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A CASE STUDY ON GRAIN LEGUMES GENETIC RESOURCES AVAILABLE FOR USE IN BREEDING FOR SUSTAINABLE AGRICULTURE - A REVIEW

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Abstract

Plant genetic resources are essential for sustainable agriculture and for securing the global food supply. Sustainable agriculture and global food security depend on the availability of well-described plant genetic resources. The work presents challenges related to the availability of grain legumes genetic resources for use in breeding for sustainable agriculture, germplasm held in gene banks, and approaches to enhance the use and access to conserved resources. A better understanding of the stability and potential of investigated traits can be achieved by considering data from different experiments, thereby improving the prospects of using genetic resources in novel breeding programs. Consequently, genetic resource collections can become more utilized through enhanced cooperation and sharing not only of seeds, but also the accumulated knowledge gained over many years of resource regeneration and/or research. Legumes are a vital group of crops that include beans, lentils, chickpeas, lupins, and many others, contributing significantly to global food security, nutrition, and sustainable agriculture. The genetic resources of legumes are essential for breeding programs aimed at improving yield, disease resistance, and adaptability to changing climates. However, these genetic resources face several safeguarding challenges.

Key words*: sustainable agriculture, germplasm, crops, genetic variation.*

INTRODUCTION

Sustainability is imperative, particularly within agri-food systems, where it becomes even more critical amid experienced global challenges, as climate changes, conflicts, and pandemics. Agrobiodiversity conservation, sustainable agricultural practices, and food security demand feasible solutions that are both economically competitive and environmentally beneficial. Enhancing sustainability is essential, particularly for agri-food chains, given the current global challenges related to climate changes, food security and need to preserve the quality of environment. The grain legumes species, featured by unique biological and nutritional characteristics, play a pivotal role in addressing critical societal issues related to agri-food, including agrobiodiversity conservation, sustainable farming practices, food security, and human health.

Capturing the full diversity of grain legumes and ensuring availability and access to well-described, well-managed genetic resource collections is of paramount importance for advancing grain legume crops. This is essential for achieving a competitive level of agronomic performance and sustainability.

Legumes stand out as a sustainable, cost-effective, water-efficient, and low-carbon footprint crop, making them a vital component of environmentally conscious agriculture. Globally, grain legumes represent approximately 15% of the 7.4 million accessions preserved in gene banks (Tripathi, et al. 2020). However, same authors stated that a significant challenge is that over half of this germplasm lacks essential characterization and evaluation data, which severely limits its use in legume improvement programs. The comprehensive characterization of gene bank accessions is crucial for unlocking their full potential.

Recognizing the importance of accessible and well-documented grain legumes genetic resources, the establishment of a robust framework for selection and creation of practical, harmonized research plans become an imperative. These efforts aim to promote the utilization of plant genetic resources, thereby securing long-term economic, environmental, climatic, and socio-economic advantages.

Grain legumes become components of sustainable agriculture, driven by emerging research opportunities in key areas. A major challenge in this endeavor is securing adequate expertise and funding to ensure the network's sustainability and continued impact.

A critical task involves strategically selecting legumes, species and cultivars that can be effectively integrated into diverse cropping systems. This selection process must carefully balance specific challenges as economic yield, environmental and agronomic benefits, ensuring both profitability and ecological resilience.

It is crucial to pinpoint the traits valued by end-users (breeders, farmers, technicians), necessitating improved documentation of legume germplasm diversity in *ex situ* collections. This process involves several steps which may include characterizing genetic material through DNA markers, evaluating responses to specific biotic and abiotic stresses, and assessing organoleptic qualities as well as health-related attributes or anti nutritional profile of legumes

Most of the current strategies are focussed on modernizing and refining pre-breeding and breeding techniques for legumes by exploring genetic resources - such as crop wild relatives, landraces, minor crops, cultivars, and breeding lines - to maximize benefits for human nutrition, environmental sustainability, and end-user needs within divers agri food systems. These approaches will facilitate the development of advanced methods for evaluating and breeding legume cultigens, ultimately leading to a more diverse and efficient pipeline of improved cultivars. Additionally, addressing abiotic stress limitations, particularly water deficit, salinity, and thermal shocks, requires extensive investigation to develop resilient legume varieties.

