to 2020 we obtained a similar picture of diversity distribution, but emerging some future regional decoupling. A primary result (Fig. 3c) suggests that over half of the territory examined (60% of the area) will not undergo changes in the number of species, while there will be an increase in areas mainly at Patagonia and a decrease in places along the Andes.

Figures 3d and 4 show the potential unbalanced trade-off with locations gaining up to four species against others with a more dramatic loss of up to ten species. The most sensitive places were located in the central-western area of Argentina and Chile, coinciding with the area of current greatest richness of the genus.

Biogeographic regionalization

The ‘elbow’ criterion (Salvador and Chan 2004) found 5 optimal clusters of squares for β_{sim} explaining 56% of variance in species composition (Fig. 5). A larger number of clusters lead to little interpretable and not meaningful regions. We referred these clusters according to their geographical location and adjusting as far as possible to the nomenclature of previous phytogeographical proposals (Table 1).

The dendrogram firstly separated the cluster corresponding to the Malvinas/Falklands archipelago with a very high β_{sim} value of about 1.0 due to a whole replacement of the insular species with respect to the continental ones (Fig. 6). Next divisions were also supported by high β_{sim} indexes and separated two wide and rich areas, Subantarctic Province from Puna and Monte Province, and two lesser clusters, the Patagonian Province from the Central Chilean Province. The detailed composition of the resulting areas was presented in Table 1.

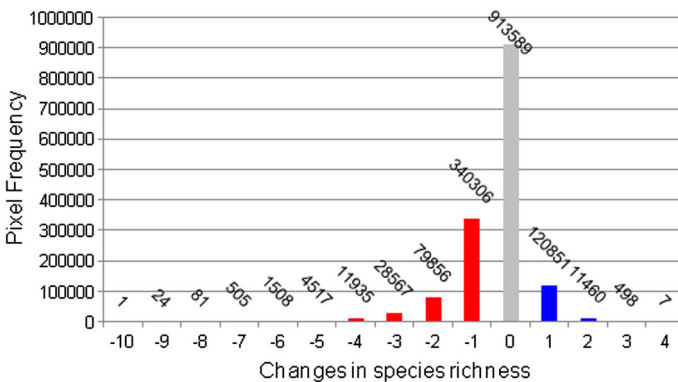


Fig. 4 Frequency of pixels regarding the future trend in species richness of *Nassauvia* based on the map of Fig. 3d. Negative figures indicate the amount of species lost (in red), positive values indicate species gain (in blue). Major part of the territory will keep the same amount of species richness (in grey). Note that at this latitude each pixel corresponds to about 0.65 km². (Color figure online)

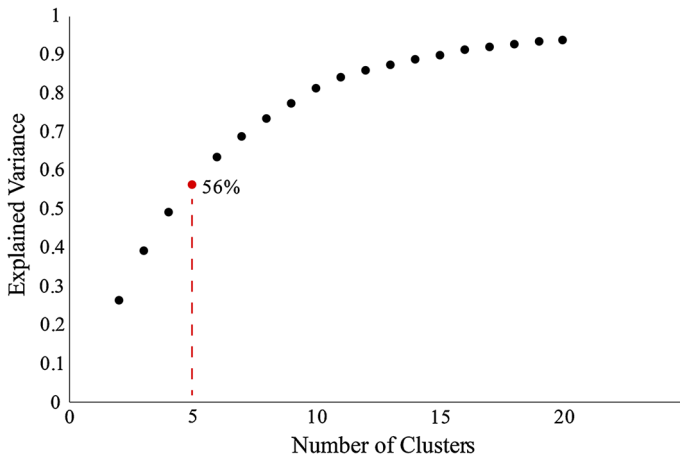


Fig. 5 Threshold of explained variance identifying the optimal number of clusters from $n = 2$ –20 groups for beta diversity. The ‘elbow’ criterion (optimal cluster number) is shown by the red line. (Color figure online)

Table 1 Relation of five clusters of grid squares (provinces) selected by UPGMA analysis

Area	# Squares	# Species
1. Malvinian/Falklandian province (orange)	4	3
2. Patagonian province (yellow)	22	16
3. Subantarctic subregion (green)	51	30
4. Puna and Monte province (dark blue)	58	25
5. Central Chilean province (light blue)	6	10

