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Effects of crop evolution under domestication and narrowing genetic bases of crop species

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ABSTRACT

The study was aimed to evaluate the effects of crop evolution under domestication and narrowing genetic bases of crop species. The adaptation of plants to cultivation was vital to the shift from hunter-gatherer to agricultural societies, and it stimulated the rise of cities and modern civilization. The amount or quantum of genetic diversity available in a breeding population is referred to as genetic base of that population. In other words, genetic base represents spectrum of genetic variability in a plant breeding population. Genetic improvement by conventional breeding has made substantial changes when the efforts have been long-term. Characters improved include productivity, quality, and resistance to diseases, insects, and stress. There were, however, limits to the progress of conventional breeding, due to limitations of the sexual system, it was not possible to incorporate genes from nonrelated species or to incorporate small changes without disturbing the particular combination of genes that make a particular type unique.

Keywords: Domestication; Evolution; Genetic base; Genetic erosion.

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Introduction

The origin of agriculture can be traced back to more than 10,000 years ago when the first crops were domesticated in the Fertile Crescent (Brown *et al*., 2009). The identification (phenotyping) and deliberate selection of off-type plants by the hunters and gatherers were the initial efforts in plant breeding. The first plants to undergo domestication are thought to be the cereals wheat, barley, millet and emmer (Sang, 2009). Early phenotypers selected plants with increased grain size and loss of seed shattering. The rise agriculture which occurred approximately 10,000 years ago was one of the most transitions human histories. During the Neolithic revolution, the domestication of plant species led to a major subsistence shift, from hunter-gatherers to sedentary agriculturalists that ultimately resulted in the development of complex societies. The process of plant domestication led to striking morphological and behavioural changes in domesticated organisms compared with wild progenitors.

Traditionally this process has often been viewed as human directed, involving strong bottlenecks in the domestication population (founder events due to the selection of only few individuals at the beginning of domestication) and reproductive isolation between wild and domesticate forms. This straightforward model provides an attractive theoretical framework for geneticists, because the key events such as the geographic origin and timeframe of domestication are well defined. Agriculture and genetic resources are critically interdependent. All agricultural commodities, even modern varieties, descend from an array of wild and improved genetic resources from around the world.

Furthermore, agricultural production depends on continuing infusions of genetic resources for yield stability and growth.The process of domestication is one aspect of transition from hunting, gathering to agriculture. It is generally through that is transition has taken several millennia (Smith, 1995a).Domestication process is a continual process starting with the wild species, then formation of the cultivated species, then selection of improved strains of the species by growers (called landraces), then to modern cultivars from scientific breeding. The use of diverse genetic resources is important for breeding crop varieties (Glaszmann*et al*., 2010). Crop species with narrow genetic diversity are susceptible to emerging pathogens or other constraints leading to loss of productivity and this may lead to a serious decline in the areas of adaptation (Dyer *et al*., 2014).Crop improvement refers to the genetic alteration of plants to satisfy human needs. This process of domestication involved the identification of certain useful wild species combined with a process of selection that brought about changes in appearance, quality, and productivity. The selection of naturally occurring variants is the basis of crop improvement.

Conventional plant breeding can be defined as systems for selection of superior genotypes from genetically variable populations derived from sexual recombination. The system is powerful because it is evolutionary; progress can be cumulative, with improved individuals continually serving as parents for subsequent cycles of breeding. Genetic improvement by conventional breeding has made substantial changes when the efforts have been long-term. Characters improved include productivity, quality, and resistance to diseases, insects, and stress. There are, however, limits to the progress of conventional breeding. These are due to limitations of the sexual system, because it is usually not possible to incorporate genes from nonrelated species or to incorporate small changes without disturbing the particular combination of genes that make a particular type unique.Crop genetic resources are the genes and gene combinations available for crop improvement.Genetic improvements have arisen in several ways.

