



Full Length Article

Plant Genetic Resources and Breeding: Current Scenario and Future Prospects

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ABSTRACT

Variation in any plant population is very important for breeders. Basic aim(s) of the plant breeding is/are high yield, quality and quantity, development, resistance or tolerance of adaptation ability to stress factors, etc. They are being utilized from the genetic variation to be able to manage all these component(s). On the other hand, an accomplished adaptation to environmental conditions and 'success' of the plant breeding is limited with genetic base (or gene pools) of the organism. Therefore, this wideness is measured by density of the biological diversity or biodiversity/bioversity. Aboveall, variation (genetic, among species, ecosystems, etc.) is essential for all kind of the plant breeding activities and obtained from the PGRs fundamentally (such as breeding lines, landraces, local varieties, primitive forms, wild & wide relatives, weed races, etc.). © 2011 Friends Science Publishers

Key Words: Genetic resources; Biodiversity; Biotechnology; Yield; Yield formation

Abbreviations: PGRs, plant genetic resources; CGIAR, Consultative Group on International Agricultural Researches; CWR, crop wild relatives; MA, marker-assisted PCR; GMOs, genetically modified organisms; DNA, Deoxyribonucleic acid; PCR, polymerase chain reaction; AFLP, amplified fragment length polymorphism; QTL, quantitative trait locus; eQTL, expression quantitative trait loci; SNP, single nucleotide polymorphism

INTRODUCTION

Plant breeding is an art and science, and it describes related methods for the creation, selection, and fixation of superior plants in the development of improved cultivars suited to the needs of growers and consumers (Moose & Muhm, 2008). About 250,000 angiosperms, 650,000 gymnosperms, 12,000 ferns, 14,000 bryophytes and 40,000 algae are taxonomically studies up to now (Govaerts, 2001; Hodkinson *et al.*, 2007). But, less than 3% plants are available to agriculture, and economically important 15–30 species responsible for the world's food, shelters, etc. (wheat, rice, maize, sorghum, cotton, lentil, flax, sunflower, tobacco, etc.). Especially, from them, cereals are very important, and this has a very significant and strategic role. It is estimated that some cereals such as rice (*Oryza sativa* L.), wheat (*Triticum* spp.) and only maize (*Zea mays* L.) provide about 50% of the calories people consume each day (Anonymous, 2007b; Bertrand & Mackill, 2008; Mondeil & Setboonsarng, 2009). But, about 840 million people (about 14% of the total population) have no adequate food (Anonymous, 2008a & 2008c) and more than 700 million people suffer from malnutrition in the world. Since 1960, world food production has been grown faster than the human population. The main reason of this positive development is green revolution; introgression of genes

reduced the plant height and increased the disease and viral resistance in wheat (Poehlman, 1979). According to the FAO (1999) (Cited by Mondeil & Setboonsarng, 2009), major causes of genetic erosion in crops are land clearing, population pressure, environmental and land degradation, pest/weeds/diseases, over-exploitation of species, overgrazing, collateral damages caused by conventional agriculture, contamination by genetically engineered or transgenic crops, and finally global climate change replacement local cultivars and changing agricultural systems.

Importance of plant biodiversity: The term of "biodiversity" is not only limited to "plant species richness", but are also related to all living components in the flora (Büchs, 2003). The diversity of PGRs from which the world's food crops are derived is steadily declining, due in part to the reliance of modern agriculture on a limited number of improved varieties (Mondeil & Setboonsarng, 2009). There are three types of biological diversity in the nature (i) intraspecific (genetic), (ii) species and (iii) ecosystem diversity (Hammer, 2000). The importance of genetic diversity (biodiversity) in plant breeding was recognized by the 1960s and Sir Otto Frankel coined the term "genetic resources" in 1967 to highlight the relevance and need to consider germplasm as natural resource for the long-term breeding of crop plants (Yunbi, 2010).

