



# Plant Genebanks: Present Situation and Proposals for Their Improvement. The Case of the Spanish Network

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Genebanks were created by the middle of the twentieth century to preserve cultivated biodiversity when landraces began to be substituted by modern varieties. This move was generally accepted as a necessary step to safeguard the future. After about 75 years of collecting and maintaining genetic resources, the increasing ability of biotechnology to create new variability brings the roles of genebanks in the present and near future into question. As a continuation of several workshops that started in 2014, staff of some representative genebanks have met to discuss how the Spanish Plant Genetic Resources Network can be improved, identifying the following major shortcomings: lack of efficient coordination in the distribution of species among genebanks; too many genebanks; existence of detected and undetected duplicates; insufficient rate of regeneration; insufficient phenotyping, genotyping, and epiphenotyping; unsatisfactory rate of use by end users; and, insufficient funding. As a considerable increase in public funding is unlikely, we propose some strategies to increase the efficiency of the system. The most urgent tasks are to strengthen the rationalization of the network by establishing a clear hierarchy and functions, to improve the information in the base collection by deep characterization including not only phenotypes but also uses and utilities, to progressively replace the active collections with focused core collections constructed to meet users' needs, to optimize regeneration protocols, to limit new collecting expeditions of Spanish crop wild relatives to those growing in threatened habitats, and to develop user-friendly platforms to access germplasm documentation, including a unified system of descriptors and classification categories. Current advances in biotechnology, and especially those in gene editing will have without doubt an impact on the role of genebanks. However, the high number of genes and gene combinations created by evolution they hold cannot be

produced by these techniques at present. So, these reservoirs of variability will continue to be indispensable for the near-medium future while the function of all the genes is unveiled. In turn, biotechnologies and gene editing will allow us to take advantage of the information held in genebanks in a more efficient and fast way, contributing to a better rationalization and functioning.

**Keywords:** genetic variability, phenotypic variation, *ex situ* conservation, landraces, crop wild relatives, seedbanks, gene conservation, plant genetic resources

## INTRODUCTION

The *ex situ* conservation of plant genetic resources started by the mid-twentieth century as a reaction to the rapid loss of agricultural biodiversity, mainly due to the replacement of landraces by improved varieties (Gepts, 2006; Van de Wouw et al., 2009; Khoury et al., 2014). This replacement was made possible by enormous energy inputs into agrarian systems in the form of machinery, fertilizers, pesticides, herbicides, irrigation, protected cultivation, etc., which make environmental conditions more uniform, thereby allowing a limited number of improved varieties to be grown everywhere, replacing landraces adapted to microenvironments, local cultivation methods, and cultural elements of use. It has been estimated that 70% of currently cultivated crops are of foreign origin, while the traditional crops indigenous to each area are disappearing (Khoury et al., 2016).

When genebanks were created, they were intended to preserve genetic material (fundamentally gene combinations) with the aim that they might be used in the future (Fowler and Hodgkin, 2004), either directly or as material in breeding programs (Tanksley and McCouch, 1997) to face potential changes in environmental conditions or societal needs, even before discussions about climate change started. After decades of experience with genebanks, the advantages and disadvantages of this strategy with respect to conservation *in situ* have been discussed extensively [(Gómez et al., 2005; Gepts, 2006; Veteläinen, 2009; Negri and Tiranti, 2010)]. To date, it seems that *ex situ* conservation has had more success than *in situ* conservation, probably because of its lower cost (about 100 times less than *in situ* conservation; De-Zhu and Pritchard, 2009) and greater ease for users to access the material. Since the first plant genebanks were established, biological technologies have evolved immensely, so breeders now have more tools available to generate variability and also new data sources. Thus, it is time to evaluate to what extent genebanks' main functions (collection, documentation, regeneration, distribution, and conservation) should be reconsidered.

The Iberian Peninsula's diverse climates (Mediterranean, Atlantic, Continental, and Alpine) and soil types, together with its location and history, have made it an important center of agricultural diversity. Its proximity to the area of domestication of the Fertile Crescent, and colonization by the Muslims facilitated the arrival of plants from Asian and African domestication zones (Hancock, 2004). Later, its participation in the colonization of America also made it an expansion zone for many American cultivated plants and a secondary center of diversity for some of them, such as the tomato *Solanum*

*lycopersicum* L.; (Cebolla-Cornejo et al., 2013) or common bean (*Phaseolus vulgaris* L.; Santalla et al., 2002). These circumstances have generated a wealth of landraces, which are largely preserved in genebanks.

This paper aims to review the system of Spanish genebanks to: (i) examine their activities, (ii) review the present and expected demands of society on genebanks, and (iii) evaluate to what extent genebanks' activities and their organization should be modified to optimize their present work and to adapt them to meet new needs. An analysis of the situation in our country should help firstly in rearranging national system but can be also considered within an international perspective.

## GENEBANKS IN SPAIN

The first Spanish genebanks, derived from breeders' seed banks, were linked to research institutions, mainly the regional centers of the National Institute for Agricultural and Food Research and Technology (INIA) devoted to regional crops. Rather than unique to our country, this situation is the general rule around the world, as many of the most important genebanks started in this way (Engels and Thormann, 2007). In the mid-1980s, political decisions resulted in the partial transfer of the INIA's tasks to regional governments, although the Program for the Conservation and Utilization of Plant Genetic Resources National Network (PCURF), established by Ministry of Agriculture in 1993, maintained a certain level of coordination. Later, new initiatives appeared, including regional banks and new public and private banks set up by breeders and conservation organizations.

The Spanish Plant Genetic Resources National Center (CRF), dependent on the INIA, is entrusted by law with the mission of preserving backup copies of the seeds from all Spanish institutions and managing the Collection Network (that includes also vegetative propagated material) and the National Inventory of Plant Genetic Resources (Figure 1 and Table 1; the readers are referred to Table 1 for detailed information about the acronyms cited in this section), in addition to its role as active collection of grain legumes, winter cereal and industrial crops. Then, other genebanks maintain active collections of national scope for specific crops or groups of crops, such as the COMAV and the CITA, which hold horticultural crops, or the CICYTEX, which hold forages/grassland and lupine crops (Figure 1 and Table 1). Additionally, there are banks that are clearly devoted to specific regions (e.g., IMIDRA in Madrid, SERIDA in Asturias, IMIDA in Murcia, CCBAT in the Canary Islands), others that maintain

collections oriented toward breeding (MBG-CSIC and IHSM-UMA-CSIC) (Figure 1 and Table 1). Besides, in close connection with the network, there are still others that combine regional collections with breeding activities (Fundació Miquel Agustí in Catalonia, FMA). Finally, there are the community genebanks that belong to conservation organizations, which have a local scope and frequently do not follow the standard procedures for collecting, documenting, and conserving materials. On the other hand, seed companies have their own banks with materials they have obtained for or from different breeding programs, although it is difficult to know exactly what materials they have, since they are not freely available.

The reflections we present here are based on the data from a group of five genebanks dedicated to seed conservation: CRF, CITA, COMAV, MBG-CSIC, and FMA. The materials in these banks represent about 85% of the 62,470 accessions stored in the seed genebanks included in the National Network (without considering the base collection of the CRF). Here we describe their main characteristics.

The CRF genebank (<http://wwwx.inia.es/coleccionescrf/>) (Table 2), the most important bank in Spain, dates back to 1977 (Bueno and Alaman, 1982). It currently coordinates the country's plant genetic resources, conserves the base collection containing a backup copy of more than 43,000 seed accessions, and is the national documentation center. The CRF also maintains the active collection of legumes, cereals, and species for industrial use, which contains more than 22,000 accessions from 233 species. With a long experience in collecting missions (>35), it is currently the only institution that conducts collecting activities, especially targeting wild relatives of cultivated plants (CWR); it has the capacity to regenerate over 700 accessions per year in collaboration with other institutions. On average, between 2013 and 2017 it delivered 1,362 samples per year in response to 61 requests per year, most of which came from researchers and farmers.

CITA (<https://sites.cita-aragon.es/BGHZ/>) and COMAV (Table 2) are the two main active genebanks for horticultural crops. CITA began operations in 1981 and currently maintains a collection of more than 17,000 accessions of 245 species of horticultural crops, underutilized species, and CWR. With help from other institutions it regenerates about 190 accessions per year. Between 2013 and 2017, it distributed an average of 600 accessions per year, mostly to farmers and researchers. It collaborates with numerous associations of farmers, transferring materials and providing advice to the sector.

