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M Hemalatha
Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India

VK Deshpande
Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India

Corresponding Author
M Hemalatha
Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India

Plant genetic resources

M Hemalatha and VK Deshpande

Abstract
Plant genetic resources are the biological basis of food security. Plant genetic resources for food and agriculture comprises diversity of seeds and planting materials of traditional varieties and modern cultivars, crop wild relatives and different wild plant species. It provides wealth and food diversity for humans and animals, fiber, fuel, healthful plants, affects water regulation in nature, prevents soil erosion and degradation, allows the development of sport, recreation and ecotourism. Users of Plant Genetic Resources (PGR) will probably utilize these capacities to significantly increase the efficiency and effectiveness of their efforts to conserve, discover and utilize novel qualities in PGR and facilitate to accomplish the Sustainable Development Goals (SDGs). During this review it's discussed about efforts for the conservation of resources and sources.

Keywords: Plant genetic resources, gene banks, PGR management, crop wild relatives, modern cultivars and traditional varieties

1. Introduction
Germplasm is living genetic resources such as seeds or tissues that are maintained for the purpose of animal and plant breeding, preservation, and alternative analysis uses. These resources could take the shape of seed collections stored in seed banks, trees growing in nurseries, animal breeding lines maintained in animal breeding programs or gene banks etc. [1]. Germplasm collections will vary from collections of wild species to elite, domesticated breeding lines that have undergone extensive human selection. Germplasm collection is very important for the maintenance of biological diversity and food security.

2. Plant Genetic Resources
Plant genetic materials of actual or potential value describe the variability within plants resulting from human and natural selection over thousands of years. Its intrinsic value relates mainly to agricultural crops. In state of the World's Plant Genetic Resources for Food and Agriculture (1998), the FAO defined plant genetic resources for food and agriculture (PGRFA) as the diversity of genetic material contained in traditional cultivars and modern cultivars, as well as in wild-cultured relatives and other wild plant species, which can be used now or in the future for food and agriculture [2]. The conservation of plant genetic resources is becoming increasingly important as more and more plants are threatened or become rare. At the same time, a growing world population and rapid climate change have prompted people to search for new resilient and nutritious crops.
Plant conservation strategies generally combine elements of on-farm conservation (as part of the crop production cycle, where it evolves and supports farmers' needs), ex situ or in situ [3]. Mostly in situ conservation concerns crop wild relatives, source of genetic variation for crop improvement programs. Plant genetic resources preserved by either of these methods are often referred to as germplasm.

3. Efforts for the Conservation of Plant Genetic Resources
Efforts to conserve plant genetic resources after World War II came primarily from breeder organizations in the US and Europe, resulting in crop-specific collections primarily located in developed countries (e.g., CIMMYT, IRRI). Harvesting and conservation of plant genetic resources against genetic erosion is carried out by organizations such as the European Society for Breeding Research (EUCARPIA) and the Rockefeller Foundation [4]. A pivotal event in the conservation of plant genetic resources was the establishment in 1974 of the International Board on Plant Genetic Resources (IBPGR) (or Biodiversity International), whose directive was to encourage and support worldwide efforts to collect and conserve the necessary plant germplasm for future use research and production.

As a sign of international recognition of the importance of genetic resources, the IBPGR trained scientists to build a global network of gene banks.

Regarding genetic resources, international agreements require a competent and valuable global system to ensure that distinctive genetic diversity is permanently preserved and available for use. The Global Plan of Action for the Conservation and Proprietary Use of Plant Genetic Resources for Food and Agriculture (GPA), adopted by several countries at the 1996 International Technical Conference on Plant Genetic Resources, publicized the benefits of the global system. A reasonable system supports more planning and coordination, costs can be reduced and the conservation work can be placed on a scientifically sound and financially viable basis. This would set the foundation for extended consumption of plant genetic resources for food and agriculture, in the context of more capable conservation [5].