Nevertheless, the global spread of commercial cultivars is reducing the genetic diversity that needed to continue crop improvement. The overall objective of the plant breeding is to improve of the agro-economic traits such as yield and yield components in the plant species' parts like leaf, stem, tuber, root, flower, fruit, seed etc (Gepts, 2002; Ulukan, 2008). From them, plant genetic diversity refers to any variation in the nucleotides of genomes of organisms (Hawkes, 1991; Kasha, 1999; Ulukan, 2008). Genetic studies, therefore cannot be conducted if no variation exists within plant species. The germplasm centre(s) of cultivated plants species was/were for the first time offered by a researcher *la Candolle* (Engels *et al.*, 2006), later, after the publication of Vavilov's "*On the Origin of Cultivated Plants*" and some researchers suggested sub-centers of origin (or gene centers) and totally their number has reached to 13-14, but mainly its number is 8 (Vavilov, 1926, 1951; Perrino, 2005; Ulukan, 2010; Fig. 1). However, these centers are not always equivalent to the biodiversity centers, because they may have originated in one geographic area, but domesticated elsewhere. Today, many plant species have been lost or under threat for their genetical components and their genetic bases have narrowed or are being narrowed. Several species have lost their resistance potential against biotic and abiotic stresses. This point is especially important for minimizing the effects of stress factor(s). A clear category of plant genetic diversity has been summarized in Fig. 2. Two approaches are accepted for the maintaining techniques of the germplasms (Table I) and all of them are related with measurement of the genetic variation (Table II) including *in situ* and *ex situ* approaches. In *in situ* conservation, the maintenance is made in their natural habitat, but in *ex situ* conservation, the germplasms is collected in proper form and preserved in the chambers (centers, institutes, gene banks, seed banks, etc. Table III) under controlled conditions such as temperature, humidity, light, etc. (Engels *et al.*, 2006). During 1980s and 1990s, application of genetic engineering to crop improvement allowed genes from distantly related and even non-related taxa to be incorporated into crops, thereby broadening the value of CWRs by expanding their usefulness into secondary and tertiary crop gene pools. Because *ex situ* conservation is developed as the preferred approach to safeguard the PGRs during the 1970s and 1980s when *in situ* conservation of landraces in particular was thought to be impractical, the agricultural scientists did not embrace the *in situ* CWR conservation until the 1990s, despite the fact that influential crop scientists like Frankel (1970) and Jain (1975) (Cited by Meilleur & Hodgkin, 2004) had called for its use earlier.

Role of plants as a member of the PGRs and their utilization: The plant breeding activities started in its most primitive form since the first farmers saved the seeds of their best plants from one season to the next more than 10,000–12,000 years ago (Hawkes, 1983; Suslov *et al.*, 2002; Fowler & Hodgkin, 2004; Ulukan, 2010). Throughout

Table I: Maintenance methods and their relative worth for different categories of diversity (Modified from Hammer *et al.*, 2003)

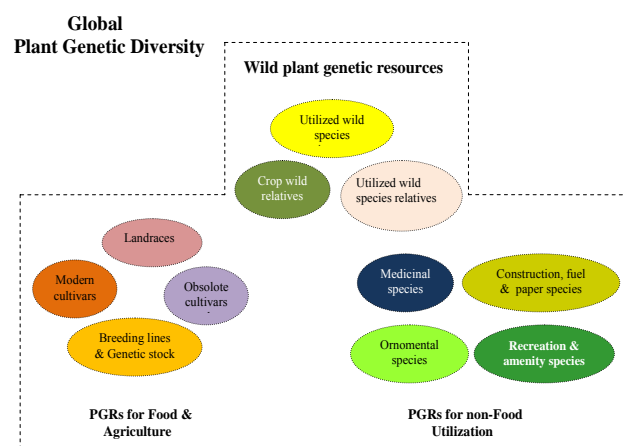
Category of Diversity	Methods of Maintenance		
	<i>Ex situ</i> (gene banks)	On-farm (agro-ecosystems)	<i>In situ</i> (other ecosystems)
Intraspecific diversity	C** W*	C** W ⁰	C ⁰ W***
Species diversity	WP* C** W*	WP** C*** W ⁰	WP* C ⁰ W***
Ecosystem diversity	WP* C ⁰ W ⁰ WP ⁰	WP** C** W ⁰ WP**	WP* C ⁰ W*** WP ⁰

The relative meaning of the methods for the different categories of diversity is illustrated by the number of stars: * = little meaning; ** = important; *** = very important; ⁰ = unimportant; C = cultivated plants; W = wild plant related to cultivated plants; WP = weedy plants