Before the development of modern varieties, farmerscultivated landraces. Landraces are varieties of crops that evolved and were improved by farmers over many generations, without the use of modern breeding techniques. These varieties are generally very diverse within species, because each was adapted to a specific environment. The pace of improvement accelerated as modern breeding techniques were developed that facilitated selection of specific desirable traits. Within most types of crops, breeders have crossed different parental material and selected traits resulting in high yields. Quality changes have also been the subject of breeding effort. Other goals of breeding have included rapid and simultaneous germination, flowering, and maturation of crops. Likewise, plants have been bred for uniform stature to ease mechanical harvesting. These advances in yield, quality, and other desired traits have resulted from the use of genetic resources. Breeders have also sought resistance to pests and diseases, and tolerance to non-biological stresses, such asdrought. Because pests and diseases evolve over time, breeders continually need new and diverse germplasm from outside the utilized stock, sometimes using wild relatives and landraces to find specific traits to maintain or improve yields (Duvick, 1986).USDA has estimated that new varieties are resistant for an average of five years, while it generally takes 8-11 years to breed new varieties (USDA, 1990).

The economic importance of non-biological stresses can also change over time, although less rapidly than pests and diseases. Plant breeders often rely on landraces or wild relatives as a last resort, but when used, genes from these materials have "often had a disproportionately large and beneficial impact on crop production" (Wilkes, 1991). In short, the plant breeding process is a continual one, in which diverse genetic resources remain a critical input in the agricultural production process.The advent of biotechnology and genetic engineering may increase the demand for genetic resources. One goal of genetic engineering is to simplify the process of incorporating desired traits in new varieties. The use of genetic engineering and other techniques such as molecular markers may make it easier to incorporate the beneficial characteristics of landraces, and wild relatives of agricultural crops. Genetic engineering also can be used to incorporate traits from very disparate species, exemplified by research that is using flounder genes to prevent frost damage in plants. On the frontier of biotechnology research are efforts to increase the genetic material that breeders can access. Organisms may carry within their DNA many genes that are not expressed as traits, some of which are of interest to crop breeders. In the future, scientists may be able to determine how these unexpressed genes operate, and make use of them in the breeding of new varieties. The objective of the study was to evaluate the effects of crop evolution under domestication has led to increase productivity of crop species and know crop evolution under domestication has narrowed genetic bases of crop species.

CROP Evolution under domestication and narrowed genetic bases

Genetic Diversity

Domestication is an evolutionary process in which selection (both natural and artificial) operates to change plants genetically, morphologically, and physiologically. Species that become completely domesticated often are unable to survive when reintroduced into the wild. The selection process that drives domestication strips plants of natural adaptive features and mechanisms that are critical for survival in the wild. Information about the genetic variations present within and between various plant populations and their structure and level can play a beneficial role in the efficient utilization of plants (Cole CT, 2003).The loss of genetic diversity in a species, also called genetic erosion, has been identified in many commercially important crops. One reason for this decline in diversity has been the loss of landraces and wild relatives of cultivated crops. The loss of wild relatives occurs mainly through habitat conversion. Because the economic values of wild relatives can rarely be appropriated (or captured) by land owners, the use of land to preserve habitats for wild relatives remains undervalued compared with alternative uses such as clearing for agricultural or urban use. Although many habitat reserves have been established worldwide, as a rule, wild relatives of agricultural species are covered only by accident (FAO, 1996).Habitat preserves often focus on areas rich in species diversity. These are not necessarily the areas with the greatest crop genetic diversity, while there is some potential for overlap in habitat conservation for wildlife resources and genetic resources, efforts to achieve these two goals often focus on different habitats. Genetic erosion of crop varieties can be furthered as landraces are displaced by commercially developed modern varieties. When choosing varieties, farmers consider yield potential and consumption attributes. Sometimes landraces offer superior yields and consumption traits, but often they do not. While maintenance of a diverse set of landrace varieties may prove valuable to current or future plant breeding, individual farmers do not directly capture these benefits.