The development of a global system under active international agreements required that international efforts on plant genetic resources (1983) be reviewed in accordance with the Convention on Biological Diversity (1992). This led to the international agreement on plant genetic resources for food and agriculture. (ITPGRFA), which ultimately has the specific goal of conserving and sustainably using plant genetic resources for food and agriculture, and thus the equitable and equitable distribution of the benefits [6].

To fill the gaps in financial resources that continue to plague ex situ conservation efforts, recognizing that sustained funding would be needed, and to support the growth and maintenance of the rational global system identified in ITPGRFA and GPA, the Global Crop Diversity Trust was established by the Food and Agriculture Organization of the United Nations (FAO) and Bioversity International on behalf of the Consultative Group on International Agricultural Research (CGIAR). The Trust's goal is to offer the world's leading ex situ crop collections, a reliable and sustainable source of funding. Further conservation effort for plant genetic resources is yet more necessary. Greater efforts to conserve plant genetic resources are all the more necessary. A 2016 global study of over 1,000 species of wild crop relatives rated 70% as a high priority for further collection to improve their representation in seed banks and found that 29% were fully committed to ex situ conservation were missing [7]. A conceptual overview of the role is given in "The Role of the Global Crop Diversity Trust in Helping Guarantee the Long-term Conservation and Availability of PGRFA "(Global Crop Diversity Trust 2007c) [8], and activities are described on the Trust website (www.croptrust.org). In combination, the approaches give a comprehensive view on the present problems concerning the conservation and use of plant genetic resources, and therefore the views on better arrangements within the future for their management.

In order to fill the gaps in the collections and to save the unique diversity, the collection needs of plant resources, before it is uprooted, has been in situ for decades (Frankel and Bennett 1970, Hawkes 1971, Harlan 1972, Wilkes 1977) [9-12] and remains to be highlighted (Zedan 1995, Vetelainen *et al*. 2009, Hammer *et al*. 2003, Kiambi *et al*. 2005, Wilkes 2007, Maxted and Kell 2009, Johnson 2008, Burke *et al*. 2009, Damiana 2008) [13-21]. FAO (2009b) [22] emphasizes the necessity for collection particularly for unnoticed crop diversity. Many of the international gene banks within the CGIAR are presently highlight the necessity to gather CWR (Halewood and Sood 2006) [23], and U.S. germplasm professionals ranked getting further materials because the preferred funding priority for the U.S. germplasm system (Zohrabian *et al*. 2003) [24]. Despite these attempts, the accessions variety collected annually on the average weakened since the mid-1980's (FAO 2009b, Fowler *et al*. 2001) [22, 25].

Regarding regeneration backlogs, each approach that assesses current regeneration desires acknowledges substantial ex situ issues resonated in assessments and analysis of the status of plant genetic resources conservation (FAO 2009b, Dulloo *et al*. 2008, Imperial college Wye 2002, Engels and Rao 1998, Hammer *et al*. 2003, Fowler and Hodgkin 2004, Schoen *et al*. 1998, Qualset and Shands 2005, Hammer 2004) [22, 26, 27, 28, 15, 29, 30, 31, 32]. A 2020 study found that 93.3% of crop wild relatives native to the us were poorly delineated in exsitu conservation repositories, whereas 93.1% were inadequately preserved in their natural habitats [33].

4. Seed Collections and Gene Banks

The aim of the conservation method is to expand genetic diversity with as few gene pools as possible. Attempting to do this requires knowledge of target genetic diversity, environmental requirements, breeding system, population composition, and geographic distribution. The classification, conservation, location, and examining of genetic diversity in a very bound natural location ought to so be incorporated within the conservation of the wild species component. The elementary model for establishing a natural reserve conservation includes site evaluation, coming up with the reserve, political and socioeconomic factors, style of the reserve, assessment of reserve sustainability, establishment of the reserve, initiation of the reserve management set up, handling and watching the reserve, use of reserve traditionally or professionally, management plan style and linkage to ex situ conservation (complimentary) analysis programs and academic organizations. An intensive example of the creation and monitoring of a conservation area is the Ammiad experiment in Israel, which focuses on the natural diversity of wild species of *T. turgidum* [34].