Fig. 1: Vavilov's suggested eight gene centers



Fig. 2: Distinct categories of plant genetic diversity (Modified from Maxted *et al.*, 2008)



the centuries, application of selection processes have had gradually become more effective (in a scientific way), bringing great qualitative and quantitative improvements (Hawkes, 1991). The aims are to re-establish or redesign these heritcal units for improved productivity (Anonymous,

Table II: Advantages and disadvantages of some methods of measuring genetic variation (Modified from Hammer *et al.*, 2003)

Method	Variation Detected	Sample through-put	Loci analyzed per assay	Reproducibility between assays	Analyzed Character		Required Techn. level
					Type	Inheritance	
Morphology	L	H	L number	M	Phenotypic trait	Qual./Quan.	L
Pedigree analysis	M	(n.a.)	(n.a.)	G	Degree of ancestry	(n.a.)	"
Isozymes	"	M	L number	M	Proteins	Co-Dominant	M
RFLP (L copy)	"	L	L number (specific)	G	DNA	"	H
RFLP (H copy)	H	"	H number (specific)	"	"	Dominant	"
RAPD	H to M	H	H number (random)	P	"	"	M
DNA sequencing	H	L	L number (specific)	G	"	Co-Dominant/Dominant	H
Seq taq SSRs	"	H	M number (specific)	"	"	Co-Dominant	"
AFLPs	M to H	"	H number (random)	M	"	Dominant	"

(n.a.) = No access; L: Low; H: High; M: Medium; G: Good; P: Poor; Qual.: Qualitative; Quan.: Quantitative

Table III: List of the some biodiversity conservation centers of the CGIAR's (Modified from Anonymous, 2009; Nagel *et al.*, 2009)

Centers	Target
CIAT (Centro Internacional de Agricultura Tropical)	Rice, Beans, Cassava, Forages, Pasture.
CIFOR (Center for International Forestry Research)	Forest conservation and Sust. Development.
CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo)	Maize, Wheat, Barley, Triticale.
CIP (Centro Internacional de la Papa)	Potato and Sweet potato
IPGRI (International Plant Genetic Resources Institute)	Conservation of gene pools for crops and forages.
ICARDA (International Center for Agricultural Research in the Dry Areas)	Wheat, Barley, Chickpea, Lentil, Pasture, Legumes, Small. ruminants.
ICLARM (International Center for Living Aquatic Resources Management)	Fisheries to imp. efficiency and Productivity of culture and capture fisheries.
ICRAF (International Centre for Research in Agro-forestry)	Land-use systems in developing countries.
ICRISAT (International Crops Research Institute for the Semi-Arid Tropics)	Cropping systems in Sorghum, Millet, Chickpea, Pigeonpea and Groundnut.
IFPRI (International Food Policy Research Institute)	Food Policy and Socio-economic Research & Institution- Building in Developing Countries.
IIMI (International Irrigation Management Institute)	Irrigation in developing countries.
IITA (International Institute of Tropical Agriculture)	Crop imp. and land manag. in humid and sub-humid tropics, farming sys. in maize, cassava, cowpea, yam, plantain, soybean, rice
ILRI (International Livestock Research Institute)	Livestock productivity and animal health
IRRI (International Rice Research Institute)	Global rice improvement
ISNAR (International Service for National Agricultural Research)	Strengthening and developing national agricultural research systems
WARDA (West Africa Rice Development Association)	Rice imp. in West Africa with research on rice in mangrove and inland swamps, upland conditions under irrigated conditions.

2008d). In practice, the plant breeding is a very complex and time-consuming procedure. Depending on the crop type, climate, environment, practices and economic or socio-economic conditions forms the similarity or difference in any plant breeding programs. Plant breeders adapt old crops to the new localities increase yields, improve resistance to pest and disease, enhance the nutritional quality and flavor of the fruits and vegetables; and develop traits that are useful for storage, shipping, processing of foods etc., (Prance, 1997; Anonymous, 2008c). Newly developed plants would give more nutritional values and sometimes easier to process, e.g., during cultivation, harvesting and post-harvest. For example, the malting barley (*Hordeum vulgare* L.) cultivar "Morex" has a high percentage of total malt extract released in 1978 (Hayes *et al.*, 2003). Development of the rapeseed (*Brassica rapa*) cultivars with a low content of the erucic acid improved the value of oil and extended the under cultivation areas (Jauhar, 2001). Resistance to various pathotypes is found in a number of different wild species and in the cultivated tetraploid subsp. *andigena*, which is the originally a

