

The Contribution of Traditional Plant Breeding to Ensuring Food has Safe Amounts of Naturally Occurring Toxins

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Introduction

This article covers how plant breeders create secure new food crop varieties using traditional breeding techniques. Two categories are used to classify crops: 1) Crop plants with no detectable plant toxins; and 2) crop plants with recognised plant toxins. Examples and crop case studies from each category are used to demonstrate how plant breeding practises are altered before commercialization depending on whether the crop produces a known natural toxin when breeding these economically significant crops. The great majority of food crops that shoppers find in the produce sections of supermarkets are the result of traditional plant breeding. Even cultivars like seedless watermelon, pluots, apriums, and tangelos-which are frequently wrongly believed to be the result of cutting-edge genetic engineering technologies-are the results of traditional breeding techniques. In reality, only a small number of food crops, including maize, soybean, canola, rice, potato, papaya, squash, and apple, have varieties produced by genetic engineering, which the USDA defines as a process that uses contemporary biotechnology tools to introduce, eliminate, or rearrange specific genes [1].

Description

In traditional plant breeding, selecting parent plants with desirable traits is done to produce advantageous pairings in the following generation. More than 10,000 years ago, the method of choosing excellent plants for food, feed, and fibre products was developed; nevertheless, in the last century, it has undergone significant refinement. Early farmers depended on genetic diversity still present in groups of wild plants and chose particular species with desired qualities. Today's plant breeders increase genetic variation by choosing genetically different parents that can or cannot reproduce sexually in nature. Plant breeders choose plants for interesting qualities and characterise criteria crucial for each crop using well-established scientific methodologies in order to discover the best individuals in the progeny [2].

Although few foods have been rigorously evaluated for whether or not any harm might occur when foods are consumed, consumers anticipate foods from conventionally produced crops to be safe and nutritious. This consumer expectation that crop plants will produce safe foods is based on either their own personal history of eating such foods without incident or their knowledge that people have historically prepared and consumed foods from a particular crop without any evidence of harm or unfavourable effects. Foods with a "history of safe consumption" can be attributed to a variety of factors, such as the length of time they have been consumed, measures taken to prevent the buildup of

toxins after harvest, knowledge of whether the crop contains endogenous plant toxins, and if so, accepted preparation techniques [3].

The practise of conventional breeding has developed over time, resulting in an efficient framework that enables the development of foods that are both safe and nutrient-rich as well as improving crop performance. Making judgments about which parents to select, which parents to cross-pollinate, and which progeny to progress are all part of the process of breeding plants. Contrary to animal breeding, plant breeding has the advantage of being able to produce very large populations (depending on the crop, into the tens of thousands), in which the vast majority of plants (often >99%) are discarded while only a few specific plants are chosen to move on to subsequent breeding rounds. The ability to choose a small number of individuals from enormous populations is a crucial component in plant breeding and is used to: A trait-related DNA marker that segregates, or is consistently co-inherited, with the trait has now been established as being genetically linked to the trait after mapping the genetic basis for the trait of interest within a chromosomal region. The development of a DNA marker-based assay then uses this trait-linked marker. In place of more time-consuming and resource-intensive phenotyping techniques, DNA marker-based assays enable breeders to quickly screen thousands of progeny plants for the genetic basis of an interest characteristic. Breeders can now identify and choose certain plants with the desired trait using the DNA marker-based assay for the next phase of breeding of trait introgression [4,5].

Characteristic introgression's goal is to introduce a desirable trait from the source parent plant into parental varieties' germplasm that are already well-characterized for other traits that are acceptable for commercialization (e.g., uniform yield performance, adaptability to different environments). The trait-linked marker created through trait mapping and the genome-wide markers from the commercial-track varieties are the two types of DNA markers that breeders utilise for trait introgression. A trait-related DNA marker that segregates, or is consistently co-inherited, with the trait has now been established as being genetically linked to the trait after mapping the genetic basis for the trait of interest within a chromosomal region. The development of a DNA marker-based assay then uses this trait-linked marker. In place of more time-consuming and resource-intensive phenotyping techniques, DNA marker-based assays enable breeders to quickly screen thousands of progeny plants for the genetic basis of an interest characteristic. Breeders can now identify and choose specific plants with the desired trait using the DNA marker-based assay for the next phase of breeding of trait introgression.

Conclusion

Characteristic introgression's goal is to introduce a desirable trait from the source parent plant into parental varieties' germplasm that are already well-characterized for other traits that are acceptable for commercialization (e.g., uniform yield performance, adaptability to different environments). The trait-linked marker created through trait mapping and the genome-wide markers from the commercial-track varieties are the two types of DNA markers that breeders utilise for trait introgression. These crops have a lengthy history of being safe to eat, thanks to centuries of domestication and breeding techniques, such as maize. Incorporating characteristics that increase yield, improve nutrition, and increase abiotic (like drought) and biotic (like microbial infection) stress tolerance of crops in this category requires using the framework of conventional breeding procedures. Crop breeders in this group concentrate on agronomic factors as advancement criteria to assess variety

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performance under various environmental factors, such as different soil types and geographic locations, as well as diverse management techniques.

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Conflict of Interest

None.

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