There are 5 necessary sources of germplasm collections [35]. They're the Centre of diversity, gene banks, gene sanctuaries, Seed companies, and Farmers fields. Based on the utilization and length of conservation, seed collections are of 3 types:

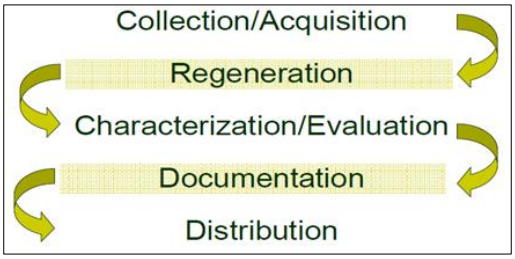
1. **Base collections:** It includes the most range of accessions on the market in a crop. These are meant for future conservation (up to 50 years or more) and are stored at 18 or 20ºC in hermetically sealed containers. The seeds are dried to 5 (+-1) % moisture and have over 85% initial seed viability. These collections are distributed just for the aim of regeneration and are used only germplasm from alternative sources isn't available to be used in breeding
2. **Active collections:** This class of germplasm is actively used in breeding programmes and are preserved for medium term (8-10 years or more). These collections are stored at zero degree Celsius with moisture content around 8%. Germination check is carried out once every 5-10 years to assess the reduction in seed viability.
3. **Working collection:** These collections are oftentimes utilized by breeders in their crop programmes. These are stored for a brief term (3 to 5 years). The seed is stored at 5-10 ºC with moisture content of 8-10%.

