Diversity and conservation of wild crop relatives for source of resistance to major biotic stress: Experiences in Ethiopia

Tewodros Mulualem[1]* and Zelalem Bekeko[2]

[1]Jimma Agricultural Research Center, Po Box 192, Jimma, and [2] Haramaya University, School of Plant Sciences, Po Box 138, Dire Dawa, Ethiopia.
*Corresponding authors: tewodrosmulualem@gmail.com, zelalembekeko@yahoo.com

Abstract

Naturally, crops can defend themselves against insect pests in different ways. Although, wild crop species are important as sources of genes for resistance to major biotic stress, they are widely neglected by research and development programs in Africa in general and in Ethiopia in particular. The significant features of crop wild relatives are: ecologically sound, economically pragmatic and publicly acceptable. The current alarming global crisis and extinction of biodiversity affect negatively the planet's biosphere. Conservation of biodiversity is one attempt to alleviate the pending extinction of the biosphere by humans. Genetic diversity, the basis of evolution by natural selection, is gravely threatened in the progenitors of cultivated plants and its exploration, evaluation, conservation in situ and ex situ is imperative to guarantee sustainable development. So far limited attention has been given to assess the diversity and conservation of indigenous wild crop genetic resources and research is at its rudimentary stage for the identification, description and evaluation of these genetic resources for resistance to major disease and insect pests. As a result, some of the wild crop genetic resources in Ethiopia are endangered, and unless urgent efforts are taken to characterize and conserve, they may be lost even before they are described and documented. Besides, the majority of wild crop genetic diversity is found in the country where documentation is scarce and risk of extinction is highest and increasing. Therefore, there is a need to characterize, conserve and utilize our indigenous wild crop genetic resources as agriculturally important traits have paramount importance. Consequently, this review article helps to assess the use, diversity, threats and conservation strategies of wild crop relatives in Ethiopia for sustainable resistance of biotic stress.

Keywords: Breeding, Crop wild relatives, Conservation, Diversity, Gene, Resistance.

Introduction

Agriculture remains the mainstay of Ethiopia's economy. About 85% of the economically active population lives in rural areas, particularly in the central highlands (FAO, 1996). The majority of the population has a subsistence mode of crop and livestock production. This form of agriculture contributes a large share of the growth national products (GNP). Estimates of the contribution of crop to total agriculture vary from 65-70% (Carlos and Gritzner, 2003). However, under natural condition, cultivated crops are attacked by different disease and pests and causing considerable economic damage. Use of pesticides as the main option to control disease and insect pests, but it has high cost and difficult to apply. Chemical control sometimes results in development of insect resistance, residue problems on crops and causes risks to human health and environmental pollution.

Thus, economical potential and environmental benefits of improved crop production and quality through breeding with crop wild relatives have tremendous impact for sustainable crop production in the country (Sharma, 2009; Tewodros *et al.*, 2013).

The use of crop wild relatives may lead to potentially environmental friendly methods of managing insect pests and safe for beneficial soil living organisms (Sharma, 2009). The main important features of crop wild relatives are: i) ecologically sound, ii) economically pragmatic, and iii) publicly acceptable (Sharma and Ortiz, 2002). Naturally, crops can defend themselves against insect pests in different ways. Although, wild crop species are important as sources of genes for resistance to major biotic stress (Xiao et al., 1996), they widely neglected by research and development programs in Africa in general and in Ethiopia in

particular (Muluneh, 2006; Tewodros, 2008).

In Ethiopia, there is a marvelous wild crop diversity that is distributed over a wide range of agro-ecological zones in the country. Currently, the indigenous wild crop genetic resources are becoming seriously endangered owing to the high rate of genetic erosion resulting from natural calamities. Furthermore, displacement of indigenous landraces by genetically uniform/modern varieties, changes in crop pattern and land use have largely affected the magnitude of the wild crop genetic diversity in the country. If this trend continues, the gene pool of wild crop relatives could be lost in the near future. This threat is in line with the FAO report (FAO, 1999), which states that crop genetic resources in developing countries in general and in Ethiopia in particular, are being eroded through the rapid transformation of modern agricultural system and introduction of exotic genetic resources, before proper characterization, utilization and conservation of wild crop genetic resources. Besides, genetic dilution due to foreign or exotic germplasm use, changes in production systems, markets preferences and environments, natural catastrophes, unstable policies from public and private sectors and the availability of very limited funds for conservation strategies are deteriorate the diversity of wild crop relatives in the country (Rege and Gibson, 2001).

Moreover, limited attention has been given to assess the diversity and conservation of indigenous wild crop genetic resources and research is at its rudimentary stage for the identification, description and evaluation of these genetic resources for resistance to major disease and insect pests. As a result, some of the wild crop genetic resources in Ethiopia are endangered, and unless urgent efforts are taken to characterize and conserve, they may be lost even before they are described and documented (Rege, 2003). Besides, the majority of wild crop genetic diversity is found in the country where documentation is scarce and risk of extinction is highest and increasing. Therefore, there is a need to characterize, conserve and utilize our indigenous wild crop genetic resources as agriculturally important traits have paramount importance. Moreover, analysis of diversity on wild crop relatives has tremendous impact for conservation and a basis for resistance to major biotic stress in Ethiopia.

Wild crop genetic diversity:

The importance of the genetic diversity of wild crops can be examined from two different perspectives. From one perspective, genetic diversity may be a necessary condition to achieve high 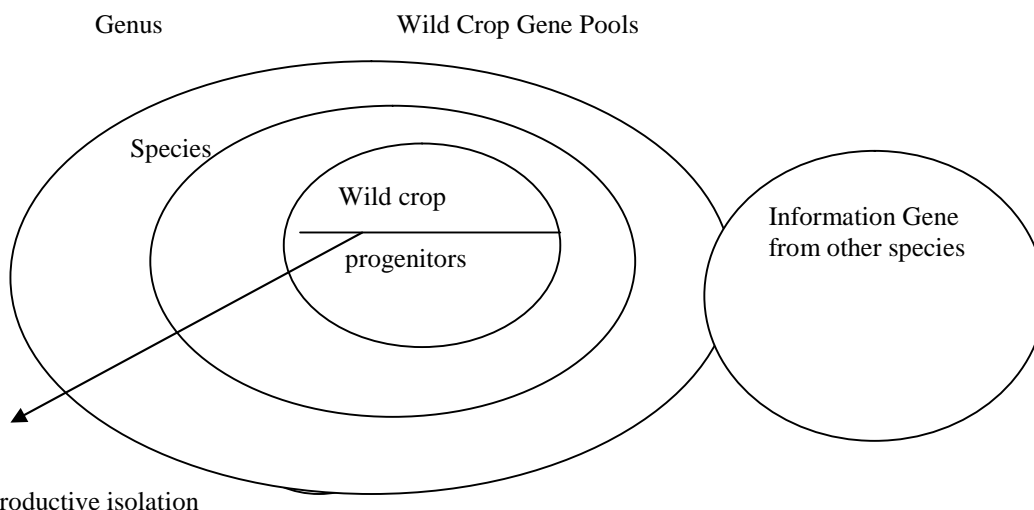productivity and yield stability. From the other perspective, genetic diversity is the raw material used by plant breeders over the long term to develop improved resistant plant varieties. In agro-ecosystems, diversity in a simplified version compared to natural ecosystems also leads to higher total yields. This is illustrated by the many types of multiple cropping and agro-forestry systems in use in the world, mainly in developing countries in subsistence agriculture settings. In these systems, careful choice of the genotypes of the individual crops and the actual planting arrangements can lead to a cropping system where the total biomass produced is larger than the sum of the biomasses of the individual components grown in monoculture.