Amid rising demand for plant-based products like proteins and oils, coupled with increasing economic and environmental pressures on agroecosystems, grain legumes are set to play a pivotal role in shaping the future of sustainable cropping systems. Their ability to enhance soil health, reduce input dependency, and provide nutritious yields positions them as indispensable allies in addressing global agricultural challenges.

This work aims to strengthen a strategic approach that leverages genetic variation of grain legumes to enhance the access and the share of plant genetic resources, in a context of actively engaging European farmers, advisory services, research institutes, breeding companies, and food producers across diverse socioeconomic contexts.

BACKGROUND AND CASE STUDY DOCUMENTATION

A search for studies that link legumes genetic resources and their role for food and resilient agriculture was undertaken by screening case studies, reviews, projects, initiatives and open access data bases from the ScienceDirect, Scopus and Google Scholar databases. Peer-reviewed literature was complemented, where appropriate, with relevant project reports and databases. Sector-specific searches were undertaken to ensure adequate coverage legumes genetic resources, as their diversity to meet breeding objectives like nutritional quality, yield, and tolerance to a diverse source of biotic and abiotic stresses, role, and the impact of *ex situ*, *in situ* and *on farm* conservation. The search results, consisting in 56 sources were reviewed to determine which threats were overrepresented and which might represent research gaps. The conclusions and recommendations of this thematic study are built upon the reviews papers, which include background literature on the various sectors and topics addressed. Case studies, projects, databases were included in the analysis met the following criteria: include a description of legumes diversity, address one or more ways in which biodiversity contributes to coping with or managing environmental stresses and change in production systems. Based on this search specific recommendations to facilitate the use and the share of plant genetic resources are provided.

THE CONTEXT OF PLANT GENETIC RESOURCES CONSERVATION

The tasks of preserving and characterizing genetic resources are requiring expertise, labour, equipment, and significant funding. A systematic approach is mandatory for effective plant genetic resource management. This will maximize the value and use capacity, adhering to high-quality standards. According to Genetic Resources Strategy for Europe, 2021, this systematic approach includes implementing agreed-upon ontologies and following FAIR principles (Findable, Accessible, Interoperable, Reusable) for open data sharing, documentation, and archiving. Moreover, conservation of genetic resources requires interventions to ensure the ecological or management processes necessary for the preservation of populations *in situ* (including on-farm), and to support the collection and management of population samples in dedicated *ex situ* facilities. The success of screening programs in crop breeding, focused on identifying valuable traits, hinges on the availability of a broad and genetically diverse pool of plant resources sourced globally. Following the screening process, only a few breeding lines are ultimately chosen to develop the final, commercially viable variety (Ebert et al., 2023).

Based on our experience and also stated generally, traditional plant variety innovation in agriculture relies heavily on centralized efforts by seed companies, scientists, and experts, who develop new varieties using the vast genetic diversity stored in germplasm banks. However, this model limits plant genetic resource utilization to a small group of contributors, resulting in innovative varieties reaching farmers only after a lengthy process (10–20 years). This slow, narrow approach minimally contributes to agricultural diversification and hinders the adoption of minor crops, especially when rapid transitions are needed.

Participatory and decentralized innovation strategies, rooted in localized plant genetic resources conservation (essential for supporting plant breeding programs), offer a promising alternative to promote agricultural diversification and climate-economic adaptation. To maximize their effectiveness, these strategies should integrate cutting-edge technologies, including data analytics, genomics, metabolomics, high-throughput phenotyping, digital tools. Additionally, leveraging satellite-based weather data and developing crop-specific climatic predictions can enhance resilience to environmental variability, as developed and implemented by pulsesincrease.eu.

Another critical factor is the development of new food products, based on genetic resources conserved and explored in breeding programs. According to FAO reports, most food products derive from a limited number of species, varieties, and market classes, constrained by the scale of industrial production. To overcome this bottleneck, diversifying food types requires not only farmer and stakeholder involvement but also broader societal engagement. This collective effort can drive cultural and economic innovation in agricultural and food production systems.

Due to the rising demand for plant-based products, such as proteins and oils, coupled with increasing economic and environmental pressures on agro-ecosystems, grain legumes play a significant role in future cropping systems. Improving the nutritional quality of food, especially plant-based proteins, is essential for enhancing human health. Achieving this dual goal of quantity and quality is further complicated by environmental shifts, including unpredictable rainfall patterns, extreme weather events like floods and storms, and rising temperatures, which can lead to soil erosion, pest infestations, and reduced crop yields. Additionally, transitions to low-input agricultural systems, driven by evolving farming conditions and regulatory policies on land and energy use, may exacerbate food production challenges.

