

FUTURE TRENDS IN CORN GENETICS AND BIOTECHNOLOGY

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INTRODUCTION

Commercial corn breeding and trait integration have changed modern corn production. In recent years, technology advances for control of insects, weeds, and diseases have improved corn yield levels significantly. Conventional breeding continues to be the foundation of new inbreds (parent lines) for hybrid development. Another method of inbred development is called doubled haploids. This methodology results in non-segregating or fixed inbreds lines. These are coupled with biotechnology applications such as transformation, genomics, and molecular markers. These applications help researchers better understand plant function and allows for development of improved yield performance or disease resistance.

Conventional Breeding

Conventional corn breeding leverages the theory of heterosis or hybrid vigor. Heterosis may be defined as the occurrence of the greatest possible number of loci with a dominant allele (1). This imparts improved vigor, size, yield, disease resistance or tolerance to environmental effects. In short, the single cross hybrid or progeny of the two inbred lines is superior in performance than either of the parents independently.

In corn, inbreeding is used to create near-homozygous inbred lines with desirable traits. The most common method of inbred line development is based on pedigree breeding. It is a method of breeding that utilizes knowledge or records of all lines of descent of the individuals of each generation. For example, a breeder may be selecting for improved disease resistance. Knowing the background of specific inbred lines will help in determining the crosses to be made to have a desirable affect on the disease resistance. Key traits that are targets for genetic improvement are generally specific to a region. Once the traits are identified, selection for improvement can begin. Common traits include disease resistance, stalk strength, root strength, plant height and others.

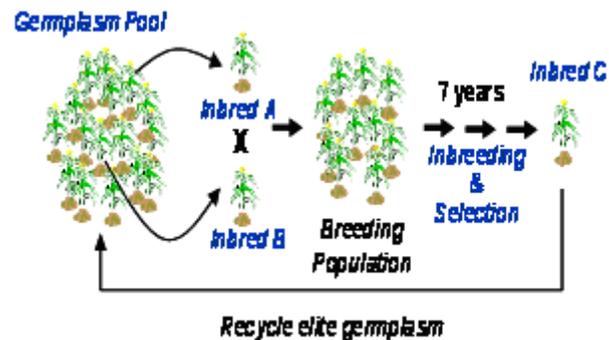


Figure 1. Inbred development process flow.

The process of pedigree breeding is to cross two known inbred lines of interest to create a segregating population. Once the population is created, individuals may be self pollinated and selected from the population. These individuals are then tested for increased disease resistance

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or other key traits. Individuals that demonstrate improved performance continue to be self-pollinated to develop a more uniform line (Figure 1).

Once an inbred line is finished, after seven generations or years of inbreeding, it can be used in combination with other finished inbred lines to create single cross hybrids. These hybrids are then tested in yield trials and/or disease nurseries to determine if the candidate inbred is delivering improved performance. Generally, yield is the first key selection criteria. If the new inbred is deemed improved, it may be incorporated back into the germplasm pool and crossed with other inbreds to create new segregating populations for further inbred development.

Doubled Haploids

Like traditional breeding, Doubled haploids are a method of breeding that creates inbreds. Two key differences between the Pedigree and Doubled haploid (DH) methods are that with DH inbreds are completely homozygous and developed in 1-2 years versus 7 for traditional breeding.

There are several advantages to creating inbreds using this method. They include, improved breeding efficiency and effectiveness by generating inbred lines with 100 percent purity in just two generations, increased options for per se selection of key traits like parental traits, disease, and maturity, breeding impact; more complex pedigree selection away from home nursery, and finally, increases precision of molecular markers (Figure 2).

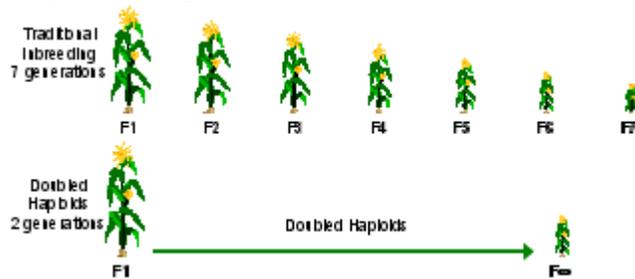


Figure 2. Comparison of Conventional inbred line development to Doubled haploid inbred development

Doubled haploids are created by a special genetic process and have one set of chromosomes. They undergo chromosome doubling through a chemical process that produces a completely homozygous, fertile doubled haploid plant. Conventional inbred development, it takes seven generations to do this, and the plants are still not 100 percent pure. The purity and genetic uniformity of doubled haploid lines make it easier to measure characteristics and reduce product development time.

Like conventional inbred development, hybrids are created from the new inbreds and tested in various environments to determine if a genetic improvement has been made. If performance is improved the inbred will be recycled into the germplasm pool to create new sources of genetic variation for corn improvement.

Biotechnology

Biotechnology has been widely used in corn breeding. It covers many different technology applications that influence the understanding of gene function. Biotechnology tools include transformation, genomics, molecular markers, and gene sequencing. Application of these technologies does not occur independently of conventional breeding, but in association with it.