Plant breeders have selected genotypes specifically for improve yield, high resistance to different insect pests under these multiple cropping conditions and nutritional quality (Francis, 1985). Recently, Zhu et al. (2000) showed that a simple mixture of rice varieties (Oryza sativa L.) was effective in limiting the infection of rice blast (Magnaporthe grisea (Hebert) Barr.) compared to a rice monoculture. In developing countries, nevertheless, farmers may grow mixtures of plant varieties not only to maximize yield, but also to satisfy different needs, such as different types of culinary preparations or other uses, and to minimize risk. The second perspective on wild crop genetic diversity deals with the utilitarian aspect of genetic resources in breeding. Until the advent of plant transformation technologies, access to genetic diversity in breeding programs was limited by sexual incompatibility. Plant breeders recognized three major gene pools based on the degree of sexual compatibility (Gepts, 2000).

Crosses within the primary gene pool, which includes the crop and its wild progenitor, do not encounter any reproductive isolation, in contrast to crosses between the primary gene pool, on one hand, and the secondary and tertiary gene pools, on the other. Plant breeders have traditionally emphasized closely related, well-adapted domesticated materials within the primary gene pool as sources of genetic diversity (Kelly et al., 1998). More recently, however, plant transformation and genomics have led to a fourth gene pool. Transgenesis allows us to bypass sexual incompatibility barriers altogether and introduce new genes into existing cultivars. It should be emphasized here that the major function of transgenic technologies is not the creation of new cultivars but the generation of new gene combinations that can be used in breeding programs (Gepts, 2002). Comparative genomics provides the means to identify sequences in a crop

of agronomic interest based on homology of DNA sequences, transcription patterns, etc., with similar data in model systems such as Arabidopsis (*Arabidopsis thaliana* (L.) Heynh.) and rice (Gepts, 2000). Over the last few decades, awareness of the rich diversity of exotic or wild germplasm has increased. This has led to a more intensive use of

this germplasm in breeding (Rick, 1982; Stalker, 1983). The use of molecular markers has facilitated the identification of genes of agronomic interest in wild germplasm through the dissection of quantitative traits using linkage-map based approaches (Tanksley and McCouch, 1997).

Figure (1): Wild crop gene pools as sources of genetic diversity for breeding purposes

Wild crop relative Diversity of in Ethiopia

The Ethiopian region is characterized by a wide range of agro-climatic conditions, which account for the enormous diversity of biological resources that exist in the country. Probably the most important of these resources is the immense genetic diversity of the various crop plants grown in the country. The indigenous crop plant species, their wild relatives, the wild and weedy species which form the basis of Ethiopia's plant genetic resources, are highly prized for their potential value as sources of important variations for crop improvement programs.

Populations of these forms of plant species also represent sources having the greatest potential for genetic diversity and can therefore serve as invaluable means to fill the gaps that still exist in the available base of genetic diversity in the world collection of many major crop species. Among the most important traits which are believed to exist in these materials are earliness, disease and pest resistance, nutritional quality, resistance to drought and other stress conditions, and characteristics especially useful in low-input agriculture. Preservation of the indigenous stock has a particular significance in the country's breeding programs as a source of resistance for disease and adaptation needed by breeders to solve acute

national problems exist in these materials (IBC, 2008).

The most important domesticated crop plant species in Ethiopia are: sorghum, barley, teff, chickpeas, and coffee, largely represented in the country by landraces and wild types that are uniquely adapted, genetically diverse forms of these various crops. The genetic diversity found in Ethiopian wild crop relatives has been used worldwide in developing new resistant crop varieties and addressing acute yield constraints. Much of this crop diversity is found in small fields of peasants who, aided by nature, have played a central role in the creation, maintenance, and use of these invaluable resources. Peasant farmers in Ethiopia translate their deep understanding and use of different wild plants, or the general biology of their surroundings, to farming systems that are best adapted to their own circumstances.

The existence of genetic diversity has special significance for the maintenance and enhancement of productivity in agricultural crops in a country, which is characterized by highly varied agro-climates and diverse growing conditions. Such diversity provides security for the farmer against diseases, pests, drought, and other stresses. Genetic diversity also allows farmers to exploit the

full range of the country's highly varied microenvironments differing in characteristics such as soil, water, temperature, altitude, slope, and fertility.

Diversity among species is especially significant to Ethiopia as it represents an important resource to subsistence farming communities throughout the country. A wide variety of wild plant species provide material for food, feed, fiber, and medicinal uses (IBC, 2008; Kebebew, 2010). Such diversity is also crucial to sustain current production systems, improve human diets, and support biological systems essential for the livelihood of local communities. Maintenance of species and genetic diversity in farmers' fields is, therefore, crucial to sustainable agriculture, especially for resource-poor farmers practicing agriculture under low-input conditions in marginal lands. The major wild and landrace crops of Ethiopia include the following:

Table (1): Major wild and landrace crops in Ethiopia

Crop type	Total number of collected and donated accession	%	No. of accessions collected by PGRC/E	%	% of total number of accessions
Cereals	28849.0	73.1	8219.0	56.4	28.0
Oilseeds	4490.0	11.4	2355.0	16.2	52.0
Legumes	4170.0	10.6	2890.0	19.8	69.0
Spices	749.0	1.9	520.0	3.6	69.0
Coffee	702.0	1.7	140.0	0.9	20.0
Medicinal	62.0	0.1	61.0	0.4	98.0
Others	452.0	1.2	397.0	2.7	88.0
Total	39474	100	14582	100.0	

Source: PGRIE (1991)

The use of crop wild relatives for resistance against insect pests in some major crops

Wild relatives were developed during evolution of crops with many features that have enabled them to survive in extreme conditions. They are a source of genes for resistance of major biotic and a biotic stress, for example in the saline environment, wild crop relatives that provided genes to the cultivated plants conferring high tolerance of salinity, so the plants can be irrigated with one-third sea water. The main source of resistance is found in wild plants and their close relatives that have been the most exploited in plant breeding (Ramanatha Rao and Hodgkin, 2002).

The use of wild relatives has continued to increase the number of crops with cultivars containing genes from wild relatives, the number of wild species used to provide genes, and the range of traits obtained from wild relatives. Currently, many wild crop species were identified in many crops and over a 100 traits having been transferred. Those crops where use of wild relatives were well established and to be dominant in terms of numbers of species used and numbers of traits transferred in many major crops, namely, tomato, wheat, rice, potato, and sunflower. Nonetheless, novel traits are continually being incorporated from new wild relatives in most of these and other crops, with more promised in the pipeline.