The genebank of the COMAV (<https://www.comav.upv.es/index.php/databasesgermplasm/bancoger>) (Table 2) began its collecting missions in 1981 and it currently has a collection of about 13,000 accessions of almost 200 different species. With the collaboration of IMIDA it regenerates some 200 accessions per year. Between 2013 and 2017, it distributed an average of 2,700 accessions per year, mainly to researchers, seed companies, and farmers. The COMAV participates in various European projects and maintains collaborations with numerous farmers and seed companies.

The *Brassica* genebank of MBG-CSIC (<http://www.mbg.csic.es/es/>) (Table 2) started its activities in 1985. In the present paper,

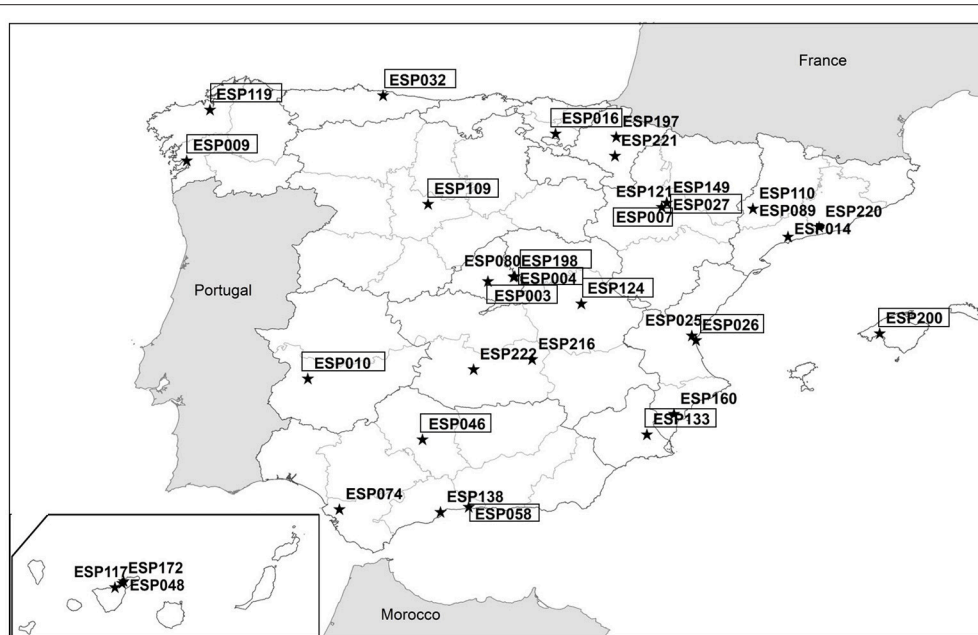
we will focus only on the collection of Galician *Brassica* crops belonging to the species *Brassica oleracea* L., *B. rapa* L. and *B. napus* L., which houses 644 accessions. *B. oleracea* includes kales (*B. oleracea* var. *acephala*), cabbages (*B. oleracea* var. *capitata*), and Tronchuda cabbage (*B. oleracea* var. *costata*). *B. rapa* groups the turnips, turnip greens, and turnip tops; and *B. napus* appears only in the form known as “nabicol” or leaf rape. The difficulty of the controlled multiplication of these crops (allogamous with strong inbreeding effect) and their long growth cycles, limit the institution's regeneration capacity to about 40–50 accessions per year. It is an important collection of *Brassica* germplasm, adapted to the Atlantic conditions with high intra- and inter-variety variability (Cartea et al., 2003; Soengas et al., 2008). More than half of the requests come from farmers and associations, and the rest come from national and foreign research centers.

The newest genebank considered belongs to the FMA (<http://fundaciomiquelagusti.com/>) (Table 2). It started its activities in the late 1990s with efforts to recover the common bean (Casañas et al., 1997). The bank keeps 1,774 accessions of 25 different species. Its most important collections are of tomato (884 accessions) and Ganxet common bean (627 accessions). The collection consists almost exclusively of landraces collected in Catalonia (Casals et al., 2017). For most of the materials, data are available on agronomic and morphological traits. For some materials, sensory and/or chemical data related to organoleptic traits are also available. Initially, the collection was entirely dedicated to varietal recovery programs carried out in collaboration with farmers and cooperatives; however, the current collection is a representation of the genetic variability of the area, so it tends to function as a regional horticultural genebank.

The functioning of genebanks has come under discussion, with publications by Fu (2017) and Byrne et al. (2018), among others. In February 2018, representatives of the aforementioned banks met to discuss their main concerns and, by extension, those of the Network of Spanish genebanks. The aim was to examine to what extent the banks were fulfilling the challenges of meeting the changing needs of their scientific, technical, and social environments and to evaluate possible changes in their activities to assume new roles. We will focus only on genebanks holding seeds, as the problems associated with their management can be different from those of genebanks conserving vegetative propagated crops.

## SYSTEM WEAKNESSES, EVALUATION OF ALTERNATIVES AND RECOMMENDATIONS

The activities of the Spanish Plant Genetic Resources Network have facilitated the creation of large collections while avoiding the loss of many potential interesting accessions. However, several weaknesses of the system were detected by Guasch et al. (2016) in a workshops series structured by crops, conducted in 2014 and 2015, to perform a Strengths, Weakness, Opportunities and Threats analysis. In our survey of the Network we have confirmed several interconnected weak points, that need substantial improvement (Table 2), coinciding with the scenario



**FIGURE 1** | Location of the genebanks included in the Conservation and Utilization of Plant Genetic Resources Spanish Network. Institutions with framed codes store exclusively seeds or seeds and vegetative propagated crops.

drawn by FAO in other countries (FAO, 2010). In the following sub-sections we describe the weaknesses and interconnections found (Table 3), and suggest actions for improving the key points.

## Rationalization of the System and Coordination Among Genebanks Weaknesses

As explained above, all the banks were started up by breeders in certain crops and extended to include new species based on the findings in collecting expeditions and on the exchange of accessions with other genebanks. So, many of the same species are kept in different banks. This is mainly because they were set up in the late 1970s and early 1980s, and it was not until 1993 when the former Ministry of Agriculture, Fisheries and Food created the first Conservation and Utilization of Plant Genetic Resources Program and the CRF was assigned the responsibility of documentation. During that period, as mentioned, some of the INIA activities were inefficiently transferred to regional governments, making coordination more difficult. The result was a clear need for profound rationalization and coordination among genebanks.

### Suggested Actions

The organization of genebanks differs greatly between countries. Sometimes these disparities derive from the differences in biological diversity among countries, but in any case the goal should be to enable the most efficient use of germplasm (Halewood et al., 2018). In Spain, there are some genebanks with similar or repeated activities; the Program for the Conservation and Sustainable Use of Plant Genetic Resources National

Network (<http://wwwx.inia.es/inventarionacional/Instituciones.asp>) comprises 35 institutions, 19 of which maintain seeds. If we were trying to optimize the network, from the scratch, it would be necessary to conceive the needed structure banks, defining their characteristics, functions, and number. Taking this into account we have to establish the adaptation measures to rearrange the network to fit into the theoretical structure.

The reference bank that houses the backup copies of the Spanish seed collections would still be the CRF. It would be advisable to have active banks specialized in large groups of related crops (cereals, legumes, vegetables, fruit trees, etc.). However, for horticultural crops currently both CITA and COMAV hold a large number of accessions from different sources. Thus, the National Programme should determine the actions to make them work with common specific standards and let them harmonise the activities of the other banks holding also horticultural crops. The main advantage of nested/grouped genebanks, is the ease with which users can access unified data from characterizations trials done under similar conditions. At a third level, there would be other banks, smaller, more focused on the crops grown in specific agro-climatic zones. Familiar with the materials grown in their areas, these banks would have more direct contact with farmers and would know their needs through interacting with them. Thus, farmers working with these genebanks can be trained in the techniques of conservative selection or can provide populations not yet collected. Current banks operating along these lines are the FMA, IMIDA, IMIDRA, MBG-CSIC, etc., which are already playing an important role in the recovery and enhancement of landraces in their respective areas in cooperation with farmers. The following level would be

Q4

**TABLE 1** | Institutes in the Spanish Genebanks Network, full name, acronym, institute code, and kind of crops preserved in the banks.