tetraploid subspecies of *S. tuberosum* (Bradshaw *et al.*, 2006). Evidence is building up that this type of resistance has penetrated into the cultigens from a wild resistant tetraploid, *S. oplocense* Hawkes (Hawkes, 1998). The F₁ hybrid of this cross, which has been named *S. sucrease*, is well-known weed species in Central Bolivia (Bradshaw *et al.*, 2006). The most famous example is the inclusion of eyespot resistance from the wild species (*Aegilops ventricosa* Tausch.) in wheat (Valkoun, 2001). Again, some resistant genes have been identified against coffee rust (*Hemileia vastatrix*) in the cultivated coffee (*Coffea arabica* L.), wild coffee species (*C. liberica* Hiern.) and (*C. canephora* L.). Likewise, resistance to bacterial leaf streak has been found in spontanea varieties of *Oryza sativa* L., the Asian cultivated rice, and in the related wild rice species (*O. rufipogon* Griff.) in Southeast Asia (Leroy *et al.*, 2006) (See also Table I). Wild plants have desirable traits but, as known and at the same time, they also contain many undesirable characters such as low yielding, low quality, susceptibility to pests and diseases, etc. Breeding effort to backcross such wild types with commercial varieties to the point where we

Fig. 3: Model of plant genetic conservation (Modified from Maxted *et al.*, 2008)

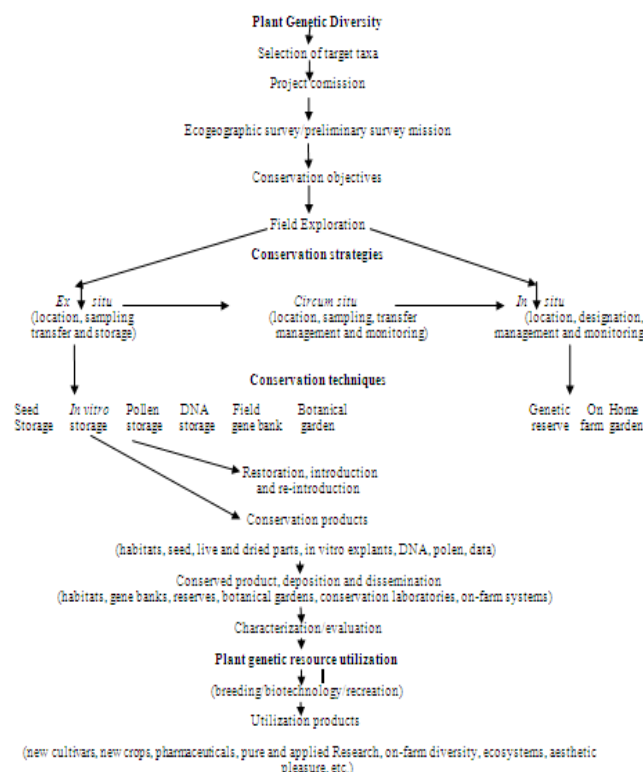
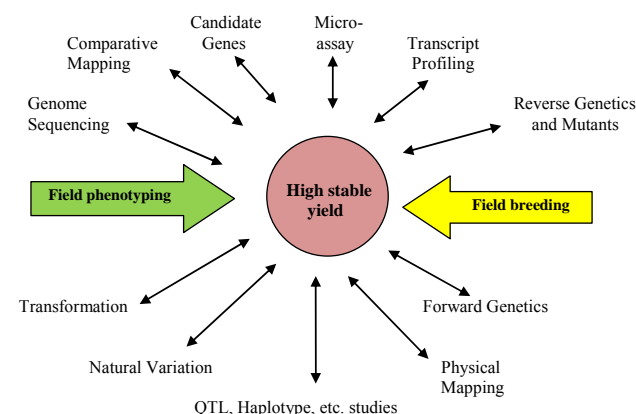