Pest and disease resistance is still the leading reason why breeders look to the wild relatives, resulting predictably in a dominance of pest and disease related wild gene introgressions. Many study confirm that pest and disease resistance derived from wild crop relatives, approximately 80% of the 14 crops reviewed for release cultivars have more than just biotic stress tolerance traits incorporated from wild relatives, with most also incorporating abiotic stress tolerance or enhanced yield and quality traits. The characteristics of wild relative resistance to cold or extreme conditions and resistance to insect pests and diseases have been transferred from wild relatives to cultivated plants (Perez et al., 1997). The knowledge and conservation of crop wild relatives is of utmost importance in global food production. Unfortunately, "modern" agricultural practices as the use of herbicides and other chemicals have led to a gradual loss of biological diversity and populations of wild relatives of cultivated plants have been drastically depleted (Peralta et al., 2005; Vargas, 2008). Therefore, conservation of wild crop relatives is vital as a source of resistance gene for many biotic and a biotic stresses.

Breeders have exploited wild relatives for resistance to diseases for over a century (Prescott-Allen and Prescott-Allen, 1986) and they continue to search extended gene pools for genes that convey resistance to major crop diseases and pests, of the 13 crops with incorporated wild genes in released cultivars, all except barley and chickpea have cultivars with disease resistances derived from

wild relative genes. However, only maize, banana and groundnut have disease and pest resistance as the only beneficial trait derived from the wild.

Most prominent among these: Oryza nivara S.D. Sharma & Shastry providing resistance to grassy stunt virus in rice; *Solanum demissum* Lindl. providing resistance to potato late blight; the many tomato disease resistances introgressed from wild species, mostly from *Lycopersicon pimpinellifolium* Mill.; and, stem and leaf rust resistance from *Agropyron elongatum* Host ex. *P. Beauv* and *Aegilops umbellulata* Zhuck., respectively, in wheat (Prescott-Allen and Prescott-Allen, 1986). Since then, the discovery and use of new resistance genes from the wild have steadily increased in these crops and others. Resistances found in tomato wild relatives have been reported at a rate of about one per year since 1982 (Rick and Chetelat, 1995), with virtually all disease resistance genes currently in commercial cultivars having been bred from wild genetic resources. Over 40 resistance genes have been derived from *Lycopersicon peruvianum* (L.) Mill., L. cheesmanii Riley, L. pennellii (Correll) D'Arcy, and several other wild relatives.

In rice, Oryza nivara genes still provide strong and extensive resistance to grassy stunt virus on millions of hectares of rice fields in south and south-east Asia (Barclay, 2004), and resistance to at least six other major diseases in rice have been obtained from different wild species (Brar and Kush, 1997). In potatoes, besides several new resistances from other wild relatives, resistance to potato late blight obtained from *Solanum demissum* and *Solanum stoloniferum* Schltdl and Bche´ continues to be effective in some areas, and currently 40% of the total area of the most popular potato cultivars in the United States have *Solanum demissum* in their ancestry, a considerable increase from 11% of the total area in 1986. Along with these wild relatives, *Solanum chacoense* Bitt., *Solanum acaule Bitt.*, and *Solanum spegazzinii Bitt.* have provided resistance to several viruses and pests (Ross, 1986; Love, 1999).

Breeders continue to isolate and introgress genes from wheat wild relatives for resistance to leaf and stem rust (Hoisington *et al.,* 1999), yellow dwarf virus, root lesion nematode, powdery mildew and wheat streak mosaic virus. Spring wheat germplasm lines derived from *Aegilops tauschii* Coss for resistance to Hessian fly, a major insect pest causing multimillion dollars crop losses in the US, have recently become available to breeders (Suszkiw, 2005). The prevalence of wild genes in providing pest and disease resistance has increased in many other crops as well (Table 2).

Disease resistances in wild sunflowers have been exploited for decades, with multiple sources of genetic resistance to all the known races of downy mildew, as well as rust, verticillium wilt, and broomrape, continually being transferred from wild *Helianthus annuus* L. and H. praecox Engelm. & A. Gray into a new sunflower hybrid. The most recent trait from wild *H. annuus L.* is herbicide resistance to imidazolinone and sulfonylurea chemicals used to control broomrape (Seilerand Gulya, 2004). These resistance genes have been transferred into cultivated hybrids under the trade name 'Clearfield', and are expected to be worth millions of dollars globally.

Table (2): Use of crop wild relatives in the past 20 years in released cultivars of 13 crops of international importance

Crop	Pest and disease resistance	Abiotic stress	Yield	Quality	Male sterility or fertility restoration	Total no. of contributed traits
Cassava	+	-	-	+	-	3.0
Wheat	+++++++++++	-			-	9.0
Millet	+	-			+	3.0
Rice	+++++++	+++			+	12.0
Maize	+	-			-	2.0
Sunflower	+++	-			-	7.0
Lettuce	+++	-			-	2.0
Banana	++	-			-	2.0
Potato	+++++	-			-	12.0.
Groundnut	+	-			-	1.0
Tomato	++++++++++	++			-	55.0
Barly	_	+			-	1.0
Chickpea	_	+			-	2.0

A Plus signs indicate number of wild relatives that have contributed beneficial traits to crop varieties in each category of traits. Minus sign indicates wild relatives have not contributed beneficial traits in that category. Total number of individual traits obtained from wild species are indicated in the last column for each crop

In cassava, less well known are the Tropical Manioc Selection (TMS) cassava cultivars, developed by the International Institute for Tropical Agriculture (IITA) using crosses with *Manihot glaziovii* Mü ll. Arg., and adopted by a number of African countries in combating the devastation caused by cassava mosaic disease and bacterial blight. Disease resistance derived from the wild relative has contributed to a 40% yield increase in Nigeria (Nweke, 2004), and has led to a gain in popularity for these cultivars in neighboring countries, with, for example, 25% of Western Kenyan households planting one of the cultivars. The cultivars are now planted on an estimated two million hectares.

In millets, rust and *Pyricularia grisea* resistances were introgressed from wild relatives. Although the rust resistance was overcome quickly, *Pyricularia* resistance is still effective (Wilson and Gates, 1993). Striga resistance has been identified in millet's primary gene pool (Wilson *et al.*, 2000), but the work remains at the early stages of gene transfer. In sorghum, recent success in hybridization between Sorghum macrospermum and Sorghum bicolor promises to help in introducing several pest and disease resistance traits to cultivars (Price *et al.*, 2005). In bananas, 'Calcutta 4' (*Musa acuminata Colla*), a wild, non-edible diploid banana has been used as a source of resistance in banana hybrids to black sigatoka, the most serious constraint to banana production globally caused by the fungus *Mycosphaerella fijiensis* (Escalant *et al.*, 2002). The new generations of these hybrids, distributed since the 1990s, are resistant to black sigatoka and Fusarium wilt (Vuylsteke *et al.*, 1993). However, resistance to black sigatoka has been overcome in the Pacific, and breeders have once again turned to wild *Musa acuminata* for more resistance genes (Escalant *et al.*, 2002).

The vast majority of modern lettuce cultivars have benefited from wild relatives. All lettuce downy mildew, *Bremia lactucae*, and lettuce aphid, *Nasonovia spp.*, resistance is derived from the wild (Eenink *et al.*, 1982; Crute, 1992). For downy mildew, cultivars with resistance derived from wild germplasm have been released regularly since the 1980s. Fungicides have limited effectiveness against the pathogen, thus without the introduced genes it would not be possible to grow lettuce in many parts of Europe. However, resistance genes appear to be overcome rapidly, and breeders are constantly returning to wild germplasm for new resistance genes (Crute, 1992).

