

Chapter 4: Assessing the threat of genetic erosion

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Abstract

The world community has confirmed its commitment to the conservation of plant genetic resources that provide valuable traits for meeting the challenges of the future, such as adapting crops to changing climatic conditions or disease outbreaks. However, this plant diversity is threatened by “genetic erosion”, a term coined by scientists for the loss of individual genes or combinations of genes, such as those found in locally adapted landraces. 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 bush fires. Genetic erosion can also occur on the level of germplasm collections and genebanks due to improper management and inadequate regeneration procedures. There is a need to strengthen the conservation and sustainable use of plants and seed systems, and the crucial linkages between them, through a combination of appropriate policies, use of scientific information, farmers’ knowledge, and action. Traditionally, efforts to counter genetic erosion have concentrated on conserving seeds in crop genebanks (*ex situ*). Today, it has become clear that the best strategy combines *ex situ* conservation with on-the-ground (*in situ*) conservation by farmers in their agro-ecosystems and of crop wild relatives in, for example, areas protected for their environmental value. While such mechanisms are vital, the sustainable use of plant genetic resources is likewise essential because plant genetic diversity increases options and provides insurance against future adverse conditions, such as extreme and variable environments. The threat of genetic erosion has been reported by many countries and is discussed in this chapter.

Current status

This chapter discusses the concept of genetic erosion in crops, defined as the loss of variation in crops due to the modernization of agriculture. Two stages leading to genetic erosion are recognized: the initial replacement of landraces by modern cultivars and further trends in diversity as a consequence of modern breeding practices. It may occur at three levels of integration: crop, variety and allele (Rogers 2004) and is often magnified or accelerated by human activities. In native plant populations, genetic erosion results from habitat loss and fragmentation, but it can also result from a narrow genetic base in the original collections or by practices that reduce genetic diversity. Although species-specific guidelines are not available, the risk of genetic erosion can be minimized by familiarity with the biology of the affected species (including breeding system, mode of reproduction and pattern of genetic diversity).

The loss of biological diversity has traditionally been measured by the frequency of species extinctions; however, genetic diversity does not only underlie species diversity—being concomitantly lost along with

This chapter is a synthesis of new knowledge, procedures, best practices and references for collecting plant diversity since the publication of the 1995 volume *Collecting Plant Diversity: Technical Guidelines*, edited by Luigi Guarino, V. Ramanatha Rao and Robert Reid, and published by CAB International on behalf of the International Plant Genetic Resources Institute (IPGRI) (now Bioversity International), the Food and Agriculture Organization of the United Nations (FAO), the World Conservation Union (IUCN) and the United Nations Environment Programme (UNEP). The original text for Chapter 4: Assessing the Threat of Genetic Erosion, authored by L. Guarino, has been made available [online](#) courtesy of CABI. The 2011 update of the Technical Guidelines, edited by L. Guarino, V. Ramanatha Rao and E. Goldberg, has been made available courtesy of Bioversity International.

species extinctions—it has also been recognized in its own right as one of three levels of biological diversity recommended for conservation by the World Conservation Union (IUCN) (McNeely et al. 1990). Below, we review the different approaches to measuring genetic erosion in crops.

The first publicized use of the term “genetic erosion” was in reference to the loss of primitive races and varieties of cultivated plants as they were gradually replaced in agriculture with newer and more productive crop varieties. It was a topic of discussion in the international agricultural community in the mid-1900s and received prominence with the twin catastrophic outbreaks in 1970 of southern corn-leaf blight in the United States and of coffee rust in Brazil. These events illuminated the consequences of genetic erosion, stimulated international discussions and provided a major focus at the United Nations Conference on Human Environment in Stockholm in 1972 (Rogers 2004). The lesson was that “genetic uniformity is the basis of vulnerability to epidemics and, more generally, to biotic and abiotic stresses” (Scarascia-Mugnozza and Perrino 2002). Concerns about genetic erosion resulted in the initiation of a global network of genebanks to conserve agriculturally important genetic resources. In the agricultural sphere, there is ongoing concern and attention to genetic erosion at all levels, including the Food and Agriculture Organization of the United Nations (FAO).

