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Mapping suitable habitat for the 'Coco mushroom', *Phlebopus bruchii* (Speg.) Heinem. & Rammeloo (Basidiomycota) in central Argentina: a case study integrating citizen science in fungal conservation

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Abstract

Phlebopus bruchii is a culturally important and culinary valued fungus endemic to the Montane Chaco forests of Córdoba and San Luis, Argentina. Recently, the species has been categorized as Critically Endangered following the International Union for Conservation of Nature criteria, primarily due to habitat loss. This work aims to identify and predict its remaining suitable habitat based on citizen science collaborations, a fundamental step in developing effective conservation strategies for the species. Species Distribution Models and the collection of presence data throughout different social media platforms were carried out. The resulting habitat suitability map was analyzed considering vegetation units, current land cover, and areas affected by fires in 2024. A total of 84 occurrence records of *Phlebopus bruchii* were compiled from Córdoba and San Luis provinces. After removing duplicates that fell within the same raster cell, 70 unique records were retained for modeling. We first developed an initial habitat suitability model (Map 1) using 35 records. This model was then validated and updated with 35 additional records obtained in the subsequent 2024 season. The final model (Map 2) presented a high performance, with results indicating moderate to high habitat suitability in remnant patches of Montane Chaco forest in Córdoba and San Luis provinces. Approximately half of the predicted suitable habitat is located in areas still facing intense anthropogenic pressures, including intentional fires, agricultural expansion, livestock grazing, and urban development. These findings highlight the urgent need for targeted conservation actions in native forest remnants and demonstrate the critical role of citizen science in documenting rare fungal species. Additionally, the conservation status of *P. bruchii* is reassessed, and its categorization is suggested to be kept based on new generated data.

Keywords Threatened species, Wild edible mushrooms, Endemic fungi, Boletinellaceae, Mycogeography, Species distribution models, MaxEnt

1 Introduction

Phlebopus bruchii (Speg.) Heinem. & Rammeloo (Boletinellaceae, Boletales, Basidiomycota), commonly known as the "hongo del coco" or "hongo del molle", is a characteristic fungal species of the Montane Chaco forests of central Argentina [1, 2]. It is the only native edible mushroom species of high culinary value documented for use and trade in the central region of Argentina [3, 4]. Morphologically, is characterized by its robust basidiomata with a dark brown pileus and white context that turns an intense blue-greenish color when exposed [2, 3, 5] (Fig. 1).

Phlebopus bruchii has been reported to occur exclusively in the Montane Chaco forest of the Sierras Chicas and Sierras Grandes in the provinces of Córdoba and San Luis, Argentina, at altitudes ranging from 600 to 1400 m above sea level [6]. It has been suggested that *P. bruchii* is associated with patches of mature "coco" [*Zanthoxyllum coco* (Gill.) Engl., Rutaceae] and "molle" [*Lithraea molleoides* (Vell.) Engl., Anacardiaceae] forests, and that its distribution would extend through the Montane Chaco forest from central Argentina along the central northern mountains to southern Bolivia [6]. However, to date there are no confirmed records outside the provinces of Córdoba and San Luis, and the current distribution of the species, both in areas where it has been recorded and, more importantly, in areas where its presence has been suggested, is still unknown. Although local people recognize sites they call "hongueras" where basidiomata are found near mature *Z. coco* and *L. molleoides* trees, *P. bruchii* does not establish an ectomycorrhizal relationship with these tree species [1, 7]. However its basidiomata, in terms of size and biomass, are more similar to those of ectomycorrhizal fungi than to those of saprophytic fungi. Though the larger size of ectomycorrhizal fungal fruiting bodies,

Fig. 1 Morphological features of basidioma of *Phlebopus bruchii* in their natural habitat: **A**. Basidiomata general view. **B**. Top view of the pileus. **C**. view of the pore surface and stipe. **D**. Longitudinal section through the basidioma showing the whitish context and blue reaction upon exposure. **A**, **D** Photos by G. Robledo, **B**, **C** Photos by L. Thornton

compared to those of many saprotrophic fungi, can be explained by their greater access to carbon provided through the symbiotic association [8].

This culturally important mushroom has been categorized as Critically Endangered (CR) in the IUCN Red List of Threatened Species™ (hereafter Red List), mainly due to habitat loss, both in area and quality [6]. The Montane Chaco forest is currently fragmented and highly threatened. More than 90% of its area was lost between 1969 and 1999, and at present is in various stages of arable agriculture, pasture or secondary succession [9, 10]. Wildfires are one of the main disturbances, which may have an important role in shaping vegetation dynamics along elevation [11]. In the region, most fires are human-induced, either by accident or linked to agricultural practices [11]. Another threat is that this fungus is one of the most sought-after species within the Boletinellaceae family, and its exploitation lacks a regulatory framework for a sustainable management plan. As a result, the primary actions proposed in the Red List assessment to prevent the decline of this species, includes habitat protection and the reduction of harvesting pressure. However, poor knowledge of species distribution can hinder the identification of key areas for conservation [12]. In order to implement such management, the potential distribution of the species must first be estimated.

Species distribution models (SDMs), also known as habitat suitability or ecological niche models, model the observed occurrence of a species as a response to environmental variables [13]. Over the past two decades, SDMs have been increasingly used to model fungal distribution [14]. One of the most popular methods for predicting species distributions for fungi is maximum entropy (MaxEnt) [15–19], which is characterized by a data-friendly algorithm and can use presence-only data [20]. Moreover, MaxEnt has been shown to perform better than other algorithms when working with extremely scarce records, as it is less sensitive to small sample sizes [21]. While models of species distribution are widely used in biogeography and ecology [22], experimental validation of their accuracy is rarely performed.

Phlebopus bruchii is a suitable candidate for modelling because the taxonomic identification of current available records is accurate. However, available geo-referenced records are extremely scarce. Citizen science (CS) offers an alternative approach to collecting occurrence records of the species compared with only traditional records from fungaria vouchers, which can be used to advance fungal conservation efforts [23]. Local CS initiatives in mycology can provide valuable insights into the distribution and ecological interactions of fungal species through the collection of species occurrence data [24, 25]. In addition, the informal educational aspect of CS activities also helps to reshape the traditional process of knowledge production and democratize science by facilitating information sharing between experts and non-experts [26]. *Phlebopus bruchii* appears to be a key species for a CS project due to its morphological and ecological uniqueness, which allows for reliable identification through photographs and interaction with people recording the observations.

In this study, we aim to estimate suitable habitat areas for the target species using SDMs, incorporating citizen science data for occurrence records. Additionally, we seek to validate and enhance the accuracy models as well as analyze the predicted potential habitat in relation to current vegetation types, phytogeographic patterns, and recent fire and urbanization events. Given that *P. bruchii* produces fruiting bodies of larger size and biomass than those observed in comparable saprophytic fungi [2], it is expected that the

most suitable sites for finding them will be associated with higher vegetation productivity and, consequently, with greater amounts of soil organic carbon. In addition, although it has been suggested that *P. bruchii* occurs in rainy mountain ecosystems further north in Argentina, even reaching Bolivia, the distinctive characteristics of the forests of the Southern Montane Chaco, e.g., floristic composition and climate, likely defines the ecological niche of the species, thereby explaining its restricted distribution. Other *Phlebopus* species, as *Phlebopus beniensis* (Singer & Digilio) Heinem. & Rammeloo, distribute wideliy in subtropical forests of South America, reaching Bolivia and Nw Argentina (authors' unpublished molecular data) [27]. Consequently, SDMs are expected to predict high habitat suitability in these areas, and no verified records of *P. bruchii* should occur further north.

For culturally known but poorly geo-referenced species such as *P. bruchii*, citizen-science collaborations are expected to provide essential and reliable occurrence data that greatly expand the number and spatial coverage of records available, thereby enabling the development of more robust species distribution models. Additionally, the habitat suitability map will facilitate the development of public policies aimed at restoring and protecting native forests and supporting existing forest restoration programs. Finally, since the conservation status of *P. bruchii* was previously assessed with limited occurrence data, the incorporation of the expanded dataset and improved models presented here will allow a more accurate reassessment of its extinction risk, providing a stronger basis for evaluating its conservation category under IUCN criteria.