Landraces become extinct through disuse if farmers stop planting and maintaining them. Widespread adoption of genetically uniform crop varieties makes the crop population more susceptible to a widespread disease or pest infestation. Nonetheless, as pests and diseases evolve to overcome host plant resistance, genetic uniformity increases the likelihood that such a mutation will be an evolutionary success. The evolved pest or disease has a greater crop base that it can successfully attack, which could increase its efficiency. Instead of a particular disease harming only a small percentage of varieties on a limited area of land, the disease now could affect vulnerable varieties accounting for a greater proportion of a crop's production. Genetic uniformity contributed to the spread of the Southern Corn Leaf Blight that led to a 15 percent reduction in the U.S. corn crop in 1970. Since 1970, the National Research Council (1993) has concluded that the genetic vulnerability of wheat and corn is less of a problem in the U.S. (in part because of efforts to breed in greater diversity). However, the Council also determined that genetic uniformity of rice, beans, and many minor crops is still a concern. The genetic uniformity of many crops has raised concerns that crop yields and production will become more variable (Swanson, 1996). Individual farmers have limited incentives to consider the consequences of genetic uniformity, and when choosing which varieties to plant may perceive the benefits of uniform varieties to be greater. The ability of plant breeders to keep ahead of pests and diseases through temporal diversity depends directly of the quality of germplasm collections in public gene banks and in private breeder collections. Because many of the benefits of raw germplasm cannot be appropriated, private breeders rely on the public sector to collect, characterize and perform pre-breeding enhancement of genetic materials to make them accessible for private use (Duvick, 1991).

The Role of Landraces and Modern Varieties in Narrowing Genetic Bases of Crops

It is a widely held belief that modern agriculture, particularly the transition from landraces to modern varieties as exemplified in the "Green Revolution," has profoundly narrowed the genetic base of modern crop varieties. In the broadest sense, however, genetic alteration and narrowing began with the first domestication of wild plants. The advent of scientific plant breeding, along with changes in crop management practices, almost certainly contributed to genetic narrowing (Porceddu*et al.*, 1988). Management of genetic resources found in "modern" varieties is related to but distinct from management of genetic resources found in more diverse "traditional" crop varieties.

Therefore, knowledge of where different types of crop varieties are currently grown would aid the development of both in situ and ex situ conservation strategies. However, precise global estimates of landrace use are very difficult to obtain. First neither industrialized nor developing countries regularly collect detailed information about what crop varieties are being planted by farmers. Second, the limited data which are collected has usually focused on the estimation of areas planted to "modern" varieties, and not to landraces. For example, in wheat and rice, "modern" is usually defined as "semi-dwarf." Earlier tall, but scientifically improved varieties are thus excluded from the definition. Finally, landrace use is affected by a variety of factors, including whether the crop is a major staple or not, the mode of reproduction (for example, through seed or tubers, cuttings), and whether the crop is primarily a food or industrial crop. As a result, genetic resource specialists may have detailed knowledge of landrace use, but it is not available in the more aggregated fashion needed by policy makers. Fortunately, some information is available for the world's three major cereals: wheat, rice, and corn (or maize). These cereals form an important part of the world's food supply, as their direct consumption by humans accounts for over 45 percent of all calories consumed. Landraces for these three crops illustrate the point that genetic resources of importance for major commercial crops are often found in developing countries.

Almost all varieties planted in industrialized countries are results of modern plant breeding (Morris and Heisey, 1998). For example, while wheat landraces from Europe have made important contributions to the modern wheat germplasm pool (Smale and McBride, 1996), today wheat landraces are probably only planted in small isolated areas in Mediterranean Europe. Furthermore, even in developing countries a large proportion of cropped area is often planted to scientifically bred varieties. In the 1990s, approximately 10 percent of the developing world's wheat area and about 15 percent of its rice area was planted to landraces. Wheat landraces were concentrated in West Asia or North Africa, with some also found in Ethiopia, China, the Indian subcontinent, and small areas in Latin America. The proportion of wheat area planted to landraces varied by wheat type and environment. For example, a considerable percentage of the area planted to durum wheats is still sown to landraces, while the percentage of spring bread wheat area in developing countries under landraces is quite low (Lantican and Dubin, 1999).

Rice landraces are concentrated in Southeast Asia, with some also found in the Indian subcontinent (Cabanilla, Hossain and Khush, 1999). As in wheat, rice landrace use varies by environment, with a much lower percentage of rice area in the irrigated lowlands being planted to landraces than in the more difficult rainfed lowland, flood prone, or upland environments. This may be because modern varieties tend to be bred with irrigated lowlands in mind. In addition, upland rice grown in West Africa often is a different species of upland rice than the rice planted in Asia, and much of the upland West African rice area also consists of landraces (T. Dalton, personal communication).Corn demonstrates how differences in a crop’s mode of reproduction may influence the use of landraces and genetic changes in a crop over time. Wheat and rice self-pollinate, which means that most of the time the pollen that fertilizes a given plant comes from the same plant. As a result, wheat and rice populations tend to be more genetically stable over time. In contrast, corn cross-pollinates, which means that a given plant is often fertilized by a different plant. Because of this feature, corn populations are inherently less stable.Therefore, landraces, improved open pollinated varieties, and hybrids whose seed has been re-used may be very diverse genetically. As a result, it is more difficult to define and measure what constitutes a landrace and what is "improved germplasm" (Morris, Risopoulos and Beck, 1999).