Instcode	Acronym	Seeds (S), vegetative propagated crops (V)	Name
ESP003	UPM-BG	S	Genebank “César Gómez-Campo”
ESP004	INIA-CRF	S	National Center for Plant Genetic Resources
ESP007	Aula Dei	S, V	Experimental Station “Aula Dei”
ESP009	CSIC-MBG	S, V	Spanish Council for Scientific Research, at the Misión Biológica de Galicia
ESP010	CICYTEX	S,V	Agricultural Research Institute “La Orden-Valdesequera”
ESP014	IRTA-MB	V	Institute of Agrifood Research and Technology, Center “Mas Bové”
ESP016	NEIKER-Tecnalia	S,V	The Basque Institute for Agricultural Research and Development
ESP025	IVIA	V	Valencian Institute of Agricultural Research
ESP026	COMAV	S	Genebank of Institute for the Conservation and Improvement of Valencian Agrodiversity
ESP027	CITA-HOR	S	Vegetable Genebank of Aragón
ESP032	SERIDA	S,V	Regional Service for Agri-food Research and Development
ESP046	IFAPA-COR	S,V	Andalusian Institute of Agricultural and Fisheries Research and Training. Center “Alamada del Obispo”
ESP048	ICIA	V	Canarian Institute of Agricultural Research
ESP058	CSIC-La Mayora	S,V	Superior Council of Scientific Research at the Experimental Station “La Mayora”
ESP074	IFAPA-CAD	V	Andalusian Institute of Agricultural and Fisheries Research and Training. Center “Rancho de la Merced”
ESP080	IMIDRA-Vid	V	Institute of Research and Rural Development from Madrid
ESP089	UdL	V	School of Agricultural Engineering. University of Lleida
ESP109	ITACYL	S	Research Center of Zamadueñas
ESP110	CITA-FRU	V	Fruitculture Department of Aragón
ESP117	ICIA-La Orotava	S	La Orotava Acclimatisation Gardens
ESP119	CIAM	S,V	Agricultural Research Center of Mabegondo
ESP121	GOB ARAGON	V	Rural Development and Sustainability Department of Aragón
ESP124	IRIAF-Albaladejito	S,V	Agricultural Research Center of Albaladejito
ESP133	IMIDA	S,V	Murcia Institute of Agri-Food Research and Development
ESP138	IFAPA-MAL	V	Andalusian Institute of Agricultural and Fisheries Research and Training. Center “Churriana”
ESP149	CITA-FOR	V	Forest Resources of Aragón
ESP160	UMH	V	Polytechnic High School. University Miguel Hernandez
ESP172	CCBAT	S,V	Centre for the Conservation of Agricultural Biodiversity in Tenerife
ESP197	UPN	V	School of Agricultural Engineering. Public University of Navarra
ESP198	IMIDRA-Varietades locales	S	Genebank of landraces of Madrid
ESP200	IRFAP	S,V	Institute of Agricultural and Fisheries Research and Training of Balearic Islands
ESP216	IRIAF-Vid	V	Institute of Vine and wine of Castilla La Mancha
ESP220	INCAVI	V	Catalonian Institute of Vineyard and Vine
ESP221	EVENA	V	Viticulture and Enology Station of Navarra
ESP222	IRIAF-Chaparrillo	V	Agricultural Center of “El Chaparrillo”

made up of the banks managed by conservation associations. These banks do not perform breeding work; rather, they are dedicated to the collection, conservation, and dissemination of genetic heritage (Jarvis et al., 2011). Standardizing the work done at these banks and linking them to the general network should be a priority. Finally, as public breeders’ banks gave rise to the collections, they should be linked to or associated with the network, although maintained with funds obtained in competitive research projects or special calls. We propose the maximum coordination between the different levels to obtain maximum efficiency by avoiding unnecessarily repeated functions.

Part of this work is being done at present as much effort is being put into nesting and organizing genebanks in Spain. To

introduce hierarchy into their functioning they are being grouped according to the type of crops they hold (cereals, leguminous, and industrial crops; vegetables; forage and meadow species; and aromatic, medicinal, and wild plants). In each of these broad categories, one genebank coordinates all the genebanks holding these species.

### Conservation: What and How Much Germplasm Do We Need to Conserve? Weaknesses

There are two main problems related with accession conservation: incomplete seed viability information and material regeneration. Not all the genebanks have the capacity

TABLE 2 | Relevant information on the genebanks surveyed.

Genebank	Foundation year	Place	Crops	Number of accessions	Conservation conditions	Number of accessions regenerated per year	Online request form	Available information online	Number of accessions delivered per year (mean of 5 years)
CRF	1977	Alcalá de Henares	All crops (seeds) <sup>a</sup> Leguminous and cereals <sup>b</sup>	42,586 <sup>a</sup> 22,041 <sup>b</sup>	-18°C <sup>a</sup> -4°C <sup>b</sup>	657 with other institutions	Yes	Passport and partial characterization	1,375
BGHZ	1981	Zaragoza	Cultivated and neglected vegetables crops	17,461	-18°C	190 with other institutions	Yes	Passport	600
COMAV	1981	Valencia	Cultivated vegetable crops and wild relatives	13,556	4°C	200 with other institutions	No	Passport and partial characterization	2,700
MBG-CSIC	1980	Pontevedra	Vegetable Galician Brassica crops	644	4°C	40-50	No	No	70
FMA	1992	Barcelona	Catalonian vegetable crops	1,774	4°C	100	No	No	50

<sup>a</sup>Base collection<sup>b</sup>Active collection

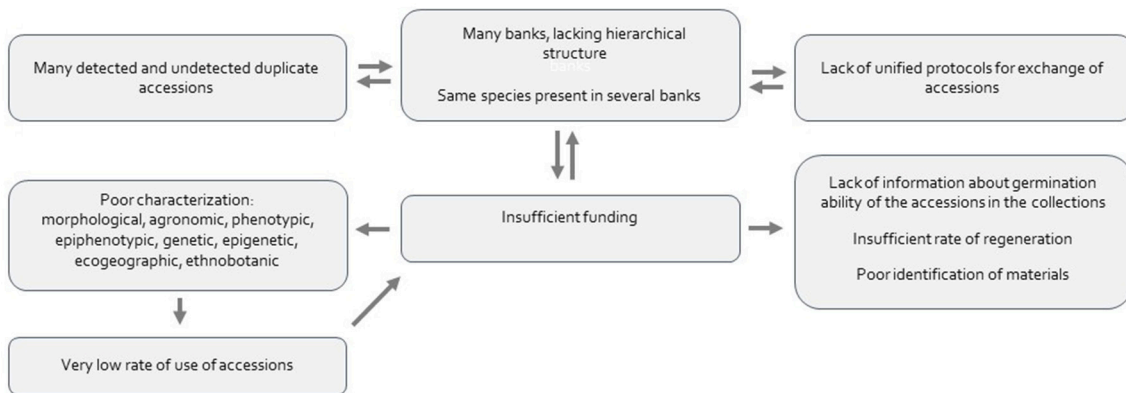
to perform regular seed monitoring. For some of the samples of CRF's base collection, initial data on germinability were not available, but the ongoing FAO recommended intermediate tests is allowing to monitor their viability. In some other cases, there are no seed viability data due to the scarce number of seeds conserved. The constant underfunding has led to a bottleneck in regeneration, with the consequent loss of some accessions. These problems are not unique to Spanish collections as they affect many genebanks and all species (FAO, 2010). Thus, it is essential to raise questions such as: Are we able to retain all materials currently stored? or What type of materials must we prioritize: cultivated or wild species, national, or foreign samples?

### Suggested Actions

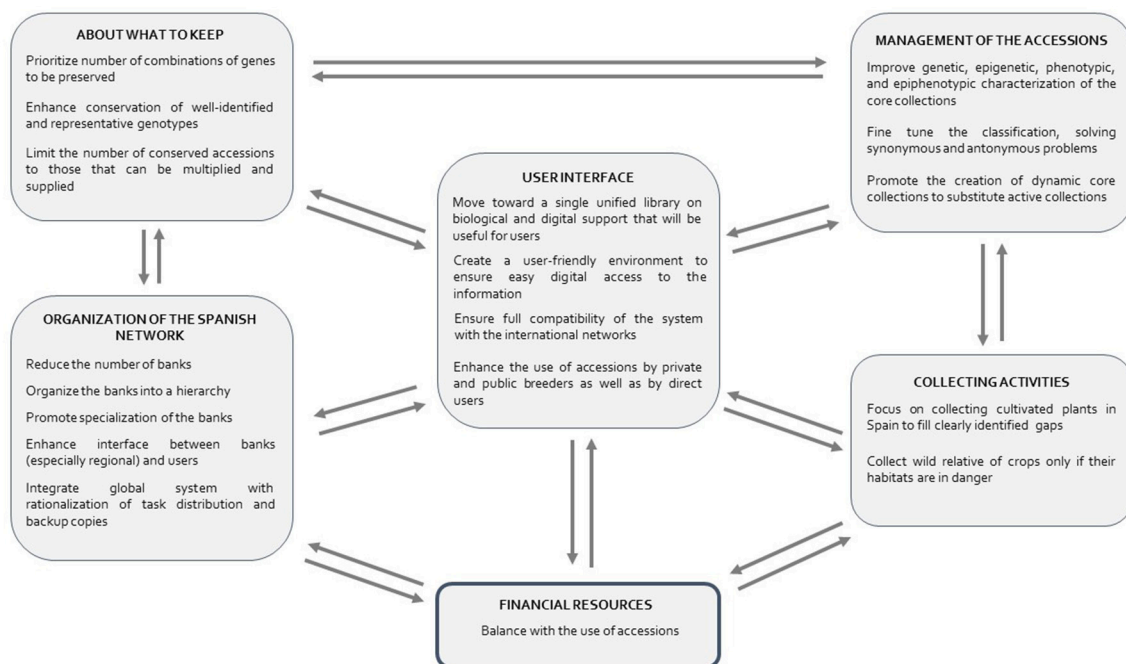
We propose to introduce protocols and scoring systems to prioritize *ex situ* conservation of the species cultivated in Spain and their wild relatives, especially if they are endemic or found in threatened habitats. Interest in wild species is growing; multiple examples of their use in breeding (Hajjar and Hodgkin, 2007; McCouch et al., 2013) underline the need to create national *in situ* inventories to encourage conservation of CWR (Maxted et al., 2007). In Spain, an in-depth study on CWR has resulted in a list of species chosen according to their ability to cross with cultivated species, endemism, and risk of extinction (Rubio et al., 2018). This study can serve as a guide to examine the current state of conservation of these species, and its results should be taken into account for future plans. In addition to landraces and wild species, materials coming from breeding programs (pre-breeding populations, collections of mutant inbreds, improved varieties, obsolete registered varieties, etc.) must also be preserved in gene banks, since they are of special interest for researchers and breeders.