2 Materials and methods

2.1 Study area

The selection of the geographic extent of the study area was based on literature where *P. bruchii* had been found, where it could potentially extend to, and where sampling would be feasible. Fungi disperse through microscopic spores, theoretically capable of traveling long distances through the air without obvious dispersal restrictions [14]. Thus, the study area encompassed the Dry Chaco ecoregion [28], which includes fragments of the Montane Chaco forest, where the fungus is expected to be present (Fig. 2). Additionally, the study area covers nearby ecoregions such as the Monte of Sierras and Basins and the Yungas, both of which also contain montane forests [28] (Fig. 2). The Monte of Sierras and Basins harbors transitional forests between the Chaco and Monte ecoregions, while the Yungas support montane forests along the eastern slopes of the Andes, providing potential habitat continuity for the species. Other ecoregions included in the study area, such as the Espinal, Pampa, and Monte of Plains and Plateaus, do not contain montane forest but were considered due to their proximity to the Dry Chaco. The inclusion of areas where the fungus might not be present but could have arrived via dispersal was based on the need to differentiate suitable and unsuitable areas for the species. All the geographic data used in this study for calculations are based on WGS 1984 datum. Any data from external sources provided in other coordinate systems were transformed prior to analysis.

2.2 Occurrence data

Georeferenced occurrence records of *P. bruchii* were collected from publications, observations by local mycologists, field trips conducted by the authors and from Citizen

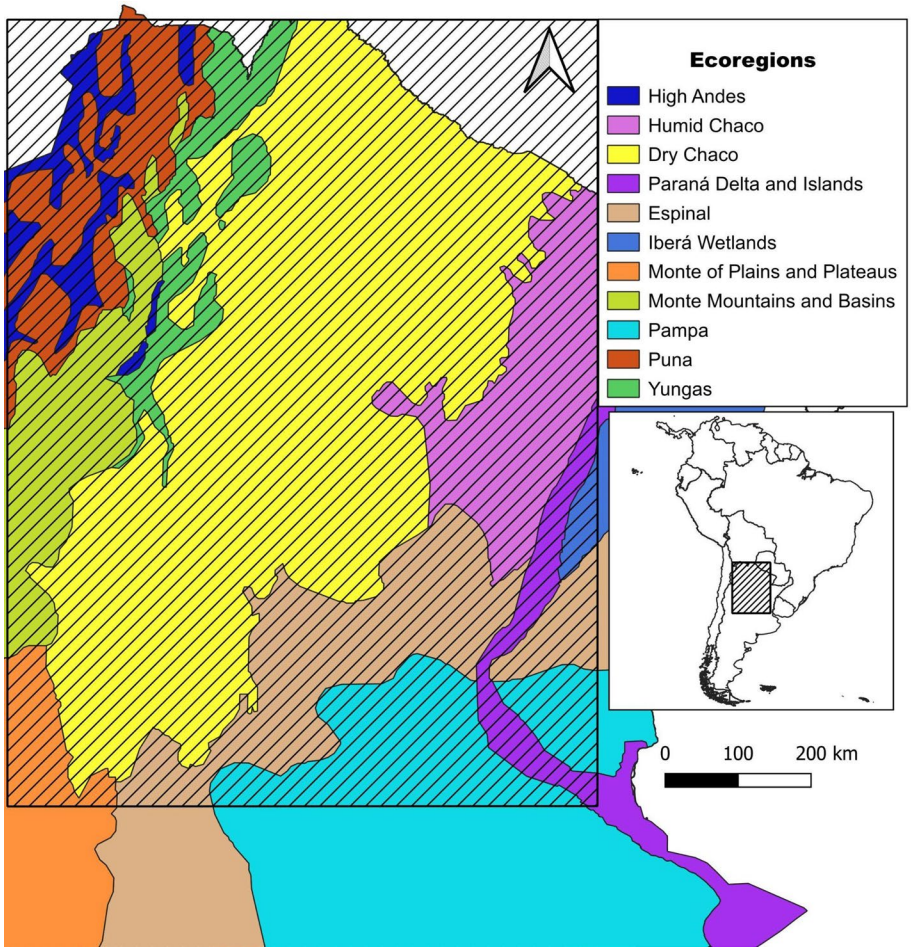

Fig. 2 Study area (diagonal striping) and its corresponding ecoregions. The map displays the different ecoregions present within the study area, following the classification of Morello et al. [28]. The inset shows the location of the study area within South America

Science. Additionally, we searched for georeferenced records in online platforms such as GBIF, iNaturalist, and Mushroom Observer, but no data or no reliable data were found. A promotional flyer was created to alert the community about the search for *P. bruchii* records (see Fig. S1) and distributed since January 16, 2023 throughout different social media platforms such as Facebook mycological groups and WhatsApp. Moreover, a dedicated Instagram profile was created for the conservation of this species (https://www.instagram.com/hongo.del.coco), providing relevant information for its accurate identification, sustainable collection, and other relevant details. The profile also included detailed information on the importance of obtaining geolocated records of the species. Following a structured protocol, a brief introduction and key questions were developed to engage with individuals who believed they had found the species (Doc. S2). The purpose of these questions was to initiate a dialogue in which the individuals would feel safe and trust that the information they provided would be used for research purposes. Since many people who collect the fungus sell it as a source of income, sharing the locations where they harvest it can be sensitive. Additionally, questions were designed to ensure accurate remote species identification, and participants were asked to provide photos.

The validity of the information was then assessed based on confirmation of the record's identity and whether these details were consistent with the georeference.

Out of a total of 84 records obtained, 63 validated presence records were collected through citizen science: 28 during the 2023 "coco" mushroom season, and 35 in 2024; sixteen records were gathered by the authors during fieldwork conducted in the summer seasons of 2023 (12 records) and 2024 (4 records); two presence records were obtained from published scientific papers [1, 4] and three were observations made by local mycologists. A total of fourteen records were discarded due to being located less than 0.86 km from each other, as MaxEnt automatically excludes such records by default, considering them duplicates. All of the occurrence records were divided into two datasets: dataset 1 with 35 records collected in 2023 season (December 2022–March 2023) and dataset 2 with 70 records (2023 and 2024 seasons).

To assess the spatial autocorrelation of occurrence records, we applied Moran's Index test in the two datasets [29] with `spdep`, `sf`, `spatstat`, and `raster` R packages [30–33]. The values obtained for dataset 1 (Moran's I = 0.88, z-score: 11.19, $p < 0.001$) and for dataset 2 (Moran's I = 0.93, z-score: 14.99, $p < 0.001$) indicated a strong and significant spatial autocorrelation among presence points, suggesting a potential sampling bias. To address this issue, we generated a *bias file* that reflects the spatial intensity of occurrence data. This file was created by converting the occurrence points into a point pattern object and estimating their spatial density using a Gaussian kernel function (σ = 0.1) with the `spatstat` R's package. The resulting density surface was then resampled to match the resolution and extent of the environmental raster layers and exported in ASCII format. During MaxEnt calibration, the bias file was used as a sampling mask so that background points were preferentially drawn from areas with higher sampling probability, thereby reducing the influence of clustered records and controlling for sampling bias.

2.3 Environmental variables

A total of nineteen bioclimatic variables recorded from 1970 to 2000 were obtained from WorldClim2 [34], together with their corresponding altitudinal data, in a spatial resolution of 30 arc-seconds (0.86 km^2) in raster format. Four edaphic variables, i.e. soil organic carbon (SOC), cation exchange capacity (CEC), soil pH (pH), and total nitrogen (N), were obtained at a resolution of 250 m from SoilGrids 2.0 [35] and resampled to a coarser resolution using bilinear interpolation to match the resolution of the bioclimatic indicators. Topographic variables (e.g., slope, orientation) were not considered because field observations confirmed that *P. bruchii* occurs in both flat and sloping areas, across different orientations, and including non-relevant predictors would only increase model complexity without ecological justification.

