

IMPORTANCE OF CROP WILD RELATIVES AND LANDRACES GENETIC RESOURCES IN PLANT BREEDING PROGRAMMES

Abstract

Plant genetic resources are the biological basis of global food security. Agricultural diversity and genetic resources should be used more effectively to sustain the current level of food production and to solve future problems. The importance of plant genetic resources in the improvement of varieties with new features is indisputably known. The most effective use of plant genetic resources is undoubtedly in plant breeding and improvement of new varieties. In other words, it is used as a genitor. Since the cultivars are often inadequate in many genes, especially biotic and abiotic stress factors (diseases, pests, cold, drought, etc.), breeders constantly search for new sources of genetic materials. This review is based on reports in the landraces (primitive) varieties and crop wild relatives to explain the importance of genetic resources in plant breeding of reviewing scientific literature to pass.

Key words: plant genetic resources, landraces, crop wild relatives, plant breeding

Plant Genetic Resources

Conservation of genetic resources in a better way and new varieties are developed by taking advantage of their diversity. For this purpose, many international, regional and national institutions organized activities for better conservation and use of plant genetic resources. Therefore among countries and a large number of agreements involving the sharing of information and material use, it has been signed. According to Kate and Laird (1999), the financial value of using plant genetic resources is 500-800 billion US dollars per year. When faced with climate change, the yield of basic food plants does not diminish or be sustained, depending on the characteristics that can be transferred from wild species (Petit, 2001).

Plant breeders are supplied from the materials provided by the following centers (Frankel 1970).

1. Agricultural Centers
 - a) Cultivars in current use
 - b) Obsolete cultivars
 - c) Landraces (primitive) varieties
2. Plant Breeding Centers
 - a) Special genetic stocks such as resistance stocks, genetic and cytogenetic material
 - b) Induced mutations
 - c) Indroduction material
3. Centers Origin
 - a) Crop wild relatives
 - b) Weed species

Landraces Varieties

Since von Rünker in 1908 first used the term landrace (Zeven, 1998). It is a landraces (primitive) varieties, developed by farmers used selection and/or with natural selection, before modern plant breeding studies, which have local characteristics (taste, odor, color, etc.), each of which is known by local names. These varieties are very well adapted to the conditions of the geographical region where they are grown. They are very valuable as a gene source in the crop improvement of new varieties. However, because they cannot compete with the modern varieties which is developed by formal breeding methods, they are composed of heterogeneous genotype mixtures that are open to genetic erosion. Landraces varieties (village varieties) have played a very important role in agriculture production and breeding activities throughout the world. They have existed since the beginning (origin) of agriculture (Zeven 1998). In this process, they have undergone genetic modification.

Throughout history, farmers provided the seed requirement for the next year's cultivation from the products they regularly produce. These seeds, which are reserved for sowing by the breeder, are generally chosen from the best of the product, consciously or unconsciously. As a result of this process, the varieties of the landraces, which are local to the ecology specific to that ecology, emerged from the wild plant species. Landraces varieties, as well as having local cultural importance, include a portion or all of the following features (Camacho Villa et al., 2005):

- High genetic diversity.
- Local genetic adaptation.
- Recognizable features (geographic identity).
- Lack of modern plant breeding
- Associated with traditional farming systems.
- History and links in a specific locality.

It can be difficult to distinguish landraces varieties from old commercial varieties that are not long in production and are only protected by seeds (Negri et al. 2009). As a result, two different landraces varieties can be defined, which can be listed as:

- Primary landraces varieties: Without modern plant breeding, they are developed based on the selection of unique properties in the natural environment by the grower.
- Secondary landraces varieties: those that have been developed by plant breeding but currently only under protection for grower preference and seed in their natural environment.

Instead of landraces varieties; many terms such as local varieties, primitive variety, primitive diversity, primitive form, variety of farmers, traditional varieties, village variety and folk varieties were used as synonyms. However, there are inconsistencies in the application for each term. The use of terms such as “diversity” and “variety” in local varieties is confusing, considering these concepts are used to describe the material that has been improved with more plant breeding.

