Chapter 8
Exploration and Collection of Quinoa's Wild Ancestor in Argentina

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Abstract In this paper we tested the performance of the Species Distribution Models (SDMs) to provide reliable guidelines for planning a collection mission for quinoa's wild ancestor, *Chenopodium hircinum*, across Argentina. A model was constructed by combining a prediction of the species' geographic distribution based on bioclimatic variables and herbarium specimen records. Annual temperature and precipitation seasonality, and mean temperature of the wettest quarter were the bioclimatic variables with the highest mean contribution to the model. Northwest and Central Argentina were the regions predicted with the highest habitat suitability. Then, SDMs predictions were tested by conducting a field-collection trip during February 2017 to previously unsampled localities. In each locality we determined whether or not *C. hircinum* was present. The model performed relatively poorly, as a significant number of collected populations came from localities with a low estimated probability of occurrence. On the other hand, the Humid Pampas, a region with abundant previous reports, yielded just one sample. This result is relevant for the development of new SDMs to plan subsequent field-collection trips for *C. hircinum* and points to further improvement of these models based on information gathered here. The field-collection trip produced 59 samples of *C. hircinum* populations covering a wide range of contrasting environments in terms of latitude, elevation, temperature and precipitation regimes. Moreover, a large number of collected populations came from Dry Chaco and High Monte ecoregions, which are very hot environments with maximum

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R. Choukr-Allah and R. Ragab (eds.), *Biosaline Agriculture as a Climate Change Adaptation for Food Security*, https://doi.org/10.1007/978-3-031-24279-3_8

temperatures often higher than 25 °C during *C. hircinum*'s growing season (spring–summer). A comparative analysis of adaptability ranges between quinoa cultivars from the whole range of the species distribution and collected wild *C. hircinum* populations from Argentina reveals that quinoa's wild ancestor explores a hotter range and suggests it can increase quinoa's adaptation range and yield stability by providing new allelic variation to breeding programs.

Keywords Argentinean lowlands · *Chenopodium hircinum* · Germplasm collection · Maxent · Quinoa · Plant genetic resources

1 Introduction

Quinoa is a highly nutritious crop of Andean origin that evolved in harsh environments. Although characterized as a stress-tolerant species, the recent global expansion of its production exposed the crop to new challenges. One of those challenges is warm temperatures during reproductive growth (Hinojosa et al. 2019). *Chenopodium hircinum* Schrad., quinoa's wild ancestor and with which it is easily crossed to produce fully fertile offspring, is distributed throughout Argentina, including mountains and plains and along a wide latitudinal range (Wilson 1988, 1990). Argentinean populations of *C. hircinum* thrive in some of the hottest environments in South America (Jellen et al. 2011). Accordingly, some of those populations could express useful traits which if transferred to quinoa could improve the crop's adaptation to warm locations.

Recently, Curti et al. (2017) evaluated the conservation status of pseudocereal CWR species and revealed a null percentage of Argentina's *C. hircinum* wild populations are currently conserved in the country's Germplasm Bank Network (INTA GBN), or even in international gene banks. These severe gaps in ex situ collections indicate that collection efforts for quinoa CWR species must be intensified, especially as quinoa's cultivation at high altitudes is threatened by the effects of anthropogenic climate change (Castañeda-Álvarez et al. 2016).

Plant collecting missions have benefited from the application of Geographic Information Systems (GIS) and the development of fast-computational algorithms such as Species Distribution Models (SDMs) (Jarvis et al. 2005; Ramírez-Villegas et al. 2010; Fois et al. 2018). By conducting spatial analyses of species distributions, gaps in collections can be prioritized in a more objective manner and targeted for collecting missions (Cobben et al. 2015). Species Distribution Models (SDMs) have previously been used for PGR collections and positive results have been reported in terms of number of populations collected, since the models predict the potential collection sites based on the most favorable environment for the target species (Villordon et al. 2006; Parra-Quijano et al. 2012b; Fois et al. 2015). Since germplasm collectors and curators have few records for the occurrence of rare species and they urgently need reliable tools for planning future collection missions, SDMs have potential utility for optimizing collecting mission while minimizing the risk of over- or under-estimation

(Jarvis et al. 2005; Fois et al. 2018). In this context, we used SDMs to: (i) model the potential distribution of *C. hircinum* across Argentina and (ii) explore the feasibility of using these models to planning future collecting mission for this species.