The layers (each bioclimatic and edaphic variable) were clipped to the extent of the study area using the R software, version 4.3.1 [36] and the `raster` package [33]. To test for multicollinearity in the SDM, the 'vif' function was used, in the `usdm` R package [37], to remove variables with a Variance Inflation Factors higher than 10 [38], the remaining variables are listed in Table 1. Additionally, a mask was created for Ansenuza Sea, a highly saline endorheic lagoon, using a shapefile obtained from https://hub.arcgis.com/. This mask was designed in QGIS 3.28.2 [39] to match the extent and resolution of the

Table 1 Variance inflation factor (VIF), percent contribution, and permutation importance of environmental variables used in habitat suitability models for *Phlebopus bruchii* in map 1 (2023) and map 2 (2024)

Variable	VIF	Contribution % Map 1	Permutation importance Map 1	Contribution % Map 2	Permutation importance Map 2
Bio2	3.73	7.3	1.6	0.5	0.8
Bio4	2.17	7.2	5.1	19.7	12.1
Bio9	2.81	36.1	28.9	50.6	73.4
Bio14	7.29	23.1	28	6.6	6.9
Bio15	7.15	1.6	35.2	0	0
Bio18	3.85	0.2	0.2	0	0
CEC	4.33	10	0	4	0
N	4.95	0	0.1	0	0
pH	3.89	13.2	0.9	18.5	6.8
SOC	4.02	0	0	0.1	0

Bio2: Mean diurnal range (mean of monthly (max temp – min temp)), Bio4: Temperature Seasonality (standard deviation ×100), Bio9: Mean Temperature of Driest Quarter, Bio14: Precipitation of Driest Month, Bio15: Precipitation Seasonality (Coefficient of Variation), Precipitation of Warmest Quarter, CEC: Cation Exchange Capacity, N: Total nitrogen, SOC: Soil Organic Carbon

study area raster, with NA values applied over the lagoon, ensuring that the model does not predict suitability in that area.

2.4 MaxEnt model configuration

A first potential distribution map of *P. bruchii* was modeled using data set 1 (35 occurrence records), hereafter referred to as Map (1), to evaluate the change in the model's prediction with the addition of new records. A second potential distribution was modeled, incorporating all records (data set 2, 70 records), hereafter referred to as Map (2). Both models were generated using MaxEnt 3.4.3k [40]. First, we optimized the Maxent models by adjusting the feature classes and the regularization multiplier using the *ENMeval* package in R [41]. Regularization multiplier values ranged from 0.2 to 2.0, increasing by 0.2 each step. Seven feature class combinations including one or more transformations were tested: Linear (L), Linear + Quadratic (LQ), Hinge (H), Linear + Quadratic + Hinge (LQH), Linear + Quadratic + Hinge + Product (LQHP), Linear + Quadratic + Hinge + Threshold (LQHT), and Linear + Quadratic + Hinge + Product + Threshold (LQHPT). These settings resulted in a total of 70 parameter combinations. After evaluating the 70 candidate models, we examined model complexity using delta AICc values. Lower AICc values were considered to indicate higher predictive performance.

Accordingly, MaxEnt was configured to perform 5 (Map 1) and 10 (Map 2) replications, fit response curves using H feature, use a regularization multiplier of 1 for Map 1 and LQHT with regularization multiplier of 1.6 for Map 2, set a prevalence of 0.5, 10,000 pseudo-absences (background points), 500 iterations, and return logistic output as the result. Models were fitted using ten-fold cross-validations to provide a highly robust estimate of predictive performance and iteration [42], 75% and 25% of the presence data were randomly selected for use as training and testing datasets, respectively. To address spatial autocorrelation of presence records, a bias file was only applied in the modeling process of Map 2, where its use led to improved predictive performance. In contrast, for Map 1, incorporating the bias file resulted in poor model predictions, and thus it was excluded from that analysis.

The Area Under Receiver Operator Characteristic Curve (AUC) was estimated to determine the accuracy of the MaxEnt model for current geographic distribution [43]. In theory, the model is considered to perform well when the value of AUC is more than 0.8 and excellently when the value is more than 0.9 [44, 45]. Additionally, the model performance was evaluated using the true skill statistics (TSS) [46]. For each map, the thresholds were chosen for two reasons: (1) they correspond to the highest thresholds at which TSS remains maximal, and (2) they are ecologically meaningful. Variable importance to the models was evaluated based on the permutation value, percent contribution and jackknife resampling produced by MaxEnt [43].

Finally, logistic output models were produced and uploaded to a GIS "Geographic Information System" map using QGIS version 3.28.2 [39]. The average model was geographically projected dividing the probability of habitat suitability into five categories: "unsuitable" < 0.2, "low" 0.2–0.4, "medium" 0.4–0.6, "high" 0.6–0.8, and "very high" >0.8. Our reclassification of the continuous suitability values into five categories follows previous studies that applied similar thresholds to facilitate the interpretation and visualization of habitat suitability maps [19, 47]. This classification does not alter the model outputs, but rather provides a more intuitive representation of the distribution patterns across the study area.

2.5 Experimental validation

New geolocated records collected during the 2024 mushroom season were used to validate the initial habitat suitability map (Map 1). The `raster` [33] and `dplyr` [48] R packages were employed to assess the number of records within the different suitability categories predicted by the model. The accuracy of the model was calculated as:

$$Accuracy = \frac{VR}{TR} \times 100$$

where, VR was the number of validated records in the "very high", "high" and "medium" categories, and TR was the total number of records.

2.6 Evaluation of model prediction with current land cover and phytogeographic scenario

To assess the most approximately "real" suitable area for *P. bruchii*, the most up-to-date land cover raster (2022–2023) for Córdoba Province was obtained from https://www.mapascordoba.gob.ar/#/mapas [49]. The predicted suitability layer, modeled using all records (Map 2), and the land cover layer were then aligned to the same extent in QGIS 3.28.2 [39]. Subsequently, the land cover layer was resampled to match the resolution of Map 2 using the nearest neighbor method in R version 4.3.1 [36] with the `raster` [33] and `terra` packages [50]. A habitat suitability mask was then created for areas with suitability values greater than 0.5 (medium to high suitability), and the land area covered by each land cover category was calculated. The threshold value was selected to generate a high-confidence map for conservation purposes. Finally, a bar chart was generated using the `dplyr` [48] and `ggplot2` packages [51] in R.

Additionally, Sentinel-2 L2A satellite images in raster format from September-October 2024 were obtained from the Copernicus Open Access to identify areas affected by fires, specifically using SWIR bands [52]. These images were processed in QGIS version 3.28.2 [39] to create a raster layer with all burned areas within the study region, assigning a

value of 1 for burnt zones and 0 for no fire. This layer was aligned in extent and resolution with the habitat suitability map. Subsequently, similar analyses were conducted in R Studio to calculate the proportion of areas with a habitat suitability index greater than 0.5 that were affected by fires in 2024.

To assess the phytogeographic units suitable for *P. bruchii*, the most recent categorization of vegetation units was obtained from Oyarzabal et al. [53]. The Physiognomic-Floristic map layer was rasterized to match the extent and resolution of the suitability map using the `terra` package [50]. A habitat suitability mask was then created for areas with suitability values greater than 0.5 (medium to high suitability), and the area covered by each vegetation unit category was calculated. Finally, a barplot was generated to visualize the categories and the suitable habitat.

2.7 Conservation status assessment

The conservation status of *P. bruchii* was reassessed following the International Union for Conservation of Nature (IUCN) criteria [54, 55]. Population size was calculated by combining the number of potential sites of suitable habitat, as indicated by distribution models results, with field-based estimates of the number of mature individuals per site (2–8). Past population decline was estimated as directly correlated with the loss of Montane Chaco forest, based on historical data and published literature [9, 10, 56, 57]. These estimates were then used to evaluate species against IUCN subcriteria previously applied in the Red List assessment.

3 Results

3.1 Environmental variables for modelling

According to the models, Bio9 (Mean Temperature of the Driest Quarter) emerged as the dominant predictor across both datasets. In Map 1 (35 records), Bio9 explained 36.1% of percent contribution (permutation importance = 28.9%), while in Map 2 (70 records) its influence increased sharply to 50.6% (permutation importance = 73.4%) (Table 1). Soil pH showed a moderate but consistent contribution, rising from 13.2% (permutation = 0.9%) in Map 1 to 18.5% (permutation = 6.8%) in Map 2. Bio14 (Precipitation of the Driest Month) was relatively important in Map 1 (permutation importance = 28.7%) but declined in Map 2 (6.9%), whereas Bio4 (Temperature Seasonality) gained weight in Map 2 (19.7%). Other edaphic variables (CEC, SOC, N) contributed minimally in both models. Overall, these results highlight the critical role of climatic conditions—particularly temperature during the driest quarter—in shaping *P. bruchii* suitability, with soil pH acting as a secondary driver that becomes more relevant with larger sample size. The Jackknife test (Table S3) corroborated the central role of Bio9, showing that its exclusion led to the largest drop in training gain, indicating that no other variable provided equivalent information.