Landraces varieties still play a key role in food safety (Brush 1995). However, local varieties are very important not only in this aspect, but also; they are alternative farm systems such as organic agriculture (Negri et al. 2000). However, as a result of the spread of high-yielding commercial varieties, the attractiveness of landraces varieties has decreased. However, they are of great importance as a gene source. They are still being cultivated for marginal areas and

for small-scale markets (niche). As previously emphasized, however, they are open to erosion under the pressure of rapidly spreading commercial varieties. Therefore, they need to be taken under emergent protection.

Crop Wild Relatives

Crop wild relatives are the wild ancestors of cultivated crops. Geographical origins are closely related to a cultivated crop, which extends into areas known as crop origin centers of Vavilov, and are wild-type plants. They are either a wild ancestor of cultivated crops or a taxa that is closely related to it. Crop wild relatives of the crops provide significant resources to researchers for adaptation to climate changes in terms of their resistance to biotic and abiotic stress factors that they contain (Maxted et al. 2008; Lane and Jarvis 2007). Crop wild relatives have contributed millions of dollars to agriculture, both directly and indirectly, using biotic and abiotic stress to enhance the resistance of crops. (Dwivedi et al. 2008). It is a well known fact that, many plants such as sugar cane, tomato and tobacco would not be able to cultivate these plants commercially if they were not given resistance to diseases from their wild relatives (FAO, 1997). Generally these are important in terms of having high adaptability genes, environmental pressures, resistance to diseases and pests. In many species; in particular, polyploid species, culture types of relatives of the breeders in terms of the use of very important gene stores constitute. Nowadays, these relatives are used successfully in breeding. The possibility of eliminating some problems encountered in practice with biotechnological methods gradually increases the future importance of these species (Özgen and Akar 1993).

Wild species have been utilized for 39% diseases, 17% pests, 13% abiotic stress factors, 10% yield increase, 11% quality increase and 4% cytoplasmic male sterility and fertility restoration (Maxet and Kell 2009). The monetary value of the varieties developed with the use of wild relatives in breeding of crops is estimated to be approximately 115 billion dollars per year. It is not difficult to guess that this value has increased even more with the continuation of studies and improvement of new varieties since then (Hopkins and Maxted 2011). The use of wild gene resources in plant breeding has increased especially after 1990s. But this is not newly discovered. Wild relatives of plants have played a role in scientific plant breeding programs during the 20th century, especially in the case of new diseases and pests and in the damage caused by the cultivated varieties (Hijmans et al. 2000). Plant wild relatives were first used primarily in important crops such as wheat and maize. However, it constitutes an important potential for many other plants.

Wild relatives of cultivated plants play an important role in ensuring food safety. They have more genetic diversity than cultivated crops. This is because they have not been selected from a larger population to be domesticated, and may occur in a wide range of climate, soil and other factors. In addition, wild species, climate and other environmental factors continue to adapt to their environment as they change. While the crop plants can be protected from pests, diseases and drought by spraying and irrigation, wild-type populations naturally have the genetic composition to withstand such stresses. This situation carries potential genes in plant breeding for adaptation to adverse effects of climate change, resistance to new diseases and pests, and varieties to be improved in terms of tolerance to drought.

The large proportion of global food production is derived from a small number of varieties that have been improved in narrow genetic diversity and modern breeding. These new varieties damaged approximately 75% of the global plant genetic diversity due to the replacement of a much larger number of genetically diversified traditional products (FAO 1998).

The approach that best describes the relationship between cultivated plants and their wild relatives was made by Harlan and de Wet (1971). This approach describes three gene pools (Gene Pool Concept).

Gene pool 1: In this pool, the cultivated plants themselves (gene pool 1A) wild forms grow as weeds in agricultural areas (gene pool 1B).

Gene pool 2: This pool contains species that are less associated with the culture plants. These are wild relatives that are more difficult to produce using conventional breeding techniques, although gene transfer to cultured plants is possible.

Gene pool 3: Cultures include species where no gene transfer is performed from wild relatives. To take advantage of these resources, advanced genetic engineering techniques need to be used.