For every cluster the number of grid squares and the number of covered species is shown. Colors correspond to those used in Fig. 6

Dispersal-vicariance analysis (DIVA)

The results of DIVA analysis (Fig. 7) showed Patagonia (area E) as the probable ancestral area for *Nassauvia*. The tree of *Nassauvia* showed 48 dispersal (including the dispersal events in the terminal taxa) and nine vicariance events (see Supplementary Information, Online resource 4 showing the events of dispersal or vicariance at each node of the tree of Fig. 7). There were multiple dispersals from the Patagonian province to the Valdivian Forest, Magellanic Forest and Santiagan provinces. The most frequent vicariance events occurred between Patagonian with other areas, mainly between Patagonian and Malvinas/Falkland, Magellanic, and Santiagan provinces. Furthermore, the DIVA analysis shows three dispersal and three vicariance events to Malvinas/Falklands Islands.

Conservation status of the species according to IUCN categories

At global level, 15 species were categorized as threatened while 13 and 11 were classified as Least Concern and Near Threatened, respectively. The assessment of national categories of threat emphasized that both Bolivia (1 species) and Malvinas/Falkland islands (3

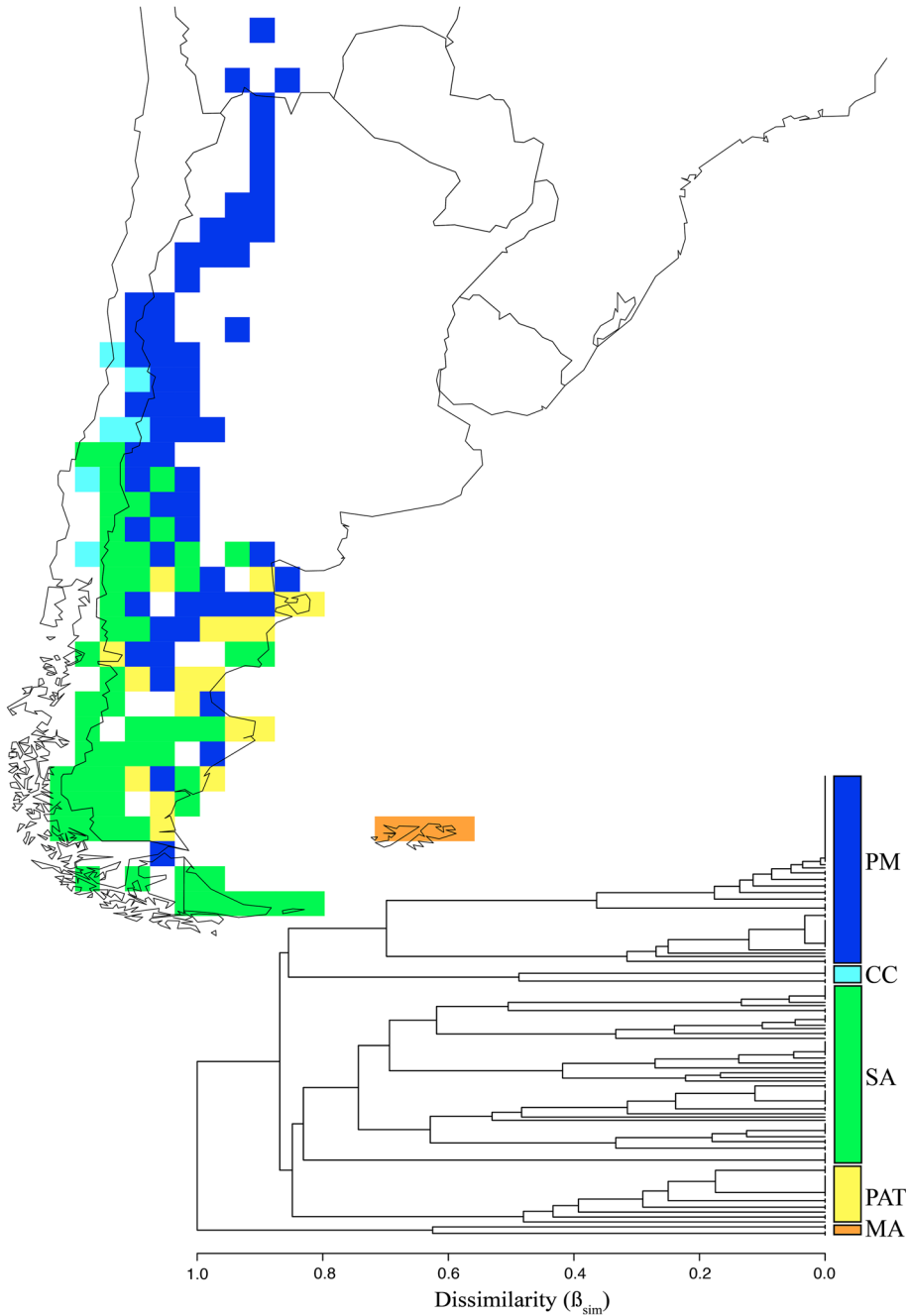


Fig. 6 Map (top) and dendrogram (bottom) resulting from UPGMA analysis of the distribution of *Nassauvia* species along the Andean-Patagonian region. Every square in the map represents an UTM cell of c. 100 km side. The 5 provinces correspond to those showed in Table 1: PM Puna and Monte; CC Central Chilean; SA Subantarctic; PAT Patagonian; MA Malvinian/Falklandian. (Color figure online)

