

Chapter 3

Assessment of Effects on Genetic Diversity

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Abstract

Phenotypic diversity among maize landraces is obvious in kernel color, ear and kernel shape and size, and agronomic traits such as plant height and length of the growing cycle. Traditionally, this phenotypic diversity has been used to classify populations into “races.” Currently, 59 races of maize have been described in Mexico. According to DNA analyses, these races are organized as a continuum and their differentiation is mainly due to isolation by distance. Recent genetic studies of landraces in Oaxaca (Mexico) have shown that gene flow between maize populations is quantitatively important but that management of seed by farmers maintains strong agromorphological differentiation between maize populations.

In traditional agricultural systems, farmers play a wide range of roles with regard to seed production and maintenance. They conserve the genetic resources; they select and plant seed from their varieties; and, after harvest, they are the main consumers of their products. In Mexico, the traditional system coexists with the modern agricultural sector but the subsistence-oriented system is much more widely distributed. In this system, landraces are the result of continued evolution influenced by various factors: 1) *Seed recycling*: Saving seed from one season to the next is an almost universal practice among small-scale Mexican farmers. At least from the farmer’s perspective, seed selection may also be fundamental to maintaining the integrity of a landrace, which can be lost easily through hybridization; and 2) *Seed flows*: Mexican farmers commonly acquire seed from other farmers or sources within or outside the community for several reasons, including experimentation, starting to farm, and lack of sufficient seeds. Thus, traditional farmers actively maintain landraces as dynamic entities.

Farmers are willing to modify introduced maize cultivars through recurrent hybridization with the local genetic material (process of creolization) to improve their local performance and consumer acceptability. They do not consider this process as “contamination.” However, if the introduction of modern varieties becomes a permanent and pervasive process, a threshold could be reached above which gene swamping from those cultivars would reduce or eliminate the genetic diversity of local landraces. Furthermore, the evolution of landraces, which is based on hybridization, recombination, and selection, may follow paths unsuspected for modern varieties. Through recombination, genes belonging to a specific variety can migrate into new genetic backgrounds where new linkages and gene interactions may modify the expression of transgenes in an unpredictable fashion.

Teosinte, the closest wild relative of maize, is considered a weed in Mexico and farmers attempt to control it in their fields. Co-occurrence of maize and teosinte exists in several places in Mexico (Balsas, Chalco, the Central Plateau). Teosinte usually flowers two to three weeks later than maize but overlap in flowering times may occur. Furthermore, there are genetic systems that limit but do not completely exclude crossing between maize and teosinte. Evidence of the extent of introgression of maize alleles into teosinte is mixed. The most convincing example of introgression is provided by *Z. diploperennis*. In contrast, Kato (1984) was not able to find genetic evidence for introgression. The presence in the fields of plants that appear to be F₁ hybrids between maize and teosinte is well documented, but information is lacking about the behavior of the advanced hybrid generations. It also remains to be determined whether hybridization between different genomes results in genome instability and gene movement within the maize genome.

Different agroecosystems are likely to present very different selection pressures. Thus, any beneficial effects of a transgene, for example, in an industrial agricultural setting cannot be assumed to exist in a traditional agriculture setting or among wild-growing relatives such as teosinte. Major pests of maize in Mexico are Lepidoptera, which may be susceptible to most of the Bt varieties that have been commercialized in the United States. However, further information is needed on how limiting these pests are in traditional maize agriculture and in teosinte. If herbicide tolerance genes are introduced into other genotypes, these in turn may become herbicide tolerant. This could be of benefit for local farmers, if they can or are willing to use the appropriate herbicides, and if the patent owner tolerates this inadvertent escape without suing the farmers. If herbicide tolerance is introduced through gene flow into teosinte, a potential tool for control of teosinte in maize fields may be lost.

Whether or not a transgene will spread into landraces or wild populations depends on a number of factors, including the level of gene flow in any given growing season and in successive seasons, and the selective effect of the transgene. If transgenes are selectively favored, selection may lead to a reduction of genetic diversity in the genomic vicinity of the gene in question. The size of the affected region subject to reduction in genetic diversity (“genomic window”) is proportionate to the selective advantage of the gene under selection and inversely proportionate to the level of recombination. In maize, which has high rates of recombination, the region showing reduced diversity as a result of selection on a single gene would be small (one hundredth of one per cent). Thus, any effects of a single transgene on the genetic diversity of a landrace or of teosinte are likely to be insignificant from a biological point of view, unless there are high levels of gene flow from transgenic cultivars to landraces and teosinte populations, in which case the native genetic diversity may be displaced by the limited diversity of the transgenic cultivars.

The consensus at this stage is that transgenic sequences are present in Mexican maize landraces in the field although not in the CIMMYT gene bank. However, this leaves many open questions, including the geographic magnitude of the transgenes (how widespread are they?), their local intensity (what is their local frequency?), the identity of the transgenes (are they only from commercialized varieties, such as those conferring Bt and herbicide resistance, or are they from as yet uncommercialized genotypes, such as

maize transformed for pharmaceutical production?), their possible presence in teosinte, their source(s) (local government stores, emigrants to the United States, seed companies, or other origins), the fate of transgenes in landraces and teosinte, and the role of farmers and others in gene flow by pollen and seed, involving transgenic sequences.

The processes that generate and maintain the genetic diversity of maize are very dynamic and preservation of diversity should be based on the preservation of these processes as well as the conservation of landraces, per se. We contend that establishing more effective selection schemes on the part of farmers may constitute an effective incentive for farmers to maintain their landraces. Farmers can actually be trained to conduct some degree of plant breeding, if they do not already do so. This type of outreach would require an active extension service, a network of NGOs or local cooperatives, or a network of technical schools. Preservation of genetic diversity can be achieved through more active use of the diverse landraces and their diverse products, especially in urban areas where many of the maize products are currently very standardized and uniform. Education of urban consumers about diversity of maize and its products would help promote the use of products from these landraces, permitting the conservation of the diversity in the fields. Additional research is needed in the areas of flowering biology, gene flow, and reproductive isolation of maize. Furthermore, studies that document the extent of the distribution of transgenes among maize landraces and teosinte populations need to be conducted and published in peer-reviewed journals, following protocols that rely on replications and blind tests under the supervision of outside advisors.