The use of wild genes in groundnut and maize has not been as successful so far. Groundnut cultivars with root knot nematode resistance derived from *Arachis cardenasii Krapov.* and *W.C. Greg.* (Simpson and Starr, 2001) were released, but were never grown on a significant area because of a lack of resistance. Introgression of genes from *Tripsacum L.* into maize cultivars has not had any successes since cultivars released between the 1950s and 1980s with resistance to *Helminthosporium and Puccina*. However, both these crops have cultivars in the pipeline, with wild-derived disease resistant groundnut germplasm available to breeders (Rao et al., 2003), and rootworm resistant, drought and aluminum-tolerant, nutritionally-enhanced maize cultivars with *Tripsacum* gene introgression currently being field tested, expecting to be released in 2007. There are no cultivars identified and released after the mid-1980s that have incorporated disease resistance from wild relatives in soybean, chickpea.

Soybean cyst nematode resistance has been successfully transferred from wild perennial soybean, *Glycine tomentella Hayata.* (Riggs et al., 1998), but cultivars are still in an experimental stage. Unsuccessful attempts have been made to transfer resistance to Maruca pod borer to cultivated cowpea from crosses with *Vigna vexillata* (L.). Chickpea lines derived from *Cicer reticulatum Ladizinsky* and *Cicer echinospermum P.H. Davis* are currently being developed for resistance to root lesion nematodes and *Phytophthora* root rot, but these are still undergoing backcrossing programs to recover the domesticated phenotype. *Phaseolus* wild relatives are currently being screened for resistances to web blight, rust, white mold, bean golden yellow mosaic, bruchids, and seed storage insects (Gallepo, 1988; Singh, 2001).

Gene transfer to cultivated crops from crop wild relatives

The natural defense mechanisms in crop plants have been lost during intense selection for high yield, wider adaptability and improved nutritional quality. Due to this reason, most of improved cultivars lack its defense mechanism of their wild progenitors which makes them vulnerable to stresses and this necessitate the utilization of crop wild relatives in crop resistance which constitutes an enormous reservoir of genetic variability (Bioversity International, 2011). An estimated 50-60,000 crop wild relatives species exist worldwide, of which 10,000 may be considered of high potential value to food security, with 1,000 of these being very closely related to the most important food crops but about 75.0% of these species may be threatened in the wild. Agriculturally, crop wild relatives have been commonly used in the disease and pest resistance, with 39.0% of use associated with improving disease resistance, 17.0% with pest

resistance, 13.0% with a biotic stress, 11.0% with quality improvement, 10.0% with yield increase, 6.0% with husbandry improvement and 4.0% with cytoplasmic male sterility and fertility restoration (Maxted and Kell, 2009). Another report showed that between 1986 and 2006, about 60 wild crop species have contributed more than 100 beneficial traits, mainly related to disease resistance and abiotic stress tolerance, to 13 major crops including wheat, rice, tomato, and potato (Hajjar and Hodgkin, 2007).

Diseases and pests are the major causes of yield losses in crops, but high levels of resistance to these diseases and pests have been reported in many wild crop relatives of cultivated species (Dwivedi *et al.*, 2008). The contribution of wild crops to yield increase was estimated to be about 30.0% of production (Pimentel et al., 1997) and the introgression of new genes from wild relatives contributes approximately $115 billion toward increased crop yields per year worldwide (Hajjar and Hodgkin, 2007).

The research success in transferring desirable resistant genes differs from wild crop relatives to cultivated crop species. For instance several disease resistance genes were introgressed from wild relatives to cultivated rice (Khoury and Guarino, 2010; Bioversity International, 2011) and a biotic stress resistance genes in rice (Zamir, 2001). *Helicoverpa armigera* and other pest (i.e bollworm, tomato fruit worm, or legume pod borer) resistance genes have been successfully transferred from wild relatives of legume crops (Sharma *et al.*, 2005). Dwivedi *et al.* (2005) reported the successful transfer of insect resistance genes from wild relatives to crop for resistance to nematodes (*Heterodera* spp.) in soybean, and bruchid (*Zabrotes subfasciatus*) in common bean, southern corn rootworm (*Diobrotica undecimpunctata howardi*). Wild relatives as a source of genes for resistance to biotic and a biotic stress

Cultivated crops in the semiarid tropics play an important role in human diet, in both developed and developing countries. Despite its high production potential, the actual yields on farmer fields are quite low because of due to the presence of diseases and insect pests. More than 350 species of insects damage cultivated crops in different parts of the world of which aphids (*Aphis craccivora* Koch, a vector of groundnut rosette virus in Africa), thrips [*Scirtothrips dorsalis* Hood, *Caliothrips indicus* Bagnall, *Frankliniella schultzei* (Trybom), and *Thrips palmi,* a vector of peanut bud necrosis virus in India], leafhoppers (*Empoasca kerri* Pruthi) and leaf miner (*Aproaerema modicella* Deventer) and an estimated loss of $720million annually (Stalker and Campbell, 1983).

Traditionally, insect control in crop is dependent on insecticides. With the development of insecticide resistance in insect populations, occurrence of pesticide residues in food and food products, and adverse effects of pesticide use on the environment, the alternative methods of pest control have begun to receive considerable attention. Host plant resistance is one of the most economical and environmental friendly methods of keeping insect pest populations below economic injury levels. In the germplasm accessions of cultivated crops screened to date, moderate levels of resistance have been observed against *A. modicella, S. litura, S. frugiperda*, and white grubs (Wightman *et al.,* 1990). Some attempts have also been made to identify sources of resistance in the wild relatives in specific crops (Lynch, 1990). Currently, introgressing genes from the wild relatives into cultivated crops for resistance to different insect pest are common. For example, in ground nut rust, *Puccnia arachidis* Speg. and late leaf spot, *Cercosporidium personatum.* Selected resistant genes from wild relatives and inserted in to cultivated (susceptible) crops and these derivatives are less susceptible to insect pests than commercial cultivars. Because there is considerable variation in insect infestations under field conditions,

Wild relatives contributing genetic resistance to abiotic stresses in major crops have reached the stage of cultivar release although many wild relatives with potential have been described. Important recent advances in this field include the development of a chickpea cultivar with introgressed wild genes'BG1103' for drought and temperature tolerance are derived from *Cicer reticulatum*, and is already a leading cultivar in Northern India. Six barley cultivars with drought tolerance derived from *Hordeum spontaneum* genes have been exploited for tolerance of soils with high acidic-sulfate content in Vietnam (Nguyen *et al.,* 2003), and *O. longistaminata A. Chev. & Roehrich* genes for drought tolerance in cultivars in the Philippines, allowing the spread of rice production to previously unusable lands. In tomatoes, *L. chilense and L.pennellii* genes have been used to increase drought and salinity tolerance (Rick and Chetelat, 1995). Sunflower and bean cultivars with genes from crop wild relatives will soon be released. Salt tolerant sunflower hybrids, which promise to yield 25.0% more in salt impacted soils, are still under development (Lexer *et al.,* 2004); although maintainer lines have already been released. Bean cultivars with tolerance to low temperatures and salinity derived from wild

Phaseolus are in the pipeline.