3.2 Potential distribution maps

The first potential distribution map (Map 1) is shown in Fig. S4. A. The model showed high performance, with an average test AUC of 0.994 across replicate runs (standard deviation = 0.002). Additionally, the average TSS was 0.98 at a threshold of 0.19, which both maximizes TSS and makes ecological sense for a rare species like *P. bruchii*. High uncertainty values, as indicated by the coefficient of variation of the average model, were

concentrated around the Sierras Chicas and Sierras Grandes from Córdoba (see Fig. S4.B).

The second potential distribution map (Map 2) is shown on Fig. 3. which had a high AUC value. The average test AUC for the replicate runs was 0.993, and the standard deviation was 0.003. Although the mathematical threshold maximizing TSS was 0.07, this value predicted presence almost everywhere and lacked ecological realism. Therefore, we applied a more conservative threshold of 0.2, which still provided a high TSS (0.90) and more plausible predictions. Low uncertainty values, as indicated by the coefficient of variation of the average model, were concentrated around the Sierras Chicas and Sierras Grandes from Córdoba (Fig.S4.D).

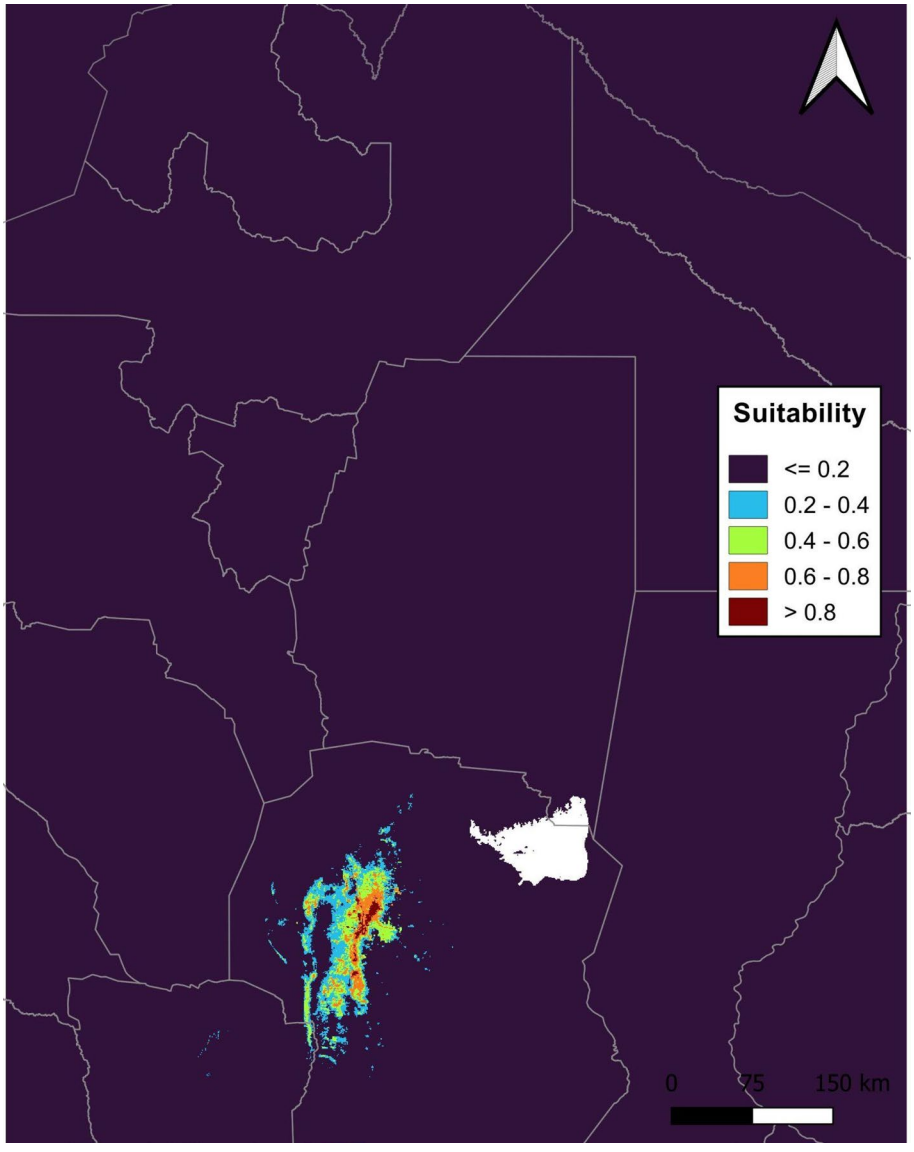

Fig. 3 Geographic projection of the distribution of suitable habitat of *P. bruchii* modFinally, in the northeastern portion of the Sierras, Map 2 assigns slightly higher suitability than Map 1 (green tones in Fig. 4C), although these values remain relatively low."eled with all presence records in the study area evaluated (map 2). The suitability value represents the predicted distribution probability (in logistic value) for environmental layers used in the niche modeling

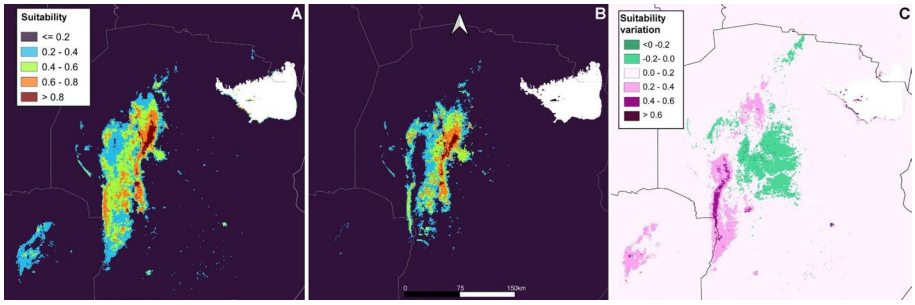

Fig. 4 Predictive performance of the model with additional presence data: **A**. Map 1, modeled with presence records from the 2023 season. **B**. Map 2, modeled with all presence records. **C**. Suitability variation: difference in values between Map 1 and Map 2 (positive values indicate higher suitability in Map 1, while negative values indicate higher suitability in Map 2). Geographic projection expanded to include the Sierras de Córdoba, and San Luis

Table 2 Distribution of 35 geolocated records across habitat suitability categories based on the validation of the initial habitat suitability map

Habitat category	Number of records	Percentage
Medium	11	31.4%
High	9	25.7%
Very high	6	17.1%
Low	6	17.1%
Unsuitable	3	8.57%

Categories are defined as follows: *Very high* (> 0.8), *High* (0.6–0.8), *Medium* (0.4–0.6), *Low* (0.2–0.4), and *Unsuitable* (< 0.2)

To assess how the predictive performance of the model improves with additional presence data, we first present uncertainty maps (see Fig. S4). Map 1 (Fig. S4.B) shows a broader area and high values of uncertainty compared to Map 2 (Fig. S4.D). Additionally, we compared variation of suitability between both habitat maps. This variation was calculated as the difference between suitability values of Map 1 and Map 2 (Fig. 4). Positive values indicate areas where Map 1 assigned higher suitability, while negative values indicate areas where Map 2 predicted higher suitability. Map 1 shows a broader and more continuous area of high to medium suitability, especially in the central-western region (Sierras Grandes and surrounding areas), with a patch with medium to low suitability in central-north of San Luis province. In contrast, Map 2 shows a more restricted distribution of highly suitable areas. While it still highlights the Sierras region, the extent is smaller and some peripheral zones visible in Map 1 are missing. Finally, in the northeastern portion of the Sierras, Map 2 assigns slightly higher suitability than Map 1 (green tones in Fig. 4C), although these values remain relatively low.

3.3 Experimental validation

The validation of the initial habitat suitability map was conducted using 35 new geolocated records obtained during the 2024 mushroom season. The distribution of all the records across the five habitat suitability categories is summarized in Table 2. The majority of the records were located in areas classified as having a "medium" habitat suitability index (31.4%) or "high" suitability (25.7%). Six records (17.1%) were located in areas classified as having "low" habitat suitability, while three of the records fell into areas deemed "unsuitable" (8.57%). The accuracy of the model was 74.29%, which indicates that 74.29% of the records were correctly predicted within the categories considered as "suitable" for the species ("high," "medium," "very high").

