



Setting conservation priorities for Argentina's pseudocereal crop wild relatives



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ABSTRACT

Although the considerable value of crop wild relatives (CWRs) as gene donors is well known, in many crop complexes they are subject to increasing threats from anthropogenic factors. The development of a prioritized inventory of CWR species is an essential step towards the conservation of this vital resource, so in this study, we developed a national inventory of pseudocereal CWR species in Argentina and established *ex situ* and *in situ* conservation priorities. The resulting prioritized inventory consisted of 16 species, almost all of which were under-represented in national and global *ex situ* gene banks. Similarly, the extant reserve network was found to be insufficient for the preservation of pseudocereal CWRs, especially *Chenopodium* diversity. Three hotspot groups were identified in the Andean region: northern, central and southern. The northern group has the highest conservation priority because it harbours CWR species from the primary and secondary gene pools, but the central and southern groups are also important because they harbour endemic species that are poorly represented in the extant reserve network. Therefore, new priority areas for protection are necessary for their conservation. This study emphasizes that the conservation of pseudocereal CWRs in Argentina must be maximized using a complementary *in situ* and *ex situ* approach.

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1. Introduction

Crop wild relatives (CWR) are plant species that are valued for their relatively close relationship to crops. Although CWR species have been identified as vital to food security and environmental sustainability, many are subject to increasing threats from anthropogenic factors such as urbanization, habitat fragmentation, agricultural intensification, and climate change (Maxted and Kell, 2009). Therefore, there is broad interest in the conservation of this group of plants.

The first step in developing a national management plan for CWR conservation is to create a checklist of the CWRs present in a country and then inventory the priority species (Maxted et al., 2007). After filtering the checklist following the incorporation of ancillary information (such as nomenclature, application of the gene pool or taxon group concepts, ecogeography, uses, threats and conservation status), the resulting final inventory is the starting point for the conservation of these important plant resources (Maxted et al., 2007).

At present, several countries have a prioritized inventory of CWR species for major crops (Kell et al., 2015; Houry et al., 2013; Vincent et al., 2013), but many important crop complexes and political regions

still lack such an inventory. Therefore, it is crucial to foster the development of this information because conservation actions are urgently needed to secure these vital resources, which are necessary to sustain food production in the world (Maxted and Kell, 2009; Redden, 2015).

The Andean region in South America is an important centre of the origin, domestication, and dispersion of high-protein pseudocereal crops (Jimenez et al., 2013), which includes species from the genus *Chenopodium* (hereafter referred to as chenopod), known as quinoa (*C. quinoa* Willd.); the semi-domesticated cañahua (*C. pallidicaule* Aellen); and species from the genus *Amaranthus* (hereafter referred to as amaranth), known as kiwicha (*A. caudatus* L.) and chaclión (*A. mantegazzianus* L.). However, only quinoa has gained attention worldwide, and it is now cultivated beyond the Andean frontiers (Murphy and Matanguihan, 2015). Although some of the other species have been shown to have similar nutritional and functional properties or have distinctly adapted to harsh climatic conditions, all have remained as local crops (Jimenez et al., 2013; Vargas et al., 2011).

The genus *Chenopodium* has been included in the recently prioritized Harlan and de Wet Inventory of CWR species, but most of the included species are from the Northern Hemisphere (Vincent et al., 2013). Many native and endemic species from South America have been poorly studied in terms of their relationships with crop species and thus remain as only potential allele donors (Jellen et al., 2011), whereas none of the species of the genus *Amaranthus* have been included in the above

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prioritized inventory, although they were staple crops of ancestral American cultures. Moreover, amaranths remain important agricultural commodities in several Latin American countries, and their drought tolerance and environmental plasticity are attractive traits that could promote their cultivation in areas that are challenging to traditional crops (Brenner et al., 2000).

As part of the Andean centre of domestication, Argentina contains important plant genetic resources for major and local food crops, but only a few of its CWR germplasms of globally important crops, such as potatoes and common beans, have been collected, characterized and evaluated (Galván et al., 2006; Jansky et al., 2013). In addition to the weak inclusion of CWR species in gene banks, the state of their *in situ* conservation has rarely been assessed (Marfil et al., 2015), so a critical evaluation of the conservation status of Argentinean pseudocereal CWRs is needed. In this group, *A. mantegazzianus* (a cultivated species) stands out because it is considered to be the only crop to have been domesticated in the country (Parodi, 2010). In addition, a species in the primary wild quinoa gene pool, *C. hircinum*, is distributed from the northwest to the south-eastern lowlands of the country (Wilson, 1990), and many wild amaranth species are sympatric with wild chenopods. Since Argentina contains species in the primary and secondary chenopod and amaranth gene pools, we believe that the diversity of pseudocereal CWRs in Argentina may contribute to future breeding programmes.

In this context, we evaluated the diversity of amaranth and chenopod species in Argentina to set conservation priorities. We expected to find a high diversity of pseudocereal CWRs in the northwest of the country, which is part of the Central Andes hotspot (Myers et al., 2000) and the major centre of plant diversity in Argentina (Juárez et al., 2007). As pseudocereals have been largely neglected and underutilized in the economy of this country, we expected to find the pseudocereal CWRs of Argentina to be underrepresented in *ex situ* collections and *in situ* protected areas. Specifically, we address the following questions: (i) What is the taxonomic diversity of the pseudocereal CWRs in Argentina? (ii) What is the degree of relatedness between Argentinean pseudocereal CWR species and cultivated species, and how are they distributed in the country? (iii) What is the current degree of representation of Argentinean pseudocereal CWRs in *ex situ* gene banks and *in situ* protected areas? (iv) Which are the most important established reserves for the conservation of prioritized pseudocereal CWRs? (v) What are the conservation priorities for Argentinean pseudo-cereal CWR?