There is another category of seed collections referred to as core collection. It refers to a subset of the base collection that represents the large collection or base collection. In alternative words, the core collection is a limited set of accessions derived from existing germplasm collections, chosen to represent the genetics within the whole collection.
Common crop varieties under numerous cropping schemes are maintained by farmers among traditional farming systems and develop an area of those conservation techniques. For example, Landraces are planted and harvested, and also the farmer frequently saves some of the harvested seed for resowing in following seasons. During this situation, it's the farmer who is saving the germplasm, whether or not wittingly or accidentally. The conservationist can keep a watch on things however isn't curious about the actual conservation [36]. While it is beneficial to preserve landraces in this way, it is dangerous within the sense that farmers can still amendment from evolving landraces to modern cultivars, and so miss a vital resource for the future [37].
Gene banks worldwide held 5.43 million accessions by the end of 2019 [38] and only 5.8% of those accessions are kept as living field collections and also the remainder of these accessions are cryopreserved and accumulated as DNA [39]. 290 gene banks across the world up to Dec 2019 are ready to preserve 96,000 of around 1700 species with a major interest for IUCN, as well as wild relatives of crops that are essential for domestic and global food stability [40]. The USDA-ARS National Plant Germplasm System is that the world's largest supplier of plant genetic capital, with 595,451 accessions covering 15,970 plants. Nevertheless, the bulk of them are yearly species command as seeds, with the National small Grains Set accounting for 25% of all accessions [41, 42] whereas woody perennials are less depicted [43, 44]. of these major collections of annual fruit crops are preserved at institutes that contain the National Fruit collection within the United [45], the N.I. Vavilov All-Russian Science research Institute of Plant Industry's fruit collection [46], and also the Foreign Centre for analysis in science [47, 48]. The Crop Trust's CGIAR gene bank Platform permits CGIAR gene banks to fulfill their fiduciary duties below the International pact on PGRFA to sustain and provide additional accessions of crops and trees [49]. The eleven CGIAR gene banks are absolutely set as crop diversity hotspots, guaranteeing that germplasm acquisitions and distributions are world in range, with a various choice of partners and users [38].
In field gene banks across forty four countries, covering six geographic regions, the ICRAF platform alone has 11,000 accessions of sixty industrially valuable tree and nut species, primarily from Asia and Africa. Around one third of all recognized plant species (over 120,000) are found in botanical gardens worldwide [49, 50]. Most botanical gardens started as medicative plant collections or farming exhibits and ever since, several have developed into foremost analysis establishments dedicated to the preservation of worldwide plant biodiversity [51]. In response to a request from the XVI International botanic Congress to safeguard the world's vulnerable plant diversity, botanical Gardens Conservation International (BGCI) was founded in 2000 [52]. many accessions worldwide is found on on-line databases like Genesys [53], BGCI's Plant Search [54], and also the FAO's international information and Early Alert System on Plant Genetic Tools for Food and Agriculture (WIEWS) web site [55]. Forages are understated in ex situ collections compared to food crops [56], with solely concerning 182,000 accessions covering about a thousand species of grasses, legumes, and fodder trees spent in eighty national and international sequence banks registered in Genesys, compared to about 7.4 million plant accessions saved in around 1750 gene banks worldwide [57].
Through germplasm summary from varied research centres located in foreign countries and germplasm collection from within the country and around the world, the National Bureau of Plant Genetic Resources (NBPGR) patterned within the improvement of various crop plants, intensification and diversification of agriculture in India and conservation therefrom comprising the foremost vital variety of 452,212 accessions [58]. the foremost important number of species was preserved by germplasm banks corresponding to the U.S.A. National Plant Germplasm System (USDA), EMBRAPA (Brazil), and IBONE (Argentina), with regarding 48, 51, and seventy two species, respectively [59, 60, 61].
Users of Plant Genetic Resources (PGRs) get to use these resources to boost the potency and effectiveness of their efforts to safeguard, explore, and use novel qualities in PGRs, in addition as support to the accomplishment of the property Development Goals (SDGs) [62]. The United Nations sustainable Development Goals require the preservation of genetic diversity of seeds through well-controlled seed and field gene banks at national and international scales as an important step against world hunger [63].

5. PGR Management

5.1 Activities

Plant Genetic Resources consist of the subsequent management activities.



PGR Informatics is the management (creation, storage, retrieval and presentation) and analyses (discovery, exploration and extraction) of diverse information (facts, figures, statistics, knowledge and news).
PGR Informatics has supposed importance because of the following factors:

1. Increased awareness about PGRFA,
2. Availability of information in text, images, maps, videos, etc.,
3. Various international agreements (CBD, GPA, ITPGRFA) coming into force,
4. Technologies to record, link and archive such varied types of information,
5. Increasing power (falling costs) of computers and internet to ease access and retrieval.

Basic advantage of an organized digital data system is that it provides truthful and just chance for all to access. On-line portals, as a consequence of PGR Informatics, modify non-exclusive access to PGR info to an oversized variety of users concerned in overlapping analysis areas on PGR management. Typically, information is collected on details of multitude of passport knowledge as well as taxonomy, biogeography, and

ethnobotany of the germplasm acquisitions (domestic collections and exotic introductions), their seed health, multiplication for supply and conservation, regeneration, experimental data on characterization and analysis resulting in utilization. Additionally, to field data, it additionally contains organic chemistry and genomic data furthermore as publications. Once the data is digitized and saved, computer technologies permit organization and analysis no matter the scale and kinds of information resulting in higher visual image and predictions.

ICAR-NBPGR hosts the second largest genebank in the world. The operations are managed by Germplasm Evaluation, Divisions of Plant Exploration and Germplasm Collection, Genomic Resources and Plant Quarantine, Germplasm Conservation additionally to the Units of Germplasm Exchange and Tissue Culture and Cryopreservation. ICARNBPGR has the network of ten Regional Stations in India covering completely different agro-climatic zones to perform PGR activities together with characterization, evaluation, collection and maintenance of various crops.