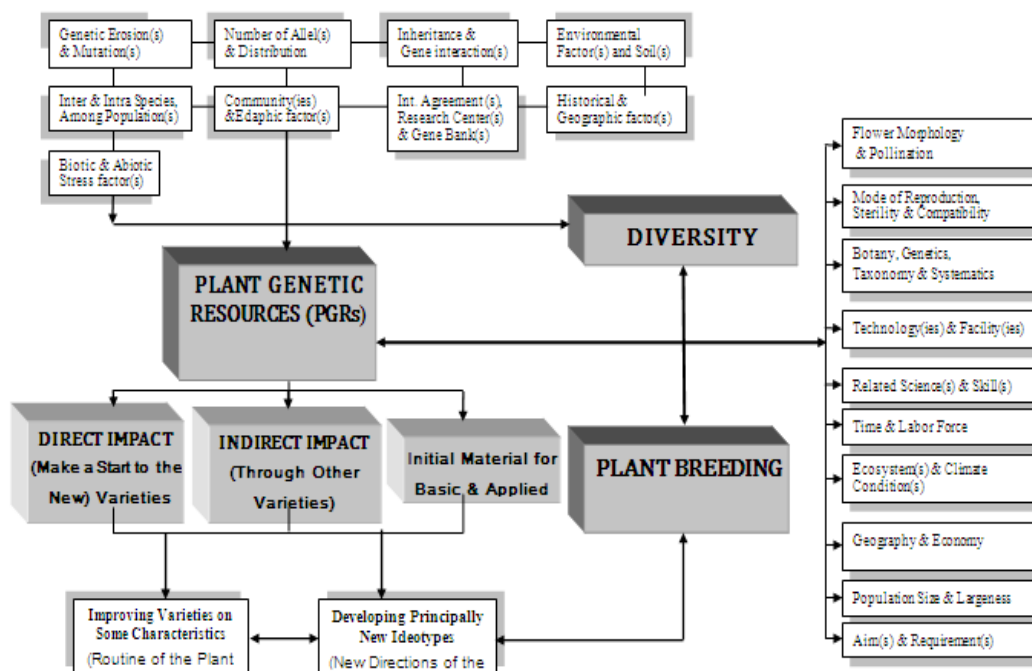
Fig. 4: Tools used in genomics and allied fields (Modified from Edmeades *et al.*, 2004)



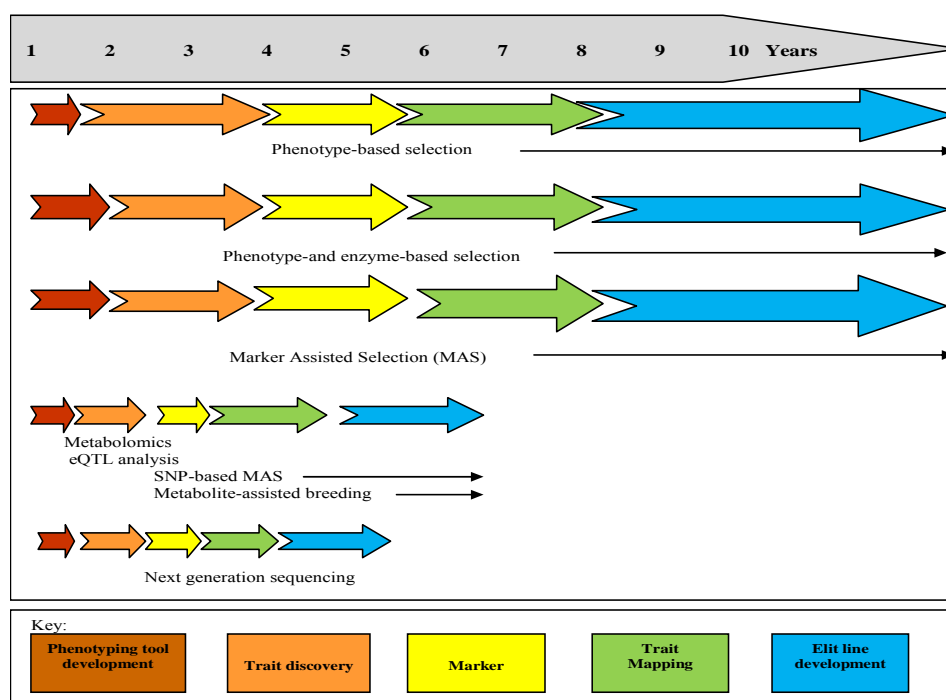
have the best of both (Ulukan, 2009). In addition to wide crossing, genetic engineering techniques enable of plant breeders to possibly find and introduce many important foreign genes into plants, provides valuable opportunities to modifying their genotypes, for resistance to stress factors and improving the quality components such as protein content, fiber content, etc. (Scharma *et al.*, 2002). The PGRs of wild species and traditionally grown landraces adapted to specific environments or showing specific traits, such as resistance to pest and disease or other environmental stresses (heat, drought, cold, etc.) can be pivotal in

