



Original research article

In situ conservation of wild potato germplasm in Argentina: Example and possibilities



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ABSTRACT

The potato is the third most important food crop worldwide and in situ conservation of its wild relatives is considered an urgent priority. Although regions of the Americas with high wild potato species richness have been identified, the need to identify specific sites for establishing genetic reserves is still pending. Matching distribution data of Argentinean wild potato species to existing protected areas (PA), two priority sites were identified. The creation of genetic reserves in these two PA would make possible to preserve populations of species that have been successfully incorporated into the crop and are listed in the global priority Crop Wild Relative inventory. While the presence of target species in PA could ensure a passive conservation, in situ conservation programs require to actively intervene in selected areas. From a field study performed on populations of the wild potato *Solanum kurtzianum* naturally growing in a PA, the Villavicencio Natural Reserve (Mendoza province), a baseline with distribution, biotic interactions, sprouting behavior, population dynamics, AFLP and pollen viability data was established. Based on a systematic work in this Reserve we have generated a working protocol to be implemented at national and regional levels for the in situ conservation of potato wild relatives.

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1. Introduction

Nowadays it is undeniable that conservation and sustainable use of biological diversity is of critical importance for meeting the food, health and other needs of the ever-growing human population. Concerns about the considerable reduction of biodiversity due to human activities was one of the factors that led to the celebration of the Convention on Biological Diversity (CBD) in 1992, whose objectives are the conservation of biological diversity, the sustainable use of its components and the fair and equitable sharing of the benefits arising from the utilization of genetic resources.

From all sources of living organisms, the conservation of plant genetic resources for food and agriculture (PGRFA), which represent the basis of global food security, has occupied a prominent position in the efforts undertaken by the international community. The PGRFA comprise, chronologically ordered, the diversity of genetic material contained in: (i) the crop wild relatives (CWR), which include crop progenitors and their closely related, (ii) landraces or traditional varieties, and (iii) modern cultivars. The crops tend to contain limited genetic diversity compared with their wild relatives, as a product of the

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successive bottlenecks imposed by the ancestral domestication, about 10 000 years ago and, then, by the successful application over the past century of modern plant breeding methodologies that have produced the high-yielding crop varieties (Tanksley and McCouch, 1997). For any crop, a broad genetic base from which new varieties can be developed is increasingly required to meet the ever changing and often unpredictable needs, and the opportunities and challenges of the future. CWR offer large and diverse gene pools to address these demands, providing plant breeders with potentially useful traits, such as pest and disease resistance, abiotic stress tolerance, quality and cytoplasmic male sterility (Hajjar and Hodgkin, 2007).

Although Nicolai Vavilov documented in the 1920s and 1930s the potential of CWR as gene donors in plant breeding programs (Vavilov, 1949), his collections consisted mainly of cultivated varieties, with a relatively poor representation of wild species (Zohary, 1970). As a consequence of an alarming deterioration of natural resources, agricultural scientists stressed CWR as a target group for conservation in the 1970s (Frankel and Bennett, 1970; Frankel and Hawkes, 1975), and currently, in the face of climate change, there are argument to consider them as the most important component of PGRFA. Taking actions to conserve CWR diversity is no longer an option but an urgent priority (Ford-Lloyd et al., 2011; Maxted et al., 2012; Vincent et al., 2013).

There are two fundamental approaches for the conservation of plant genetic resources: ex situ and in situ (Maxted et al., 1997a). The ex situ conservation method that has historically dominated the preservation actions around the world and involves exploration, collection and maintenance of plant genetic materials outside the native habitat, exhibit limitations for the effective conservation of CWR germplasm (Meilleur and Hodgkin, 2004; Maxted and Kell, 2009). The in situ conservation of CWR, first proposed in the 1970s (Frankel, 1970; Jain, 1975), took relevance by the late 1980s in response to the unsatisfactory progress in conserving these irreplaceable resources for agriculture. At the present time, the adoption of a complementary strategy that incorporates both ex situ and in situ techniques is considered an ideal scenario for conserving the gene pool of target species (Maxted et al., 2007).