Legumes are essential in tackling these challenges, as they provide food, fodder, energy, and nutritional security, while simultaneously benefiting the environment through their nitrogen-fixing capabilities and promotion of agrobiodiversity in cereal-centric systems. (Bellucci et al., 2021). Enhancing the European production of grain legumes crops is amongst the first steps in the protein transition. The most cultivated grain legumes species in Europe are faba bean (*Vicia faba* L.), pea (*Pisum sativum* L.) and soybean (*Glycine max* (L.) Merr.) (Eurostat, 2023, Sepngang et al., 2020). Expanding legume cultivation would substantially strengthen regional protein supply independence. Leveraging diverse genetic resources in legume breeding and incorporating new cultivars into both conventional and organic farming systems offers significant potential to develop climate-resilient production systems for current and future needs.

STRATEGIES TO CONSERVE THE GRAIN LEGUMES DIVERSITY

Despite the abundance of grain legumes genetic resources, their application in breeding remains underdeveloped, yielding suboptimal results. Key barriers include insufficient metadata (such as essential passport data and user-relevant descriptors), heterogeneity among accessions, and non-standardized data formats. These challenges not only hinder the effective use of genetic resources but also impede efforts to secure funding for their conservation (Bellucci et al., 2021). The main strategies and initiatives to conserve plant genetic resources and information related their taxonomy are summarised in Figure 1.

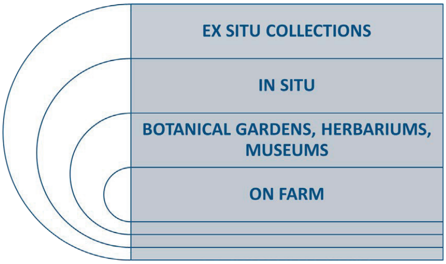

Figure 1. Ways to conserve grain legumes genetic resources

Ex Situ Germplasm Collections - gene banks host valuable plant genetic resources that require multiplication, regeneration, and thorough evaluation to promote their use. Additionally, there is a wealth of advanced materials and data from various projects and activities that could be integrated and broadly shared with stakeholders throughout the European agri-food chain.

▪Chickpea and lentil are two crops present in worldwide collections, according to the querying of the most important online platforms, Genesys (Virtual Gene bank of Plant Genetic Resources for Food Agriculture, https://www.genesys-pgr.org) and EURISCO (European Search Catalogue for Plant Genetic Resources, https://eurisco.ipk-gatersleben.de/apex/eurisco). Gene banks across the world conserve about 97,400 accessions of chickpea germplasm. (Brezeanu et al., 2024).

Based on GENESYS (https://www.genesys-pgr.org) data cited by pulsesincrease.eu the largest collections of chickpeas are maintained at International Centre for Agricultural Research in the Dry Areas (ICARDA) and International Crops Research Institute for the Semi-Arid Tropics. (ICRISAT), centres of Consultative Group for International Agricultural Research (CGIAR) with unique accessions estimated at more than 15,000 and 20,000, respectively. California's UC Davis houses the world's most extensive collection of wild materials and their derived introgression lines.

▪ Current lentil cultivars suffer from a limited genetic base, making them vulnerable to diverse biotic and abiotic stresses. The solution to these challenges lies in the genetic diversity preserved within gene banks. This germplasm diversity is of paramount importance, as it enables the identification of valuable genes that can serve as essential resources for lentil breeding programs. There are currently over 58,000 lentil accessions held in various gene banks worldwide. Genesys displays information for about 70% of these (https://www.genesys-pgr.org/c/lentil).

ICARDA, with 12,463 accessions, is the centre with the largest lentil collection (Figure 2).

ICRISAT and ICARDA continue to provide global leadership in the conservation of chickpea and lentil germplasm. Over time, both collections have expanded substantially, and today, the two institutes collectively safeguard 33.9% of chickpea and 43.5% of lentil accessions in their facilities (Piergiovanni, 2022).