3.4 Habitat suitability map and current land cover

The total suitable habitat area with a suitability index greater than 0.5 (moderate to high suitability) across the entire study region amounted to 3344.677 km^2 located within the province of Córdoba, with different land cover types. The proportional representation of various land cover types in regions where the latest model predicts suitability above 0.5 is shown in Fig. 5. The dominant land cover categories include Shrubland (31%), Forest (30%), Urban (13%), Natural grassland (9.8%), Crops (3.4%), Shrubland/Grassland with rocks or bare soil (3.3%), Water (3.3%) and Pastures (2.9%) with minor contributions from burned woody vegetion (1.4%) and other land covers types. The land cover types most suitable for the species—Forest and Shrubland—collectively account for 61% of the total suitable area in Córdoba Province (2040.25 km^2). Additionally, 3.3% of the suitable habitat in Córdoba remains uncategorized in terms of land cover type.

3.5 Suitability map and most recent fires

The area affected by fires within the study region in 2024, with a suitability index greater than 0.5 (Map 2), indicates a total of 127.1727 km^2 (Fig. S5). This represents 7.5% of the total area classified as moderate to very high suitability for *P. bruchii*.

3.6 Suitability map, phytogeography and Human-altered areas

The vegetation units, as categorized by Oyarzabal et al. [53], that overlap with areas having a suitability index greater than 0.5 were assessed. These vegetation units include: "Xerophytic Forest with *Schinopsis marginata*" (68.75% of the total area), "Grassland of Stipeas and Festuceas" (18.11% of the total area), and "Sclerophyllous Forest with *Prosopis nigra* and *P. alba*" (13.14% of the total area), as shown in Fig. 6. To better visualize the currently suitable habitat for the 'coco' mushroom, a refined map that excludes areas considered unsuitable, such as grasslands, croplands, pastures, salt flats, urban zones, and water bodies, is shown in Fig. 7. The map also highlights the extent of xerophytic forest as defined by Oyarzabal et al. [53], along with regions impacted by major wildfires in 2024.

3.7 Conservation status assessment

Based on the new compiled data, *P. bruchii* remains restricted to the subxerophytic forests of the Montane Chaco ("Bosque Serrano") in the Sierras Chicas and Sierras Grandes

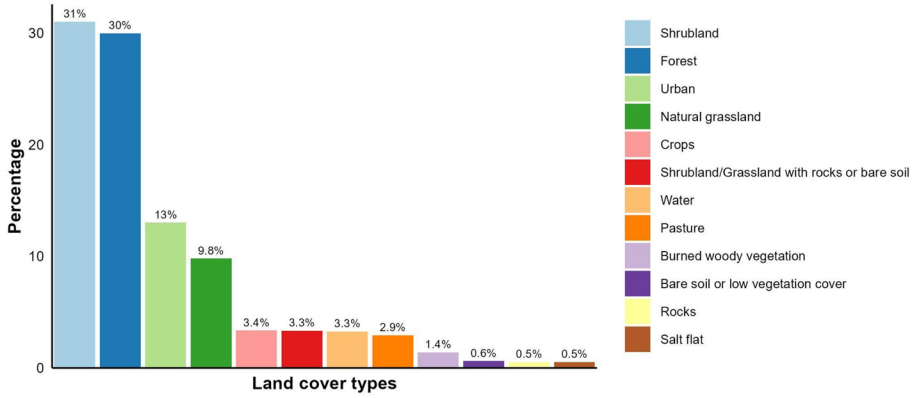

Fig. 5 Percentage of land cover types where the latest modeling predicted suitability greater than 0.5 for *P. bruchii* in Córdoba province

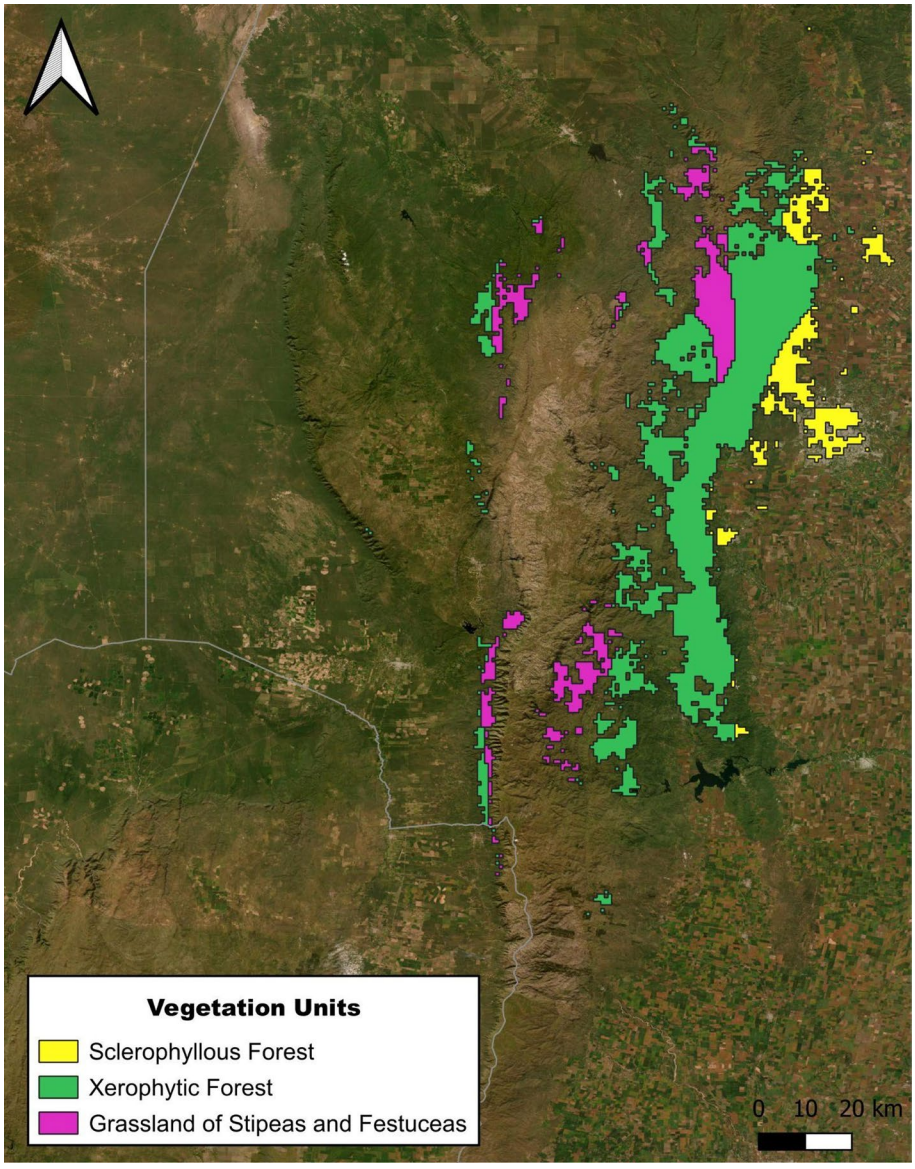

Fig. 6 Overlap of areas with a habitat suitability index for *Phlebopus bruchii* greater than 0.5 and vegetation units [53], zoomed in on the Sierras de Córdoba and San Luis

of Córdoba and San Luis provinces, central Argentina, between 600 and 1,400 m a.s.l. The inclusion of CS data refined the understanding of the species occurrence throughout its range, but did not expand its distribution range. Aided by distribution models results, prior expert knowledge and new records generated by the CS campaign and targeted sampling efforts, we estimate that *P. bruchii* currently persists in approximately 50–100 sites of suitable habitat. The data generated here supports a small density of mature individuals throughout *P. bruchii* range. Thus, assuming two to eight mature individuals per site, this corresponds to a population size of 200 to 1,600 mature individuals. The distribution models showed that the species has a restricted potential distribution, that along with severe population decline inferred from habitat loss (see Discussion), and its total population size estimated here, make *P. bruchii* threatened.