Wild relatives as a source of genes for crop improvement

Crop wild relatives, which include the progenitors of crops as well as other species more or less closely related to them, have been undeniably beneficial to modern agriculture, providing plant breeders with a broad pool of potentially useful genetic resources. Wild relatives were used in crop improvement in different crops in the first half of the 20th century. Their utility was recognized in breeding programs of major crops, and wild gene use in crop improvement gained in prominence by the 1970s and 1980s with their use being investigated in an increasing wide range of crops. Many information recognize the economic and production importance of crop wild relatives in many areas of the world. They calculated that yield and quality contributions from crop wild relatives to US-grown or imported crops amounted to over $340 million a year (Prescott-Allen, 1986). Significant advances have been in made in the 20 years since the both in the molecular technologies and hybridization procedures available for breeding and cultivar development that allow for the incorporation of more distantly related taxa, and in our knowledge of the wild relatives available for use in these programs. Tanksley and Mc Couch (1997) pointed to the potential role of genome mapping in efficiently utilizing the genetic diversity of wild relatives, and suggested that the continued sampling of wild germplasm would result in new gene discoveries and use. While many articles have reported the importance of wild species in providing beneficial traits to particular crops, information is lacking on the extent to which these are incorporated in new cultivars developed.

Yield increase

Wild crop relatives have poor agronomic performance and it is therefore used to enhance yield in modern cultivars. Yield improvements of the selected crop cultivars have mostly been associated with other beneficial traits, namely biotic or abiotic stress tolerance, provided by the wild relatives. For example, chickpea cultivar 'BG1103' yields approximately 40.0% more than competing cultivars, but this increase is due to wild genes conveying increased drought and temperature tolerance, rather than specifically targeting yield. Similarly the TMS line of cassava, derived from an initial cross with a wild relative, gives a 42.0% yield increase (Nweke, 2004), although this is mostly a result of disease resistance provided by the wild genes. Of target crops, it has found only one example of a released cultivar using wild germplasm to specifically increase yield: rice cultivar NSICRc112 released in the Philippines in 2002 from the cross of *Oryza sativa* and *O. longistaminata* is known to be high yielding.

Nevertheless, there are an increasing number of cases of high yielding derivatives of hybrids created with the use of wild relatives, of which synthetic hexaploid wheat are a good example. Produced by the International Maize and Wheat Improvement Center (CIMMYT), synthetic hexaploid wheat are a cross between durum wheat and the wild relative *Aegilops tauschii* that has undergone artificial chromosome doubling to produce a hexaploid with A, B and D genomes (Mujeeb-Kazi *et al.*, 1996). These lines are then back crossed to elite bread wheat cultivars, to produce wheat with superior quality, disease resistance and yield (Hodgkin and Hajjar, 2008).

Breeding programs designed to increase yields and make use of wild germplasm in *Phaseolus* and cultivars with increased yield derived from a Colombian wild bean are in the pipeline. In a recent study, pyramiding of three independent yield promoting genomic regions introduced from *Solanum pennellii*, a green-fruited wild relative of tomato, has led to hybrids with a 50.0% increased yield over a leading variety (Gur and Zamir, 2004). High-yielding hybrid derivatives created with the use of cytoplasmic male sterility (CMS) derived from wild relatives have also gained in prominence. A major advantage of producing F_1 hybrids is fixing heterosis in the population, often resulting in higher yields, frequently through the use of male sterility. Cytoplasmic male sterility has been found in an increasing number of wild species, resulting in much hybrid research and a few released cultivars. Cytoplasmic male sterility based on using wild *Helianthus annuus* and *H. petiolaris* Nutt. has been used in high yielding commercial sunflower hybrids, significantly expanding the sunflower industry (Prescott-Allen, 1986; Hodgkin and Hajjar, 2008).

Currently, 100.0% of sunflower production in the US and approximately 60–70% of production worldwide is estimated to be from these hybrids. With rice, 95.0% of hybrids grown in China are derived from crosses using cytoplasmic male sterility from wild *Oryza sativa f. spontanea L.*. These hybrids are currently planted on approximately 45.0% of China's rice-planting area. More recently, cytoplasmic male sterility found in wild millet has been used to produce popular high yielding and disease resistant hybrids.

For improved quality

Tomatoes have provided many classic examples of improved quality traits from wild genes, from increased soluble solid content, fruit color, and adaptation to harvesting. Since then, QTL mapping

and analysis has aided the discovery of useful quality controlling genes, such as fruit size, in unlikely candidates such as the small-fruited tomato ancestor *L. pimpinellifolium* (Tanksley and McCouch, 1997). A handful of other advances in quality traits can be attributed to wild relatives: a doubling of protein content in a Brazilian cassava cultivar, ICB-300, derived from *Manihot oligantha Pax. & K. Hoffm.* and increased protein content in wheat cultivars derived from *Triticum dicoccoides (Ko¨ rnicke) G. Schweinfurth* (Hoisington *et al.,* 1999). The increased alpha acid content of a cultivar of hops derived from wild hops, but this cultivar has since been discarded due to adverse aroma components that had a severe negative impact on beer flavor. Better grain quality synthetic hexaploid wheat cultivar 'Carmona' has been released in Spain and future releases of synthetic hexaploid wheat with higher content of essential minerals such as iron or zinc are expected (CIMMYT, 2004).

Sources of genes for resistance to Insect pests

The sources gene for resistance depends on the magnitude of genetic variability within the species, heritability of the trait and the level of selection intensity applied (Gemechu *et al.,* 2011). The higher the levels of these components for a given trait, the higher will be the genetic gain expected from each cycle of selection. In many crops, different sources of resistance to insect pests have been identified from cultivated varieties, landraces, species of wild relatives and mutants (Chen, 2007). Naturally, complete resistance genes to insect pests hardly occur. Nevertheless, a few cases of complete resistance were also reported in cultivated and crops of wild relatives in legumes (Ishimoto, 1996). Insect resistance may involve morphological, physiological and biochemical features of the host plant.

Morphological features

Plants have different morphological features for resistance to insect pests; the most common morphological features are hairiness, color, thickness and toughness of the tissue. These features are highly resistance to many insect pests.

Hairiness:

Hairiness of leaves is associated with resistance to many insect pests in at least 18 genera of insect pests for many crops. eg. in cereals to cereals leaf beetle, in cotton in jassids, turnip to turnip aphids. Moreover, in cotton hairy genotypes are highly resistant to jassids, while non-hairy types are susceptible level of resistance. However, the length of hairs is of prime importance and dense hairs without adequate length are in effective. Hairiness in cotton is governed by two polymeric genes H^p_1 and H^A_2; an epistatic gene E^A, is also known (Sing

BD, 2007).

Color of the plant

Plant color may contribute to non-preference in some cases. For example, red cabbage and red leaves Brussel's sprouts are less favored than green varieties by butterflies and certain other Lepidoptera for oviposition. Similarly ball worms prefer green cotton plants to red ones. Yellow green varieties of pea are less preferred by aphid than are blue green varieties.

Thickness and toughness of the plant

Thick and tough plant tissues present mechanical obstruction to feeding and oviposition, and there by lead non preference as well as antibiosis. For example, thick leaf lamina in cotton contributes to jassid resistance, while solid stem leads to resistance to wheat stem fly. Wheat stem becomes solid due to the development of pith inside the stem; this is affected by the environment. Wheat varieties with the same degree of stem solidness may vary in their relative resistance to stem saw fly. Similarly, thick and tough rind of cotton boll makes it difficult for the bollworm larvae to bore holes and enter the bolls (Sing BD, 2007).