Another uncontested question is if we have to conserve genes or gene combinations. Since landraces evolve to adapt to changing environments, it seems that a rigorous conservation policy should store all genes and combinations of genes that are created over time. This would require adding accessions continually. The other extreme, favored by biotechnology, would be to preserve cloned genes or even only nucleotide sequences that can be reproduced by genetic editing. Since preserving everything is unfeasible, a compromise solution would be to conserve combinations of adaptive genes or those that translate in high yields along with Mendelian genes of interest. The progress of biotechnology will surely guide the balance between these two strategies (Halewood et al., 2018) and will reduce the number of genotypes to be conserved.

How many accessions can we keep in a reasonable way? The conservation of germplasm is inevitably linked to the system's capacity for regenerating the conserved material, and most Spanish genebanks are overwhelmed. To ensure a good representation of the types of germplasm listed above, we must refine our definition of what is really valuable, and we must redesign our organization to be more efficient. Since the real bottleneck lies in regeneration, the distribution of accessions among the different types of genebanks should be optimized. The base collection, with good facilities to conserve



**FIGURE 2 |** Main shortcomings of the Spanish Plant Genetic Resources Network and relations between them.



**FIGURE 3 |** Key points to be improved in the Spanish Plant Genetic Resources Network. As all aspects are related, the corrective actions should be chosen to improve the system with minimum financial increase, favoring the accessions used by breeders and producers. Increase of business and social return of germplasm preserved would help financial returns to the system.

accessions at  $-18^{\circ}\text{C}$  for long periods of time, should hold the country's complete seed germplasm collection, which must be conserved under good conditions and well-documented. On the other hand, all the active collections (e.g., COMAV and CITA) should focus on part of the base collection. This part would comprise accessions of specific interest and should represent the total diversity of the base collection. These active collections should be dynamic, changing their priorities according to the interest of the different end users, who should suggest the traits for which the variability represented, should

be maximized. As new breeding objectives arise, prioritization would change and strategic materials will be regenerated and made available to users. In this way, active collections can be considered a mixture of core collections, each of which has been constructed to meet specific objectives (Byrne et al., 2018; Wambugu et al., 2018). In the end, this is a question of introducing economic criteria in the composition of active collections and rationalizing base collections, which should be broad, without redundancies, and especially well-documented.

## 799 Identification of the Accessions: 800 Delimitation of the Concept of Variety and 801 Classification of Accessions 802 Weaknesses

803 Efficient organization of a genebank optimizing the search for  
804 information requires clear categories for classifying the materials.  
805 The concept of accession is not problematic as it refers to a  
806 sample taken in a certain area and linked to its respective passport  
807 data or to pre-breeding or breeding materials that are kept  
808 independent and identified. Following the definition given by  
809 Zeven (1998), an autochthonous landrace is a variety with a high  
810 capacity to tolerate biotic and abiotic stress, resulting in high yield  
811 stability and intermediate yields under a low-input agricultural  
812 system. Whereas, there is a consensus to include all materials  
813 that farmers have cultivated for a long time in the landrace  
814 category, it is often more complicated to ascribe an accession to  
815 a particular landrace. The names and definitions of landraces are  
816 lax: collectors have generally accepted the information provided  
817 by farmers (cultivation time in the area, name, etc.) without  
818 checking its reliability, and this has introduced a certain level  
819 of uncertainty as synonymous and homonymous occur (Lema  
820 et al., 2010). So, it is complex to assign accessions to a variety or a  
821 landrace.  
822

## 823 Suggested Actions

824 Fortunately, protocols today are much more rigorous  
825 (ecogeographic data are included in databases at collection  
826 time), but the material stored in genebanks comes from both old  
827 and recent sources. Additionally, the primary characterization  
828 carried out during multiplication considers only botanical  
829 descriptors related to the morphology of the crop and the  
830 reproductive cycle. Nevertheless, landraces' main value does not  
831 lie solely in primary characterization data; rather it is linked to  
832 their role in the ecosystem and to their adaptation to specific  
833 territories, cultural practices, and uses. Data about these aspects  
834 are much more informative and should be used together with  
835 the descriptors of Bioversity International (formerly IBPGR  
836 and IPGRI) and/or the International Union for the Protection  
837 of New Varieties of Plants (UPOV) to assign an accession to  
838 a variety or varietal type. Molecular characterization can also  
839 help to determine the degree to which different accessions of,  
840 presumably, the same variety are related, as well as to identify  
841 alleles of agronomic interest (Prada, 2009).  
842

843 Accessions must be classified based on exhaustive  
844 characterizations by specialists through field trials designed  
845 to enable statistical analyses. This is especially important when  
846 the names and characteristics of landraces are linked to legal  
847 aspects such as conservation varieties or varieties linked to  
848 geographical quality labels. The public bodies should look  
849 to specialists to define the limits of the varieties; however,  
850 we recognize the difficulties in this approach, so we suggest  
851 replacing the term variety with varietal type to favor grouping  
852 together materials with some key traits in common but variability  
853 for many others, as proposed by (Camacho Villa et al., 2005)  
854 regarding the definition of crop landrace. In the next future  
855 concepts such as "landrace" or "varietal type" need to be

reconsidered to ensure that accessions are correctly classified  
(Casañas et al., 2017). 856 857 858

## 859 Characterization: Thorough 860 Characterization as a Strategy to 861 Encourage Germplasm Use 862 Weaknesses

863 No characterization data are available for many accessions,  
864 greatly hindering the use of the conserved samples. A rough  
865 estimation made in 2010 revealed that less than a 5% of  
866 the accessions stored in banks have been characterized for  
867 quality traits (Romero del Castillo et al., 2010). Also lacking  
868 is information about the "epiphenotype" (data about the  
869 relationships between the plant and the environment, including  
870 ethnobotanical aspects), which in many cases was not recorded at  
871 the time of collection.  
872

## 873 Suggested Actions

874 Exhaustive phenotyping of the material stored in the genebanks  
875 and of new candidates is key, and the relevant data must  
876 be publicly accessible in websites as well as through publicly  
877 available Application Programming Interfaces (API) that allow  
878 for automatic data requests. These conditions will allow  
879 researchers to explore easily the phenotypic variability stored  
880 in genebanks (Zamir, 2013). The more information available  
881 about the materials in a germplasm collection, the more useful  
882 the conserved material will be for farmers and/or researchers  
883 (McFerson et al., 1996; Engels et al., 2001).  
884

885 Each accession should be characterized by its morphological  
886 traits, which reflect the expression/variation of botanical aspects  
887 and are useful for taxonomical classification. However, as  
888 mentioned before, it is just as important to provide an accurate  
889 description of its agronomic characteristics, its relationship  
890 with the environment, other quality-related properties, and  
891 its use. This approach would also allow the makeup of the  
892 collection to be adapted to users' needs and preferences. At  
893 first, farmers and breeders were interested in increasing yields;  
894 then we realized that resistance and tolerance to biotic and  
895 abiotic stresses were important components of production  
896 and adaptation, so genebanks were screened for these aspects  
897 (Tanksley and McCouch, 1997). Later, there was also an interest  
898 in nutritional quality and the balance of components that would  
899 enable the population to be fed with a few species. Now,  
900 consumers have incorporated new elements in their decision  
901 making, beginning with the product's appearance and continuing  
902 on with various additional sensory traits. But multiple other  
903 factors are also important (e.g., industrial, cultural, landscape-  
904 related, and medicinal factors, as well as the equilibrium of  
905 the ecosystems, territorial distribution of the population, etc.).  
906 The more information we have about the materials preserved  
907 in the base collections, the easier it will be to change the  
908 active collections to meet users' demands (core collections in  
909 accordance with users' demands, as described above).  
910

911 Phenotypic and "epiphenotypic" characterization must be  
912 complemented with genotypic characterization, especially now  
913 that genotyping is already less expensive than good phenotyping.