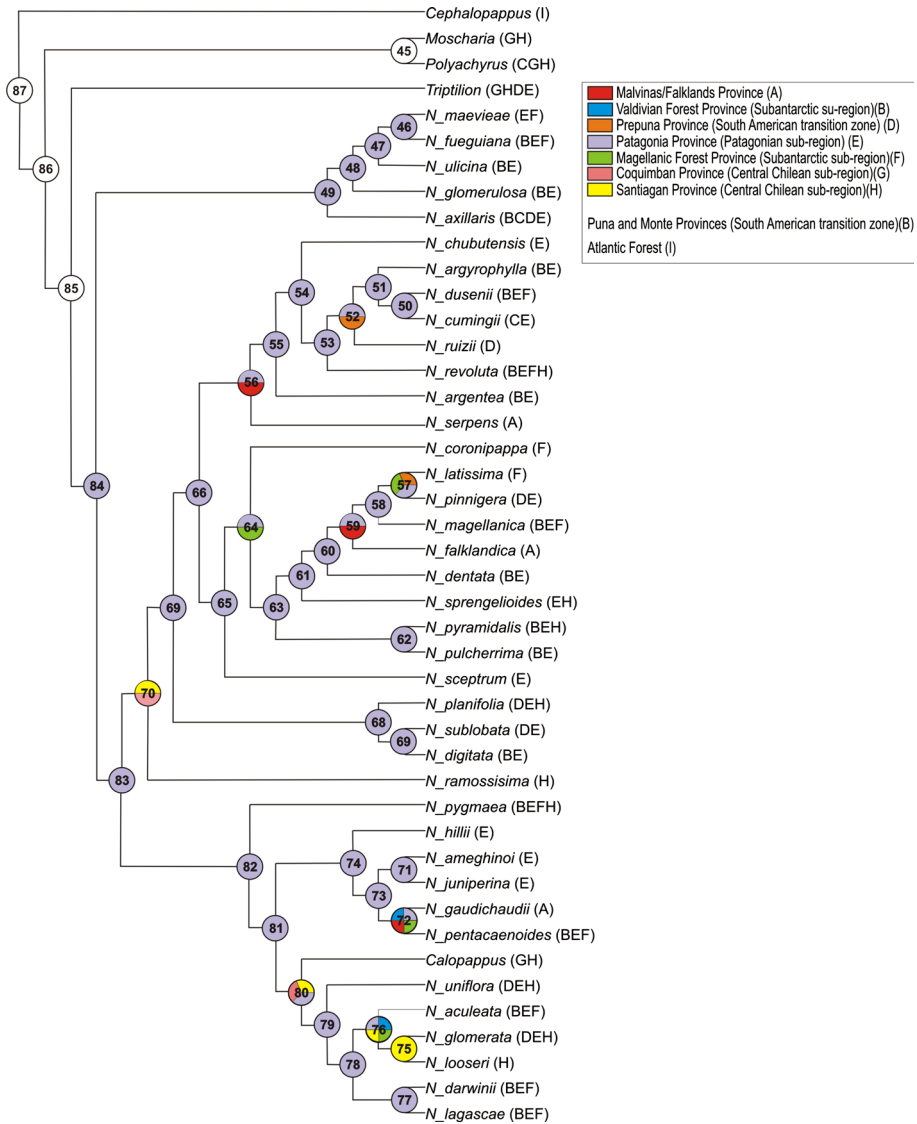


Fig. 7 Dispersal-vicariance analysis for the genus *Nassauvia*. Circles show the reconstruction of ancestral areas on each node (the correspondence between the different colors and the areas is shown in the box and represents probabilities of alternative ancestral ranges). The letters next to each species name indicate the current distribution of each taxon. Only the reconstructions of the nodes corresponding to *Nassauvia* are shown. (Color figure online)

species) had all their *Nassauvia* taxa threatened, Chile had 18 of its 24 species threatened, whilst in Argentina 11 of its 34 species were included in any category of threat (Table 2; Fig. 8) (see Supplementary Information, Online resource 5 for number of localities, sub-populations and calculated EOO and AOO area values for each species). Note that the use of ENMs instead of the MCP to evaluate the EOO can lead to the modeled presence of

Table 2 Summary of the 39 *Nassauvia* species assessed against the IUCN Red List Categories scheme

Region	LC	NT	VU	EN	CR	Assessed by region	Threatened sp.
Global	13	11	7	7	1	39	15
Argentina	13	10	6	5	0	34	11
Bolivia	0	0	0	1	0	1	1
Chile	1	5	9	5	4	24	18
Malvinas/Falkland	0	0	1	2	0	3	3

Assessments were conducted for the entire distribution but also at regional level for each country where every species occurred

LC Least Concern; NT Near Threatened; VU Vulnerable; EN Endangered; CR Critically Endangered

some species in countries where such are currently unrecorded. Such situation has been pointed out in 13 species.

Gap analysis