Genetic erosion, or the steady loss of genetic diversity in on-farm agriculture, is perhaps the key pressure on the sustainable management of domesticated plant genetic resources (Brown and Brubaker 2002). Therefore, the term “genetic erosion” is now more generally applied to loss of genetic diversity, including the loss of diversity in native plant species. Also, the term “genetic erosion” is more often used in the context of human-driven or -related losses in genetic diversity that are faster in rate or larger in scale than would be expected under natural processes alone.

Genetic erosion has also been 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. It is important to recognize that genetic erosion could be of two kinds: specifically, loss of alleles/genes, which can be noticed on farmers’ fields and in habitats of crop wild relatives and, more generally, the loss of entire genotypes, the landraces. It can also occur at another level: i.e., at the level of germplasm collections and genebanks due to improper management and inadequate regeneration procedures.

Monitoring changes in the rate of genetic erosion strictly requires directly comparable, if not identical, measures of the state of a system at several points in time. Alternatively, it is possible to measure the major agents of erosion (e.g., deterioration or destruction of habitat due to urbanization, land clearing, overgrazing, salinization, drought, climate change, etc.). However, such indirect measures are very broad and have other and possibly more profound impacts than causing loss of diversity (Brown 2008). Brown (2008) also suggests that neutral or trivial changes could mask critical changes when summed over loci, genotypes, populations or species. A temporal indicator should reveal and be most sensitive to the changes of concern and not be swamped by relatively unimportant changes. For example, the loss of a few alleles at a highly polymorphic microsatellite locus is likely to be of trivial or no importance compared with the loss of disease-resistance alleles. An additional problem lies in stressing combinations of alleles: in sexual species, all multilocus genotypes are unique and ephemeral. Thus, when a claim is made that some percentage of distinct clones or genotypes has been lost from a region or a species, this is not necessarily genetic erosion. The life of each genotype is finite in sexually reproduced species, although vegetative reproduction might prolong that life (such as in named cultivars of fruit trees). A reduction in population size, and not increased recombination, is the primary agent of erosion (Brown 2008).

The relationship between population size and loss of genetic diversity has been well established and quantified, with Wright’s (1931) work being seminal. Generally, smaller populations tend to lose genetic variation by genetic drift much more quickly than larger populations. And the shorter the generation length (that is, time to reproductive maturity), the more rapid the loss of diversity in absolute time (Frankham et al. 2004). There has been considerable theorizing and empirical research on the relationship between population size and genetic diversity (Ellstrand and Elam 1993; Falk and Holsinger 1991). This relationship has also been examined at the species level, and various reviews have found restricted or rare species generally less genetically diverse than more common plant species (Cole 2003; Gitzendanner and Soltis

2000; Hamrick and Godt 1990; Karron 1987, 1991). It is important to note, however, that there may be different processes underlying the relationship between genetic diversity and size in populations, as compared to species.

Genetic drift has a second consequence with a negative impact on genetic diversity. Simply put, smaller populations are more likely to have higher rates of inbreeding (Frankham et al. 2004).

For indicators of genetic erosion, it is more important to focus on the loss of genes or genotypes of concern within specified regions or production systems than to work with inclusive concepts and measures of the whole dynamics of diversity in the full geographic context. Fluctuations in the diversity of all rare gene combinations over time and in particular patches of a spatial distribution can be a distraction, unless they are indirectly measuring the loss of important components of the genome. Far more critical is the loss of highly localized alleles, locally adapted complexes or unique specific uses, if they cannot be replaced by a recombination of genes from other populations. Even if we had fully detailed inventories of genotypes in space and at two points in time, we would still require expert assessment of genepool changes in order to be in a position to speak about significant genetic erosion (Brown 2008).