913 Genotyping allows us to establish the structure of the genetic  
914 variation and, in some cases, the geographical migration of  
915 an accession (Reif et al., 2005) or to scan a collection to find  
916 genes of agronomic interest (Prada, 2009; McCouch et al., 2013;  
917 Wambugu et al., 2018), providing elements that can help organize  
918 the collections.

919 To date, ethnobotanical studies have been largely independent  
920 from agronomic studies. Moreover, we are only beginning  
921 to understand the role of crops in ecosystems because it  
922 has been difficult to develop a comprehensive vision of the  
923 biosphere. Therefore, genebanks' databases are not usually cross-  
924 referenced with information from cultural studies (Meyer, 2015)  
925 and are rarely linked with data from studies about ecological,  
926 landscape-related, or economic aspects. This is unfortunate  
927 because ethnobotanical data can reveal transcendent information  
928 about the properties of a variety (Clawson, 1985; Ahmed  
929 et al., 2014) without which it would be impossible to fully  
930 understand its agricultural and ecological value. Since landraces'  
931 future value is related to their cultural aspects and their  
932 integration at higher levels, these data should be merged into  
933 a single database. In this direction now a project is underway  
934 to create a tool that would fill in the gaps between the  
935 botanical and ethnobotanical approaches: The Spanish Inventory  
936 of Traditional Knowledge related to Agricultural Biodiversity  
937 (IECTBA) (Tardío et al., 2018). Furthermore, future collecting  
938 missions should include exhaustive questionnaires about the  
939 history and culture associated with each of the accessions, as  
940 well as its role in the functioning of higher-level ecosystems  
941 (Bioversity and The Christensen Fund, 2009).

## 943 Online Information Accessible Through 944 Search Engines: Seed Banks as Libraries 945 Storing Information in Biological and 946 Digital Formats 947 Weaknesses

949 Without adequate public databases, information about materials  
950 held in genebanks cannot be accessed. In Spain the most  
951 complete database is the National Inventory that holds data of a  
952 big proportion of the accessions conserved in Spanish genebanks.  
953 However, most part of this information is about passport data.  
954 With regard to characterization data, in most cases the existing  
955 information is not available to community of users in easily  
956 accessible formats, as there are no databases that exhaustively  
957 collect characterization or ecogeographic data. Furthermore, the  
958 lack of standardization of descriptors between datasets greatly  
959 complicates the creation of shared databases.

## 961 Suggested Actions

962 Considerable efforts have already been devoted at an  
963 international level to merging documentation from different  
964 sources. The most complete database worldwide, Genesys  
965 (<https://www.genesys-pgr.org/en/welcome>) (Arnaud et al.,  
966 2010), contains passport data for more than 3.5 million  
967 accessions from 458 institutions. This first step enables  
968 wide-reaching searches for information on plant genetic  
969 resources.

970 In Spain, the CRF manages the documentation system for  
971 Spanish germplasm published in the National Inventory. At  
972 present, the INIA is funding a project to create an informatics  
973 platform to optimize documentation with the aim of facilitating  
974 the management of information within the CRF and adding  
975 characterization data and images to supplement the passport  
976 data. This informatics platform will also allow duplicated  
977 accessions to be easily identified and the information about  
978 the germplasm preserved in all Spanish institutions to be easily  
979 accessed.

980 This system would benefit from including all data from  
981 publicly funded research and development projects on food  
982 and agriculture to expand the characterization of germplasm  
983 currently available and thus favor its use. As the researchers who  
984 receive the material from the genebanks are those who collect  
985 these data, arranging for their findings to remain confidential  
986 for a short period would allow them to take advantage of this  
987 information before transferring it to the public domain.

988 In addition, in some cases genebanks' participation in research  
989 projects has allowed them to get access to the genotype of  
990 some of their accessions. Analyzing these data can benefit the  
991 management of these accessions, for example by helping to  
992 identify duplicates, to structure collections, or to create core  
993 collections. Although it would be feasible to include these data  
994 in the genebanks' databases, the benefits for the genebanks  
995 themselves are unclear because their staffs are generally not  
996 trained in interpreting raw data from genotyping.

997 Beyond eliminating barriers to create a single large database,  
998 it is important to accelerate the addition of data from genotypic,  
999 epigenetic, phenotypic, and epiphenotypic characterization to the  
1000 passport data. Additionally, the use of digital object identifier  
1001 (DOI) system would connect different data sources and increase  
1002 traceability of accession use. Merging all these data is a medium-  
1003 term objective that will require time and efforts, and we should  
1004 also strive to ensure that new accessions have these levels of  
1005 information. The new informatics platforms must facilitate the  
1006 storage and management of these four levels of information.  
1007 Also, these platforms must have a user-friendly interface not  
1008 only for researchers or breeders but also for farmers, farmers'  
1009 associations, etc. Map search engines dealing with ecogeographic  
1010 and epiphenotypic layers should also be developed.

## 1011 Funding of Germplasm Banks 1012 Weaknesses

1013 Genebanks belonging to the National Network are primarily  
1014 funded through competitive research grants from the INIA and  
1015 their own institutions. The first result of the above-mentioned  
1016 RD199/2017 was the approval of its Action Plan for Conservation  
1017 and Sustainable Use of Plant Genetic Resources for Food and  
1018 Agriculture (2018–2022), which will be the starting point for  
1019 new calls based on a newly organized, crop-driven collection  
1020 network, connected with the working groups of the European  
1021 Cooperative Program for Plant Genetic Resources (ECPGR). This  
1022 funding must cover the “permanent activities,” which include  
1023 ensuring the sustainable conservation of plant genetic resources,  
1024 promoting their regeneration and primary characterization, and  
1025 delivering materials to users, based on the accomplishment of  
1026

specific standards. In addition, the institutions in which the banks are located contribute by providing facilities and equipment (conservation chambers, phytotrons, greenhouses, experimental fields, etc.) as well as permanent staff in some cases. This arrangement has resulted in a steady state that allows for the maintenance of the collections, but is insufficient for adequate regeneration and phenotyping and provides no funds whatsoever for genotyping.

### Suggested Actions

We must find alternatives that provide genebanks with additional funding. One such alternative is to charge a fee for each accession delivered. Several genebanks already use this measure, which helps to filter out unjustified requests for germplasm. Its usefulness, however, depends on the bureaucratic requirements for its application and the fees charged. In Europe, the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) decided in July 2016 to introduce a handling fee for distributing its samples. Similarly, the World Vegetable Centre (AVRDC) also introduced different rates depending on the country and requesting entity and the type of material (landrace/breeding material) to contribute to the expenses of maintaining the collection, the fifth largest in the world in the number of accessions preserved. An exhaustive economic study by the AVRDC quantifies the large expenses involved in maintaining germplasm (Schreinemachers et al., 2014). Despite a reluctance to apply fees in some areas and the inconvenience involved, we think there are sufficient arguments for using this approach in our genebanks.

Another alternative is co-financing, as is done with other public services. Alternative financing options could be explored with public and private breeding companies. Expanded characterization data saves work for breeders and could command higher prices. A further option would be for users to pay according to the benefit obtained, which is feasible because the material can be tracked by studying the genomes. Finally, contributions to the conservation of seeds could be sought from the general public through sponsorship, etc. In an analysis of vulnerability of plant genetic resources conserved *ex situ*, Fu (2017) suggests alternatives such as partnership with the private sector. Another indirect way to “socialize” the materials in genebanks is through the creation of public, private, or mixed companies that produce and distribute “heirloom” or “vintage” seeds or seedlings to be used in family gardens. This is already a flourishing business in some countries.

In Spain, there is a lack of correspondence between the conservation of cultivated germplasm, which is mainly managed by public organisms, and plant breeding, which is mainly managed by private companies. Entities responsible for conserving germplasm are chronically underfunded and can barely get by through public subsidies, while breeding generates significant profits. The access under the multilateral system provided by a standard material transfer agreement includes a contribution to the profit-sharing fund, but its functioning is under discussion and the funds are not directed to the genebanks providing the seeds. It is difficult to impose solutions, but we

must seek approaches that allow us to move toward a greater presence of genebanks in the business sector.