Regarding only threatened species, out of the 15 globally threatened only four (*Nassauvia maeviae*, *N. pulcherrima*, *N. sprengelioides* and *N. sublobata*) had at least part of their range included in a National Park within the study area. Now, if we consider the national IUCN categories of threat for these plants, the results were more uneven since Argentina had four of its 11 threatened species included (*N. digitata*, *N. pulcherrima*, *N. sprengelioides* and *N. sublobata*), Chile had three of its 18 threatened species included (*N. argyrophylla*, *N. dentata* and *N. maeviae*), but none of the Bolivia nor the Malvinian/Falklandian species are under the protection of a national park (Broughton and McAdam 2005) (Table 3).

One-third of the species of *Nassauvia* (13) were within the boundaries of the Nahuel Huapi National Park in southwestern Argentina. Close to this is the Lanin National Park which hosts 10 species. Far from these values are the Chilean Bernardo O'Higgins National Park and the Argentinian Los Glaciares and Perito Moreno National Parks with five species each (see Supplementary Information, Online resource 6 for the effectiveness of the different national parks to ensure in situ conservation of the genus *Nassauvia*).

Discussion

Patterns of richness and geographical distribution

The greatest richness of *Nassauvia* species occurred in the central-western area of Argentina and Chile, between the 35° and 41°S, in the Andes at both sides of the Chilean-Argentinian boundary. This region comprises an ecotone between temperate forests, steppes and high Andes, producing a mixture of geographical and ecological elements and thus elevating the species richness. Many authors have emphasized such transitional zones as areas with the co-occurrence of floristic components belonging to distinct biotic elements typical of adjacent communities (e.g. Odum 1983; Walker et al. 2003; Ferro and Morrone 2014). A second prominent area is at the latitude of Río Gallegos (52°S), roughly coinciding with a further transition zone between steppes and Andes. Even when the