Physiological factors

Some physiological factors such as osmotic concentration of cell sap, various exudates, etc. may be associated with insect resistance. Leaf hairs of some *Solanum* species secrete gummy exudates. Aphids and Colorado beetels get trapped in these exudates and are unable to feed and reproduce. The exudates from secondary trichomes of *Medicago discifrmis* leaves have antibiotic effects on alfalfa weevil at lower concentrations; it retards the growth of weevil, while at high concentration it is lethal. In cotton, Jassid resistance is associated with high osmotic concentration of the cell sap (Sing BD, 2007; Annadana *et al.,* 2002).

Biochemical factors

Several biochemical factors are known to be associated with insect resistance in many crops. It is believed that biochemical factors are more important than morphological and physiological factors in conferring non preference and antibiosis. A well-known example is the association between high concentration of gossypol, a phenolic compound, and resistance to several insect pests in cotton. Plants produce a variety of chemicals that affect insect behaviour; these are called allelochemicals, or allelochemic factors. Allelochemic is a general term that describes non nutritional chemicals produced by an organism of one species, which affect growth, health, and behaviour or population biology of another species. These chemicals are two basic types, 1) allomones and 2) Kairomones. Allomones affect insect

activities in such a way as to result in an adaptive advantage to the plants. That may affect orientation of insects and force them to move away from plants, induce increased walking or flying, inhibit biting, piercing or feeding, interrupt egg-laying or oviposition or disturb the normal physiological processes of the insects. In contrast Kairomones, affect insect behaviour and physiology in such a way as to result in an adaptive advantage to insect pests. Kairomones may attract the insect to the host plant and help it in locating the host from among non-host plants. They may slow down insect movement and promote colonization.

In many cases, resistance is highly associated with the chemical composition of host plants. Host plant resistance to insect pests has been observed in different plants including vegetables, ornamentals and wild plants. Low concentrations of total aromatic amino acids in cucumber, pepper, lettuce, and tomato, compared to total leaf protein, were correlated with a decrease in damage by insect pests. Over expression of cystein-protease inhibitors in transgenic chrysanthemums was not related to thrips resistance (Annadana *et al.,* 2002), while multi domain cystein protease inhibitors in transgenic potato were affiliated with thrips resistance (Sing BD, 2007). Potential interference of these multi domain proteins with basic cell functions has hindered a practical function for pest management so far. Recently, two pyrrolizidine alkaloids, jaconine and jacobine, as well as the flavonoid kaempferol glycoside have been identified to be related to thrips resistance in the wild plant. A metabolomics approach to study insect pests resistance in chrysanthemum identified chlorogenic and feruloyl quinic acid as resistance factors (Leiss *et al.,* 2009a).

Mechanisms wild relatives for resistance to insect pests

In many case, the desired resistance may not be available in the cultivated crop species. In such cases, the resistance should be searched in the wild relatives of the concerned and crops. There are many cases where insect resistance has been transferred from a related wild species to a crop species. In some cases, it is possible to transfer insect resistant genes from un-related organism in to plants through recombinant DNA technology. The cry gene of *Bacillus thuringiensis* is so far the most successful example. The mechanism of resistant to insect pests are varying and depends up on the type of the crop and ways of reproduction to transfer resistant gene from wild relatives to cultivated plants. Naturally, wild crops have own mechanisms to resist insect pests before and after infection the most common are:

Formation of cuticular waxes on the surface of plants

Wild relatives are highly responsible regulate the level of cuticular waxes in the plant cell. The amounts of wax are varying depending of the species and degree of infestation. Both insect pests and predators that attack them must attach effectively to plant surfaces, which imply that they must attach to the waxy materials that cover these surfaces. The cuticle of the primary organs of wild plants consists of a polymeric cutin matrix and cuticular waxes soluble in organic solvents such as hexane or dichloromethane. A portion of plant cuticular waxes is located outside the cuticular matrix and, hence, is exposed on the immediate surface of the plant. These ''epicuticular waxes'' create unfavorable condition for insect oviposition and reduced damages done by insect pests (Eigenbrode, 1996).

Plants are exposed to a large number of insect pests. However, only a small proportion of these attacks and invasions are successful and result in disease. This is because plants have evolved to defend themselves from invading pests and pathogens (Walling, 2000; Dangl and Jones, 2001). The first line of defense is passive and includes physical barriers like waxy or thick cuticles and the presence of specialized trichomes that inhibit insects or pathogens from settling, penetrating plant surfaces, and successfully colonizing plants. In addition to these physical barriers, there are two overlapping yet different forms of active plant defense. The first is known as the basal plant defense that restricts the invasion of a virulent pathogen or insect. The second involves specific recognition of the invading pest or pathogen by plant resistance (*R*) genes. Upon recognition of the attacking organism, plant defenses are initiated that serve to localize the invasion of the pathogen or deter feeding of the insect.

Gene-for-Gene insect resistance

Active plant defense, also known as gene-for-gene resistance, is triggered when a plant resistance (*R*) gene recognizes the intrusion of a specific insect pest or pathogen. Activation of plant defense includes an array of physiological and transcriptional reprogramming. A number of single dominant *R* genes have been mapped, and molecular markers linked to these loci have been identified (Tan *et al.,* 2004). The majority of the mapped genes are in staple crops like wheat and rice. The largest number of these mapped genes confer resistance to Hessian fly, *Mayetiola destructor*, which in addition to the Russian wheat aphid, *Diuraphis noxia*, is considered one of the most serious insect pests of wheat (Webster *et al.,*

2000). In addition to these mapped genes, several single dominant aphid *R* genes have been identified that confer resistance to a single species of aphid. An example is the *Nr* (resistance to *Nasanova ribisnigri*) gene in lettuce conferring resistance to *N. ribisnigri*. During the last decade, a large number of *R* genes have been cloned from a number of wild plant species. Although these genes confer resistance to diverse groups of organisms, such as bacteria, virus, fungi, oomycetes, nematodes, and insects, their products share striking structural similarities. These structural similarities are also shared among *R* gene products from monocots and dicots, indicating that recognition and activation of plant defense signal transduction has been maintained throughout evolution.

Production of secondary plant metabolites

In the past, selection of crop species for improved agricultural value has been associated with reduced levels of herbivore resistance (Kennedy, 2007). This loss of herbivore resistance is linked to diminished amounts of particular secondary plant metabolites. The secondary plant chemicals, present in the ancestors of the domesticated cultivar, provided natural resistance to insect pests (Berlinger, 2005). For example 2-tridecanone content in cultivated tomatoes has decreased to 1.5% of the wild tomato species (Williams *et al.,* 1980). Therefore, wild relatives provide valuable source material for insect and disease resistance (Kennedy, 2007).

In the wild tomato, it has been reported to be resistant to many tomato insect pests. Specifically, accessions of *S. pennellii* showed high levels of resistance to the whitefly, *Bemisia tabaci* (Kennedy, 2003; Berlinger, 2005), the aphids, *Macrosiphum euphorbiae and Myzus persicae*, two-spotted spider mites, *Tetranychus cinnabarinus* and *T. urticae*, as well as to the larvae of corn earworm, *Helicoverpa zea*, and beet armyworm, *Spodoptera exigua*.