achieving improvements in crops. For instance, in Africa the use of modern breeding techniques and diversity in *Cardaba gaddat* and *Musa balbisiana* allowed for the breeding of improved bananas (Anonymous, 2010a). Maize was originated in Mexico from a weed-grass plant, *teosinte* (David *et al.*, 1999; Anonymous, 2008d). Tomatoes and potatoes first time appeared in South America. At the time of their origin, tomatoes had small fruits to the size of a grape, and potatoes had knobby tubers with high concentrations of a family of bitter chemicals called glycoalkaloids, toxic to the humans (Hawkes, 1983). The majority of the traits associated with domestication of the crop plants (such as seed setting, early maturity, easy harvesting, greater size of harvested seeds or fruits, changes in plant growth form, reduction or losing bitter & toxic compounds, etc.) were already accomplished by the time of historic agricultural civilizations such as Egyptian, Chinese, or Mayan (Hawkes, 1983). In addition, these primitive crops were adapted to local ecologies; therefore, they remained genetically diverse for quality and quantity components. Numerous examples are available witnessing the increased productivity of crops. Beginning in the 1930s, plant breeders developed techniques to allow them to develop plants from two parents that could not normally produce viable ancestor. An example is the technique called “*embryo rescue*” (Anonymous, 2008b; Ulukan, 2009). In 1950s, plant breeders developed new methods of creating variation in an organism's genetic structure with some physical and chemical agent(s), through “*mutation breeding*”. In addition to this, many techniques have been developed today such as *tissue culture*, *anther culture*, *genetic engineering*, *molecular breeding*, etc., (Anonymous, 2000; Jauhar, 2001; Suslov *et al.*, 2002; Şehirli & Özgen, 2007; Ulukan, 2009; Yunbi, 2010).

To provide a stable food supply, agriculture needs diversity in crop plants and cultivars. So, most interesting developments occurred in maize cultivation in this respect. Development of double-cross hybrids to replace allogamous plants during the 1930s was responsible for about 7.0–12.0% increase in yield. Genetic improvement resulted in a grain yield increase of about 28.0% from 1930s to 1960s (Contreras, 2007). The adoption of single-cross hybrids in the 1970s resulted in further improvement in maize yield. The total yield improvement of single-cross hybrids over open pollinated cultivars were more than 50% (Jain, 1982). Similarly, noticeable yield improvements were recorded in wheat and rice during the 1960s and 1970s, which played a major role in increasing of the world food production. On the other hand, huge plant germplasms or genetic resources enabled the plant breeders to create novel gene combinations and select them according to their necessities in various part of the world (Glaszmann *et al.*, 2010). The diversity and availability of the PGRs are also increases when a crop is attacked by a disease or when unexpected challenges are needed to overcome (Anonymous, 2010a). This trend and the increasing

Fig. 5: Schematically relationships among the plant genetic resources (PGRs), biodiversity and plant breeding (Modified from Merezhko, 1998)**Fig. 6: Breeding technology timeline from past to present to future**

The breeding pipeline from 1980 to that envisaged in 2020. In the past, trait discovery was mainly based on phenotypic observations, whereas marker development was restricted to phenotypic or enzymatic or protein markers. Thus, trait mapping and elite line development was a laborious task. The technological advances of molecular biology in the 1980s and 1990s enabled the application of molecular markers and improved the speed of trait mapping and commercial material development. Today, the application of marker-assisted selection in combination with new -omics approaches, such as metabolomics or transcriptomics (e.g. eQTL studies) enabled rapid discovery of new traits and allelic variation and, thus, improves the time to market by several years. In the future, the progress in trait discovery tools, plus simultaneous whole genome sequencing for marker development and trait mapping should shorten the market introduction of new varieties to $\approx 4-5$ years (Modified from Fernie & Schauer, 2008)