▪Common bean genetic resources are secured in some focal points, based on GENESYS data the most important *P. vulgaris* collections are maintained at Centro Internacional de Agricultura Tropical (CIAT) and USDA-ARS, at Washington State University (USA), with more than 24,000 and 18,500 accessions respectively. In Europe large collections are conserved at Leibniz Institute of Plant Genetics and Crop Plant Research-IPK (~8,500 accessions) as it is shown in Figure 2.

▪Lupinus has its largest number of accessions held in two gene banks: the Australian Grains Gene bank and IPK possess majority of *L. albus*

(800 accessions) and *L. mutabilis* (ca. 700 accessions), respectively. Other important lupin resources are maintained at Plant Breeding and Acclimatization Institute (IHAR-PIB, Poland, ~300 accessions) and IGR-PAN (~300 accessions), according to pulsesincrease.eu.

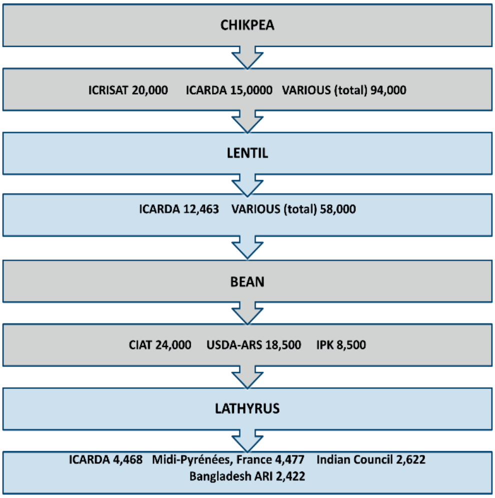

Figure 2. Representative centers for legumes genetic resources conservation and the number of conserved accessions

The largest collections of *Lathyrus* are held by the Conservatoire botanique national Midi-Pyrénées, France (4,477), ICARDA, Lebanon (4,468), the Indian Council of Agricultural Research National Bureau of Plant Genetic Resources, India (2,622), and the Bangladesh Agricultural Research Institute, Bangladesh (2,422) (Singh et al., 2024). The *Lathyrus* (Figure 2) conservation strategy highlight the importance of enhancing documentation systems, ensuring safe multiplication and duplication, and adopting international standards to manage existing collections (Global Crop Diversity Trust Strategy, 2007).

Botanical Gardens, Herbariums and Museums were established to respond to the growing interest for taxonomy, and no provision has been made for biodiversity conservation and although the Convention on Biological Diversity (CBD) mentions the opportunity of capacity building, if countries will take the necessary steps. Dixon (2007) mentioned botanic gardens as "mandated with conserving the world's flora" but in fact there is no such mandate and the task of making and maintaining the necessary *ex situ* collections of wild species has largely fallen to botanic gardens. Research conducted at botanical gardens has highlighted the importance of addressing the risks associated with hybridization in *ex situ* conservation efforts for threatened plant species. Studies have demonstrated that spontaneous hybridization within these facilities can compromise the genetic integrity of preserved collections, potentially leading to contamination of open-pollinated seeds or seedlings (Ye et al., 2006; Zhang et al., 2010).

In Situ Conservation of Crop Wild Relatives of targeted species is even more acute than that for *ex situ* conservation as discussed by Heywood & Dulloo (2006). Conducting multi-crop gene pool analyses, potentially focusing on legume species found in each of the Vavilov Centres, should be a globally important priority. Once *in situ* locations are identified, they should be leveraged to enhance global food security, maintaining as it possible the original selection pressures exerted. This necessitates understanding plant (and human) demography, the diversity of bean mixtures, the variety of selection pressures, and allowing sufficient time for continued evolution (Smýkal et al., 2014).

Planty populations of wild bean relatives can thrive in protected areas across different regions, mainly the Americas. The challenging issue remains the absence of published records, assessing which species and populations are currently conserved and were. Similarly, the absence of published inventories makes monitoring the success or failure of *in situ* conservation equally difficult (Debouck, 2014).

On-farm conservation of landraces is feasible if sustainable economic mechanisms are applied, and farmers are financial supported for the conservation of higher diversity. This was previously suggested (Zeven 1996) for the conservation of landraces in western Europe – he raised the attention on the fact that farmers will only have an interest to grow landraces when and if they are paid to do so. Some exceptions can work in case of specialty markets asking for specific landraces as in central Italy (Negri and Tosti 2002), in any case, markets may change.