5.2 They are as follows

- **Shimla (Himachal Pradesh):** Established in 1960 - Temperate crops.
- **Jodhpur (Rajasthan):** Established in 1965 - Agri-horticultural crops germplasm of arid and semiarid zones.
- **Shillong (Meghalaya):** Established in 1978- Agri-horticultural crops germplasm of north-eastern region involving Sikkim and parts of north Bengal.
- **Bhowali (Uttarakhand):** Established in 1985 - Agri-horticultural crops germplasm of sub-temperate region.
- **Thrissur (Kerala):** Established in 1977 - Agri-horticultural crops germplasm of southern peninsular region with particular emphasis on spices and plantation crops.
- **Akola (Maharashtra):** Established in 1977 - Agri-horticultural crops germplasm of central India and Deccan Plateau.
- **Cuttack (Odisha):** Established in 1985 - Agri-horticultural crops germplasm of eastern peninsular region with major importance on rice germplasm.
- **Srinagar (Jammu & Kashmir):** Established in 1988 - Agri-horticultural germplasm of temperate crops.
- **Hyderabad (Telangana):** Established in 1985 - Quarantine clearance of Agri-horticultural crops germplasm of Telangana, Andhra Pradesh and adjoining areas.
- **Ranchi (Jharkhand):** Established in 1988 - Germplasm of tropical fruits and other field crops of West Bengal, Jharkhand eastern Uttar Pradesh and Bihar.

5.3 Through Molecular Markers

The management of genetic resources of the plant by molecular markers can be achieved through the use of markers such as Isozyme markers, RFLP, RAPD, ISSR, AFLP, Microsatellite markers [64], single-nucleotide polymorphism (SNP) and sequence-based markers.

Molecular markers are commonly used to achieve the analysis of the germ-plasm diversity and the DNA fingerprint. By the range of germplasm analysis, biological process relationship, core collection development and gene flow studies can be realized. DNA fingerprinting can achieve germplasm identification, genetic purity/genetic stability, specific germplasm identification and validation. The utility of molecular markers and genomic analysis is for PGR in crop improvement. This suggests that genomic research is ultimately unlocking the genetic potential of wild and cultivated germplasm resources for the benefit of society (Tanksley and McCouch, 1997) [65].

The utility of molecular markers and genome analysis within the context of using PGR for crop improvement include

- Diversity screening to detect genetically similar or different accessions,
- Gene mapping to identify purely heritable markers in close proximity to genetic factors associated with quantitative traits (QTLs)
- Association studies to directly extract genetic diversity from PGRs and identify these alleles useful for the necessary agronomic properties.

Recent publications that integrate the technologies offered and their application within the analysis of germplasm collections, the population of wild plants and plant breeding incorporates those by callow *et al*. (1997) [66], Henry (2001) [67] and Newbury (2003) [68].

The increasing availability of molecular marker systems opened new possibilities for the evaluation of PGR cultivars to be used for crop improvement (Bretting and Widerlechner, 1995; Karp *et al*., 1997, Karp *et al*. al., 1998) [69-71]. For an efficient assessment of diversity, molecular markers should ideally be selection-neutral, extremely polymorphic, well distributed across the genome, and inexpensive and labor-efficient (Bretting and Widerlechner, 1995; Van Treuen, 2000) [69, 72]. Genetic markers that meet these requirements are protein markers (i.e. isoenzymes) and DNA markers resembling fragment length polymorphisms (RFLPs) and microsatellite or direct sequence repeats (SSRs). Since the latter two types of markers require prior information from DNA sequences, several types of universal dominant molecular markers have also been used in PGR diversity studies, such as e.g. B. Random Amplified Polymorphic DNA (RAPD) and Amplified Fragment Length Polymorphisms (AFLP). However, for example, the latter do not seem to be suitable for assessing mating behavior or PGR status.