industrialisation of agriculture are key factors in what can only be called genetic erosion and the disappearance and displacement of diverse, local populations of crops (Vernoy & Yiching, 2004). Cultivated plants under the various effects (especially improvement) of humankind and after 1950, massive genetic erosion begun (Lande, 1998). So, many valuable and desirable traits were lost due to this factor. In many parts of the world, many plants were not properly adapted to diverse cultivation practices. Many local varieties or crops were replaced with high yielding (with narrow gene pools) cultivar(s). As a result, many important and local plant gene resources disappeared without recognizing or describing properly from the flora. But, in some areas of the Mediterranean, cultivated land races are still grown on up to 25% of cropland (Hammer, 2000). The PGRs have emerged through years of evolution and natural processes (Linhart & Grant, 1996; Engels *et al.*, 2006). The cultivated PGRs are classified into three broad categories, namely (i) modern cultivars, (ii) high yielded cultivars (products of plant breeding in the formal system & typically have a high degree of genetic uniformity) and (iii) farmers' cultivars or traditional varieties e.g., product of breeding or selection carried out by farmers, either deliberately or not, continuously over generations (Harlan, 1975). Wild relatives together with weedy species, which have evolved over a long period of time and have coevolved with pests and diseases contributed to plant improvement (Harlan, 1981). It was first time used in 1993 (Hammer, 2000; Hammer *et al.*, 2003) and perceived as "common heritage" against to stress factors (Hammer *et al.*, 2003; Rao & Hodgkin, 2004; Buanec, 2005; Faizi & Ravichandran, 2008) and guarantee fighting against agricultural handicap(s). When called as the common heritage of the PGRs in 1920, they were perceived as national richness of owned country, and still the discussion continues on the ownership of the PGRs. Plant breeders commonly use wild species as gene donors to improve pest and disease resistance among the species and PGRs (Harlan, 1981).

Plant genetic diversity is not only a basis for adapting varieties and agriculture to different environmental conditions and constraints such as drought, outbreaks of pest and disease epidemics or climatic change, etc. but also a major contributor to the food production (Ulukan, 2010). Breeding new and high yielding crops varieties with better resistance to disease and adaptation to changing climates is important for ensuring the food security (Anonymous, 2010a). But, these crops are known not new. They had derived from currently grown commercial varieties, breeding lines and stocks, induced or natural mutations, old land races, primitive forms, weed races and wild species, etc., (generally from the PGRs) (Fehr, 1987). For instance, from them "weed races" exists as a part of the crop (weed complexes) in gene centers of the world. Similarly, they incorporate useful genes derived from wild types or related wild species that have moved from weedy forms into crops. In these instances nature has helped the breeder enabling

them to insert genes (useful for the agricultural aims) from wild species into a "Cultivated" genetic background (Şehirali & Özgen, 2007). "Wild relatives and species" that occur sometimes in the gene centers of cultivated plants, sometimes far outside them, and that can be crossed with the cultigens (which means, Latin *cultus*—cultivated & *genus*—kind; a cultivated/domestic organism) and we are already using them as crops and are still dependent upon the broad genetic base that exists in their wild relatives (Hawkes, 1983). Often, however, the term of genetic resources refer more specially to the types of "land races, primitive forms, weeds and wild forms" (Poehlman, 1979; Hawkes, 1983; Şehirali & Özgen, 1987; Nevo, 1998; Gepts, 2002; Wale, 2008), but the selected and cultivated form of plant germplasms have originally evolved from a wild plant population called "landrace" (Şehirali & Özgen, 1987; Nevo, 1998; Ulukan, 2010). Before breeding, each crop was a landrace, a mixture of many, sometimes hundreds of cultivars. In addition, they were far away from the uniformity. Despite all negatives, some landraces were better though they had come through selection by farmers over generations and had evolved to survive conditions on that particular farm (Moore, 2001). The maize was threatened by corn blight disease (CBD) in the US. But, thanks to the PGRs, problem was quickly solved by using the PGRs, and transferred the blight resistance genes from its wild form to cultivars in 1970. Similarly, bacterial wilt (*Pseudomonas solanacearum* E.F. Smith) resistance was re-established in this way using the PGRs in potatoes cultivation. Similarly, the world collection of potatoes was screened for wilt resistance until introduction of six lines of a primitive diploid cultivated species, *Solanum phureja*. Potatoes breeding for resistance to nematodes followed same pattern. In that the resistance genes to the potato "Cyst" nematodes are localized to Peru, Bolivia, and Northwestern Argentina (Gepts, 2002). As evident from the models of plant conservation techniques (Fig. 3), the integration of *in situ* and *ex situ* conservations of biodiversity (Rao & Hodgkin, 2004; Faizi & Ravichandran, 2008), the possibility of collaboration between plant breeders and growers and the use of the new biotechnological or advanced methods for exploring and manipulating the genetic basis of crop phenotypes are very important (Cleveland, 2001). Of these, *ex situ* gene banks play a pivotal role in preserving the wild relatives of crop plants as well as local varieties, which are grown in many places. As known, plants are often improved or better protected by using genes from wild species. These species found in the PGRs and they provide the basic input to all plant breeding programs, whether traditionally or transgenically based (Ullstrup, 1972; Anonymous, 2008f; Ulukan, 2010).