Relevant measures of genetic erosion include some subjective assessments of the significance of any loss, based on expertise and local knowledge. The inclusion of such evaluative information in measuring erosion is desirable. The challenge is to format it in such a way that at least a tentative quantitative treatment is possible. The FAO survey and database of reported instances of genetic erosion has the potential to provide the basic information for constructing such a measure (Diulgheroff 2004). Many of the records so far assembled by FAO are in a descriptive, narrative style of local expert opinion; summarizing these stories over crops or regions or time periods requires converting them to quantitative estimates, which is a significant challenge. Therefore, we should adopt a retrospective procedure that can look back, where the researcher has before him/her a genepool containing some variation and asks the question as to what proportion of diversity that was known or assumed to have been present a decade ago remains. The estimate of what was previously extant should rely on as much evidence as possible. Initially, one could work with a richness concept of diversity. Alternatively a predictive or prospective procedure might be appropriate. In this case, two quantities would be essential for any reported instance:

1. A measure of the significance if the part of the genepool in question were to become extinct. This is approached by estimating the extent of the total diversity at risk, which could, in turn, be based on the area cultivated or the number of varieties or populations, using a factor of 0.20 as an estimate of the proportion of all diversity (in this case allelic richness) that is locally common (Brown and Hardner 2000). Suppose, for example, that 20% of the area or of the varieties are deemed to be at risk in a particular area. This amounts to $0.2 \times 20\% = 4\%$ of the total genetic diversity in the crop imperilled in the area in question.
2. A category of the likelihood of loss under the current situation with no intervention (in some time period such as one decade). Classes: C = almost certain ($p > 90\%$), L = likely ($p > 50\%$), U = unlikely but threat still real ($p < 50\%$), V = very unlikely ($p < 10\%$). This might be affected by the area growing these varieties (Brown 2008).

Both these are subjective estimates but, ideally, could be based on local knowledge of the specific crop and threats to it. Any existing survey data could be used within this framework to support the estimates. While individual estimates and predictions may be prone to error, this framework is a way to codify the best opinion, and the averages will converge to give a trend. Finally, the predicted erosion can be estimated as the proportion of the resource under threat of erosion multiplied by the estimated probability of loss.

Future challenges/needs/gaps

Although there is undeniable evidence of the erosion of crop genetic diversity, and several innovative responses have been developed, there are important gaps in our knowledge that limit our capacity to decide among the various alternatives. Appropriate measures for diversity still need to be developed in order to better characterize the current situation and to evaluate changes in the future.

The capacity to evaluate genetic material in the laboratory is growing rapidly, but these are still expensive techniques, and more robust markers and measures are required to follow the progress of the conservation of genetic resources. When better measures of genetic diversity are devised, they will contribute to a clearer understanding of what exactly needs to be conserved.

Currently, there are only very general ideas about what portion of a plant population needs to be maintained in order to conserve particular genetic traits. This information is crucial to the efficient design of *in situ* conservation projects. More studies are also required to understand the causes of plant genetic erosion. Monitoring various putative causative factors is clearly one possible approach to assessing the risk of future genetic erosion within a gene pool in a given area. However, the relationship between such factors and genetic erosion may not be straightforward. It might be non-linear and site-specific and might involve complex interactions among factors.

Once a past association between genetic erosion and different causative and countervailing factor(s) have been investigated in temporal and/or spatial comparisons, a predictive model could be constructed based on the assumptions that the association will continue into the future. Thus, a temporal comparison study could suggest that a particular factor might be responsible for genetic erosion in a particular gene pool.

For agricultural crops, solutions or mitigations have focused on *ex situ* conservation: seed banks, genebanks, and others. This approach allows genetic diversity to be maintained even if it is not currently represented in agricultural practice. In addition, genetic research on some agriculturally important crops compares genetic diversity between modern and historic cultivars—and even with the progenitor wild plant species—where possible. This information helps to illuminate current or to predict future problems of genetic erosion, allowing an appropriate management response. For native plant species, the focus is on conservation of genetic diversity *in situ*, although *ex situ* conservation methods are certainly an appropriate parallel conservation strategy, particularly for rare or endangered species or those experiencing high mortality or rapid loss of habitat (Brown and Briggs 1991; Guerrant et al. 2004). However, *ex situ* conservation is not an effective or reasonable substitute for *in situ* conservation. These are complementary, rather than alternative, conservation strategies (Falk 1987; Given 1987). *Ex situ* collections, for example, are only a sample of the natural range of genetic diversity in the species. They are removed from the influence of natural selection and thus cannot accrue new adaptations over time. They are also vulnerable to financial constraints or downsizing, as well as chronic losses in diversity due to storage methods, catastrophic losses from equipment failures or fires, among other things (McGuire and Qualset 1990). Further, many of the world's genebanks do not meet minimum international standards for long-term storage, and most countries do not have facilities for the long-term storage and conservation of plant genetic resources. In a number of countries, genebanks are in a state of rapid deterioration; many accessions need to be regenerated and re-grown periodically in order to maintain seed quality. Avoiding losses of habitat or fragmentation of habitat are also important management practices (Rogers 2004).