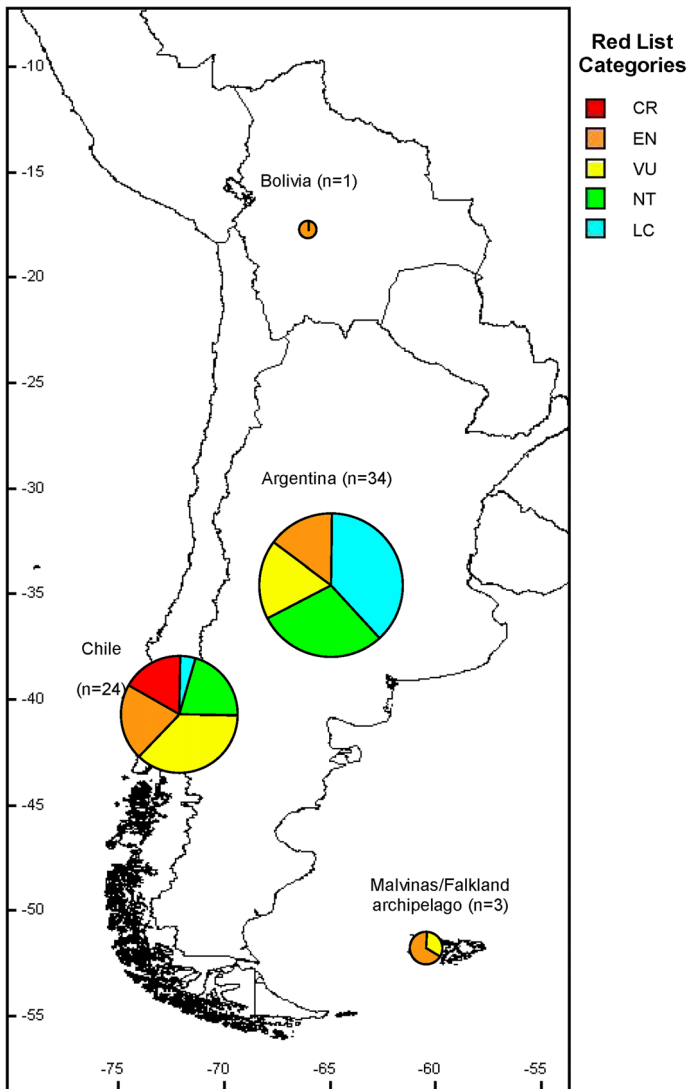


Fig. 8 Graphical representation of the spectrum of national threat categories within the *Nassauvia* species. Pie size is proportional to the amount of species by country. (Color figure online)

Patagonia steppe holds the major number of species of *Nassauvia*, it harbors a lower density of species, such as the Andes in northern Argentina and in southern Bolivia.

We used two approaches to describe species richness and their results match to some extent. The total number of species per grid cell represents a kind of density of recorded taxa along the study area. This has been the approach usually employed in many other studies and represents little operational difficulty (i.e. Cron et al. 2009; Menini Neto and Campostrini Forzza 2013). Its usefulness partly rests on the degree of accuracy of the chorological records and on the grid size. But, once the number of species observed in an area depends to some extent on the effort invested in recording there (Yang et al. 2013),

Table 3 Species of *Nassauvia* covered by the network of national parks

Taxon	Argentina	Bolivia	Chile	Malvinas
<i>N. aculeata</i>	Protected	n.r.	Unprotected	n.r.
<i>N. ameghinoi</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. argentea</i>	Protected	n.r.	Unprotected	n.r.
<i>N. argyrophylla</i>	Protected	n.r.	Protected	n.r.
<i>N. axillaris</i>	Protected	Unprotected	Unprotected	n.r.
<i>N. chubutensis</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. coronipappa</i>	n.r.	n.r.	Unprotected	n.r.
<i>N. cumingii</i>	Unprotected	n.r.	Unprotected	n.r.
<i>N. darwinii</i>	Protected	n.r.	Unprotected	n.r.
<i>N. dentata</i>	Protected	n.r.	Protected	n.r.
<i>N. digitata</i>	Protected	n.r.	Unprotected	n.r.
<i>N. dusenii</i>	Protected	n.r.	Unprotected	n.r.
<i>N. falklandica</i>	n.r.	n.r.	n.r.	Unprotected
<i>N. fuegiana</i>	Protected	n.r.	n.r.	n.r.
<i>N. gaudichaudii</i>	n.r.	n.r.	n.r.	Unprotected
<i>N. glomerata</i>	Unprotected	n.r.	Unprotected	n.r.
<i>N. glomerulosa</i>	Protected	n.r.	Unprotected	n.r.
<i>N. hillii</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. juniperina</i>	Protected	n.r.	n.r.	n.r.
<i>N. lagascae</i>	Protected	n.r.	Protected	n.r.
<i>N. latissima</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. looseri</i>	n.r.	n.r.	Unprotected	n.r.
<i>N. maeviae</i>	Unprotected	n.r.	Protected	n.r.
<i>N. magellanica</i>	Protected	n.r.	Protected	n.r.
<i>N. pentacaenoides</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. pinnigera</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. planifolia</i>	Protected	n.r.	Unprotected	n.r.
<i>N. pulcherrima</i>	Protected	n.r.	n.r.	n.r.
<i>N. pygmaea</i>	Protected	n.r.	Protected	n.r.
<i>N. pyramidalis</i>	Unprotected	n.r.	Protected	n.r.
<i>N. ramosissima</i>	Unprotected	n.r.	Unprotected	n.r.
<i>N. revoluta</i>	Protected	n.r.	Protected	n.r.
<i>N. ruizii</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. sceptrum</i>	Unprotected	n.r.	n.r.	n.r.
<i>N. serpens</i>	n.r.	n.r.	n.r.	Unprotected
<i>N. sprengelioides</i>	Protected	n.r.	Unprotected	n.r.
<i>N. sublobata</i>	Protected	n.r.	Unprotected	n.r.
<i>N. ulicina</i>	Protected	n.r.	n.r.	n.r.
<i>N. uniflora</i>	Protected	n.r.	Unprotected	n.r.

