IS THE GENETIC INTEGRITY OF NATURAL PLANT POPULATIONS *EX SITU* PRESERVED WITH THE CURRENT SAMPLING, CONSERVATION AND REGENERATION APPROACHES?

LA INTEGRIDAD GENÉTICA DE LAS POBLACIONES NATURALES DE PLANTAS ¿SE PRESERVA *EX SITU* CON LOS ENFOQUES CORRIENTES DE MUESTREO, CONSERVACIÓN Y REGENERACIÓN?

Camadro, E.L.

E.E.A. Balcarce, Instituto Nacional de Tecnología Agropecuaria (INTA)-FCA, Universidad Nacional de Mar del Plata (UNMdP) and Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET)
Ruta Nacional 226, km 73.5, 7620 Balcarce, Buenos Aires, Argentina

camadro.elsa@inta.gob.ar

ABSTRACT

Acceleration of environment degradation and climate change poses serious threats to both natural and agricultural ecosystems. In fact, the number of endangered plant species at the global level has increased yearly in the last decades, due to anthropic interventions that sum up to the climate change. Samples of natural plant populations, particularly of wild crop relatives, are *ex situ* conserved in germplasm banks, which have become active in the provision of genetic resources to breeders. The aim of this article is to generate discussion on the adequacy of (a) current protocols for sampling and *ex situ* conservation of the natural genetic diversity and (b) the actual species paradigm in plants, due to their consequences for this and future generations.

Key words: biological species, *ex situ* conservation, *ex situ* regeneration, plant genetic resources, taxonomic species

RESUMEN

La aceleración de la degradación ambiental y el cambio climático presenta serias amenazas para los ecosistemas naturales y agrícolas. De hecho, el número de especies de plantas en peligro de extinción a nivel global se ha incrementado anualmente en las últimas décadas, debido a intervenciones antrópicas que se suman al cambio climático. Las muestras de poblaciones naturales de plantas, particularmente de parientes silvestres de los cultivos, se conservan *ex situ* en bancos de germoplasma, los que se han transformado en activos en la provisión de recursos genéticos a los mejoradores. El objetivo de este artículo es generar discusión sobre la adecuación de (a) protocolos corrientes de muestreo y conservación *ex situ* de la diversidad genética natural y (b) el paradigma actual de especie en plantas, por sus consecuencias para esta y futuras generaciones.

Palabras clave: especie biológica, conservación *ex situ*, regeneración *ex situ*, recursos genéticos vegetales, especie taxonómica

INTRODUCTION

The situation

In the last decades, the acceleration of environmental degradation processes and climate changes has posed serious threats to the stability of both natural and agricultural ecosystems, highlighting their vulnerability in a scenario of increasing global food demands by an ever-growing human population (Miller et al., 2010). The number of endangered plant species is raising annually due to anthropic interventions (road constructions, deforestion and expansion of the agricultural frontiers, among others) which add up to global climate changes (Jarvis et al., 2008). The narrow genetic base of some of the most important crop plants constrains the breeding efforts. But, fortunately, crop wild relatives (CWR) represent a relevant source of genetic diversity for crop improvement (Maxted et al., 2008). As Jansky et al. (2013) have stated, the value of CWR –historically unappreciated by both agricultural scientists and conservation scientists- is now becoming more apparent to policy makers (see, as examples, https://unfccc.int/meetings/copenhagen…2009/meeting/6295.php; www.croptrust.org/; Hoffman et al., 2014). Consequently, it has become necessary to develop strategies for sampling natural populations in a way such as to preserve their genetic integrity in accessions of germplasm banks, for both germplasm enhancement of crop plants and conservation of biodiversity for other human uses (e.g. economic, spiritual, cultural, aesthetic).

Germplasm banks

In a historical perspective, most plant germplasm banks were created in the 20st century for conserving biological samples of the natural diversity. By the mid of that century, and due to the narrow genetic base of the most important world crop which, as previously said, slowed the genetic progress in breeding, CWR became an important source of desirable genes for breeding and other applied purposes. Thus, in addition to the original objective, germplasm banks became active in the provision of reproductive propagules (mainly as botanical seeds) to researchers.

Sampling and ex situ conservation/regeneration protocols

Although the conservation focus was, then, changed from the "biological" to the "genetic" resource (that is, from conserving plants or their propagules to conserving genes), many accessions are the result of the application of protocols (if any, particularly for the oldest ones) that were developed without taking into account the genetic structure of the sampled populations. In various current protocols aimed at preserving the "genetic integrity" of natural populations, the mode of plant reproduction (either asexual or sexual, by allogamy or autogamy) is mainly considered (e.g. Marshall and Brown, 1975), although other factors such as propagule dispersion strategies, heterogeneity of macro and microenvironments, phenotypic plasticity, among others, should also be taken into consideration (Jain, 1975). Morever, accessions are usually incorporated into germplasm banks with specific status, assigned on the basis of morphological phenotypes in comparison to holotypes using the Taxonomic Species Concept (TSC). The TSC was developed in the 18st century, well before the publication of Darwin´s Theory of Evolution (1859), Mendel´s laws of inheritance (1865) and the dilucidation of the DNA structure (1953) (Grant, 1970; see Camadro et al., 2012). It presupposes that living organisms are at the end of the speciation process; therefore, it does not take into account the natural phenotypic and genetic variability that can be encountered in natural populations, which results from genetic and environmental causes. In contrast to the classification approach followed in plants, the Biological Species Concept (BSC) – which is based on breeding relations and reproductive isolation- is widely accepted in higher animals (see Mayr, 2000, for a discussion on various species concepts). As Camadro (2012) has discussed, hybrids (F_1 and advanced segregating generations) are usually disregarded in current protocols; in fact "out-of-type" plants are generally not sampled in the field or they are discarded during *ex situ* conservation or regeneration (see FAO 2013). So, in an attempt to conserve a given "species"(supposedly "pure", as defined by morphological phenotypes) (a) it is not considered that genes, not genotypes, are transmitted from one generation to the next and (b) the effective population size (Ne= number of parents that contribute gametes to the next generation) is reduced in sampling and regeneration, inadvertently generating genetic erosion due to genetic drift.