Dangers of Genetic Uniformity

Industrialized agriculture favours genetic uniformity. Typically, vast areas are planted to a single, high-yielding variety a practice known as monoculture using expensive inputs such as irrigation, fertilizer and pesticides to maximize production. In the process, not only traditional crop varieties, but long-established farming ecosystems are obliterated. Genetic uniformity invites disaster because it makes a crop vulnerable to attack a pest or disease that strikes one plant quickly spreads throughout the crop.

The Irish Potato Famine of the 1840s is a dramatic example of the dangers of genetic uniformity. None of the few varieties of the New World potato introduced into Europe in the 1500s were resistant to a potato blight that struck Ireland in the 1840s. The potato crop was wiped out. Over a million people died in the famine and a million more emigrated to the New World. More recently, in 1970, genetic uniformity left the United States maize crop vulnerable to a blight that destroyed almost $1 000 million worth of maize and reduced yields by as much as 50 percent. Over 80 percent of the commercial maize varieties grown in the United States at that time were susceptible to the virulent disease, southern leaf blight. Resistance to the blight was eventually found in an African maize variety called Mayorbella. A major catastrophe was averted by incorporating this resistance into commercial varieties.

The genetic diversity of our crop plants has been substantially reduced during the process of domestication and breeding. This reduction in diversity necessarily constrains our ability to expand a crop's range of cultivation into environments that are more extreme than those in which it was domesticated, including into "sustainable" agricultural systems with reduced inputs of pesticides, water, and fertilizers. Conversely, the wild progenitors of crop plants typically possess high levels of genetic diversity, which underlie an expanded (relative to domesticates) range of adaptive traits that may be of agricultural relevance, including resistance to pests and pathogens, tolerance to abiotic extremes, and reduced dependence on inputs. Despite their clear potential for crop improvement, wild relatives have rarely been used systematically for crop improvement, and in no cases, have full sets of wild diversity been introgressed into a crop. Instead, most breeding efforts have focused on specific traits and dealt with wild species in a limited and typically adhoc manner. Although expedient, this approach misses the opportunity to test a large suite of traits and deploy the full potential of crop wild relatives in breeding for the looming challenges of the 21st century. Here we review examples of hybridization in several species, both intentionally produced and naturally occurring, to illustrate the gains that are possible. We start with naturally occurring hybrids, and then examine a range of examples of hybridization in agricultural settings.

All domesticated species of plants are impacted in unintended, often negative ways during domestication and breeding (Ladizinsky, 1985) In particular; many crops lack genetic diversity and possess properties that reduce fitness in the natural environment. This problem derives both from demographic processes (genetic drift, population bottlenecks) and from changes in the nature of selection during breeding and cultivation that elevate the frequency of alleles with unique value in the agricultural environment and that permit the persistence of deleterious alleles (through selection trade-offs and selection relaxation) (Olsen and Wendel, 2013). The combination of the loss of adaptive alleles through drift and fixation of deleterious alleles through altered selection necessarily constrains our ability to expand the cultivation of domesticated species into environments beyond those in which domestication occurred, e.g., into more extreme climates, into marginal soils, into degraded agricultural landscapes, or into "sustainable" systems with reduced agricultural inputs. As part of this special issue, "Speaking of Food," we argue that there is a need for systematic efforts to introgress broad subsets of wild relative diversity into our crop plants to incorporate the range of useful adaptations for disease resistance, abiotic stress tolerance, and other agronomic challenges that are required in order to increase the resiliency and productivity of agriculture in the 21st century. Here we review the ecological and evolutionary literature on the effects of hybridization to show the capacity of hybridization to generate phenotypic novelty, and then detail examples of hybridization of crop wild relatives with domesticated plants.Wild species have an important role to play in meeting the challenges for 21st century agriculture, which must become increasingly efficient to meet humankind's demand for a more plentiful and nutritious food supply (Tanksley and McCouch, 1997; Pimentel *et al.*, 1997). Such challenges are particularly acute in the developing world, where extreme climatic conditions, marginal soils, and reduced inputs limit productivity, create increased risk, and diminish livelihoods through reduced income and malnutrition. Yet the impact of a properly implemented and well-used resource of wild germplasm would extend beyond the developing world. Many of the crop phenotypes important to cultivation in the developing world (tolerance to heat and drought, reduced dependence on inputs [e.g., nitrogen, phosphate, pesticides, water], and increased seed nutrient density) are also key to meeting the global demand for crops that incorporate traits for climate-resilience, increased sustainability, and increased nutritional value.