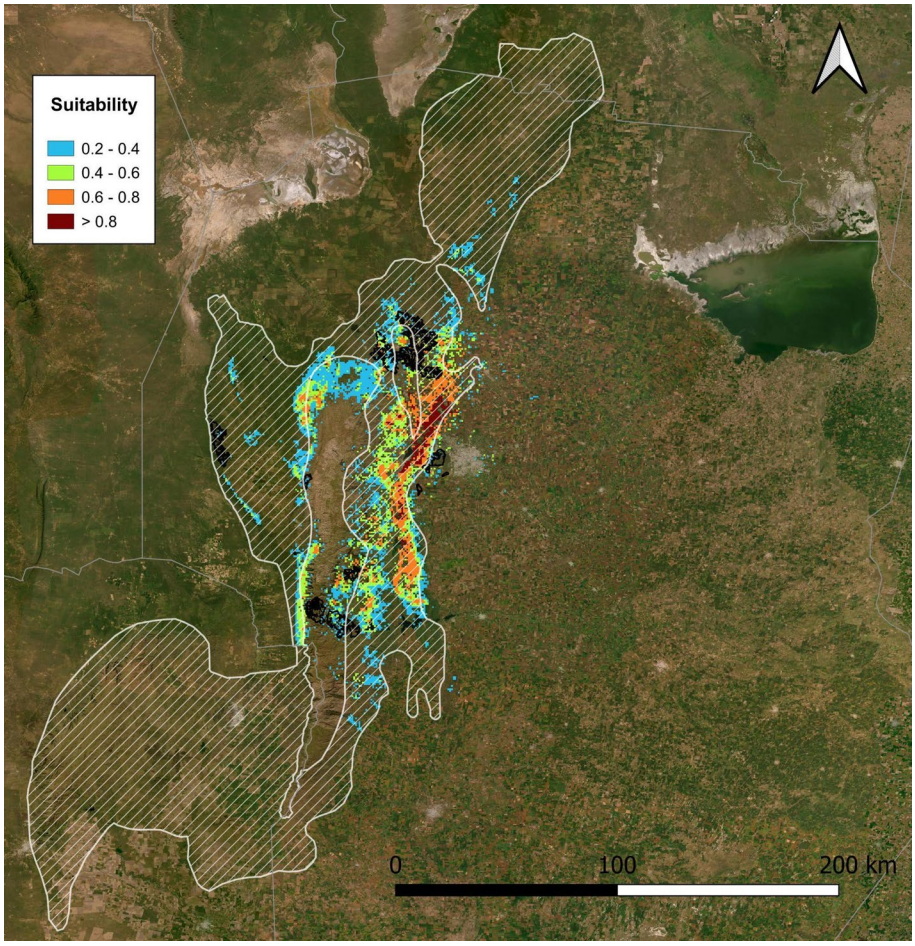

Fig. 7 Current suitability map for *Phlebopus bruchii* zoomed-in the Sierras de Córdoba and San Luis. The map shows areas predicted as suitable (threshold >0.2) after excluding land covers currently unsuitable (grasslands, croplands, pastures, salt flats, urban zones, and water bodies). The extent of xerophytic forest is indicated with diagonal white striping, following the classification of Oyarzabal et al. [53]. Areas affected by major wildfires in 2024 are marked in black, indicating areas unsuitable for the species

4 Discussion

4.1 Collection of data through citizen science

In the era of instant and global information exchange, raising awareness among local amateur mushroom collectors and residents of target areas about the search for *P. bruchii*—via social media—, proved to be both feasible and crucial for data collection. This approach is particularly effective for three key reasons. First, *P. bruchii* possesses distinctive characteristics that allow for reliable identification through photographs and direct communication with contributors. The few similar boletes in the region, with which it could be confused, are associated with exotic plants and are uncommon in the Montane Chaco Forest [2, 5], minimizing misidentifications. Second, this fungus has documented traditional uses in the region, meaning that local communities are already familiar with it [4]. Third, social media provides an accessible and efficient platform for citizen science-based data collection. While global CS databases such as iNaturalist and Mushroom Observer are widely used in mycology [23, 26], they are not commonly utilized in areas where *P. bruchii* occurs. Instead, the primary gatherers and observers of the Montane Chaco forest, the "serranos", have limited internet access and low engagement

with these platforms. Though, they do use social media such as WhatsApp, Facebook, and, to a lesser extent, Instagram. Given these factors, leveraging social networks for CS emerges as the most effective strategy for obtaining occurrence records of *P. bruchii*.

Citizen science has proven to be an efficient tool in ecological studies, particularly at large spatial and temporal scales that would otherwise be prohibitively expensive to achieve [24, 58]. This approach not only significantly contributed to the collection of presence data but also provided an opportunity to educate and engage citizens in the conservation of this CR endemic species. The CS method is especially valuable for the study of fungi, a group of organisms that has gained increasing attention globally in recent decades but remains significantly under-researched compared to the plant and animal kingdoms [59, 60]. In this context, CS plays a critical role in data collection, bridging the knowledge gap and facilitating the study of fungal biodiversity and ecology [23]. With the contribution of the general public, this study represents the first attempt to use the maximum entropy approach combined with CS data to estimate the distribution of suitable habitats for the critically endangered *P. bruchii*.

4.2 Species distribution modeling: methodological considerations, predictions, and validation

While presence-only data is generally considered less robust than presence–absence data for assessing species distributions [61], confirming true absence is inherently more challenging than confirming presence, especially in cryptic taxonomic groups [60]. This is particularly relevant for fungi: the detection of basidiomata confirms the presence of a species in a given location, but their absence does not necessarily indicate the species is not present. Environmental conditions, seasonality, and sporulation dynamics may all influence detectability, potentially leading to underestimations of the species' actual distribution. For these reasons, this approach was chosen to model the distribution of *P. bruchii*.

In this study, we generated two habitat suitability maps for the endemic *P. bruchii* (Fig. S4, Fig. 4). Both models identified similar regions as suitable for the species; however, some differences emerged between them (Fig. 4C, Fig. S4). The most notable discrepancies occurred in the Sierras de Córdoba and San Luis (Fig. 4C), where the first model estimated broader suitable areas, while the second, more data-informed model refined these predictions, reducing the extent of highly suitable habitat. Additionally, the first model showed higher levels of uncertainty, particularly around the Montane Chaco forest region, as reflected in the uncertainty maps (Fig. S4B). These discrepancies highlight the well-documented influence of sample size on model performance. As the number of occurrence records increases, model predictions tend to be more refined, reducing overestimated suitable areas and enhancing overall accuracy [21, 62]. However, a slight decline in AUC was observed when using more occurrence data and replicates (from 0.994 to 0.993, $\Delta = 0.001$), which is within the margin of error (given overlapping standard deviations, SD1 = 0.002 and SD2 = 0.003) and is not statistically meaningful in itself. Increasing sample size can introduce greater environmental and spatial heterogeneity, thereby reducing overfitting and decreasing the AUC of smaller, more restricted datasets [64]. In addition, the AUC metric has known limitations, especially for rare species such as *P. bruchii*, where pseudo-absence inflation can overestimate predictive performance and a high AUC does not necessarily imply good model fit [65, 66]. Moreover,

the AUC metric has known limitations and should be interpreted cautiously, especially when differences are minimal (i.e., "leaving the area under the ROC curve") [67]. For this reason, we did not rely exclusively on AUC but also considered uncertainty maps, the True Skill Statistic (TSS) and experimental validation. For Map 1, TSS was 0.980 at a threshold of 0.19, which both maximizes TSS and makes ecological sense for a rare species like *P. bruchii*. On the other hand, for Map 2, the threshold that mathematically maximized TSS was 0.07; however, this threshold predicts presence almost everywhere and lacks ecological realism. Therefore, we selected a more conservative threshold of 0.2 for Map 2, which better reflects the species' ecology. These results further support that the model with more occurrences (Map 2) provides robust predictions even if the AUC is slightly lower, illustrating the importance of combining statistical metrics with ecological knowledge. In other words, the model with more data doesn't actually "lose quality," but the purely statistical metrics (AUC, TSS) decrease because they reflect the real complexity of the environment and the rarity of the species.

Although species niche and distribution models are widely employed in biogeography and ecology [22], field validation to corroborate their predictions with real-world data is seldom conducted. In this study, we were able to perform such validation. We evaluated the first modeled map using new records obtained during the following basidiome season (summer 2024), achieving a 74.29% accuracy. This value is notably lower than the very high AUC (0.994) and TSS (0.98) obtained during model calibration, highlighting again the tendency of internal metrics to overestimate predictive performance and underscoring the importance of external validation in habitat suitability modeling.