Available information on germplasm banks holdings

Passport information of accessions usually includes only collection date and locality (particularly for the oldest), and geographic coordinates (see examples in http://www.grfa.org.uk/search/plants/index.html,http://

www.ars.usda.gov/Main/docs.htm,http://www.ars-grin.gov/npgs/holdings.html). However, and for most accessions, there is no (or there is scarce) information on reproductive behavior of the sampled populations, plant spatial distribution at the sampled sites, number of sampled plants and of reproductive organs sampled/plant, and how accessions were composed. For *ex situ* regeneration, there is no information on *Ne*, number of harvested reproductive organs/plant and of harvested seeds/fruit, and how the regenerated accessions were composed. Thus, in my opinion, it is not possible to ascertain if germplasm bank accessions conserve the allele frequencies of populations at the sampled sites and -assuming good practices in the handling process- if genetic drift has been avoided.

Gap Analysis

In the last years, Gap Analysis is being carried out to gather and analyze data on the distributions of CWR, to develop a list of taxa in critical need of future collection for conservation (see, as example, http://dapa.ciat.cgiar.org/cwr-gap-analysis-presented-at-conference/). The results of this type of analysis can be misleading when the TSC is used in classification and reclassifications of plant groups. In fact, when reclassifications are carried out, two or more different taxonomic species could be considered to be synonymous. As such, fewer areas would be required for conservation of the "species"; furthermore, other prioritized "species", if they are now considered synonym of a species with good conservation status, will not be sampled (Cadima et al., 2014). If breeding relations were taken into consideration, synonymous "species" could actually be assigned to either the same pool or to different gene pools. If they actually belong to different gene pools, genetic erosion would occur if the various gene pools are not sampled. In fact, if only one part of the natural genetic variability is conserved, it cannot be discarded that the rest could be lost for ever, particularly with the acceleration of the global climate change.

CONCLUSION

The formidable contribution of naturalists, biologists and botanists to the description of plant biodiversity and the conservation efforts carried out over the centuries until the present should be greatly acknowledeged. Many succesful crop varieties actually carry desirable genes transferred from wild species into the cultivated gene pool by conventional breeding techniques, and these valuable genetic resources were provided by germplasm banks (see Jansky et al., 2013). Notwithstanding, I consider that the time has come to thoroughly discuss, on objective academic grounds, the current plant species paradigm and *ex situ* conservation and regeneration strategies in the context of population genetic theory, to try to either prevent or minimize genetic erosion and to provide heritable diversity for applied purposes. Understanding natural morphological and molecular diversity of wild populations requires knowledge (and thorough comprehension) of their reproductive biology. Moreover, choice of plant materials and classification approaches have direct consequences on *ex situ* conservation of allelic frequencies of natural populations (Camadro et al., 2012; Camadro, 2012), a legacy that we ought to leave to future generations.

BIBLIOGRAPHY

Cadima X., van Zonneveld M., Scheldeman X. et al. (2014) Endemic wild potato (*Solanum* spp.) biodiversity status in Bolivia: Reasons for conservation concenrns. J. Nature Conserv. 22: 113-131.

Camadro E.L. (2012) Relevance of the genetic structure of natural populations, sampling and classification approaches for conservation and use of wild crop relatives: potatoes as an example. Botany 90: 1065-1072.

Camadro E.L., Erazzú L.E., Maune J.F., Bedogni M.C. (2012) A genetic approach to the species problem in wild potatoes. Plant Biology 14 (2012) 543–554

FAO (2013) Genebank Standards for Plant Genetic Resources for Food and Agriculture Food and Agriculture Organization of the United Nations, Rome

Grant, V. (1981) Plant speciation, 2nd Edn. Columbia. University Press, New York.

Hoffmann, A.; Penner, J.; Vohland, K. et al. (2014) Improved access to integrated biodiversity data for science, practice,

and policy. The European Biodiversity Observation Network (EU BON). Nature Conservation 6: 49–65.

Jain S.K. (1975) Population structure and the effects of breeding system. In: Crop genetic resources for today and tomorrow, cap. 4. Frankel O.H. and Hawkes J.G. (eds.). Cambridge University Press: Cambridge, London, New York, Melbourne

Jansky S.H., Dempewolf H., Camadro E.L. et al. (2013) A Case for Crop Wild Relative Preservation and Utilization in Potato (*Solanum tuberosum* L.). Crop Science 53: 746-754.

Jarvis, A., Lane A., Hijmans R.J. (2008) The effect of climate change on crop wild relatives. Agriculture, Ecosystems and Environment 126: 13–23.

Marshall D.R., Brown H.D. (1975) Optimum sampling strategies in genetic conservation. In: Crop genetic resources for today and tomorrow, cap. 4. Frankel O.H. and Hawkes J.G. (eds.). Cambridge University Press: Cambridge, London, New York, Melbourne

Maxted, N., Kell S., Ford-Lloyd B., Dulloo E., Toledo Á. (2012) Toward the systematic conservation of global crop wild relative diversity. Crop Science 52: 774–785.

Mayr E. (2006) ¿Por qué es única la biología? Consideraciones sobre la autonomía de una disciplina científica, Katz, Buenos Aires.

Miller, J.K., Herman E.M., Jahn M., Bradford K.J. (2010) Strategic research, education and policy goals for seed science and crop improvement. Plant Science 179: 645–652