In tomato trichomes serve as physical barriers and furthermore they produce different allelochemicals which are associated with pest resistance (Williams *et al.,* 1980; Kennedy, 2003). Methyl-ketones, such as 2-tridecanone, present in *S. hirsutum* f. glabratum confers resistance to colorado potato beetle, Leptinotarsa decemlineata, spider mite, *Tetranychus evansi*, the *Lepidopterous* larvae, *Manduca sexta* and *Heliothis zea* (Maluf *et al.,* 2001). The multiple pest resistance of *S. pennellii* is based on the presence of type IV glandular trichomes and the glucose and sucrose esters of fatty acids (acylsugars) that they secrete. In contrast cultivated tomato, *S. lycopersicum* does not have any type IV trichomes and does not accumulate acylsugars. Next to the secondary

metabolites produced by trichomes, glycoalkaloids and phenols are involved in host plant resistance of tomato to insects. The glycoalkaloid α-tomatine has been suggested as a possible resistance factor in tomatoes to beet armyworm, *S. exigua*, Colorado potato beetle, L. decemlineata (Kennedy, 2003). Phenolics and flavonoids are distributed widely among terrestrial plants and are likely among the oldest plant secondary compounds known as plant defense compounds against herbivores and pathogens (Elliger *et al.,* 1981).

Limitation of wild crop relatives

Inter-specific cross ability is one the major limiting factor during the use of wild relatives as a gene sources. However, using embryo rescue and other techniques to overcome inter-specific crossing barriers, it has been possible to make new hybrid combinations involving different species and to transfer many new traits. There are many examples, such as the transfer of cassava mosaic virus resistance as a result of the development of hybrids between cassava and *Manihot glaziovii* and the production of hybrids between cultivated chickpea and *C. pinnatifidum Jaub.* & Spach, with resistance to asochyta blight.

The results of many reports confirms that improved interspecific hybridization techniques have led to an increase in use of secondary and tertiary gene pools of many crops over the last 20 years. However, biological constraints still prevent successful use of wild relatives in a number of crops, where blocks to hybridization and hybrid sterility have not yet been overcome. Crossing difficulties (cross incompatibility) are the main reason why cicer wild relatives are not more prevalent in modern cultivars, with only two species, *C. echinospermum* and *C. reticulatum*, easily crossed with the cultivar. Crosses between soybean and *Glycine* species were unsuccessful in the 1970s, taking one lab 17 years to work out a successful hybridization methodology between *Glycine tomentella* and soybean cultivars. Unsuccessful crosses with *Vigna vexillata* have limited work with cowpea wild relatives.

Regardless of inter-specific cross ability, hybrid in viability, hybrid sterility and retention of undesirable agronomic traits remains a prominent technical limitation to using wild germplasm. Crosses with wild relatives usually produce lines that have poor agronomic performance, and often the undesirable traits cannot be eliminated. For example, crosses of cowpea cultivars with *Vigna unguiculata* (L.) Walp sub sp. dekindiana and pubescens which failed to produce any breeding lines with high agronomic performance or better quality traits; lines with spider mite resistance from

wild hops which were abandoned because of extreme hairiness of the leaves and strobiles of breeding populations. Efforts to reduce deleterious effects of cross breeding with wild relatives through backcrossing are costly and time-consuming, and will no doubt affect the speed with which new cultivars are released.

Molecular techniques offer a partial solution but there will likely continue to be cases where pleiotropic effects limit the use of genes from wild relatives. Improvements derived from wild species in many crops have enticed crop breeders and researchers to further explore wild genomes in search of beneficial traits. This is easily demonstrated by the literature currently available on work discussing the myriad of beneficial traits of wild relatives and the importance of broadening our crop gene pools.

The number of references increases greatly for queries on wild wheat or tomatoes. Yet some tomato scientists, working on the crop that arguably has the most incorporation of wild genes, continue to perceive this as insufficient, and blame ''a lack of appreciation and screening'' for neglect of the astonishing extent of inadequate variation in the wild. This is part of a much more general phenomenon noted by others that funding for the kind of long term research needed to study, conserve and use crop wild relatives in plant breeding has been reduced. Perhaps most promising in their potential to increase the use of wild relative genes are the advancements in the field of genomics. While introgression was not easily detectable with the genetic tools of a few decades ago, recent use of DNA markers and sequencing has helped in isolating beneficial genes and in selecting for traits which are difficult to detect based on phenotype. Marker-assisted selection is not only cost effective and efficient; it is also amenable to automation and high throughput, allowing for screening of whole collections of crop wild relatives.

Marker-assisted selection can also be increasingly applied for the maintenance of recessive alleles in backcrossing pedigrees and for pyramiding of resistance genes. The use of SNP (single nucleotide polymorphism) technology has enormous potential as the next generation of molecular marker, in that it offers a high density of markers and because SNP assays are not dependent on the rate-limiting step of electrophoresis. Genetic engineering has allowed for the introduction of new traits by overcoming crossing barriers between non-sexually compatible individuals, and these methods might be expected to increase the use of crop wild relatives. However, it has been noted that the

speed of introduction of new genes by genetic engineering, as compared to classical breeding, is overstated, due to the lack of precision in the integration point of the introduced gene requiring extensive testing of progeny, and the additional backcrossing programs that oftentimes follow successful transformation in order to introduce the transgene into the desirable genetic background. Breeders have been predicting accelerated introductions of desirable characteristics to crop plants through the development of molecular genetic techniques for more than a decade. However, while these introductions have increased greatly in number, the dramatic rate of increase predicted is not yet apparent.

The threat of wild crop genetic erosion: Experience in Ethiopian

The broad range of genetic diversity existing in Ethiopia, particularly the primitive and wild gene pools, is presently subject to serious genetic erosion and irreversible losses. This threat results from the interaction of several factors and is progressing at an alarming rate. The most crucial factors include the displacement of indigenous landraces by new, genetically uniform crop cultivars, changes and development in agriculture or land use, destruction of habitats and ecosystems, and drought. The drought that prevailed in the regions of Wello, parts of Shewa and Northern Ethiopia, has directly or indirectly caused considerable genetic erosion, and at times has even resulted in massive destruction of both animals and plants. The famine that persisted in some parts of the country has forced farmers to eat their own seed in order to survive or to sell seed as a food commodity. This has often resulted in massive displacement of native seed stock (mostly sorghum, wheat, and maize) by exotic seeds provided by relief agencies in the form of food grains. To counter losses in genetic diversity, PGRC/E has launched rescue operations during this period (1987-1988), including a strategic seed reserve program, in areas subject to recurring drought (Worede, 1991).

The extent to which the displacement of native seeds by exotic or improved materials occurs in Ethiopia has not been fully documented. Rates of displacement vary depending on regions and crops. In many cases, farmers still plant both native and exotic types interchangeably or alongside each other, at times in mixtures, depending on their particular need, market demand, or other prevailing factors. In general, native barley and durum wheat are among the crops most threatened by new varieties and/ or by other crop species such as teff and bread wheat, which are expanding within the cereal growing highlands of the Shewa, Arsi, and

Bale regions, largely because of greater market demand. Similarly, in the central highlands, including the northern Shewa and Gojam regions, introduced varieties of oats are expanding rapidly, often replacing a wide range of cereals, legumes, and pulses grown in these areas. With sorghum and millet, exotic varieties do not pose any immediate threat because expansion of such materials is at presented somewhat restricted. In the case of sorghum, however, genetic erosion is progressing on account of extensive selection and breeding of the native populations. The Ethiopian Sorghum Improvement Project (ESIP) has been doing extensive mass selection on sorghum and millet and, in some cases, selecting single lines or cultivars to develop elite materials with improved yield and/or disease (smut) and pest (stalk borer) resistance. The distribution of these materials results in a gradual displacement of the original farmers' seed stock, especially in the regions of Wello and South East Shewa. A similar situation exists with the various pulses, legumes, and oil crops grown in the country, where the bulk of the material utilized in breeding programs is represented by indigenous landrace populations. For crops such as sorghum, millet, and pulses, for which there is no immediate threat of genetic erosion, there still exists a danger of their massive displacement in the future by the expansion of other crops with better market values (e.g., maize, teff), monocropping, and shifts in cropping patterns that favor early maturing varieties.