The Gene Pool Concept normally matches a taxonomic (phylogenetic) classification, but this may not always be the case. Hybridization barriers may exist between species with the same morphological structure. The best example of this (*Oryza sativa*) is the partial crossbreeding barrier between Japonica, Javanica and Indica. (Murphy 2007). On the other hand, for example, bread wheat (*Triticum aestivum* L.) is a culture plant formed by hybridization of two different species (*Triticum* x *Aegilops*).

While some new biotechnological methods such as protoplast fusion and DNA transformation have been developed, gene transfer from wild species is generally done by hybridization methods. Success in crossbreeding depends on the knowledge of cytotaxonomic relationships, cytogenetic structure and evolutionary development of the relationship between species (Knott and Dvorak 1976).

The most successful results in transferring the resistance to environmental stress to crops are obtained from hybridization with wild species such as *Aegilops*, *Agropyron* and *Haynaldia*, which are close relatives of wheat. The resistant of some *Aegilops* species in various leaf diseases is encouraging to benefit from these as a gene source in the breeding of wheat. For example, *Ae. triuncialis* and *Ae. ovata* is known to be tolerant to yellow and black rust.

One of the earliest examples of resistant varieties was the breeding (crossing) for potato blight (*Phytophthora infestans*) disease in potatoes. Potato blight has caused major damage in the middle of the 19th century famine in some parts of Scotland and in Ireland. In the 1900s, resistance genes were transferred from the wild potato species *Solanum demissum* to the potato crops (Hawkes, 1990). There are genes from *Solanum demissum*, a wild potato species that provides resistance to potato mildew disease. Many virus disease resistance genes that cause significant damage to potatoes are also found in wild potato species such as *S. acaule*, *S. stoloniferum* and *S. chacoense* (Özgen et al. 1995).

The BNYVV (Beet necrotic yellow and virus), soil-borne parasitic fungus *Polymyxa betae* in the genus Beny virus, which was first identified in Italy in 1950s, spread to sugar beet growing areas in the world in a short time and caused 80% yield losses. Due to the fact that it is difficult to struggle and the disease survives for more than 15 years, it makes the struggle methods out of the use of resistant varieties ineffective. The disease caused a decrease in yield in the sugar beet and the abandonment of the agriculture of this plant from being cost-effective (Asher 1999, Kutluk Yılmaz and Erkan, 2003). For this purpose, in the 1980s, rhizomania disease resistance genes were found in a wild species *Beta vulgaris ssp. maritima*; it was used to improved rhizomania resistant sugar beet varieties in England, Denmark and France. In this study, resistance genes of sugar beet (root rot, leaf blot) and pests (sugar beet root maggot) were also determined (Doney and Whitney 1990). It is known that wild sugar beet species with a resistance to leaf stain, which is an important disease of sugar beet, are *Beta patellaris*, *B. webbiana*, *B. procumbens*, *B. trigyna* and *B. lomatogona* and transferred genes from them to sugar beet.

In the 1970s, corn blight (*Helminthosporium maydis*) caused a loss of more than \$ 1000 million, causing a 50% loss of product in the southern regions of USA (Stolten et al. 2006). This problem was also solved by transferring the gene to the maize crop from wild Mexican maize plants (Shand, 1993).

Tomato (*Lycopersicon esculentum*) was crossed with two wild species, *L. hirsutum* and *L. peruvianum*, for fungal diseases resistance. The genes of resistance to septoria and mosaic viruses, which are important diseases of tomato, are also found in the wild-type *Lycopersicon hirsutum*. In the genes that provide resistance to bacterial blight which is another disease of tomato, it is also from wild tomato species such as *L. peruvianum*, *L. pimpinellifolium* and *L. hirsutum* and these genes are transferred to tomato crops by successful hybridization (Özgen et al. 1995).

It is also observed that wild relatives of crops are used to improve properties resistance to pests, adaptation and quality beside resistance to diseases. *Aegilops speltoides*, the ancestor of bread wheat (*T. aestivum*), provided tolerance genes to drought, heat and salinity. The protein content of durum wheat was also increased by crossing with wild-type *T. dicoccoides* (Maxted and Kell 2009).