If for example, beans are used by the food processing industry, it is possible that interest for specific colours, colour patterns and size will continue to fall, causing little incentive for farmers to keep all that diversity on farm (Kaplan and Kaplan 1992).

CHALLENGES RELATED TO THE AVAILABILITY OF GRAIN LEGUMES GENETIC RESOURCES FOR USE IN BREEDING WORKS

The role and the importance of grain legumes in sustainable agriculture can be substantially elevated by harnessing genetic diversity across breeding programs, with a focus on enhancing yield, resilience, nutritional quality and antinutritional profile.

A key task in advancing sustainable agriculture is selection of legume species and cultivars that can seamlessly integrate into diverse cropping systems, according to the current climatic pressure. A critical challenge lies in striking a balance between maximizing yield - a primary driver of economic returns (highly demanded by farmers) and enhancing environmental and agronomic benefits (recommended by different practices, programs and strategies). Securing legume genetic resources requires a comprehensive strategy that includes robust conservation measures, supportive policies, capacity development, and the promotion of sustainable farming practices. Among the most pressing threats (Figure 3) related to the availability and utilization of genetic resources are:

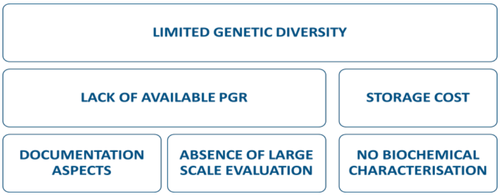

Figure 3. Threats related to the availability of grain legumes genetic resources for use in breeding works

Lack of material available for the distribution - in general, the total amount of seeds available in gene banks and research units is limited and this is challenging in terms of development of collections for research topics in frame of joint research projects. Moreover, this in a major limitation that affects the access of farmers to materials to be tested in their fields.

The narrow genetic diversity of modern legume varieties presents a substantial obstacle to their further enhancement, a critical need for addressing present and future agricultural challenges. For instance, the most widely cultivated chickpea varieties are especially susceptible to water stress and climate change impacts (Muehlbauer, 2017). To utilize available germplasm more efficiently, it is essential to broaden the genetic diversity of commercial varieties and maximize genetic gains during the breeding process (Jha, 2020). Core collections serve as an invaluable starting point for germplasm users, as they streamline the process by eliminating the time and resource-intensive task of screening large germplasm segments to identify parents with desirable traits.

The absence of large-scale germplasm evaluation is another significant limitation. Efforts to identify useful traits are often confined to a national framework, focusing on a limited set of bean germplasm from a single geographic origin. Evaluation should be done at the crop (biological) level, not at the national level. Vavilov, implemented in the 1920s an evaluation network of 400 experimental stations with 20,000 staff (Hawkes, 1990, Reznick & Vavilov 1997) in one country. The model was replicated by CIAT that followed that approach for a period of twenty years, starting at the middle of 70s. (CIAT 1973), with many useful traits disclosed (Hidalgo and Beebe 1997) and a significant impact in breeding (Voysest, 2000) unmatched to date.

The costs of storage, distribution and multiplication of materials, and costs for acquisitions of new samples (Halewood, 2020). Ensuring proper storage conditions and seeds availability to researchers, breeders, farmers and so on, represents great efforts to setting up core collections or mini core collections. These core collections consist of a minimized set of accessions that maximally represent the genetic diversity of the entire collection. This approach significantly reduces the volume of material requiring distribution and multiplication. In recent years, ICRISAT and ICARDA have developed several chickpea and lentil core collections, incorporating diverse traits such as pest resistance and morphological characteristics. However, this process remains ongoing due to the continuous acquisition of new materials and the rapid advancements in knowledge from omics techniques.

Lack of characterisation of biochemical traits – It is estimated a large percentage, up to 70% of conserved germplasm is well characterised. This is done based on distinct morpho-agronomic traits including resistance to biotic and abiotic stresses using crop-specific descriptor sets (Upadhyaya et al., 2011). Despite this, just a small percentage of collections have been characterized for biochemical traits. As model can serve a comprehensive study on common bean (*Phaseolus vulgaris*), chickpea (*Cicer arietinum*), lentil (*Lens culinaris*), white lupin (*Lupinus albus*) and pearl lupin (*Lupinus mutabilis*), at the tissue level. 3,400 metabolites covering major nutritional and anti-nutritional compounds were detected and quantified. This structure includes 224 derivatized metabolites, 2,283 specialized metabolites and 923 lipids. This kind of data ensure a foundation to advance metabolomics-assisted crop breeding and enable metabolite-based genome-wide association studies, thereby unravelling the genetic and biochemical underpinnings of metabolism in legume species (Bulut et al., 2023).