According to the CBD (1992), in situ conservation is the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings. One particular advantage of in situ conservation is that it allows the maintenance of evolving populations in their natural habitats, permitting the preservation of gene frequencies and the generation of genetic variability during the dynamic and permanent interaction of target populations with biotic and abiotic factors. The great long term challenge of in situ conservation of CWR is the creation of genetic reserves, which involves the location, designation, management and monitoring of target wild populations in their natural habitats to maintain their genetic diversity (Maxted et al., 1997b).

For the designation of a genetic reserve a series of prioritizations should be established, among which there is the selection of crop gene pools, the selection of target species and the selection of target sites (Maxted and Kell, 2009). A criterion for the selection of priority crop gene pool is to consider the most socio-economically important global food crops. According to their contribution to food security and interdependence within a multilateral system, the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) (FAO, 2009) has identified in its Annex 1 the major importance crop, and this Annex has been used to elaborate an approach for the systematic conservation of the global CWR diversity (Maxted and Kell, 2009; Maxted et al., 2012). For selection of target species, a prioritization could be based on the degree of relationship among the crop and their wild relatives. The Gene Pool (GP) concept (Harlan and de Wet, 1971), which classifies wild relatives into three gene pools according to the feasibility of incorporating their genes by sexual crossing into the crop, is often used to select priority species. The highest priority CWR are typically those in GP1B (directly crossable wild or weedy forms of the crop) and GP2 (less closely related species from which gene transfer to the crop is possible but with some manipulations) (Maxted et al., 2012). Respect to the selection of target sites, the establishment of CWR genetic reserves within already existing protected areas (PA) is largely accepted as the most efficient approach (Heywood and Dulloo, 2006; Maxted and Kell, 2009; Hunter and Heywood, 2011; Maxted et al., 2012). The PA are geographically defined areas designated, regulated and supported by legal and institutional structures to achieve specific conservation objectives, and are the cornerstone of conservation efforts in virtually all countries (CBD, 1992). One strategy to identify the most suitable PA in which to locate genetic reserves of target CWR, is matching the geographic distribution data of these species with the network of PA in a given country or region (Maxted et al., 2012).

The potato, *Solanum tuberosum* L., has been presented as an excellent case study for the importance of CWR germplasm utilization in addressing global food security needs (Jansky et al., 2013). Potato annual production has remained above 300 million metric tons during the 2003–2012 period, which ranks this crop in the fifth place worldwide behind sugar cane, maize, wheat and rice (FAOSTAT, 2014). In addition, the potato ranked third in food supply behind wheat and rice, with an average of 33.01 kg/capita/yr in the 2002–2011 decade; and it is the fourth crop worldwide in terms of protein supply, behind wheat, rice and maize, averaging 1.45 g/capita/day during the years 2002–2011 (FAOSTAT, 2014). From this data related to food and agriculture, obtained for ca. 200 countries, it is clear why the potato is identified as a crop of major importance for food security and included in the Annex 1 of the ITPGRFA. More than 200 wild potato species have been described and grouped in section *Petota*, which occur in the Americas from south-western United States to central Argentina and Chile, Uruguay, Paraguay and Brazil (Hawkes, 1990). The number of species has been reduced in recent years (Spooner and Salas, 2006; Spooner, 2009). However, a consensus in the classification of potato species has not yet been reached (Camadro et al., 2012). In the present work the Hawkes (1990) treatment was used. Potato CWR are found in a wide variety of habitats with the following ranges of ecogeographic distribution: (i) from sea level to 4697 m in altitude; (ii) from 96 to 3601 mm in annual precipitations; and (iii) from 5.6 to 22.1 °C in annual average temperature (Hijmans et al., 2002). Over 150 years ago the late blight epiphytia in Ireland precipitated the use of wild potato germplasm in breeding programs (Ross, 1966; Hawkes, 1990).

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