The potential for genetic gains from use of crop wild relatives is well documented (Pimentel *et al.*, 1997; Tanksley and McCouch, 1997; Maxted and Kell, 2009). Nevertheless, crop wild relatives have been used sparingly and typically in an ad hoc manner in many crop breeding programs (Hajjar and Hodgkin, 2007; Maxted and Kell, 2009; Brumlop *et al.*, 2013). Impediments to the systematic use of wild material in crop improvement programs include the often poor agronomic performance of crop–wild hybrids and their immediate backcrosses, and the labor intensive process of constructing large-scale, representative populations that are suitable for phenotypic assessment. For perennial crop species, which can take many years to reach reproductive age, such repeated backcrossing is prohibitively time consuming. Moreover, for many crops, the use of wild germplasm is further constrained by the limited state of international germplasm collections. Compounding the problem, many crop wild relatives are at risk of extinction from habitat loss, habitat fragmentation, changing land use and management practices, climate change, and introgression from agricultural relatives (Ford-Lloyd *et al.*, 2011).

The fact that crop wild relatives are under-used in crop improvement programs presents an opportunity. One can restructure germplasm resources, essentially de novo, guided by appropriate ecological and population genetic theory; when properly implemented, such collections would represent a diversity of source habitats and encompass the breadth of segregating genetic variation and adaptations characteristic of the target species. Genomics, phenotyping, and computational approaches can subsequently be used to infer natural adaptations in situ, for example, based on knowledge of population structure, allele frequency, and recombination history, combined with knowledge about selective constraints in individual populations. Such analyses can motivate targeted phenotyping activities and ultimately nominate candidate genes for adaptive traits, leading to increased understanding of the autecology of crop wild relatives. In parallel to the analysis of gene function in situ, purpose-built populations that are hybrids between crops and their wild relatives provide powerful tools for trait dissection, and as such they become the vehicle by which the genetic (genomic) basis of valuable agronomic traits can be understood.

Examples of such populations include nested association mapping (NAM) (Yu *et al.*, 2008; McMullen *et al.*, 2009) and multi-parent advanced generation inter-cross (MAGIC) (Cavanagh *et al.*, 2008) panels, to which the logic of association genetics can be applied (Huang and Han, 2013; Korte and Farlow, 2013), as well as advanced backcross introgression lines (Tanksley and McCouch, 1997) that capture genome intervals and their adaptive traits from wild relatives within the essential crop genome. The value of combining ecology, population genetics, genomics, and phenotyping is well documented in model species, such as Arabidopsis, Drosophila, mice and maize (Yu *et al.*, 2008; Ayroles*et al.*, 2009; McMullen *et al.*, 2009; Atwell *et al.*, 2010, Tian *et al.*, 2011; Flint and Eskin, 2012; MacKay *et al.*, 2012;Korte and Farlow, 2013), but has not been used widely in support of crop species and their wild relatives (e.g., Huang and Han, 2013). To make the most of this approach, however, we must understand more about the complex effects of hybridization. To that end, we review examples of hybridization in several species, both intentionally produced and naturally occurring, to illustrate the gains that are possible.