It has been shown that occurrence is modeled more precisely for specialist species with restricted distributions because their ranges are more strongly determined by environmental variables than those of more widespread and generalist species [62, 68, 69]. Therefore, for an endemic species like *P. bruchii*, the model demonstrated a high level of precision. The error could be attributed to the environmental variables used in the modeling, which are primarily averages of precipitation and temperature and do not account for factors such as physiognomies types or current land cover. We acknowledge that our SDMs rely on bioclimatic variables at 30-arc-second (~ 1 km^2) resolution and edaphic variables resampled from 250 m. While these datasets are widely used and provide consistent coverage, they cannot capture the fine-scale environmental conditions (e.g., microclimate, soil moisture heterogeneity, host plant associations) that often influence fungal occurrence [70, 71]. As a result, some key microhabitats may be wrongly/under- represented or masked in our models, and the predicted suitability may not fully reflect the true environmental preferences of *P. bruchii*. Future research incorporating microclimatic measurements, higher-resolution soil data, or field-collected habitat variables could refine habitat suitability estimates for *P. bruchii.*

4.3 Key environmental variables

The distribution modeling of *P. bruchii* highlighted the importance of climatic variables in determining suitable habitats. Among these, Bio9 (Mean Temperature of the Driest Quarter) consistently emerged as the dominant predictor, with its influence becoming even stronger in the model based on a larger sample size. This indicates that temperature during dry periods plays a crucial role in shaping the species' potential range.

Soil pH appeared as a secondary, yet consistent, driver, increasing in importance with the expanded dataset. This suggests that while climate exerts the primary control, edaphic conditions may modulate local suitability, potentially affecting fungal growth and mycelial activity.In contrast, other soil-related variables such as Cation Exchange Capacity (CEC), Total Nitrogen (N), and Soil Organic Carbon (SOC) had minimal to no impact on model predictions, reinforcing the idea that *P. bruchii*'s distribution is primarily driven by climate rather than soil characteristics. This finding contrasts with our initial hypothesis that soil organic carbon would be a relevant driver of habitat suitability, indicating that this factor does not explain the modeled distribution of the species. Precipitation-related predictors, such as Bio14 (Precipitation of the Driest Month), played a relevant role in the smaller dataset but lost influence when more occurrence data were incorporated, while Bio4 (Temperature Seasonality) gained importance. This shift suggests that increased sample size refined the models, emphasizing temperature variability and soil pH over moisture availability.

Temperature variables appear to be crucial for *P. bruchii* due to the climatic characteristics of the Chaco Serrano region. The dry and cold winters typical of this temperate/subtropical mountain climate [72] may act as limiting factors for the species' survival and colonization, underscoring their importance in shaping its distribution.

Similarly, various species distribution models (SDMs) for fungi have highlighted the significant role of both temperature and precipitation in determining fungal distributions [16, 19, 73]. Likewise to these findings, Wollan et al. [69] showed that precipitation was rarely a limiting factor for ectomycorrhizal and saprotrophic fungi in Norway. In this region, precipitation is seldom a limiting factor for fungal growth, whereas in the Chaco Serrano, seasonal droughts could significantly impact fungal activity.

The climate in the studied region is characterized by marked seasonal variations influenced by altitude and slope orientation [11, 72, 74]. At lower altitudes, summers are warm, with an average maximum temperature of 30 °C, and most rainfall occurs from December to March in the form of convective storms—precisely when *P. bruchii* produces its reproductive structures [1, 2, 4, 6]. In contrast, winters are cool to cold, with minimum temperatures often dropping below 0 °C at higher elevations, and precipitation is scarce, typically occurring as light drizzle or occasional snowfall in elevated areas [75]. Additionally, a slight decrease in temperature from north to south has been observed in the region [76].

Given these climatic characteristics, it is logical that temperature plays a significant role in determining the distribution of *P. bruchii*. Extreme conditions, such as temperatures below 0 °C and prolonged dry winters, could pose a threat to the fungus's survival [77], reinforcing the idea that its occurrence is closely tied to specific climatic conditions.

Soil pH was also identified as a secondary predictor, but consistent driver of *P. bruchii* suitable habitat distribution. This pattern aligns with large-scale studies based on metabarcoding and community surveys, which have repeatedly shown that pH is among the strongest predictors of fungal diversity, composition, and distribution [78–81]. Although these studies address community-level patterns rather than species-specific habitat suitability, the convergence remarks the pervasive role of soil pH in shaping fungal ecology, suggesting that local edaphic conditions may modulate the realized niche of *P. bruchii* within climatically suitable areas.

4.4 Predicted suitability and phytogeography

The literature suggests that *P. bruchii* may be distributed throughout the Montane Chaco forest of central Argentina, extending along the central-northern mountains into southern Bolivia [6]. In this study, both distribution models predicted only a few areas outside Córdoba and San Luis with low to moderate habitat suitability. Notably, Map 2, modeled with more occurrence data than Map 1, indicated even lower suitability values in the northern part of the study area (Fig. 4).

These maps, based solely on occurrence records from Córdoba and San Luis provinces and environmental variables such as temperature and precipitation averages, suggest a more restricted range than previously anticipated. The more suitable areas predicted for the fungus were the Montane Chaco Forest near the Sierras Grandes and Sierras Chicas (Fig. 4). These areas predominantly overlap (68.75% of total area) with the Xerophytic Forest with *Schinopsis marginata* (Chaco Serrano) vegetation unit (Fig. 6), proposed by Oyarzabal et al. [53] as part of the Chaco Phytogeographic Province within the Chaco Domain. This vegetation unit comprises three community types, but only one, open xerophytic forest with *Schinopsis marginata*, appears suitable for *P. bruchii* the. This community occupies shallow soils on slopes and ravines of the Pampean and Sub-Andean mountain ranges at altitudes between 500 and 1300 m a.s.l [53]. The floristic composition varies depending on latitude, altitude, soil type, and disturbance levels. The most suitable areas for *P. bruchii* are likely found on southern slopes, where *Lithraea molleoides*, *Zanthoxylum coco*, and *Trithrinax campestris* are the dominant plant species. Notably, *L. molleoides* and *Z. coco* are closely associated with the fungus, giving rise to its common names, "coco mushroom" or "molle mushroom". Historical and ethnomycological evidence supported this association, however ectomycorrhizal symbiosis does not occur [1]. The genus is considered saprophytic, however there is some controversial evidence in other species [82, 83]. Local people have traditionally collected *P. bruchii* in these areas [4]. Collectors specifically seek out "*molladas*" (groves of *L. molleoides*) or 'coco' trees (*Z. coco*), as they believe there is a particular ecological association between the fungus and these trees [4]. On the other hand, northern slopes within this community are predominantly characterized by *Aspidosperma quebracho-blanco*, and *Ruprechtia apetala*. *Phlebopus bruchii* is not typically found in close proximity to those trees and are more representative of drier areas compared to southern slopes.

The other two communities within the Xerophytic Forest with *Schinopsis marginata*.

occur at altitudes exceeding 1400 m a.s.l. and are beyond the ecological range of *P. bruchii*. Another vegetation unit that has a less prominent representation in the suitable habitat predicted in this study is the Grassland of Stipeas and Festuceas (the high grasslands), which represents 18.11% of the total area. These grasslands occupy mountain ridges and hills, forming the highest vegetation belt of the Pampean and Sub-Andean Sierras, at elevations above 1700–1900 m a.s.l [53]. Given its high-altitude conditions, this area is unlikely to be suitable for *P. bruchii*. Additionally, the Sclerophyllous Forest with *Prosopis nigra* and *P. alba* comprises 13.14% of the total predicted area. Within this unit vegetation type, the vegetation overlap with predicted suitability consists of open woodlands dominated by *P. nigra* and *Acacia caven*. These vegetation types are typically found in dry environments, where the presence of *P. bruchii* may be unlikely.

4.5 Predicted suitable area vs. current human activities

Another important factor to consider in the survival of the fungus is the current extent of native forest. For an obligate forest species, areas that were once forest and remain forested can be evaluated to provide a more precise prediction of its potential distribution [84]. In this study, we evaluated the most updated predicted suitable area (Map 2) and overlapped it with: (1) a land cover layer and (2) areas affected by fires in 2024. This approach allowed us to assess which areas the fungus could potentially occupy and what percentage of the predicted suitable area is no longer viable, either due to changes in land use or because it was affected by fire. It is important to note that the land cover layer was resampled to match the resolution of the environmental predictors used in the habitat suitability model. This procedure, while necessary for spatial comparability, may merge or dilute some categories, potentially influencing the exact proportions of land cover types reported.

We found that approximately 61% (2040.25 km^2) of the predicted suitable area in Córdoba province may represent "truly" suitable habitat (forests and shrublands). Shrublands were considered suitable because many of them may represent early successional stages of native forests, given the presence of low-stature tree species [85]. Other land cover types, such as "grasslands", "crops", "pastures", "rocks", "water" and "urban areas," are likely unsuitable for the species. Additionally, 7.5% (127.1727 km^2) of the total area with medium to high suitable index was affected by fires in 2024.