2 Materials and Methods

MaxEnt (Phillips et al. 2006) was used to model the potential distribution of *C. hircinum* in Argentina. The model predicts the distribution using species presence points as well as environmental variables covering the study area (Elith et al. 2011). Occurrence records of *C. hircinum* were obtained from the Global Biodiversity Information Facility (GBIF, available at http://www.gbif.org/) and CWR Diversity (available at http://www.cwrdiversity.org/) websites, and the environmental inputs included altitude and 19 bioclimatic variables from the WorldClim (ver. 2) website (http://www.worldclim.org). It needs to be highlighted that the model does not consider soil composition variables. The ROC curves (Receiver Operating Characteristic) and AUC (Area Under the Curve) were used to evaluate the accuracy of MaxEnt in modeling the target taxon distribution, as implemented by MaxEnt (Phillips et al. 2006). Furthermore, the MaxEnt-based variables selection procedure (jackknife-based) was used to evaluate the most important bioclimatic variables that define *C. hircinum*'s geographic distribution.

The Argentina *C. hircinum* collection expedition was used to validate and determine the utility of the MaxEnt model for germplasm collecting mission planning when applied to this species. For this, the collection mission was planned by focusing on the probability threshold values ≥ 0.90 (arbitrary threshold) of the potential habitat suitability map of this species. In each previously unsampled locality having a high estimated probability of occurrence we determined whether or not *C. hircinum* was present. As one of the goals was to include samples from environments for which there are current and past cultivated quinoa reports (Andrade et al. 2015), the collection trips also included parts of the Monte ecoregion in Mendoza and Neuquén provinces toward Patagonia, environments with low predicted values according to the model. To assess the model prediction in relation to expedition data, the predicted probability of occurrence was determined for the 30-arcsec grid cell in which a population was found. All probabilities were classified from 0 to 1.0 and the number of presence and absence locations were summed per class.

We collected passport data from quinoa cultivars currently evaluated worldwide from the GRIN-global website (https://npgsweb.ars-grin.gov/gringlobal/search.aspx) and then with ArcGIS Toolbox extracted temperature and precipitation climatic information. Density plots of the average daily maximum temperature and yearly precipitation of the native ranges of C. quinoa and *C. hircinum* were calculated using the package ggplot2 (Wickham 2016).

3 Results

According to the ROC curves, modeled *C. hircinum* potential distribution showed a high level of AUC predictive performance (training 0.96 ± 0.5; test, 0.91 ± 0.7). Based on the jackknife test, environmental predictors that exhibited the highest mean contributions were temperature seasonality (Bio4) and precipitation seasonality (Bio15) both defined in terms of annual ranges, and mean temperature of the wettest quarter (Bio8) (Table 1). Bio4 was the variable with the highest gain (>2) when used in isolation, and the same variables were the ones that decreased the gain the most when omitted. Considering permutation importance, isothermality (Bio3) defined as the ratio between mean diurnal range (mean of monthly (max temp − min temp)) and temperature annual range, mean temperature of warmest quarter (Bio10) and Bio4 were the main environmental variables affecting the potential distribution of *C. hircinum* (Table 1).

C. hircinum potential distribution map in Argentina is shown in Fig. 1. Out of 2,760,555 km^2 of the total country area, 2,162,361 km^2 (~78%) was predicted as unsuitable for *C. hircinum*; the remaining 598,194 km^2 was divided into 180,687 km^2 (6.5%) with a low potential probability (0.51–0.60), 135,950 km^2 (4.9%) with a moderate potential probability (0.61–0.70) and 281,558 km^2 (10%) with the highest probability ($\geq$0.71) of suitable ecological conditions. The majority of suitable habitats ($\geq$0.71) were located in the central and northern parts of Argentina (Fig. 1).