Some of the highly usually used molecular marker techniques used for characterizing plant genetic resources are elaborated here under:

5.3.1 Random Amplified Polymorphic DNA (RAPD)

RAPDs were the primary PCR-based molecular markers to be employed in genetic variation analyses. RAPD markers are generated through the random amplification of genomic DNA using short decamer primers, separation of the obtained fragments on agarose gel within the presence of ethidium bromide and finally, visualization beneath ultraviolet light. The major drawback of this technique is that the identification depends on reaction conditions which may vary between laboratories. Arbitrarily primed polymerase chain reaction (APPCR) and DNA amplification fingerprinting (DAF) are independently developed methods that are variants of RAPD.

5.3.2 Microsatellites or simple Sequence Repeats (SSR)

SSRs are tandem continual sequences discovered among eukaryotic genomes. These comprises sequences of repetitions, comprising basic short motifs usually between two and six base-pairs long. Polymorphisms related to a particular locus are due to the variation in length of the

microsatellite that successively depends on the amount of repetitions of the fundamental motif. Variations in the number of repeated units are primarily due to strand slippage throughout DNA replication where the repeats permit matching via excision or addition of repeats. As slippage in replication is a lot of possible than point mutations, microsatellite loci tend to be hypervariable. Microsatellites are extremely common genetic markers as they possess: high abundance, co-dominant inheritance, huge extent of factor diversity, easy assessing SSR size variation through PCR with pairs of flanking primers and high reproducibility. Nevertheless, the development of microsatellites needs in depth information of DNA sequences. The growth of genomic resources like ESTs has led to EST-derived SSRs that are very helpful for assessing functional diversity.

5.3.3 Single Nucleotide Polymorphisms (SNPs)

Individual nucleotide variations in the genome sequence of individuals in a population are referred to as SNPs. SNPs are the broadest molecular markers in the genome. They are widespread in all genomes with a variable distribution between species. SNPs are often widespread in the non-coding regions of the genome. Once a SNP is present within coding regions, it will produce either non-synonymous mutations that result in an amino acid sequence change, or synonymous mutations that do not alter the amino acid sequence. Improvements in sequencing technology and increased manageability of the ever-expanding array of EST sequences have created an analysis of genetic variation that can be accomplished directly at the DNA level. Genotyping methods, as well as DNA chips, allele-specific PCR and primer extension approaches supported SNPs, are particularly engaging for their high information output and for their suitability for automation.

5.3.4 Diversity Array Technology

DArT is a common and inexpensive genotyping technology that detects all types of DNA variations (SNP, Indel, CNV, Methylation). It had been developed to overcome a number of the shortcomings of alternative molecular marker technologies similar to RFLP, AFLP and SSR. The main advantages of DArT markers are their low cost per data point, sequence information, application-relevant marker density and platform independence, combining the most cost-effective technology with application on modern platforms. DArT markers are useful for diversity analysis and for applications in genetics and physics. Mapping, identification of quantitative trait loci (QTL), rapid introgression of genomic regions in accelerated backcrossing programs, simultaneous marker-assisted selection for many traits, genome selection, cultivar identification, and genetic purity testing.

Table 1: Indian Rice Germplasm as Source of Important Genes (Identified through SNPs) [73]

Trait	Source	Gene
Submergence tolerance	FR-13	Sub 1
Salt tolerance	Pokkali Nona Bokra	Saltol SKC1
Drought tolerance	Nagina-22 Kala Keri	(gene not characterized)
BLB resistance	O. Longistaminata Bhog Jeera 1	Xa 21 Xa 13
BPH resistance	O.nivara	-

6. Issues and Controversies

Due to the high value and complexity of plant genetic resources, as well as the number of parties involved worldwide, some issues regarding their conservation and use have arisen. Much of the material for breeding programs was collected in the southern hemisphere and sent to gene banks in the northern hemisphere, a concern that led to a strong emphasis on national sovereignty over plant genetic resources and policies to correct the imbalance [74]. The enhanced use of plant genetic data for research, for instance to find genes of interest for drought tolerance, has led to differences in whether or not and to what extent the genetic information (separate from the organism) is subject to the international ABS standards [75].