Documentation aspects at accession level might be challenging in many cases related to wide data availability on the internet. This is a crucial aspect in terms of management of collection. Documentation units have been set up in nearly every gene bank globally. These units collectively grapple with the critical task of ensuring that information about gene bank accessions is consistently maintained and effectively transferred from one generation to the next. (Weise et al., 2020)

APPROACHES TO FACILITATE THE ACCESS TO THE GRAIN LEGUMES GENETIC RESOURCES FOR A HIGH STANDING USE IN BREEDING

Facilitating proper access to grain legumes genetic resources is crucial for advancing breeding programs, as it enables researchers and breeders to harness diverse traits for improved yield, resilience, and nutritional quality. By streamlining access, breeders can more efficiently develop varieties that address global challenges such as climate change, food security, and sustainable agriculture, ultimately benefiting farmers and consumers alike.

The following tools contribute to a successful management of data and genetic diversity evaluation and utilization. The final goal is to ensure the access to unlock the stored collection and to make them useful for food and agriculture, ensuring environmental benefits and worldwide human nutrition. The useful tools and approaches for facilitating the access and use are listed in Figure 4 and described in this section. The list is non-hierarchical, and its application should be tailored to individual contexts.

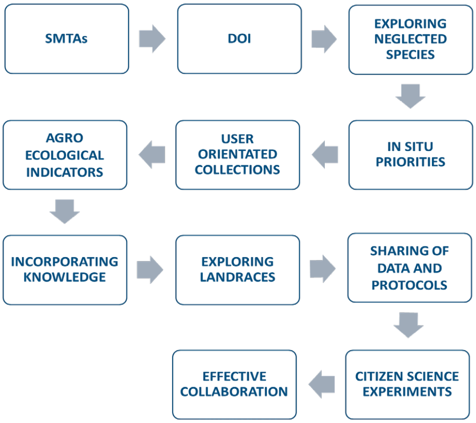

Figure 4. Approaches for a successful management of data and genetic resources

Standard Material Transfer Agreement (SMTA)
It is a tool developed to ensure the implementation of principles of the Treaty "Treaty on Plant Genetic Resources for Food and Agriculture" (ITPGRFA, "Treaty"). Its standardized format facilitates access to and fair use of plant genetic resources for food and agriculture (PGRFA) for conservation, development and training to promote sustainable agricultural development. The PGRFA allows the use or free of charge redistribution for research and breeding purposes. Farmers are invited to exploit this tool in their farm management.

Transparent exchanges will enhance accessibility and make information readily available, supported by mechanisms such as subscription systems or seed sales taxes. The primary benefit of this system lies in eliminating legal uncertainties and minimizing transaction costs for conservers, curators, and users of genetic resources, thereby enabling plant breeders to fulfil their mission more effectively.

Identity of collection - assignment of Digital Object Identifiers to avoid the difficulty of collaboration on conservation, research and breeding. Without a common standard for identification, it is challenging to locate information associated with the material. Millions of accessions are currently preserved in germplasm collections and breeding pools, yet numerous duplicates often contain valuable data that is frequently lost during transfers between custodians. Compounding this issue, diverse user groups, including plant breeders, data curators, researchers, and extensionists, often employ distinct methods to assign identifiers based on their specific requirements. This lack of standardization has historically impeded the global exchange of Plant Genetic Resources for Food and Agriculture (PGRFA) data, a longstanding barrier to their effective conservation and sustainable use. By adopting the Digital Object Identifier (DOI) standards endorsed by the Governing Body of the International Treaty, users can ensure unique and permanent identification and documentation of their plant material, significantly enhancing data interoperability across various systems. (Alercia, et al., 2018).

Explore the effects and benefits promote access to neglected grain legumes featured by resilience suitable for introduction in breeding activities - development of open and distributed seed system involving farmers and other main actors to support innovation for agricultural diversification. These species possess an extensive adaptation to poor soils and resilience to biotic and abiotic stresses, having a great potential to improve the livelihoods of smallholder farmers globally (Chandra et al., 2020; Kebede et al., 2020). Given climate change, legumes crops integrated into agroecosystems for diversification can break the cycle of pests and diseases and contribute to balancing the deficit in plant protein production worldwide (Chandra et al, 2020; Sita et al., 2020).