Conservation of wild crop relative genetic resources in Ethiopia

The importance of plant genetic resources (PGR) and threats to them has led to the creation of conservation programs to preserve crop resources for future generations. One type of crop genetic conservation is *ex situ* maintenance of genetic resources in gene banks, botanical gardens, and agricultural research stations (Plucknett *et al.,* 1987). Another type is *in situ* maintenance of genetic resources on-farm or in natural habitats (Brush, 1991; Maxtel *et al.,* 2008).

In situ conservation

There are two types of *in situ* conservation can be distinguished. First, *in situ* conservation refers to the persistence of genetic resources in their natural habitats, including areas where every day practices of farmers maintain genetic diversity on their farms. This type is a historic phenomenon, but it is now especially visible in regions where farmers maintain local, diverse crop varieties (landraces), even though modern, broadly adapted, or higher yielding varieties are available.

Second, *in situ* conservation refers to specific projects and programs to support and promote the maintenance of crop diversity, sponsored by national governments, international programs, and private organizations. *In situ* conservation programs may draw on the existence and experience of the first type, but they are designed to influence farmers in the direction of maintaining local crops by employing techniques that may not be local. This type of conservation faces daunting tasks. It must cope with continual social, technological, and biological change while preserving the critical elements of crop evolution genetic diversity, farmer knowledge and selection, and exchange of crop varieties. *In situ* conservation practices and projects in agriculture theoretically can concern the wide spectrum of genetic resources relating to crops, from wild and weedy relatives of crop species to the intraspecific diversity within crop species (Maxted *et al.,* 1997b).

There are named, farmer varieties that usually have a reduced geographic range, are often diverse within particular types, and are adapted to local conditions (Brush, 1995; Harlan, 1995). One reason for our focus on diversity within cultivated crops is that science of *in situ* conservation of cultivated resources is relatively less developed than the science of conserving wild resources such as wild and weedy crop relatives. Another reason is that *in situ* conservation of cultivated plants requires novel approaches, while *in situ* conservation of wild crop relatives can draw on theories and methods developed for conserving many different species in their natural habitats. Finally, focusing on variation within cultivated species is warranted by the fact that this type of diversity is arguably the most important one for the future viability of agricultural evolution, as it has been in the past.

Ex-situ Conservation

Plant species and varieties can be preserved under artificial conditions away from the places where they naturally grow. Ex situ plant collections have a number of uses for conservation and development, including for the revitalization of plant populations and associated economies and cultures. Ex situ conservation is the conservation of components of biological diversity outside their natural habitats (CBD, 1992). There are different methods of *ex situ* conservation among these methods, the storage of seeds in seed banks has some advantages for preserving species, but can only be used for species with seeds capable of remaining viable after long-term storage (known as 'orthodox' seeds). The typical technique used for seed storage is to lower the moisture content of the seeds to 2–6 % or less, and reduce the temperature to around 0°C or lower. Collections in seed banks

should occasionally be tested for their viability. Periodically, the seeds in seed banks should be germinated and the plants allowed to grow and produce more seeds, which are then stored as replacements for the originals. In comparison to some other common methods of ex situ conservation, the advantages of seed storage can include low cost, less risk of disease and more efficient use of space or land. Seed storage can be 50 to 500 times cheaper per collection than field gene banks or *in vitro* storage. However, there are numerous species, including many tropical forest and temperate trees, whose seeds cannot be stored in seed banks because they lose viability if their moisture contents are reduced to the required level ('recalcitrant' seeds).

Field gene banks

It can be used for conserving varieties of plants for which seed banks are unsuitable. They are mainly used for major crop plants, such as banana *Musa*, mango *Mangifera* and yam *Dioscorea*. In Ethiopia, this type of conservation is used for coffee. It is now universally agreed that Ethiopia is the primary centre of diversification for *Coffea arabica* and perhaps the only region, covering the area bordering southern Sudan and part of Uganda, where the species occurs spontaneously. The genetic diversity that exists is tremendous and this has great significance for the economy of the country and the rest of the coffee growing world. In realization of the urgent need for effective measures to preserve and utilize the existing variability, which at present is being disastrously eroded, a special effort is being made to conserve coffee in its natural growing environment. This includes conservation of the semi-cultivated coffee in areas where the forest coffee occurs spontaneously, and where large variation exists, and maintenance of the forest coffee in its natural ecosystem in certain protected areas, the so called genetic reserves (Worede, 1982). A field genebank, comprising some 700 accessions, is being established within the Kefa administrative region. In the future this gene bank will be extended into other appropriate sites as the size of the collection continues to increase. Other living collections include *Phytolacca* spp., commonly known as 'endod', *Ensete ventricosum* and several spices and root crops, maintained at different sites in the country in collaboration with existing agricultural research and other relevant scientific institutions.

In vitro storage

It refers to the maintenance of cells or tissues in sterile growth media in dishes or flasks.

Botanical gardens

It differ from seed banks and field gene banks in that their collections usually consist of small numbers of many species, rather than many specimens of a few species.

Summery

Agriculture is the back bone of Ethiopian economy. About 85% of the people directly and indirectly associated with agriculture. Agricultural production in Ethiopia constrained by biotic and a biotic stresses. From the total agricultural production, about 30-40% annual harvests lost to diseases and pests. This results increase the cost of agricultural products. Use of insecticide is the common practice to control disease and insect pests, however the use of pesticide have negative impact on the development of resistant disease and insects, environmental pollution, and reduced the quality of agricultural products. Therefore the use of wild crop relatives as a resistant to disease and insect pests are the best option to solve these problems. The use of crop wild relatives may lead to potentially environmental friendly methods of managing insect pests and safe for beneficial soil living. The main important features of crop wild relatives are: i) ecologically sound, ii) economically pragmatic, and iii) publicly acceptable.

In Ethiopia, there is a huge amount of wild crop diversity that is distributed over a wide range of agro-ecological zones in the country. Currently, the indigenous wild crop genetic resources are becoming seriously endangered owing to the high rate of genetic erosion resulting from extensive substitute of the genotypes by high value crops (coffee, spices and *Chata edulis*), Changes in production systems, markets preferences and environmental hazards, availability of very limited funds for conservation of PGR and the diversity, ethno-botanical data and culinary characteristics of the landraces have not been documented anywhere. Moreover, rapid transformation of modern agricultural system and introduction of exotic genetic resources, fever the genetic erosion of wild crop relatives in Ethiopia. If this trend continues, the gene pool of wild crop relatives could be lost in the near future before proper characterization and conservation of wild crop genetic resources. Therefore, there is a need to characterize, conserve and efficiently utilize the existed indigenous wild crop genetic resources have paramount importance.

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