Fire is one of the most prevalent disturbances that impacts biological organisms, either directly or indirectly [86]. In the Montane Chaco forest, most fires are human-induced, either by accident or linked to agricultural practices [5]. It is estimated that fires occur at intervals ranging from 1 to 11 years, typically taking place at the end of the dry season, between June and November [5, 87, 87]. In fact, 80% of the total burned area in 2024 had previously been affected by fire, with some areas burned up to 10 times between 1986 and 2023 [88]. In 2024, two megafires (>100 km^2) occurred in the region: the largest near Capilla del Monte, with 41,000 ha burned, and another in El Durazno, totaling 165 km^2. These large-scale disturbances pose a potential threat to *P. bruchii* and the biodiversity present in this ecosystem.

To date, only one study has investigated the impact of fire events on fungi in the Montane Chaco forests. Longo et al. [89] examined the effects of fire on arbuscular mycorrhizal fungi (AMF). Their findings revealed that fire events had direct negative effects on AMF spore communities resulting in decreased evenness, diversity, and richness of AMF spores in burned sites. Other studies conducted in different regions of the world have shown that the severity of the fire and the time since the fire have varying impacts on fungal community composition [90, 91].

In a subtropical peatland, low-severity fires initially increased fungal diversity, but recovery did not occur in deeper soil layers even after 30 years following high-severity fires [91]. Similarly, in boreal forests of Canada, Day et al. [90] observed that increased fire severity caused declines in the richness of total fungi, mycorrhizal, and saprotrophs, as well as reductions in the diversity of total fungi and mycorrhizas. So, the severity of the fires that occurred in 2024, must be evaluated to assess the level of damage to the flora, funga and soil.

Comparatively, in 2020, the mountains of Córdoba experienced the worst fire season of the last 31 years [56]. Of all physiognomies, shrublands and grasslands were affected

with moderate to low severity, while forests had moderate to high burn severity [56]. Given this context, the fires that occurred in 2024 in the suitable areas (forests) for the species could represent a high-severity risk for the fungus and other species.

We conclude that the area that remains suitable for the species is slightly more than half of the area predicted by the model. These efforts to evaluate the 'truly' suitable habitat and raise awareness within the community about the species' conservation status are crucial for implementing effective conservation actions. SDMs also commonly known as ecological niche models, amongst other names, are currently the main tools used to derive spatially explicit predictions of environmental suitability for species [13, 92–95]. They have the potential to play a critical role in supporting spatial conservation decision making [96, 97].

Our results indicate that *P. bruchii* is still under extinction pressure given the current threats such as fires, agricultural, cattle and urban expansion. In the past, the region was almost completely covered by forests and woodlands and has been transformed into a highly fragmented mosaic of isolated patches of forest, dense thorny scrubs, semi-natural grassland, and cultivated land [9, 85, 98, 99]. This process of replacement of forest by cultivated land is still ongoing. On the other hand, half of the remaining native forest is low vegetation, with an average height of 9 m, which indicates that very few well-developed forests are left in the mountains [57, 85, 100]. Simultaneously, the region is being invaded by nearly 40 exotic tree and shrub species, hindering the recovery of native forests after fires [11, 85, 101–107].

4.6 Conservation status of *Phlebopus bruchii*

During this study, 84 new records of *P. bruchii* were obtained, more than doubling the number of previously available high-quality records (41) used in the first extinction risk assessment [6]. These new data allowed a refined understanding of the species occurrence within its known range. The prediction models did not support its suggested presence in northwestern Argentina. Accordingly, a specimen collected in Tucumán province was identified as a different *Phlebopus* species by molecular analysis. Thus, the distribution of *P. bruchii* remains considered to be restricted to the Montane Chaco forests of Córdoba and San Luis.

The updated dataset, combined with habitat suitability modeling, indicates that the species currently persists in approximately 50–100 suitable sites, with an estimated total of 200–1,600 mature individuals. This, together with more than 90% loss of Montane Chaco forest between 1969 and 1999 [9, 10], supports the inference of an 80–90% population decline over the past 50 years.

Applying the IUCN Red List criteria, *P. bruchii* continues to qualify as Critically Endangered (CR). The species meets criterion A2cd, as the severe decline in population size is directly associated with habitat loss and degradation due to logging and fire. Subcriterion A4cd, used in the previous assessment, was excluded in this reassessment because present and future declines remain difficult to quantify with precision, given uncertainties about fire recurrence and generation length. Additionally, the species meets criterion C2a(ii), as the lower bound of the estimated population size places it well within the thresholds for CR, with most individuals occurring in small and fragmented subpopulations.

Beyond field observations, several isolations were obtained during this study and are now preserved in the CeTBIO culture collection. These strains are important for safeguarding part of the genetic diversity of the species, and they provide a basis for future research on indoor cultivation, production studies, and potential reintroduction into areas of high habitat suitability.

Phlebopus bruchii thus joins other highly threatened fungal species from the same ecosystem, such as *Kavinia chacoserrana* Robledo & Urcelay [108] and *Hericium rajchenbergii* Robledo & Hallenberg [109], which are already listed as Critically Endangered in the IUCN Red List. Notably, *P. bruchii* remains the only member of its genus formally assessed and published in the Global Fungal Red List to date [110], reinforcing both its conservation importance and its symbolic role in highlighting fungal diversity loss in the Montane Chaco ecosystem.

4.7 Management recommendations

Based on our habitat suitability models and threat analysis, remnant Montane Chaco forest patches in Córdoba are identified as priority areas for conserving *P. bruchii*. These areas should be prioritized for systematic monitoring of fruiting events and inclusion within, or expansion of, existing protected areas to maintain habitat connectivity. Because a substantial proportion of suitable habitat is affected by recurrent wildfires, agricultural expansion, livestock grazing, and urban development, urgent management actions, e.g. reintroduction, are required. Agreements with private landowners to reduce grazing pressure, limit soil compaction, and prevent conversion of native forest would further safeguard the species. Where *P. bruchii* is traditionally harvested, the development of sustainable harvesting guidelines—including leaving mature sporocarps and avoiding removal of subterranean mycelia—could help maintain viable populations. In addition, degraded but climatically suitable sites identified by our model represent potential targets for native forest restoration and experimental reintroduction or inoculation efforts. Finally, strengthening and expanding citizen-science networks is essential for maintaining up-to-date occurrence data and for enabling early warning systems for population declines. By directly linking our hypotheses and model outputs to concrete conservation actions, we provide an evidence-based roadmap to support decision makers in safeguarding this culturally significant and highly threatened fungal species.

5 Conclusion

Overall, the findings of this study provide valuable insights for making robust conservation management decisions, particularly in areas where the Montane Chaco forest still persists. Species Distribution Models (SDMs) have the potential to play a crucial role in guiding spatial conservation planning [96–97]. The development of distribution maps is not only essential for conservation strategies but also for anticipating the impacts of climate change on ecosystems. In this regard, we strongly encourage future studies to incorporate predictive models under different climate change scenarios to design effective mitigation and adaptation strategies.

Furthermore, citizen science is a powerful tool for data collection on large spatial and temporal scales. Public engagement in biological data collection can significantly improve both the quality and quantity of available information, strengthening predictive models and their applicability in conservation efforts. We encourage researchers to

actively involve communities in their studies, particularly in conservation-related projects, fostering a more inclusive and effective approach to biodiversity preservation.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1007/s44353-025-00068-6.

Supplementary Material 1

Supplementary Material 2

Supplementary Material 3

Supplementary Material 4

Supplementary Material 5

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Author contributions
Lara Thornton, Gerardo Robledo and Carlos Urcelay conceptualized and designed the study. Funding acquisition was led by Gerado Robledo and Lara Thornton. Data collection and data analysis was performed by Lara Thornton. Lara Thornton, Kelmer Martins da Cunha, Elisandro Ricardo Drechsler-Santos, Enzo Cristaldo, Ariel Ortiz, Carlos Urcelay and Gerardo Robledo contributed to interpretation of the results. The first draft of the manuscript was written by Lara Thornton and Kelmer Martins da Cunha, Elisandro Ricardo Drechsler-Santos, Enzo Cristaldo, Carlos Urcelay and Gerardo Robledo contributed to writing, reviewing, editing, and approving the final manuscript.

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Data availability
All data analyzed during this study are included in this article and itssupplementary information files, with the exception of the table of presence records of the fungus, which is available from the corresponding author upon request.

Code availability
The R code used during the current study is available from the corresponding author on request.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not Applicable.

Competing interests
The authors declare no competing interests.

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