Some of the challenges of genebank operations, particularly those that could carry hidden risks for long-term germplasm conservation and usage are:

6.1 Gene banks are generally underfunded

Several studies conducted between 1995 and 1997 established that almost all sequence banks lacked adequate funds, facilities and staff to maintain their germplasm collections (Zohrabian, 1995; U.S.A. GAO, 1997; Rubenstein *et al*., 2005) [76-78]. More than 20 years later, given the larger amount of germplasm stored in gene banks, the conclusion remains largely unchanged (Global Crop Diversity Trust, 2015) [79]. Genebank managers are still under pressure from their governments' budget constraints to do a lot with less by prioritizing genebank activities and reducing the impact on long-term conservation efforts (CGIAR, 2012) [80].

6.1.1 Task to update genebank data systems

Data management systems are critical to the management and utilization of germplasm (Fowler and Hodgkin, 2004) [29]. Several gene banks have developed their own data systems for managing germplasm. The quality of the information management system varies between institutions, which affects the use and evaluation of germplasm. A joint effort with the Crop Trust, Bioversity International and USDAARS led to the launch of the GRIN-Global system in 2011. To create more accessible germplasm, the Crop Trust has also set up a global portal called Genesys, where gene banks from around the world can be found sharing information about their gene pools. It enables automatic transfer and exchange of data from GRIN-Global to Genesys with a single click. Some of these efforts have strengthened germplasm documentation and information management in gene banks. However, each genebank needs to upgrade its IT infrastructure (servers, computers, and a backup generator) and more IT support (and IT skills) just to keep its current information. Effectively updating genebank information systems could be a major challenge that needs to be addressed.

6.2 Unfair research support

Achieving long-term germplasm management may depend on the expertise gained, the technologies designed for germplasm preservation (van Hintum *et al*., 2000) [81] and the way they are commonly used. This requires comprehensive and

integrated research programs to strengthen our information on germplasm storage, regeneration, seed viability and the growth of effective tools to assess and monitor germplasm viability. However, the role of supporting research in long-term germplasm conservation in several gene banks is diminishing. Due to budget constraints, many gene banks have streamlined research support to a lower priority, and some even have no research support policies for gene banks (McCouch *et al*., 2013) [82]. More research is important to develop new preservation technologies, especially for non-traditional seeds and vegetatively propagated plants, along with *in vitro* and cryopreservation strategies (Walters *et al*., 2013) [83]. Improvements in plant cryobiology in recent years have demonstrated the potential of cryopreservation as the most effective method for preserving the viability of unorthodox germplasm (Li and Pritchard, 2009; Engelmann, 2011; Pence, 2011; Chaudhury and Malik, 2016) [84-87]. Conservation-related research can provide better quality management systems and management of germplasm with distinct long-term biological characteristics and needs.

7. Conclusion

The global crop and regional methods signify a key undertaking in the field of plant genetic resources, mobilizing experts to design plans collaboratively for effective conservation and utilization of crop diversity ex situ. With continuing developments as new info becomes available and therefore the rational global system progresses, the strategies have the ability to serve the field into the future. Jointly the worldwide crop and regional strategies establish variety of major developments and needs in ex situ conservation of plant genetic resources.

Genetic resources are a gold mine, and that we got to build substantial long run investment for exploiting its full potential. Without associate intelligent and considered use of PGR it'll be difficult to attain sustainable advance in agricultural production. *In vitro* culture and cryopreservation are the necessary tools to gather and conserve genetic resources in difficult crops. And molecular markers techniques form a sturdy tool for PGR management in conservation, collection, utilization of PGR.

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