Figure 2 shows the presence or absence of *C. hircinum* in 75 locations sampled during the collecting expedition in February 2017 (end of the Southern Hemisphere summer and of reproductive growth of the species) in relation to the MaxEnt probabilities of occurrence. The model performed relatively poorly, as at locations with

Table 1 Estimates of average contribution and permutation importance of the environmental variables used in MaxEnt modeling of *C. hircinum* according to jackknife test (Phillips et al. 2006)

Variable	Percent contribution	Permutation importance
Bio2	3.8	4.8
Bio3	5	42.4
Bio4	46.1	9.6
Bio6	2.7	0
Bio7	1.7	0
Bio8	6.5	8.4
Bio9	4.4	0
Bio10	4.7	11.2
Bio11	6	5.7
Bio12	0.2	2.3
Bio13	0.5	5.3
Bio15	15.4	8.4
Bio18	3	1.9

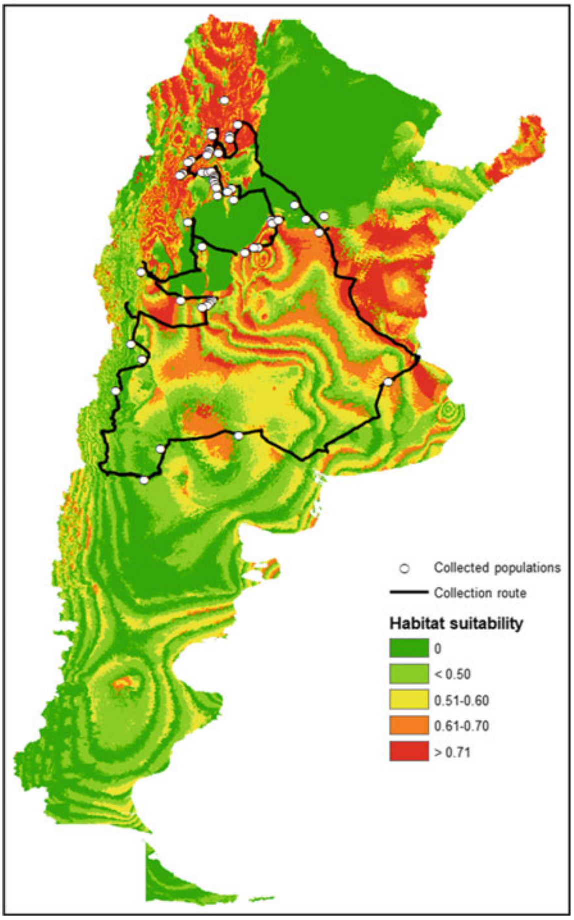

Fig. 1 Map for habitat suitability probability of *C. hircinum* according to occurrence records in Argentina. Habitat suitability classes include: unsuitable (<0.50), low potential (0.51–0.60), moderate potential (0.61–0.70) and high potential (>0.71). See color charts

low estimated probabilities of occurrence, presence of the species was comparatively higher than its absence (Fig. 2).

Fifty-nine populations of *C. hircinum* were collected from Argentina covering a large latitudinal (from –24.89 to –39.04) and altitudinal (from 32 to 2,116 m. a. s. l) range, respectively (Table 2). Most collected accessions came from Catamarca, San Luis, Salta and Santiago del Estero provinces, covering the ecoregions of Dry Chaco, High Monte and Southern Andean Yungas (Table 2).