Future prospects of PGRs: Two major technologies in this regard include biotechnology, molecular biology (Anonymous, 2008c; Fig. 4). In biotechnology, with the advances in genomics, molecular tools for plant breeding

are becoming readily accessible and more affordable and useful. Plant breeding informatics will include improved pedigree records, sophisticated statistical designs and analyses, and database management to fully incorporate molecular markers, and to better estimate cultivar performance and breeding methodology used (Edmeades *et al.*, 2004; Anonymous, 2007b; Baenziger *et al.*, 2009; Fig. 4). Molecular biology has become possible to be overcome the obstacles, which can not be overed by classical plant breeding techniques. From them, technology level for the molecular genetics' (esp. molecular marker) (Anonymous, 2007b) enables our understanding of genetic resources more than any other type of genetic data. Relationship(s) among the PGRs, biodiversity and plant breeding were given details in Fig. 5. The identification of genes and molecular markers underlying these agronomic traits will help accelerate the breeding process and lead to improved varieties with improved yield and quality, tolerance to unfavourable environmental conditions and resistance to disease, etc. (Anonymous, 2007b; Baenziger *et al.*, 2009). All these technological developments are presented in the Fig. 6 as timeline. In days to come, 14 major research areas will be very important in the plant breeding (Gale & Devos, 1998; Ortiz, 1998; Anonymous, 2000; Sharma *et al.*, 2002; Doebley *et al.*, 2006; Anonymous, 2007b; Ozias-Akins & Dijk, 2007; Swaninathan, 2007; Vasil, 2007 & 2008; Schaart & Wissner, 2009). They are: (i) grafting and apomixis to fix hybrid vigour, (ii) Agro-infiltration, (iii) direct gene transfer, electroporation, polyethylene glycol techniques and DNA-vector *Agrobacterium*, (iv) *in vitro* gene shuffling (v) homologous recombination, (vi) male sterility systems with transgenics for hybrid seed in autogams, (vii) DNA methylation, (viii) parthenocarpy for seedless, (ix) induce RNA and silencing by RNA interference, (x) virus-induced gene silencing, (xi) interfering RNAs, (xii) reverse breeding, (xiii) gene Silencing or overexpression, (xiv) genetically modified organisms induction for early flowering, (xv) cisgenesis, (xvi) intragenesis, (xvii) genomics, phenome, metabolomics, QTL, eQTL, transgenics and xenogenics, (xviii) oligonucleotide-mediated mutation induction for the stress factors and finally (xiv) converting annual into perennials.

CONCLUSION

Advanced laboratory techniques are being used in plant biology such as molecular genetics, molecular biology, genomics, metabolomics, proteomics, bioinformatics, DNA sequencing, QTL and eQTL, etc. today. No matter what, certain plant breeding techniques keep their importance as long as the PGRs and biodiversity. Some of them are tentatively, some of them are not, and some of them are hopeful in the long run and near future. However, it is open that received technology level; obtained information will be help and increase our knowledge in this area, and will bring

many solutions to the encountered problems. Thanks to contribution of new findings with the support of scientific tools and techniques such as *in vitro* breeding, molecular breeding and transgenic breeding, all limits and handicaps could be overcome. But, this point is essential that to be able to get final success identify the aim(s) and study with large, representative and healthy sample(s) as possible as.

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