The highlighted species in boldface are outside the range of all national parks throughout its distribution (n.r. not recorded within the country)

any method based only in records will be affected by sampling bias. In fact, this method only provides information where we already have some information but it does not act properly on places not previously recorded. Our second approximation is based on the elaboration of ENMs obtained from the species records and an environmental dataset, a procedure that requires some data processing and GIS environment. When we estimate the richness based on the overlap of several ENMs we get a continuous map of richness values where gaps in Patagonia or sharp discontinuities in the Andean diversity are damped. So we fulfill the gaps and minimize the effects of sampling bias. A further advantage in using the overlap of individual ENMs is that we can project them in time considering changes on some environmental descriptors and identify changing patterns. These facts give this method higher biogeographical value in areas with incomplete sampling and make it a powerful conservationist tool. On the other hand, the temporary projection of species distributions to year 2020 allows getting a prospective scenario of future changes on species richness.

The richness based on ENMs for 2010 provides a fine perspective of the expected richness for each pixel. We identify a future dramatic loss of *Nassauvia* species in the Andes and conversely a species increase in Patagonia. Therefore, the Andes area requires a substantial conservation effort, not only for hosting the greatest density of species, but also for being the area that will be most affected in view of climate change, according the projected species distribution models to 2020. The predicted lack of change in the number of modelled species in much of the range of the genus during the decade 2010–2020 does not imply in situ local persistence of the respective species, as commutations of species can be envisioned in each cell. Such projection should be considered as a trend. Aspects such as autoecology, dispersal ability and colonization or life forms will determine if a species would remain or not in a particular geographical space in just a decade.

Biogeographical scenarios

The use of an estimation of the distance between cells based on beta diversity among species assemblies has yielded a robust separation of five clusters in the first branches of the biogeographical regionalization by means of UPGMA. We have recognized five well-defined areas for *Nassauvia* with significant similarity to biogeographic regions previously recognized in classic essays using the South American fauna and flora (Cabrera 1971; Cabrera and Willink 1973; Morrone 2015).

Even when the Malvinas/Falkland archipelago shares many species with southern continental Argentina and Chile (e.g., Tierra del Fuego), the dendrogram shows a robust Malvinian/Falklandian Province with no species in common with the other areas. Nevertheless, as demonstrated by the phylogeny of the genus (Freire et al. 1993; Maraner et al. 2012) the three insular species belong to different continental clades. After the separation of insular squares, a rough latitudinal division separates a large group of southern grids from another cluster of northern grids. The first cluster groups the rich Subantarctic subregion (30 species) (within this subregion most *Nassauvia* species inhabit the high Andes) with the less diverse Patagonian Province (16 species). The second cluster gathers the Central Chilean Province with the Puna and Monte Province (25 species). This last region presents a discontinuous area along the elevations of the Andes, from 20 to 50°S following the distribution of the wider range species of the genus.