2. Materials and methods

2.1. Checklist and national inventory of Argentinean pseudocereal CWRs

The Argentinean pseudocereal CWR checklist was developed from the Catálogo de Plantas Vasculares del Cono Sur, which contains an updated database of the wild and exotic plant species in Argentina arranged by family and genus (Zuloaga et al., 2008). The checklist was compiled in a standardized format and taxonomically verified following The Plant List (2010).

Next, the national prioritized inventory of the pseudocereal CWRs of Argentina was developed from the checklist by applying the following criteria: 1) the status of each species (whether the taxon is native, endemic or exotic to the country), 2) its relatedness to its respective crop species (after applying the gene pool and taxon group concepts), 3) the *ex situ* and 4) the *in situ* conservation status. We followed these criteria because there were no agricultural statistics available to evaluate the economic value of pseudocereal crop species in Argentina, and none of the pseudocereal CWRs in the country are categorized as threatened by the IUCN. Two species of the genus *Chenopodium* and five of the genus *Amaranthus* are categorized by the IUCN, but they are not found in Argentina.

To apply criterion 1, we obtained information from the Catálogo de Plantas Vasculares del Cono Sur (Zuloaga et al., 2008), in which a species is considered native when it is naturally, although not exclusively, distributed in Argentina, while a species is classified as endemic when it is naturally and exclusively distributed in Argentina (political endemism, Cowling, 2001). According to this criterion, only native and endemic species are considered priorities.

Crop species relatedness (criterion 2) was defined in two ways. First, the gene pool (GP) concept developed by Harlan and de Wet (1971) was applied when information about inter-specific hybridization was available, and in the absence of such information, the taxon group (TG) concept developed by Maxted et al. (2006) was used. As the genus *Chenopodium* is included in the Harlan and de Wet Inventory (available at <http://www.cwrdiversity.org>), we applied the GP concept to those species from this inventory present in Argentina. For the other *Chenopodium* species, we searched for information about inter-specific hybridization, and when such information was not available, we applied the TG concept following the recent review by Jellen et al. (2011). Conversely, because the genus *Amaranthus* is not included in the Harlan and de Wet Inventory, we applied the GP concept based on the inter-specific hybridization studies reviewed by Brenner et al. (2000) and Trucco and Tranel (2011), and we applied the TG concept based on the taxonomic relationships reported in Mosyakin and Robertson (1996) and Das (2012). The species that were categorized into GP 1b, GP 2, TG 1b, TG 2 or TG 3, i.e. those most closely related to existing crop species, were prioritized.

We searched for information about the number of accessions currently maintained by the National Institute of Agricultural Technology (INTA) to evaluate the *ex situ* conservation status (criterion 3) of the species selected according to criteria 1 and 2. This institution has implemented the Germplasm Bank Network (GBN) comprising nine active plant genetic resource banks and eleven collections distributed in different ecological areas across Argentina; the GBN is the only network in the country that contributes to the *ex situ* conservation of crop species and their wild relatives. Additionally, we searched for information in the Royal Botanical Garden at Kew (<https://www.kew.org/seedlist/>) and the USDA-ARS (<https://npgsweb.ars-grin.gov/gringlobal/search.aspx>) databases. These institutions maintain collections of wild *Chenopodium* and *Amaranthus* native to the Americas and actively contribute to their *ex situ* conservation (Brenner et al., 2000; Jellen et al., 2011).

The *in situ* conservation status of the species selected according to criteria 1 and 2 was determined by evaluating the degree of representation of those species in the National Protected Areas System of Argentina (NPASA). As no checklist of pseudocereal CWRs in NPASA is available, we obtained this information by overlaying the species distribution maps on a map of the NPASA reserves. We determined the number of reserves in which the priority species are present and the percentage of their geographic distribution that is currently protected.

We used species distribution models (SDMs) to estimate the potential geographical distribution of each priority species; species occurrence records were acquired from the Global Biodiversity Information Facility (GBIF, available at <http://www.gbif.org/>) and CWR Diversity (available at <http://www.cwrdiversity.org/>). All geographical coordinates were cross-checked for inconsistencies following the methodology proposed by Scheldeman and van Zonneveld (2010). A total of 381 occurrence data points were used to model the potential distributions of all species.

The potential distribution of each species was obtained using Maxent (the Maximum Entropy Algorithm; (Phillips et al., 2006) with a set of environmental variables and species presence records as inputs. Modelling was performed at a resolution of 30 arc-sec (~1 km × 1 km cell size at the equator) (Hijmans et al., 2005), and the environmental inputs included altitude and 19 bioclimatic variables from the WorldClim database (available at <http://www.worldclim.org>). We defined species-specific geographical backgrounds using SDMtoolbox v1.1 software (Brown, 2014), in which the estimated background areas of each species were generated using the buffered local adaptive

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