Diversity in plant genetic resources (PGR) provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (yield potential and large seed, etc.) and breeders preferred traits (pest and disease resistance and photosensitivity, etc.). From the very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirement, and now it is being focused to surplus food for growing populations. In the middle of 1960s developing countries like India experienced the green revolution by meeting food demand with help of high-yielding and fertilizer responsive dwarf hybrids/varieties especially in wheat and rice. These prolonged activities that lead to the huge coverage of single genetic cultivars (boom) made situation again worse in other forms such as genetic erosion (loss of genetic diversity) and extinction of primitive and adaptive genes (loss of landraces). Today with an advancement of agricultural and allied science and technology, we still ask ourselves whether we can feed the world in 2050; this question was recently sensitized at the world food prize event in 2014 and remains that unanswered in every one hands since global population will exceed 9 billion in 2050.

The per capita availability of food and water will become worse year after year coping with the undesirable climate change. Therefore, it becomes more important to look at the agriculture not only as a food-producing machine, but also as an important source of livelihood generation both in the farm and nonfarm sectors. Keeping the reservoir for cultivated and cultivable crops species is a principle for future agriculture, just like keeping a museum of cultural and spiritual specialty of diverse civilized humans in various geography for their historical evidence for future. The former can play a very important role in providing adaptive and productive genes, thus leading to long-term increases in food productivity which is further associated with environmental detriment. This paper will indicate the significance of genetic conservation and its analytical tools and techniques that are made widely available for utilization in postgenomic era. Plant breeders introduced desirable genes and eliminated undesirable ones slowly, altering in the process of underlying heredity principle for several decades. With the advent of new biotechnological tools and techniques, this process of genetic manipulation is being accelerated and it shortened the breeding cycles, and it can be carried out with more precision (neglecting environmental effects) and fast-track manner than the classical breeding techniques. The growing population pressure and urbanization of agricultural lands and rapid modernization in every field of our day-to-day activities that create biodiversity are getting too eroded in direct and indirect way.

For instance, land degradation, deforestation, urbanization, coastal development, and environmental stress are collectively leading to large-scale extinction of plant species especially agriculturally important food crops. On the other hand, system driven famine such as, Irish potato famine and Southern corn leaf blight epidemic in USA are the two instances of food crises caused by large-scale cultivation of genetically homogenous varieties of potato and corn, respectively. Even after these historical events, the importance of PGR had only got popular recognition when the spread of green revolution across cultivated crops threatened the conservation of land races. Green revolution technologies introduced improved crop varieties that have higher yields, and it was hoped that they would increase farmers' income. Consequently, the Consultative Group of International Agricultural Researches (CIGAR) initiated gene banks and research centers of domestication for conserving PGR in most of the stable food crops around the world. Center for domestication: maize (Mexico), wheat and barley (middle/near East and North Africa), rice (North China), and potatoes (Peru). The Food and Agriculture Organization (FAO) supported the International Treaty on Plant Genetic Resources (ITPGR) and UN supported the Convention on Biological Diversity (CBD) which is the international agreements that recognize the important role of genetic diversity conservation.

Genetic diversity is the key pillar of biodiversity and diversity within species, between species, and of ecosystems. However, the problem is that modern crop varieties, especially, have been developed primarily for high yielding potential under well-endowed production conditions. Such varieties are often not suitable for low income farmers in marginal production environments as they are facing highly variable stress conditions. Land races or traditional varieties have been found to have higher stability (adaptation over time) in low-input agriculture under marginal environments, thus, their cultivation may contribute farm level resilience in face of food production shocks. This is especially true in some part of Ethiopia where agro climatic conditions are challenging, technological progress is slow, and market institutions are poorly developed and have no appropriate infrastructure.