The dispersal-vicariance approach supports Patagonia as the probable ancestral area for *Nassauvia*, in coincidence with Cabrera's (1982) hypothesis, and that from that area many dispersal and some vicariance events occurred in the past. Patagonia has also the richest

fossil record of *Nassauvieae* (Asteraceae) dated from the early Miocene (23–9 MYA) (Katinas et al. 2007), and the phylogenetically most basal species of the genus (cf. Freire et al. 1993; Maraner et al. 2012).

The numerous dispersal events from Patagonia to the Valdivian and Magellanic Forests may be the result of massive marine incursions in Patagonia during the Middle and Late Miocene, a pattern repeated in others taxa (Ortiz and Cladera 2006; Posadas 2008). The biogeography of the three species of the Malvinas/Falkland Islands (*Nassauvia falklandica*, *N. gaudichaudii*, and *N. serpens*), on the other hand, is a history of vicariance and dispersal events. The DIVA tree shows that the dispersals from Patagonia to the islands correspond to ancestral nodes whereas the vicariance between Patagonia and the islands corresponds to the speciation events leading to the three island species. A possible explanation is that during the height of the Last Glacial Maximum (26,000–19,000 years before present) the global sea levels were around 130 m lower, which exposed an enormous coastal plain off the Argentine coast, while the Malvinas/Falkland islands land mass was about four times larger than the present (Ponce et al. 2011; Austin et al. 2013). Some ancestors probably occupied this land bridge and reached the islands, being later isolated at the islands when the sea level rose again and the ocean acted as a barrier.

We emphasize the importance of the historical phenomena because in species with poor dispersal devices it could be helpful to understand the species reaction under constraining past geological and climatic changes, considering that they would retain their ancestral niche-related traits. Understanding how the species reacted, where they moved, and from where, will be extremely helpful when considering conservation actions under future global climatic change. For example, only four ancestors of the 14 threatened species of *Nassauvia* expanded their distributional range from Patagonia to other areas in the past, but several ancestors of currently non-threatened species increased their distribution. These latter species should be taken into account as a potential genetic pool reservoir in the case of future habitat threatening.

Assessment of current in situ conservation and future challenges

Using the genus *Nassauvia* as one of the few well-documented surrogates of Andean-Patagonian plant diversity, we are able to contribute to the Global Strategy for Plant Conservation 2011–2020 objectives and to examine some results of conservation policy in the countries of the region. Target 2 implies an assessment of the conservation status of all known plant species to guide conservation action. Global threat category of the 39 *Nassauvia* species have been assessed according to the IUCN criterion B, thus we provide the first IUCN category of risk for 36 species. As far as we know, only the three Malvinian/Falklandian taxa had been previously evaluated against the IUCN scheme: *N. gaudichaudii* and *N. serpens* were included with a LC (Least Concern) category in the IUCN Red List (<http://www.iucnredlist.org>; February 1, 2016), and *N. falklandica* was categorized as CR (Critically Endangered) in its description (Upson et al. 2013). Our assessment using current and projected scenarios (for both AOO and EOO) for the first two taxa gave rise to VU (Vulnerable) and EN (Endangered) risk categories, respectively. Excluding these insular species and those endemic to a single country, we have also assigned national IUCN risk categories for the first time to all species for the respective territories.

The use of ENMs combined with high-quality data on ranges can overcome the shortage of limited sampling in biodiversity rich areas (Cardoso et al. 2011; Pena et al. 2014). Data from herbaria sheets and reliable records contained in electronic repositories have been previously used to detect threatened species and assign risk categories (Sérgio et al. 2007;

Papes and Gaubert 2007; Rivers et al. 2011; Jiménez-Alfaro et al. 2012; Syfert et al. 2014). IUCN Guidelines incorporate the use of species distribution models (SDM) or ecological niche models (ENM) at least from the version 8.1 (IUCN 2010). Although the latest recommendations of IUCN (2016) continue to recognize the usefulness of the ENM for inferring population reduction under criterion A3, linking bioclimate and demographic models for criteria E, or projecting plausible threats for use in criterion D2, nothing is mentioned about the application of ENM for calculating the extent of occurrence (EOO). The EOO defined as the spatial spread of the areas currently occupied by the taxon is just measured by topological approaches (minimum convex polygon or α -hull). Such topological approaches cannot deal with future changes and does not contribute to identify future or past trends. Sérgio et al. (2007) discussed the use of ENMs but a recent work from Syfert et al. (2014) analyze, compare and also suggest an excellent set of approaches to incorporate ENM into Red List assessments. A minor contribution in the use of ENMs is that they are able to predict that certain species could be present at regions or countries which have not been registered so far, pointing out new prospecting areas that could result in an increase in local diversity.