Figure 3 shows the climatic patterns of Argentina to which the collection places are superimposed. Isohyets and isotherms maps were generated with the ArcGIS Toolbox to show the large annual precipitation (from 200 to 900 mm) and mean temperature (12 to 20 °C) ranges for the locations explored during the collection expedition. The isotherm map for mean annual maximum temperature shows that a large number of collected populations came from locations with summer maximum average temperatures higher than 25 °C (Fig. 3). In addition, density plots calculated

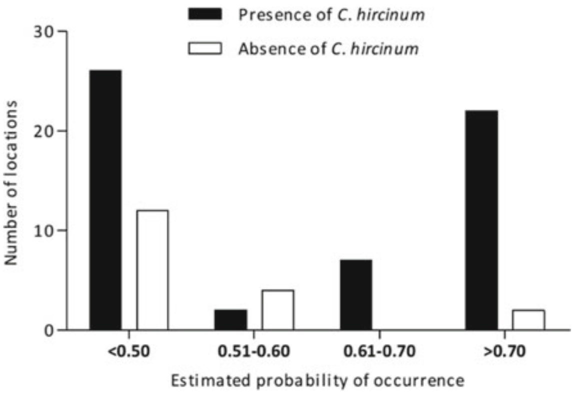

Fig. 2 Number of locations in Argentina where *C. hircinum* were present or absent plotted according to the probability classes of occurrences at these locations

for *C. hircinum* and *C. quinoa* show that wild *C. hircinum* populations grow and flower in warmer and drier (with a higher degree of overlapping for this variable however) habitats than the cultivated quinoa (Fig. 4).

4 Discussion and Conclusions

According to our results, *C. hircinum* is widely distributed across central and northern parts of Argentina covering three main ecoregions known as Dry Chaco, High Monte and Southern Andean Yungas (Olson et al. 2001), suggesting that the target taxon prefers subtropical climates (Wilson 1988; Jellen et al. 2011). This result matched with the planned collection route that allocated exploration efforts mainly to those ecoregions in which a large number of populations were collected. However, exploration of localities with a low estimated probability of occurrence for the target taxon, such as Mendoza and Neuquén provinces, and environments toward the southeastern plains of Santiago del Estero, yielded an important number of populations. These results could be explained by the data source used to construct the distribution of the species. Since herbarium data are incomplete and suffer from sampling bias, it is probable that the distribution deduced for *C. hircinum* with an associative species distribution model such as MaxEnt, wouldn't necessarily represent the complete distribution of the species. Consequently, new populations could be encountered outside the predicted distribution, for example in Northwestern Patagonia. Moreover, the species' collection points recorded in those environments should be used to redefine its predicted distribution across Argentina and direct future collection missions toward those sites.

The Pampas region, in the Center-East part of the map, deserves a special comment. Figure 1 shows a medium to high probability of occurrence for this region, which encompasses parts of Buenos Aires, Córdoba and Santa Fe provinces; however it yielded just one sample (CHIR 56 in Table 2). Additionally, this accession comes from a locality with sandy soils, perhaps the main factor explaining its survival in the

Table 2 Passport data (latitude and longitude in coordinates, elevation in m.a.s.l.) for the collected populations of *C. hircinum* in field expeditions during 2017