## THE USEFULNESS OF GENE BANKS

Genebanks were created to ensure the survival of combinations of genes (or individual genes) that were present when we realized that the biodiversity of crops had stopped increasing and started decreasing (Fu, 2017). Despite globalization, our planet has a variety of habitats and in each habitat, the maximum productive efficiency for each species is achieved with specific combinations of genes. This means that low-input agriculture faces the challenge of finding the most adapted genotypes for each environment. As we tend to decrease the amounts of inputs aimed at equalizing environments (lower irrigation and fertilization, less herbicides and pesticides, etc.), we need genotypes that are better adapted to particular environments. Many of these genotypes or their precursors are undoubtedly preserved in genebanks.

The situation is similar at the global level. Humans’ influence has not only led to changes at the level of particular habitats; rather, it is also bringing about great changes in the global habitat. Warming is changing the climatic and even geographical characteristics of many areas (Olesen and Bindi, 2002). Breeders specialized in obtaining new varieties to be cultivated in large areas of the world must also update the combinations of genes that were so successful during the twentieth century, to adapt to new conditions (Ceccarelli and Grando, 1996; Chapman et al., 2012). What has been said for “micro” adaptations also serves for “macro” adaptations. Again, gene banks hold the resources for addressing this goal (Lema et al., 2010; Wambugu et al., 2018), but these resources are useful only if they are well-documented and easily accessible.

The justification for our investments in genebanks must be based on the use of the materials they contain to meet new demands such as increased productivity, resistance, and adaptation to low input conditions, as well as improved sensory and nutritional characteristics, industrial, medicinal, landscape, and social values, etc. The genebanks also have a role in educating new generations about the importance of preserving biodiversity and the best way to go about this mission. In any case, although the formats evolve, genebanks will continue to be information libraries where to look for the meaning of genes. The greater the quantity and quality of the information stored and the better the engines we have to process and filter it, the greater the utility of the bank. In turn, the degree of utility, in the medium or long term, will determine their survival (Byrne et al., 2018).

## THE FUTURE OF THE GENE BANKS

Advances in biotechnology techniques pave the way to new scenarios that reach beyond the reflections in this article into the future. The massive sequencing of many accessions of many crops has generated huge quantities of data. One example is the work done in rice (*Oryza sativa* L.) at the International Rice Research Institute, in which numerous

1141 researchers have collaborated (McCouch et al., 2012). The  
 1142 availability of this information has in turn enabled breeding  
 1143 materials to be developed: mapping populations, homozygous  
 1144 materials essential for resequencing and allele identification,  
 1145 etc., in short, materials other than heterogeneous populations  
 1146 normally kept in banks. Before these advances, the focus  
 1147 was on landraces, wild relatives, passport data, and primary  
 1148 characterization; now the scenario is much more complex. Users,  
 1149 especially researchers and breeders, need not only accessions but  
 1150 also as much associated information as possible. In addition,  
 1151 we are beginning to glimpse the possibilities of gene editing, so  
 1152 the importance of physically preserving biological information  
 1153 (seeds or propagules) may be declining.

1154 Genebanks must start re-thinking their mission, especially  
 1155 considering users' needs and presenting information in an  
 1156 accessible and useful way (Van Treuren and van Hintum,  
 1157 2014). To advance in this direction, genebanks in Spain and  
 1158 around the world should assume their changing role and  
 1159 integrate into worldwide initiatives that have been underway  
 1160 for years, including such measures as strength collaborations  
 1161 between genebanks and the community of users. Users can  
 1162 contribute in many ways to the sustainability of the banks,  
 1163 for example, by regenerating accessions, supporting collecting  
 1164 missions, developing pre-breeding materials that can be shared  
 1165 by the scientific community, contributing their phenotyping  
 1166 and genotyping data to improve the information in databases  
 1167 and specific information portals, etc. The bidirectional flow of  
 1168 information must be encouraged, moving beyond the present  
 1169 arrangement in which information flows only from genebanks  
 1170 to users. In short, users must have a role in the maintenance of  
 1171 germplasm collections (Wambugu et al., 2018).

1172 Genebanks must present the information in a way that  
 1173 meets the specific needs and interests of the users, beyond the  
 1174 passport data. Thus, genebanks should develop portals with  
 1175 specific information for their users, for example, for lettuce  
 1176 (*Lactuca sativa* L.) breeders interested in resistance, researchers  
 1177 working with landraces of a particular crop, etc. The information  
 1178 provided should be organized differently in each case to ensure  
 1179 the maximum usefulness for the user's purpose. The CGN of The  
 1180 Netherlands has developed prototypes of these portals for lettuce  
 1181 (pgrportal.nl/lettuce) and potato (pgrportal.nl/potato).

1182 Genebanks should incorporate pre-breeding materials  
 1183 developed by researchers in their collections, because landraces  
 1184 are not the only useful source of germplasm, although including  
 1185 different types of collections may require different conservation  
 1186 and distribution protocols. Besides, we should consider the  
 1187 possibility of the participation of the researchers themselves and  
 1188 seed companies interested in the maintenance of these materials.  
 1189 Likewise, these materials can be transferred through specific  
 1190 transfer agreements.

1191 The large quantity of data about origins and characterization  
 1192 that is available in genebanks should be interconnected with  
 1193 efficiently genotyping data, annotation of genomes, etc. from  
 1194 the scientific community. The question "How will genebanks  
 1195 use and provide access to genomic data and how will  
 1196 genomic information resources give access to genebank data  
 1197 and materials?" has already been discussed recently (Finkers

1198 et al., 2015). Bioinformatics technologies allow databases  
 1199 to be interconnected through the use of publicly defined  
 1200 Application Programming Interfaces and DOIs. The automated  
 1201 interconnection of different data sources that deal with different  
 1202 aspects of the collections (e.g., passport or genomic data) should  
 1203 add value to the biological materials stored. For example,  
 1204 when the name of a specific gene is entered, the application  
 1205 can provide a list of genebank accessions containing different  
 1206 alleles as well as the available phenotyping data and passport  
 1207 data. This information can be invaluable for users requesting  
 1208 accessions of interest. McCouch et al. (2013) suggested building  
 1209 databases that integrate passport information, genotyping data,  
 1210 and phenotyping data, and coordinated work on this initiative is  
 1211 underway.

## 1212 GENE BANKS IN THE ERA OF GENETIC 1213 EDITING

1214 With the aim of going further and trying to elucidate the role  
 1215 of genebanks in the era of genetic editing, we consulted some  
 1216 significant Spanish biotechnologists and geneticists. The main  
 1217 message we got from them is that genebanks store a high number  
 1218 of genes and gene combinations created by evolution and that,  
 1219 at present, cannot be produced by biotechnology or genetic  
 1220 editing techniques. Although this would be perhaps the case in  
 1221 a future, variability reservoirs will continue to be indispensable  
 1222 for determining the gene function.

1223 Nevertheless, genetic editing techniques and other current  
 1224 biotechnology tools will allow us to take advantage of the  
 1225 information held in genebanks in a more efficient and fast way,  
 1226 contributing to the rationalization and running. Genotyping of  
 1227 the collections, both at low and high density, will allow the  
 1228 identification of duplicates, the establishment of varietal limits,  
 1229 the estimation of the population variability, the identification of  
 1230 haplotypic blocks, etc., that is, to rationalize the genebanks in a  
 1231 scenario where genotyping is much cheaper than phenotyping.  
 1232 Taking advantage of sequencing progress, genebanks should  
 1233 be collections of allelic variants of genes responsible of  
 1234 characteristics of interest and should provide information about  
 1235 the sequence associated to phenotype.

1236 Future genebanks should also conserve products of genetic  
 1237 editing and transgenics, as well as the associated information.  
 1238 Finally, they should conserve DNA, as well as all the information  
 1239 related to the sequences of the corresponding genomes. It  
 1240 seems then clear than genebanks, mainly historically born  
 1241 from breeder's collections and then segregated into individual  
 1242 new bodies, should now associate to research and breeding  
 1243 institutions to get all their sense.