Establishing in situ conservation priorities, having greater practical value and being cost efficient to establish multi-gene pool conservation targets irrespective of individual gene pool results (Smýkal et al., 2014). Development of GAP analysis according to (Maxted et al., 2008) which involves steps as: identify priority taxa, identify genetic (or ecogeographic as a proxy for genetic) diversity and complementary hotspots using distribution and environmental data, match current *in situ* and *ex situ* conservation actions with the identified genetic (or ecogeographic) diversity and complementary hotspots to identify 'gaps' formulate revised *in situ* and *ex situ* conservation actions derived from identification of the gaps.

The GAP analysis is a valuable method for diversity conservation, explored and applied by Maxted et al. (2008), to illustrate its potential utility in both *in situ* and *ex situ* genetic diversity conservation approaches. The authors outlined four key stages: (i) defining the focal species and geographic region; (ii) evaluating native biodiversity alongside potential threats; (iii) reviewing the effectiveness of existing complementary *in situ* and *ex situ* conservation measures; and (iv) refining the conservation approach by examining disparities between the natural diversity and the components of that diversity currently safeguarded through *in situ* and *ex situ* strategies.

This methodology has been previously explored for several legumes CWR groups, as vetch (Maxted, 1995), lentils (Ferguson et al., 1998), Asiatic *Vigna* (Tomooka et al., 2009), African *Vigna* species (Maxted et al., 2004), perennial *Medicago* (Bennett et al., 2006), garden pea, faba bean and cowpea as important food crop gene pools (Maxted and Kell, 2009), *Phaseolus* species (Ramırez-Villegas et al., 2010), *Lathyrus* species (Shehadeh et al., 2013).

Developing and mapping crop-specific agro-ecological indicators across current and future climate scenarios to enhance the understanding of the benefits legumes offer for improving climatic resilience and adaptive capacity. This approach provides valuable insights across a wide range of spatial and temporal conditions, supporting more informed agricultural strategies.

Development of specific user-oriented collections at gene bank level – this can include populations and genetically purified lines, complemented by novel information services, able to guide users based on their specific interest (van Treuren and van Hintum, 2014).

Incorporating knowledge of related organisms, such as pathogens and pests, into the utilization of new germplasm in breeding programs would significantly enhance the development of improved crop varieties. These varieties would be better equipped to withstand climate change challenges and contribute to more sustainable agricultural practices. By leveraging this integrated approach, breeding efforts can address both biotic stresses and environmental changes, fostering resilience and sustainability in agriculture (Erbert, 2023).

The development and sharing of guidelines, protocols and data (Piergiovanni, 2022) The characterization, maintenance, and utilization of food legume genetic resources are critical for breeding new varieties with enhanced adaptability, improved quality traits, and higher nutritional value. Recent advancements in genomics and metabolomics provide unprecedented opportunities to explore heritable diversity, identify the genetic basis of phenotypic traits, and develop genomic prediction tools. These technologies also deepen the understanding of Genotype × Environment interactions, enabling more precise breeding strategies (Rocchetti et al., 2022).

In this context, creating well-described collections based on pure single-seed-descent (SSD) lines, where phenotypic traits are directly linked to specific genotypes, offers a powerful approach to efficiently manage genetic resources and generate unique, accessible information for users. This concept, termed "Intelligent Collections" (ICs), has been proposed for chickpea, as well as for common bean (Cortinovis et al., 2021), lentil (Guerra-García et al., 2021), and lupin (Kroc et al., 2021). ICs are developed through standardized protocols, with phenotypic characterization integrated during the multiplication and seed-increase stages, ensuring a robust foundation for future breeding and research efforts.

Advanced tools such as genomics, climate-based crop suitability modelling, plant phenotyping, soil biodiversity analyses, metabolomics, and nutritional quality assessment are being increasingly explored to enhance agricultural research and conservation efforts. Additionally, breakthroughs in sequencing technologies have significantly reduced production costs, enabling the efficient analysis of large volumes of germplasm. This progress has opened new possibilities for screening gene bank collections more effectively, particularly in identifying DNA sequence variations. (van Treuren and van Hintum, 2014).

