Evolution of corn: role of single nucleotide polymorphism

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Maize (*Zea mays* L.) commonly known as corn has wider adaptability under varied agro-climatic conditions. It is cultivated on nearly 150 m ha in about 160 countries. In India, maize is the third most important food crop after rice and wheat. Globally, maize is known as the queen of cereals, because it has the highest genetic yield potential among cereals. Maize was domesticated by indigenous peoples in central Balsas valley of Mexico around 9000 years ago. Until Columbus introduced corn to Europe, it was not grown outside the Americas. The evolution of corn is a matter of controversy among scientists. Several theories have been proposed about the specific origin of maize, including the most prevalent theory of direct domestication of a Mexican annual teosinte, hybridization between a small domesticated maize (a slightly changed form of a wild maize) and a teosinte, undergoing two or more domestications either of a wild maize or of a teosinte and evolving from the hybridization of *Zea diploperennis* by *Tripsacum*. It has been accepted that the wild ancestor of corn is a grass called teosinte (Figure 1). The two plants have dissimilar appearance, maize having a single tall stalk with multiple leaves and teosinte being a short, bushy plant and especially the kernels. But cytologicaly, the two are surprisingly alike. They have the same number of chromosomes and a remarkably similar arrangement of genes. In fact, teosinte can cross-breed with modern maize varieties to form maize–teosinte hybrids that can go on to reproduce naturally. Scientists are interested in the major changes in plant and seed architecture that transformed teosinte into corn.

Figure 1. (Left) Maize ear and (right) teosinte ear (photo credit: www.google.com).

Geneticists have used advanced molecular biology tools to pinpoint the roles of some of the genes with large effects. Remarkably, genes controlling much of the morphological difference between maize and teosinte were shown to map just six regions of the genome. Among them, genes dealing with seeds of teosinte and maize are an important focus. Teosinte seeds are protected by a hard seed casing (technically a 'fruit case') that makes them impractical to eat. However, in evolved maize the structure that forms the seed case becomes the cob at the centre of the ear, leaving the seed exposed as a kernel[1,2]. The transition from encased to exposed grain greatly facilitated the use of the grain as food. The locus that largely controls this difference has been resolved to a single gene called teosinte glume architecture 1 (*tga*1) (ref. 3). The maize allele of *tga*1 disrupts the normal development of the cupulate fruit case, exposing the grain on the surface of the ear. *tga*1 encodes a squamosa-promoter binding protein (SBP), a transcription factor family that has been shown to regulate floral development[4,5]. Although *tga*1 has been identified as the major gene controlling changes in fruit case development during domestication, the causative polymorphism in *tga*1 and how this affects the phenotype has been deciphered by a team of scientists lead by John F. Doebley (University of Wisconsin, Madison, USA)[2]. They found that a single amino acid substitution in *tga*1 is the causal variant for the origin of the naked grains of maize compared to the covered grains of teosinte. However, the predominant mechanism for morphological evolution may be alterations in gene expression. They compared the *tga1* DNA sequence in 16 different maize varieties and 20 varieties of teosinte. They discovered a single fixed nucleotide polymorphism (**G**TAC into **C**TAC) in the coding sequence of the *tga*1 gene which substitutes a single amino acid (lysine to asparagine) in the TGA1 protein. This leads to major tendency to form dimers in maize and to turn TGA1 into a transcriptional repressor of its target genes, while the teosinte TGA1 did not act as a repressor. The repressing TGA target genes alter fruit case development, contributing to the naked kernel trait. These results provide an example of how selection by ancient plant breeders triggered profound structural changes in an organism through relatively minor genetic alterations, allowing new traits to evolve rapidly. A small change in the course of evolution makes a gigantic difference over a period of time.

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