## 1244 FINAL CONSIDERATIONS

1245 Spanish genebanks cannot apply all the above mentioned  
 1246 correcting measures in the short term, but we should start  
 1247 looking in this direction and the most basic aspects discussed  
 1248 should be prioritized. In fact, some genebanks at an international  
 1249 level are already genotyping a large number of accessions in  
 1250

1255 their collections by participating in research projects. In the  
 1256 ongoing project H2020 G2P-SOL ([www.g2p-sol.eu](http://www.g2p-sol.eu)), more than  
 1257 45,000 accessions of major solanaceous crops [tomato, pepper  
 1258 (*Capsicum annuum* L.), eggplant (*Solanum melongena* L.), and  
 1259 potato (*Solanum tuberosum* L.)] from 12 countries in Europe,  
 1260 Asia, and America are being genotyped. Using these genotyping  
 1261 and passport data, core collections are being built. The joint study  
 1262 of all these data will allow to elucidate the genetic relationships  
 1263 between all these inputs (practically all the collections of these  
 1264 crops worldwide), identify alleles and shared regions, locate the  
 1265 places where to look for new variation, determine the value of  
 1266 the different collections, identify accessions with rare alleles of  
 1267 interest, associate genotypes with phenotypes, etc. These actions  
 1268 represent an advance in applying the guidelines mentioned  
 1269 along the manuscript and we hope that models like that will  
 1270 inspire the Spanish Plant Genetic Resources Network to adapt  
 1271 to changing technologies and demands. The recently constituted  
 1272 Commission of the National Program for the Conservation  
 1273 and Utilization of Plant Genetic Resources for Agriculture and  
 1274 Food, besides structuring the Network, updating information on  
 1275 Spanish genebanks, and streamlining access to their repositories,  
 1276 should address the international challenge of rethinking them.

## 1277 REFERENCES

- 1281 Ahmed, S., Stepp, J. R., Orians, C., Griffin, T., Matyas, C., Robbat, A., et al.  
 1282 (2014). Effects of extreme climate events on tea (*Camellia sinensis*) functional  
 1283 quality validate indigenous farmer knowledge and sensory preferences  
 1284 in tropical China. *PLoS ONE* 9:e109126. doi: 10.1371/journal.pone.01  
 1285 09126
- 1286 Arnaud, E., Dias, S., Mackay, M., Cyr, P., Gardner, C., Bretting, P., et al. (2010).  
 1287 “A global portal enabling worldwide access to information on conservation  
 1288 and use of biodiversity for food and agriculture,” in *Information and  
 1289 Communication Technologies for Biodiversity Conservation and Agriculture*, eds  
 1290 L. Maurer Lisa and K. Tochtermann (Aix-la-Chapelle: Shaker Verlag), 168–180.
- 1291 Bioversity and The Christensen Fund. (2009). *Descriptors for Farmers' Knowledge  
 1292 of Plants*. Bioversity International, Rome, Italy and The Christensen Fund, Palo  
 1293 Alto,
- 1294 Bueno, M. A., and Alaman, M. C. (1982). Los bancos de germoplasma: una  
 1295 estrategia para el futuro. *Rev. Ext. Agrar.* 21, 65–71.
- 1296 Byrne, P. F., Volk, G. M., Gardner, C., Gore, M. A., Simon, P. W., and  
 1297 Smith, S. (2018). Sustaining the future of plant breeding: the critical role  
 1298 of the USDA-ARS national plant germplasm system. *Crop Sci.* 58, 451–468.  
 1299 doi: 10.2135/cropsci2017.05.0303
- 1300 Camacho Villa, T. C., Maxted, N., Scholten, M., and Ford-Lloyd, B. (2005).  
 1301 Defining and identifying crop landraces. *Plant Genet. Resour.-C.* 3, 373–384.  
 1302 doi: 10.1079/PGR200591
- 1303 Cartea, M. E., Picoaga, A., Soengas, P., and Ordás, A. (2003). Morphological  
 1304 characterization of kale populations from northwestern Spain. *Euphytica* 129,  
 1305 25–32. doi: 10.1023/A:1021576005211
- 1306 Casals, J., Casañas, F., and Simó, J. (2017). Is it necessary to continue to collect  
 1307 genetic crop resources in the Mediterranean area? A case study in Catalonia.  
 1308 *Econ. Bot.* 71, 330–341. doi: 10.1007/s12231-017-9392-0
- 1309 Casañas, F., Bosch, L., Sánchez, E., Romero del Castillo, R., Valero, J., Baldi, M.,  
 1310 et al. (1997). Collecting, conservation and variability of Ganxet common bean  
 1311 (*Phaseolus vulgaris* L.). *Plant Genet. Resour.* 112, 105–106.
- 1312 Casañas, F., Simó, J., Casals, J., and Prohens, J. (2017). Toward an evolved concept  
 1313 of landrace. *Front. Plant Sci.* 8:145. doi: 10.3389/fpls.2017.00145
- 1314 Cebolla-Cornejo, J., Roselló, S., and Nuez, F. (2013). Phenotypic and  
 1315 genetic diversity of Spanish tomato landraces. *Sci. Hortic.* 162, 150–164.  
 1316 doi: 10.1016/j.scienta.2013.07.044

## AUTHOR CONTRIBUTIONS

1312 MD and FC conceived the project, organized a specific meeting  
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 1314 LD, IM, MC, CM, JC, JS, AR, GA, JP, SS, JB, and JV  
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- 1326 Ceccarelli, S., and Grando, S. (1996). Drought as a challenge for the plant breeder.  
 1327 *Plant Growth Regul.* 20, 149–155. doi: 10.1007/BF00024011
- 1328 Chapman, S. C., Chakraborty, S., Dreccer, M. F., and Howden, S. M. (2012). Plant  
 1329 adaptation to climate change—opportunities and priorities in breeding. *Crop  
 1330 Pasture Sci.* 63, 251–268. doi: 10.1071/CP11303
- 1331 Clawson, D. L. (1985). Harvest security and intraspecific diversity in traditional  
 1332 tropical agriculture. *Econ. Bot.* 39, 56–67. doi: 10.1007/BF02861175
- 1333 De-Zhu, L., and Pritchard, H. W. (2009). The science and economics  
 1334 of *ex situ* plant conservation. *Trends Plant Sci.* 14, 614–621.  
 1335 doi: 10.1016/j.tplants.2009.09.005
- 1336 Engels, J. M. M., Rao, V. R., Brown, A. H. D., and Jackson, M. (2001). *Managing  
 1337 Plant Genetic Diversity*. New York, NY: Cabi.
- 1338 Engels, J. M. M., and Thormann, I. (2007). Horticultural genetic resources  
 1339 collections: Their characteristics, strengths and weaknesses. *Acta Hortic.* 760,  
 1340 33–42. doi: 10.17660/ActaHortic.2007.760.2
- 1341 FAO (2010). *The Second Report on the State of the World's Plant Genetic Resources  
 1342 for Food and Agriculture*. Rome: FAO. Available online at: [http://www.fao.org/  
 1343 docrep/013/i1500e/i1500e.pdf](http://www.fao.org/docrep/013/i1500e/i1500e.pdf)
- 1344 Finkers, R., Chibon, P. Y., van Treuren, R., Visser, R., and van Hintum, T. (2015).  
 1345 Genebanks and genomics: how to interconnect data from both communities?  
 1346 *Plant Genet. Resour.-C.* 13, 90–93. doi: 10.1017/S1479262114000689
- 1347 Fowler, C., and Hodgkin, T. (2004). Plant genetic resources for food and  
 1348 agriculture: assessing global availability. *Annu. Rev. Env. Resour.* 29, 143–179.  
 1349 doi: 10.1146/annurev.energy.29.062403.102203
- 1350 Fu, Y. B. (2017). The vulnerability of plant genetic resources conserved *ex situ*.  
 1351 *Crop Sci.* 57, 2314–2328. doi: 10.2135/cropsci2017.01.0014
- 1352 Gepts, P. (2006). Plant genetic resources conservation and utilization. *Crop Sci.* 46,  
 1353 2278–2292. doi: 10.2135/cropsci2006.03.0169gas
- 1354 Gómez, O. J., Blair, M. W., Frankow-Lindberg, B. E., and Gullberg, U.  
 1355 (2005). Comparative study of common bean (*Phaseolus vulgaris* L.) landraces  
 1356 conserved *ex situ* in genebanks and *in situ* by farmers. *Genet. Resour. Crop Evol.*  
 1357 52, 371–380. doi: 10.1007/s10722-005-2249-x
- 1358 Guasch, L. M., Fajardo, J., and de la Rosa, L. (2016). Informe de la reunión  
 1359 de coordinación de investigación agraria INIA-Comunidades Autónomas:  
 1360 propuesta de actuación sobre las colecciones de recursos fitogenéticos. Reunión  
 1361 interregional de I+D en agricultura. *Logroño febrero* 2016, 1–29.
- 1362 Hajjar, R., and Hodgkin, T. (2007). The use of wild relatives in crop improvement:  
 1363 a survey of developments over the last 20 years. *Euphytica* 156, 1–13. Q10