Effect of Genetic Erosion in Crop Plants

Genetic erosion can be defined as the "loss of genetic diversity, in a particular location and over a particular period of time, including the loss of individual genes, and the loss of particular combinations of genes such as those manifested in landraces or varieties. It is thus a function of change of genetic diversity over time (FAO, 2012c). Genetic erosion is the loss of genetic diversity within a species. The loss of variation in crops due to the modernization of agriculture has been described as genetic erosion. Genetic erosion of cultivated diversity is reflected in a modernization bottleneck in the diversity levels that occurred during the history of the crop. Two stages in this bottleneck are recognized: the initial replacement of landraces by modern cultivars; and further trends in diversity as a consequence of modern breeding practices. Genetic erosion may occur at three levels of integration: crop, variety and allele. One of the main causes of genetic erosion is the replacement of local varieties by modern varieties. Other causes include environmental degradation, urbanization, and land clearing through deforestation and brush fires. Variability refers to heterogeneity of alleles and genotypes with their attendant morphotypes and phenotypes. Population can be identified at different spatial levels from a locality to the crops global distribution. Genetic erosion implies that the normal addition and disappearance of genetic variability in a population is altered so that the net change in diversity is negative. The manifest cause of genetic erosion is the diffusion of modern varieties from crop improvement programs. Latent causes include population growth, poverty, markets, and cultural change. In the literature, three different views on methods to quantify genetic erosion can be found: (1) Genetic erosion as an absolute loss of a crop, variety or allele (Peroni and Hanazaki, 2002; Gao, 2003; Tsegaye and Berg, 2007; Willemen *et al*., 2007). The use of an absolute loss as evidence of genetic erosion ignores the dynamic nature of a farming system and population genetic processes. This approach only looks at what has been lost, and not at what has replaced this lost material. (2) Genetic erosion as a reduction in richness (Hammer *et al*., 1996; Hammer and Laghetti, 2005; Ford-Lloyd, 2006; Nabhan, 2007). A reduction in richness (that is a reduction in the total number of crops, varieties or alleles) is a better indicator for genetic erosion, as it does recognize the dynamics in the system. A reduction in richness is always accompanied by an absolute loss, but an absolute loss does not necessarily imply a reduction in richness, as a loss may be compensated for by novel diversity. A drawback in the use of richness as a criterion for genetic erosion is that very rare varieties or alleles contribute as much to the diversity as the most common varieties or alleles, and therefore richness might only poorly reflect increased levels of uniformity in agriculture. Also, the level of richness found depends to a large extent on the intensity of the investigation. A more detailed survey will most likely yield a larger number of varieties or alleles and thus shows a higher level of richness. (3) Genetic erosion as a reduction in evenness (Khlestkina *et al*., 2004; Ford-Lloyd, 2006). Genetic erosion as a reduction in evenness originates from the diversity indices used in vegetation ecology and population genetics, such as Shannon's index (Maughan *et al*., 1996) or Nei's gene diversity index (Nei, 1973), respectively.

Diversity is measured using the frequencies of alleles within a group of genotypes or using the production areas of landraces, cultivars or crop species in a region. Diversity levels are lowered due to increasing dominance of a single or small number of crop species, genotypes or alleles, even though alleles or varieties are not necessarily lost. Using evenness, rare varieties or rare alleles contribute little to the diversity. The risks of losing alleles or varieties are higher when distributions are much skewed. Using evenness as a measure for genetic erosion offers the opportunity to take action before a reduced diversity results in an absolute loss and reduced richness. Furthermore, it is not as sensitive to the sampling procedure as compared with the previous measures. Considerable overlap between these three views on genetic erosion exists, and most studies use a combination of the different approaches. The use of the concept of genetic erosion is not limited to the field of crop diversity. Genetic erosion equates genetic impoverishment and this concept is also applied to conservation ecology and animal husbandry, as the genetic impoverishment of a species or a population. Genetic erosion in ex situ collections may occur due to the loss of accessions or loss of alleles as a result of regeneration and storage practices (Parzies *et al*., 2000).

Conclusion

It was concluded that crop domestication can profoundly alter interactions among plants, herbivores, and their natural enemies. In general, domestication consistently has reduced chemical resistance against herbivorous insects, improving herbivore and natural enemy performance on crop plants. Selection exerted by humans on crop plants during the domestication process causes changes in the plants as they transit from wild species to domesticates. Many traits selected under domestication, for the satisfaction of human needs and as a consequence, fully domesticated crops may not survive in the wild without human intervention in planting and harvesting.

Ecology plays a key role in domestication of crop plants starting from the very beginning of evolutionary process and primitive life of human being. Domestication is a continuous process and bringing wild species of plants by considering the agro-ecological environment plays a significant role for the ease of adaptation. Generally domestication of crop plants with their appropriate ecologies is used to maintain sustainable yielding ability without reducing actual potential of crop plants. Variability refers to heterogeneity of alleles and genotypes with their attendant morphotypes and phenotypes. Generally, domestication is the transformation of wild progenitors to the cultivated species through continues selection for desirable traits of crop plants in order to satisfy the human demand.

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