Designing a multi-location variety testing system and evaluation networks – one successful example is EVA networks. All activities are designed to deepen understanding of valuable traits in publicly available crop germplasm, with the aim of integrating these traits into public and private breeding programs. Evaluation data from diverse environments across Europe are meant to identify adapted accessions for developing climate-resilient crops. The primary goal is to unite diverse stakeholders of Plant Genetic Resources for Food and Agriculture (PGRFA) to collectively enhance understanding of the genetic diversity preserved in gene banks and to make this material accessible for breeding and research purposes. This European Initiative holds strategic importance for Europe, offering a platform to promote the sustainable use of PGRFA, support the adaptation of European agriculture to climate change, and contribute to achieving relevant Sustainable Development Goals (SDGs). Through collaborative projects involving public and private sector partners, as well as participatory plant breeding initiatives, EVA is generating standardized evaluation data, both phenotypic and genotypic, for seven legumes crop groups (EVA legumes, 2024).

Exploring the landraces - the local germplasm, oftentimes associated with traditional sustainable farming systems, incorporates diverse and dynamic gene pools associated to adaptive traits that allow subsistence, in a changing climate. Initiatives such as (ExploDiv, 2022) are focused on exploring the potential of locally adapted and genetically diverse resources. Previous studies on landraces showed their potential to address ongoing and emerging challenges in real farms under biotic and abiotic stressful conditions. Despite their variable phenology and typically modest yields, local ecotypes often boast high nutritional value. Landraces are essential in plant breeding, possessing traits for improved nutrient efficiency and resilience to abiotic stresses such as drought, salinity, and heat. Systematic evaluation of these resources can uncover genetic diversity, aiding in the discovery of alleles that enhance both yield and stress tolerance. This strategy holds promise to increase the productivity and resilience of staple crops in environmentally vulnerable regions. (Dwivedi et al, 2016).

Citizen science experiments for creating participatory and decentralized innovation framework. The goal is to implement a decentralized approach for conserving food legume genetic resources. citizens are actively engaged in evaluation and conservation efforts, as well as in seed sharing and exchange initiatives. The gain is to disseminate knowledge related to legume biodiversity and to empower citizens to participate directly in these activities (pulsesincrease.eu).

Effective collaboration between research institutions, farmers, and international organizations is crucial to tackle these challenges and secure the enduring availability of legume genetic diversity for the benefit of future generations. As the most important directions to consolidate the availability and the access for valuable use of legumes genetic resources, some synergic and imperative activities are in progress at different levels, in national and international initiatives:

- enhancement of farm diversity and practices by preserving local biological resources and improving access to new resources and knowledge, focusing on legume traits that enhance adaptability to variable and changing climates;
- conserving the wide legume diversity, including neglected species, landraces, traditional and modern breeds, and varieties;
- preservation of the complexity and heterogeneity of farms to ensure continuous ecosystem services, support recovery from disturbances, and provide habitats for associated biodiversity;
- embrace participatory and transdisciplinary approaches in research and conservation, using a social-ecological systems framework to develop and promote locally relevant strategies that strengthen resilience, informed by local knowledge;
- strengthen research efforts, including: (i) investigating how legume resources enhance the resilience of production systems, particularly in recovering from multiple stresses; (ii) studying resilience strategies that integrate diverse legume components across scales; and (iii) conducting long-term studies to evaluate the contribution of legume genetic resources to resilience over medium and long periods;
- expand institutional and policy support to encourage the broader adoption of diversity-rich practices that enhance resilience;
- mobilizing experts to collaboratively plan for the more efficient and effective conservation and the use of legumes diversity;
- allocation of funding to generate data and to support regional strategies for *ex situ* and *in situ* conservation and utilization of crop diversity.

CONCLUSIONS

Sustainability is imperative, particularly within agri-food systems. Agrobiodiversity conservation demands feasible solutions that are both economically competitive and environmentally beneficial. Facilitated access to Plant Genetic Resources for Food and Agriculture is essential for promoting sustainable crop production and enhancing food and nutrition security. Access and utilization of genetic resources and well documented data must be streamlined. Making related information available under a Standard Material Transfer Agreement (SMTA), and combining it with additional measures, would eliminate legal ambiguities and reduce transaction costs for conservers, curators, and users of genetic resources. This, in turn, would support plant breeders and farmers in effectively fulfilling their mission.

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