Accession #	Province	Longitude	Latitude	Elevation	Ecoregion
CHIR 001	Santiago del Estero	−62.44	−29.35	83	Dry Chaco
CHIR 002	Santiago del Estero	−62.85	−28.82	98	Dry Chaco
CHIR 003	Salta	−64.97	−25.8	783	Dry Chaco
CHIR 004	Salta	−64.98	−25.81	790	Dry Chaco
CHIR 005	Tucumán	−65.28	−26.24	775	Dry Chaco
CHIR 006	Tucumán	−65.3	−26.37	769	Dry Chaco
CHIR 007	Tucumán	−65.69	−26.9	1,913	Southern Andean Yungas
CHIR 009	Salta	−65.94	−26.23	1,660	High Monte
CHIR 010	Salta	−65.97	−26.07	1,615	High Monte
CHIR 011	Catamarca	−66.05	−26.73	1,912	High Monte
CHIR 012	Catamarca	−66.06	−26.78	1,956	High Monte
CHIR 013	Catamarca	−66.1	−26.88	2,063	High Monte
CHIR 014	Catamarca	−66.14	−26.96	2,116	High Monte
CHIR 015	Catamarca	−66.72	−27.16	2,064	High Monte
CHIR 016	Catamarca	−66.84	−27.22	1,869	High Monte
CHIR 017	Catamarca	−67.03	−27.63	1,355	High Monte
CHIR 018	Catamarca	−67.1	−27.71	1,179	High Monte
CHIR 019	Catamarca	−67.14	−27.71	1,237	High Monte
CHIR 020	Catamarca	−66.33	−27.58	1,074	High Monte
CHIR 021	Catamarca	−66.1	−27.62	1,767	Southern Andean Yungas
CHIR 022	Catamarca	−65.99	−27.58	1,809	Southern Andean Yungas
CHIR 023	Catamarca	−65.88	−27.77	1,393	Southern Andean Yungas
CHIR 024	Catamarca	−65.86	−27.82	1,206	Southern Andean Yungas
CHIR 025	Catamarca	−65.88	−27.91	1,221	Southern Andean Yungas
CHIR 026	Catamarca	−65.87	−27.93	1,178	Southern Andean Yungas
CHIR 027	Catamarca	−65.87	−27.95	1,165	Southern Andean Yungas
CHIR 028	Catamarca	−65.82	−28.04	1,054	Southern Andean Yungas
CHIR 029	Catamarca	−65.79	−28.16	956	Dry Chaco
CHIR 030	Catamarca	−65.76	−28.48	500	Dry Chaco

(continued)

Table 2 (continued)

Accession #	Province	Longitude	Latitude	Elevation	Ecoregion
CHIR 031	Catamarca	−65.37	−28.32	972	Dry Chaco
CHIR 032	Catamarca	−65.21	−28.2	543	Dry Chaco
CHIR 033	Santiago del Estero	−65.12	−28.62	337	Dry Chaco
CHIR 034	Santiago del Estero	−63.72	−29.4	463	Dry Chaco
CHIR 035	Santiago del Estero	−63.7	−29.5	538	Dry Chaco
CHIR 036	Santiago del Estero	−63.69	−29.5	565	Dry Chaco
CHIR 037	Santiago del Estero	−63.47	−29.39	241	Dry Chaco
CHIR 038	Córdoba	−64.22	−30.43	834	Dry Chaco
CHIR 039	Córdoba	−64.38	−30.41	661	Dry Chaco
CHIR 040	Córdoba	−64.73	−30.58	511	Dry Chaco
CHIR 041	La Rioja	−66.3	−30.36	468	Dry Chaco
CHIR 042	La Rioja	−66.84	−29.44	488	Dry Chaco
CHIR 043	San Juan	−68.61	−31.33	1,001	High Monte
CHIR 044	San Luis	−67.12	−32.38	594	Dry Chaco
CHIR 045	San Luis	−65.94	−32.37	601	Dry Chaco
CHIR 046	San Luis	−66	−32.42	652	Dry Chaco
CHIR 047	San Luis	−66.06	−32.47	637	Dry Chaco
CHIR 048	San Luis	−66.13	−32.59	768	Dry Chaco
CHIR 049	San Luis	−66.31	−32.65	715	Dry Chaco
CHIR 050	Mendoza	−68.98	−34.03	1,211	Low Monte
CHIR 051	Mendoza	−68.56	−34.58	864	Low Monte
CHIR 052	Mendoza	−69.55	−35.74	1,730	Southern Andean steppe
CHIR 053	Neuquén	−68.5	−39.04	296	Low Monte
CHIR 054	Río Negro	−67.87	−37.92	310	Low Monte
CHIR 055	La Pampa	−64.94	−37.43	291	Espinal
CHIR 056	Buenos Aires	−59.36	−35.42	32	Humid Pampas
CHIR 057	Salta	−65.47	−24.89	1,231	Dry Chaco
CHIR 058	Santa Fe	−61.95	−29.86	89	Dry Chaco
CHIR 059	Santa Fe	−61.77	−29.23	64	Dry Chaco