With respect to the total compliance of Target 2 in these countries, our contribution is a modest amount in relation to the committed task. The Chilean flora comprises over 5,215 plant species (WWF and IUCN 1997) and its Red List covers 424 taxa including none *Nassauvia* species (<http://especies.mma.gob.cl/> April 15, 2016). The Maldivian/Falklandian flora consists in 171 species and its Red List in 23 plants (Broughton and McAdam 2002, 2005; Otley et al. 2008) including *N. serpens* and *N. gaudichaudii*. Meanwhile, neither Bolivian (a like-minded megadiverse country with 17,350 species) nor Argentinian (9,370 species) floras have red lists according to IUCN categories (WWF and IUCN 1997). However, in Argentina there is an official initiative using *ad hoc* categories based on expert criterion which has evaluated four endemic *Nassauvia* species into the top threat level: *N. chubutensis*, *N. hilli*, *N. ruizii* and *N. sceptrum* (www.lista-planear.org/ April 15, 2016).

Meanwhile, Target 7 aims to achieve more than 75% of known threatened plant species conserved in situ by 2020. The best information available to us indicates that none species of *Nassauvia* is legally protected in conservation acts at any of the countries in the region. Beyond the laws on endangered species, habitats where members of the genus extend are partially preserved. Twenty-three species have a part of their whole distribution within the limits of a national park (Category II in the IUCN Protected Areas Categories System; Dudley 2008). Out of the 15 globally threatened *Nassauvia* (IUCN categories VU, EN and CR), only four have at least part of their range included in a national park within the study area, that is 26.6% of the known threatened species of the genus. Now, if we consider the national IUCN categories of threat for these plants, the results are more uneven since Argentina has 36.3% of its 11 threatened species included, Chile has 16.6% of its 18 threatened species included, Bolivia has its unique species excluded, and the Malvinas/Falkland administration has none of its species covered by a national park. That means that at any scale the target is not achieved taking into account just national parks. Our gap analysis on the degree of in situ conservation of threatened *Nassauvia* species has to be taken with some caution. We have not evaluated the presence of the 11 threatened species out of national parks in other kind of nature reserves due to regional heterogeneity and lack of information. Of course, parks and reserves other than national parks do contribute to the conservation of species of *Nassauvia*. As the Target 2 is far from being achieved in Bolivia, Chile or Argentina, little can be said in absolute terms for the Target 7 in these countries, unless it is very doubtful that it can be reached by 2020. Other South American countries have already evaluated this Target 7 considering in its entirety their respective

networks of protected areas, and have failed as well (Fajardo et al. 2014; Lessmann et al. 2014). We propose this integration of different approaches as a model to apply in other taxa for establishing conservation areas and evaluating the degree of compliance of explicitly stated conservation targets.

Acknowledgements Our gratitude to the curators of revised herbaria. We are indebted to Andrés Moreira Muñoz for providing some localities and clarifying doubts in georeferencing Chilean records. Stephan Beck, Isabel Loza-Rivera, Manuel Macía and Santos Casado kindly shared their information on protected areas in the study region. Rebecca Upson resolved our doubts concerning plant conservation on the Malvinas/Falkland islands and the current status of *Nassauvia falklandica*. We sincerely thank to the reviewers for their valuable comments in improving the quality and presentation of this paper. MAG, MJA, MV and LK acknowledge the support of Agencia Nacional de Promoción Científica y Tecnológica (ANPCyT), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), and Universidad Nacional de La Plata (UNLP). DD is supported by postdoctoral fellowship (SFRH/BPD/100384/2014) of the Portuguese Foundation for Science and Technology (FCT). LP and JCMS acknowledge the support of Dirección General de Investigación Científica y Técnica, Ministerio de Economía y Competitividad (Project CGL2013-48768-P).

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