Conclusion

Plant diversity is threatened by “genetic erosion”, a term coined by scientists for the loss of individual genes or combinations of genes, such as those found in locally adapted landraces. It is now well documented that over a period of time, there has been significant genetic erosion of crop diversity and there are several reasons for this loss. In Africa, the degradation and destruction of forests and bush lands is cited as a main cause of genetic erosion; overgrazing and over-exploitation are the reasons for the erosion of biodiversity in Cameroon, Burkina Faso, Guinea, Kenya, Morocco, Nigeria and Senegal, as well as in Saudi Arabia and Yemen in the Near East. Wars and civil strife have contributed to genetic erosion in Africa and Asia. In Latin America, most countries report major genetic erosion of economically important forest species.

More recently, the spread of modern, commercial agriculture and the introduction of new varieties of crops has been the main cause of the loss of genetic diversity (FAO 2012a). Considerable genetic uniformity now exists in a number of crops like hybrids of rice and sunflowers. Therefore, in many cases, it is still necessary to return to the store of genetic diversity, both *ex situ* and *in situ*, to find genes conferring resistance to biotic and abiotic stresses. The complementarity between seed conservation in genebanks (*ex*

situ) and in ecosystems and natural habitats (*in situ*) should be further strengthened. Therefore, the FAO Second Global Plan of Action (FAO 2012b) also urges all countries to better manage crop diversity in farmers' fields; develop strategies to protect, collect and conserve crop wild relatives and wild food plants that are under threat; support the use of a wider range of traits for plant breeding; and strengthen seed systems, especially those of locally adapted varieties. The main focus of the Second Global Plan of Action is to strengthen the conservation and sustainable use of plants and seed systems—and the crucial linkages between them—through a combination of appropriate policies, use of scientific information, farmers' knowledge, and action. There is also an urgent need to develop improved indicators, including proxy indicators, of diversity, genetic erosion and vulnerability that can be used to establish national, regional and global baselines. These indicators should be objective and balanced, taking into account the systems in use at the national level. Local and indigenous knowledge should be recognized as an important component of surveys for assessing and inventorying genetic erosion and should be carefully considered and documented where appropriate.

Countries need to establish or strengthen systems for monitoring genetic erosion, including easy-to-use indicators. Support should be given to collecting farmers' varieties/landraces in particularly vulnerable or threatened areas, where these are not already held *ex situ*, so that these genetic resources can be multiplied for immediate use and conserved for future use. National genebank collections should be duplicated outside the country (for example, in the genebanks of neighboring countries and/or in regional or international genebanks). In some countries, the threat of invasive alien species should also be considered, as these may contribute to genetic erosion. Since the loss of plant genetic resources for food and agriculture (PGRFA) varies within countries and from country to country, support should be provided to establish monitoring mechanisms at all levels. The World Information and Early Warning System on PGRFA (WIEWS) application for remote searching, updating and reporting on genetic erosion (<http://apps3.fao.org/wiews/wiews.jsp>) should be further strengthened.

Further research is needed (1) on the use of GIS technology to monitor genetic diversity and to predict and minimize genetic erosion and (2) on the incorporation of the resulting information into comprehensive information systems. Additional study is required in order to understand the nature and extent of possible threats to existing diversity on-farm and *in situ*. And further attention must be given to the many food crops that are the main staples for millions of the world's poor—like sorghum, millet, potatoes and cassava—which do not receive enough attention or investment in terms of conservation research and development.

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Internet resources

Commission on Genetic Resources for Food and Agriculture: www.fao.org/nr/cgrfa

World Information and Early Warning System on PGRFA (WIEWS):
<http://apps3.fao.org/wiews/wiews.jsp>