Ecoregions are presented according to Olson et al. (2001)

region. The Pampas region has been extensively explored by the Argentinean authors of this paper yielding no additional *hircinum* samples. The most recent herbarium specimens of the species are several decades old; meanwhile, the Pampas have been subjected to many changes in terms of tillage (mostly no tillage today), crops (soybean started to be extensively cultivated in the 80s) plus significant changes in herbicide use (Viglizzo et al. 2011). All these factors could have dramatically altered *hircinum*'s

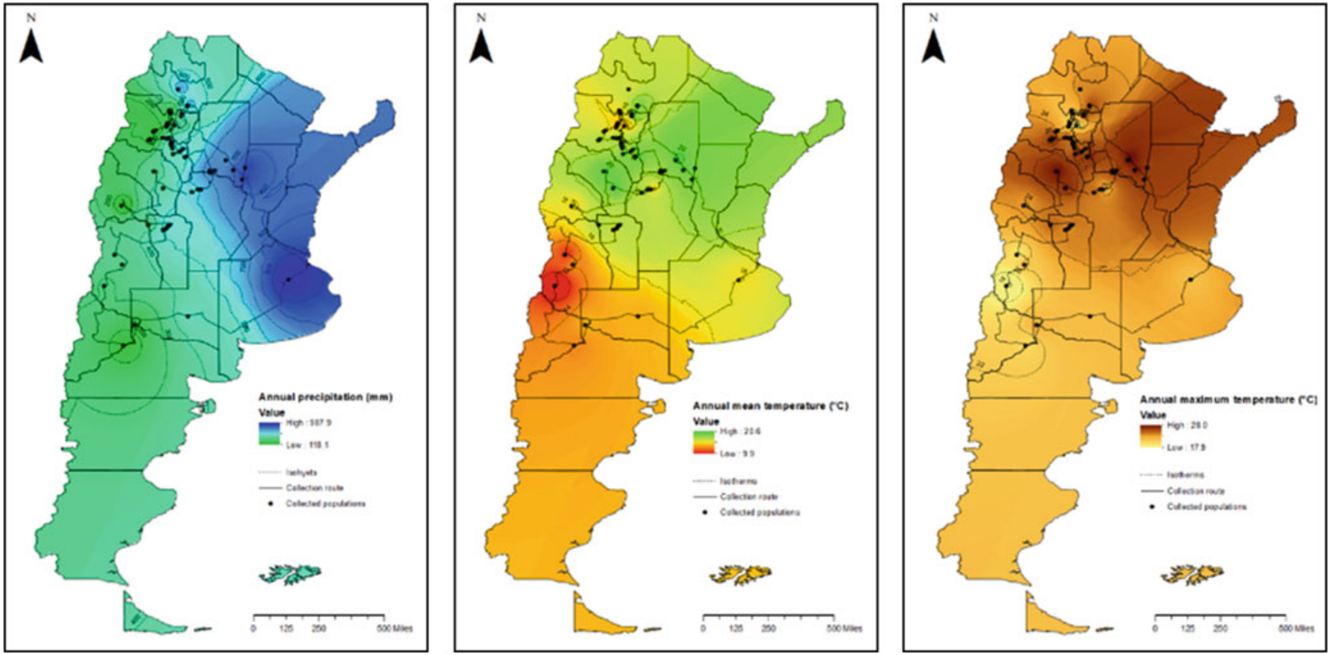

Fig. 3 Isohyets (left) and isotherms for mean (middle) and maximum (right) temperatures maps from Argentina and geographical distribution of the collected populations of *C. hircinum*. The high and low value numbers in each map legend represent the range of conditions explored by the collection