It is known that resistance to leaf beetle in wheat is resistant to *T. turgidum* and virus carrier pests in *Agropyron elongatum*. In addition, the genes for resistance to tobacco nematodes are found in *Nicotiana rependra*, potato aphid resistance genes were found in *Solanum demissum*, *S. acaule* and *S. chacoensis*; resistance genes to potato nematodes were found *S. vernei* and *S. multidissectum*; resistant gene to beet nematode was found in *Beta procumbens*, which are all crop wild relatives of these crops (Özgen et al. 1995).

One of the most important problems in agriculture is the salinity of the soil. More than half of the world's agricultural areas have salinity problems. Therefore, resistance to salt has always been one of the important issues in plant breeding. On the other hand, the emergence of salinity problem in irrigation areas increases the importance of this issue even more. It is seen from the Poaceae family that includes *Festuca* and *Agropyron* species, which are the wild relatives of wheat, have salt resistance genes and these genes are transferred to the wheat crop

(Cordukes 1981; McGuire and Dvorak 1981). In the tomato, wild-type *L. cheesmani* contains the resistance genes to salt which can be used successfully for this purpose (Rush and Epstein 1981).

With the use of crops wild relatives, which are important gene sources of crops, many successes have been achieved and genetic diversity has been increased in cultivated plants. However, many other plant gene sources are not available for gene transfer for various reasons. The main reason for the limited use of wild species by the breeders is the long time and high cost in the classical breeding methods. This is due to processes such as backcrossing from wild species to the hybrid individual through linkage and to extracting undesirable genes. However, with developed techniques for genome analysis (for example, Marker Assisted Selection, New Generation sequencing and transcriptomics), it can now shorten this process and commitment can break linkage. Via these rapidly developing new technologies, new gene resources can be used and breeding studies will have much more opportunities in the future. This situation increases the importance of wild gene resources in the face of new problems such as new disease breeds or various environmental stresses that may arise in the future. In the face of the need for new plant varieties to overcome the emerging environment-related and other possible challenges, the importance of wild relatives of crops has become more prominent in future plant breeding. This requires a more strategic approach to their protection (see Stolten et al. 2006; Maxted & Kell 2009). However, crop wild relatives are also under risk of being lost due to climate changes. According to the United Nations FAO estimates, in the last century, 75% of the plant biodiversity was lost.

Due to the fact that natural habitats and agricultural systems are under risk, it is of great importance to collect, protect and characterize wild relatives in order to reduce the effects of biotic and abiotic stress factors related to climate change. Because of the increased level of CO₂, wild-type species began to give less fruit and seeds than the cultivated plants (Jablonski et al., 2002). This situation increases the risk of extinction.

Jarvis et al. (2008) reported that approximately 16% to 22% of the wild relatives of the important species used directly in agriculture were destroyed due to climate change. Some are expected to decrease by 50%. One of the most comprehensive analyzes on the change of wild biodiversity is Thomas et al. (2004)'s research. Researchers expect that crop biodiversity is threatened by 15-37% of them due to climate change in 2050. Jarvis et al. (2008), estimates that 61% of peanut species, 12% of potato species and 8% of cowpea species will be extinct within 50 years. These results indicate that crops wild relatives of the crop varieties that are at risk due to climate change should first be identified (Jarvis et al., 2010).

Unfortunately, crops wild species are weak against climate change, as they cannot take immediate action against changing environmental conditions. Some adaptive species and endemic plants are particularly vulnerable to the direct effects of climate change. Changes in biotic interactions, including pests and changes in disease severity (Newton et al., 2008), indirect factors such as competition and symbiotic interactions may also have significant effects.

Conclusion

The review of this study determined that the conservation of genetic diversity of landraces and crop wild relatives are very critical. Genetic analysis of populations to identify genetic diversity is one of the most ideal protection strategies. The landrace conservation should be one of the primary biodiversity targets. It should allow landrace actual inventories to be widely established. On the other hand there are two basic options for the protection of wild relatives of cultivated plants. These are gene banks (ex situ) conservation and in the natural environment (in situ) conservation. Wild relatives are more suitable to in situ conservation of the environment as they are durable. The conservation of selected wild species in gene banks is also preferred as insurance and for providing material to researchers.

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