- 1369 Halewood, M., Chiurugwi, T., Sackville Hamilton, R., Kurtz, B., Marden,  
1370 E., Welch, E. et al. (2018). Plant genetic resources for food and agriculture:  
1371 opportunities and challenges emerging from the science and information  
1372 technology revolution. *New Phytol.* 217, 1407–1419. doi: 10.1111/nph.14993
- 1373 Hancock, J. F. (2004). *Plant Evolution and the Origin of Crop Species*. Cambridge:  
1374 CABI Publishing.
- 1375 Jarvis, D. I., Hodgkin, T., Sthapit, B. R., Fadda, C., and Lopez-Noriega,  
1376 I. (2011). An heuristic framework for identifying multiple ways of  
1377 supporting the conservation and use of traditional crop varieties within  
1378 the agricultural production system. *Crit. Rev. Plant Sci.* 30, 125–176.  
1379 doi: 10.1080/07352689.2011.554358
- 1380 Khoury, C. K., Achicanoy, H. A., Bjorkman, A. D., Navarro-Racines, C., Guarino,  
1381 L., Flores-Palacios, X., et al. (2016). Origins of food crops connect countries  
1382 worldwide. *P. R. Soc. B-Biol. Sci.* 283:2060792. doi: 10.1098/rspb.2016.0792
- 1383 Khoury, C. K., Bjorkmann, A. D., Dempewolf, H., Ramirez-Villegas, J., Guarino,  
1384 L., Jarvis, A., et al. (2014). Increasing homogeneity in global food supplies and  
1385 the implications for food security. *Proc. Natl. Acad. Sci. U.S.A.* 111, 4001–4006.  
1386 doi: 10.1073/pnas.1313490111
- 1387 Lema, M. P., Soengas, P., Velasco, M., and Cartea, M. E. (2010). “Las razas  
1388 locales como reservorio de variabilidad genética,” in *Mejora genética y recursos  
1389 fitogenéticos: Nuevos Avances en La Conservación y Utilización de los Recursos  
1390 Fitogenéticos*, eds J. M. Carrillo, M. J. Diez, M. Pérez de la Vega, and F. Nuez  
1391 (Madrid: Ministerio de Medio Ambiente y Medio Rural y Marino), 547–580.
- 1392 Maxted, N., Scholten, M., Codd, R., and Ford-Lloyd, B. (2007). Creation and use  
1393 of a national inventory of crop wild relatives. *Biol. Conserv.* 140, 142–159.  
1394 doi: 10.1016/j.biocon.2007.08.006
- 1395 McCouch, S., Baute, G. J., Bradeen, J., Bramel, P., Bretting, P. K., and Buckler, E.  
1396 (2013). Feeding the future. *Nature* 499, 23–24. doi: 10.1038/499023a
- 1397 McCouch, S., McNally, K. L., Wang, W., and Sackville Hamilton, R. (2012).  
1398 Genomics of gene banks: a case study in rice. *Am. J. Bot.* 99, 407–423.  
1399 doi: 10.3732/ajb.1100385
- 1400 McFerson, J. R., Lamboy, W. F., and Kresovich, S. (1996). Assessing user  
1401 perceptions of genetic resource collections in crucifer crops. *Crop Sci.* 36,  
1402 831–838. doi: 10.2135/cropsci1996.0011183X003600040001x
- 1403 Meyer, R. S. (2015). Encouraging metadata curation in the diversity seek initiative.  
1404 *Nat. Plants* 1:15099. doi: 10.1038/nplants.2015.99
- 1405 Negri, V., and Tiranti, B. (2010). Effectiveness of in situ and ex situ conservation  
1406 of crop diversity. What a *Phaseolus vulgaris* L. landrace case study can tell us.  
1407 *Genética* 138, 985–998. doi: 10.1007/s10709-010-9485-5
- 1408 Olesen, J. E., and Bindi, M. (2002). Consequences of climate change for European  
1409 agricultural productivity, land use and policy. *Eur. J. Agron.* 16, 239–262.  
1410 doi: 10.1016/S1161-0301(02)00004-7
- 1411 Prada, D. (2009). Molecular population genetics and agronomic alleles in seed  
1412 banks: searching for a needle in a haystack? *J. Exp. Bot.* 60, 2541–2552.  
1413 doi: 10.1093/jxb/erp130
- 1414 Reif, J. C., Melchinger, A. E., and Frisch, M. (2005). Genetical and mathematical  
1415 properties of similarity and dissimilarity coefficients applied in plant breeding  
1416 and seed bank management. *Crop Sci.* 45, 1–7. doi: 10.2135/cropsci2005.0001
- 1417 Romero del Castillo, R., Sabaté, J., Plans, M., and Casañas, F. (2010). “Evaluación  
1418 para características de calidad,” in *Mejora Genética y Recursos Fitogenéticos:  
1419 Nuevos Avances en la Conservación y Utilización de los Recursos Fitogenéticos*,  
1420 eds J. M. Carrillo, M. J. Diez, M. Pérez de la Vega, and F. Nuez (Madrid:  
1421 Ministerio de Medio Ambiente, Medio Rural y Marino), 383–420.
- 1422
- 1423
- 1424
- 1425
- Rubio, M. L., Torres, E., Parra-Quijano, M., de la Rosa, L., Fajardo,  
1426 J., and Iriondo, J. M. (2018). National inventory and prioritization of  
1427 crop wild relatives in Spain. *Genet. Resour. Crop Evol.* 65, 1237–1253.  
1428 doi: 10.1007/s10722-018-0610-0
- 1429 Santalla, M., Rodiño, A., and de Ron, A. M. (2002). Allozyme evidence  
1430 supporting southwestern Europe as a secondary center of genetic diversity for  
1431 common bean. *Theor. Appl. Genet.* 104, 934–994. doi: 10.1007/s00122-001-  
1432 0844-6
- 1433 Schreinemachers, P., Ebert, A. W., and Wu, M. H. (2014). Costing the *ex situ*  
1434 conservation of plant genetic resources at AVRDC - The World Vegetable  
1435 Center. *Genet. Resour. Crop Evol.* 61, 757–773. doi: 10.1007/s10722-013-0070-5
- 1436 Soengas, P., Cartea, M. E., Velasco, P., Padilla, G., and Ordás, A. (2008).  
1437 Morphologic and agronomic diversity of *Brassica napus* crops. *J. Amer. Soc.  
1438 Hort. Sci.* 133, 48–54.
- 1439 Tanksley, S. D., and McCouch, S. R. (1997). Seed banks and molecular  
1440 maps: unlocking genetic potential from the wild. *Science* 277, 1063–1066.  
1441 doi: 10.1126/science.277.5329.1063
- 1442 Tardío, J., Pardo de Santayana, M., Morales, R., Molina, M., and Aceituno,  
1443 L. (2018). *Inventario Español de Conocimientos Tradicionales Relativos a la  
1444 Biodiversidad Agrícola Volumen I*. Madrid: Ministerio de Agricultura, Pesca y  
1445 Alimentación.
- 1446 Van de Wouw, M., Kik, C., van Hintum, T., van Treuren, R., and Visser, B. (2009).  
1447 Genetic erosion in crops: concept, research results and challenges. *Plant Genet.  
1448 Resour.* 8, 1–15. doi: 10.1017/S1479262109990062
- 1449 Van Treuren, R., and van Hintum, T. (2014). Next-generation genebanking:  
1450 plant genetic resources management and utilization in the sequencing  
1451 era. *Plant Genet. Resour.* 12, 298–307. doi: 10.1017/S14792621140  
1452 00082
- 1453 Veteläinen, M., Negri, V., and Maxted, N. (2009). *European Landraces: On-  
1454 Farm Conservation, Management and Use. Bioersity Technical Bulletin  
1455 N15*. Rome: Bioersity International. Available online at: [https://www.  
1456 bioersityinternational.org/fileadmin/\\_migrated/uploads/tx\\_news/European\\_  
1457 landraces\\_on-farm\\_conservation\\_management\\_and\\_use\\_1347.pdf](https://www.bioersityinternational.org/fileadmin/_migrated/uploads/tx_news/European_landraces_on-farm_conservation_management_and_use_1347.pdf)
- 1458 Wambugu, P. W., Ndjiondjop, M. N., and Henry, R. J. (2018). Role of genomics in  
1459 promoting the utilization of plant genetic resources in genebanks. *Brief. Funct.  
1460 Genomics* 17, 198–206. doi: 10.1093/bfpg/ely014
- 1461 Zamir, D. (2013). Where have all the crop phenotypes gone? *PLoS Biol.*  
1462 11:e1001595. doi: 10.1371/journal.pbio.1001595
- 1463 Zeven, A. C. (1998). Landraces: a review of definitions and classifications.  
1464 *Euphytica* 104, 127–139. doi: 10.1023/A:1018683119237
- 1465
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