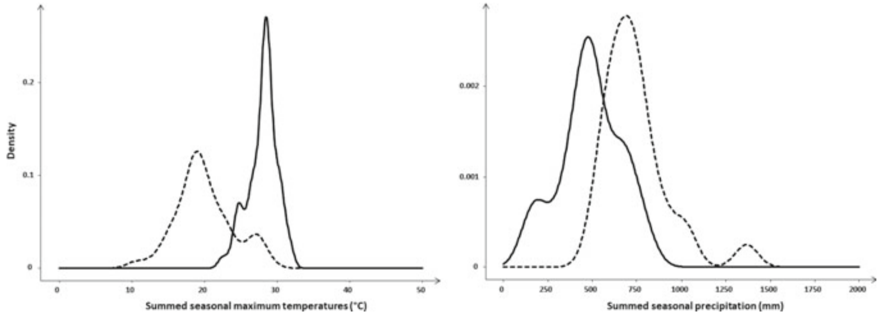

Fig. 4 Density plots representation of the average daily maximum temperature (left) during the rainy season (spring–summer) and yearly precipitation (right) of the native ranges of *C. quinoa* cultivars (dashed line) and *C. hircinum* (bold line) populations calculated from genotypes passport information and climate data retrieved from WorldClim (ver. 2) website (available at http://www.worldclim.org). Passport data from the described collection trip were used for *C. hircinum* while data from 109 locations of quinoa cultivation, spanning the whole range of distribution of the species from 2°N in Southern Colombia to 47°S in Southern Chile were used for quinoa

adaptation range in the Pampas, where the main *Chenopodium* weed today is *C. album* (Scursoni and Satorre 2010). On the other hand, *C. album* is substituted by *C. hircinum* in similar habitats (road margins and wastelands) of drier and hotter environments of the collection environments. A similar situation has occurred within the U.S. humid Corn Belt, where the North American authors of this paper have likewise struggled to find modern populations of the native, and previously abundant, North American sister-species of *C. hircinum*, *C. berlandieri*, on non-sandy coastal soils east of –96° longitude (Scursoni et al. 2006; Drewitz and Stoltenberg 2018). The ecological and management factors determining *C. hircinum* distribution are a research subject of high interest, beyond those related to species distribution maps.

For *C. hircinum*, the distribution model was to some extent useful to detect locations from where to collect germplasm, as an important number of populations were collected from localities where the model predicted the highest probability of occurrence for the target taxon. However, the performance of the model was relatively poor in those localities with low to moderate probabilities. Improvements to the model could be made by developing the ELC (Ecogeographical Land Characterization) maps that take into account information from edaphic variables (Parra-Quijano et al. 2012a, b; Marinoni et al. 2015), which to some extent seems to determine the occurrence of *C. hircinum* in the Pampa region. Furthermore, the inclusion of vegetation surveys covering a range of both habitats and landscape features (e.g. fields, hedgerows, waterways and roadsides) (Rubio Teso and Iriondo 2019; Jarvis et al. 2015) could be useful to identify the habitats and features with the highest proportion of wild *C. hircinum* populations, since these features seem to determine its occurrence in drier and hotter environments toward northern parts of Argentina.

Climatic information extracted from locations where populations of *C. hircinum* were collected revealed a large range of precipitation and temperature conditions, even for maximum temperatures. In this sense, the model guided the germplasm collectors to the preferred sites of this species, while at the same time covering a wide range of climatic conditions. Moreover, Argentinean populations of *C. hircinum* collected from hottest environments could express useful traits which transferred to quinoa and could improve adaptation to warm locations. A comparative inspection of adaptability ranges between quinoa cultivars and *C. hircinum* collected populations from Argentina reveals to what extent quinoa's wild ancestor can increase their adaptive capacity into new hottest agricultural systems by conferring new allelic variation required in breeding programs.

In conclusion, SDMs such as MaxEnt are a useful aid in planning collection missions to recover germplasm for wild populations of species with little or poor representation in gene bank collections, however improvements to the model require more consideration of expert knowledge and further refinements by including relevant information (i.e., edaphic variables, vegetation surveys and habitat features) at the species level which could be useful to determine their occurrence across different ecogeographical conditions.

Acknowledgements The authors thank Ale Lavih who assisted with the English version of the manuscript and Gordon Wellman (KAUST University) for suggestions about graphs. The *C. hircinum* collection trip was supported by grant OSR-2016-CRG5-2966 from KAUST University.

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