As superior traits are identified they may be moved within corn germplasm using the methods above.

Transformation

This tool provides scientists with the ability to improve products that cannot be accomplished with conventional breeding. In transformation, genes available from other sources can be integrated into corn to make marked improvements for a key trait. A well known example is corn that has been improved with “Bt” insect resistance. It is a naturally occurring soil bacterium that has a gene that provides protection against certain insects. Once the gene is inserted into corn germplasm, it can be used in conventional backcrossing programs to move the gene into other corn inbreds.

Genomics

Genomics is a relatively new field of study, and may be described as the science of the genetic material of a chromosome set. This tool helps scientists identify which genes determine important traits in corn, and how genes interact with each other. For example, gene interaction likely determines how drought tolerant a hybrid is in a particular environment. This is due to multiple genes controlling different plant functions during the stress period. Genomics help sort out the interaction.

Molecular Markers and Breeding

Molecular markers are pieces of DNA that are closely associated with a gene or genes responsible for a certain trait. Marker-assisted selection is the use of genetic markers to identify the presence of a specific gene or combination of genes that carry a desirable trait, such as insect or disease resistance. Knowing that a gene of interest is contained in a specific inbred allows directed use of the inbred to create specific combinations so more rapid trait improvements can be made. This saves a great deal of time in the breeding and selection process.

Molecular markers have a significant role in selection. They serve as a starting point for genes that are responsible for the phenotypic response. The phenotypic response is an interaction of the “inbred” or hybrids and its environment. This is also known as the Genotype X Environment interaction.

Another application of molecular markers is in the introgression of a desirable trait from a donor inbred into an elite inbred. When a trait is transferred from a donor, it is important to identify and recover the genotype with the desired traits. Traditionally, this was done through a process called backcrossing. This required a great deal of time, effort, and resources. Markers allow for the identification of the favorable genotype in approximately one-half the generations compared to the conventional backcross method. This improves accuracy and timeliness of key trait integration.

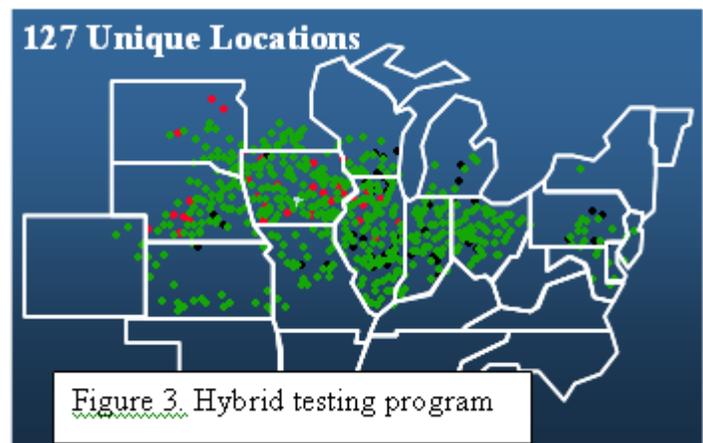
Gene Sequencing

Gene sequencing technology is used by researchers to determine the nucleotide sequence of genes or regions of the genome important for trait improvement. This technology has also been used to create a dense genetic map that helps us understand precisely where a specific gene or trait is located, the amount of genetic diversity that exists for that specific gene or trait, and to develop DNA-based diagnostic markers for the trait for use in the breeding programs. Gene sequencing makes this trait selection much more accurate, as researchers know exactly where select traits reside within the germplasm, and it allows them to understand the function of specific genes, a process that previously took years of research and testing. The technology helps us to improve plant breeding and product development systems. This allows for more rapid creation and testing of superior products by selecting the best possible traits for yield and disease resistance. The application of gene sequencing technology to native trait discovery and molecular breeding is in active area of use.

Testing

Testing is a principle component of any product development program. It is the process which identifies genetic improvement. It provides the genotype X environment interaction that will allow the selection of superior inbreds. To create hybrids for testing, unrelated inbred parents are crossed to produce experimental hybrids. These experimental hybrids are tested year after year.

The early stages of testing include a few locations. As testing continues, more locations are added for wide area testing (Figure 3). This is a very rigorous testing program that allows the experimental hybrids to be challenged by a broad range of soil types, climatic conditions, and other pressures such as diseases and insects. Measurements are taken for important traits and over a period of several years, the highest yielding and most environmentally stable hybrids are identified. The most superior inbreds from these the top performing hybrids are then recycled into to the corn germplasm pool. This defines genetic improvement.



Traits

Genetic improvement must result in improved traits. These traits result in greater harvestable yield. Traits generally fall into agronomic, disease, and/or end use categories. The targets for trait improvement vary depending on the area and the level of improvement needed. In the High Plains and Western U.S. traits may include drought tolerance, Head smut resistance, Fusarium ear mold resistance, silage yield and quality, or others. Testing programs are designed and

deployed to determine if genetic improvement is being made in the area of focus. Measurable differences are required to identify trait improvement. Figure 4 shows a typical strategy for selecting for improvement in a particular trait. Individuals sort out with varying responses. Focusing on individuals that provide measurable improvement for the trait of interest leads to genetic improvement.

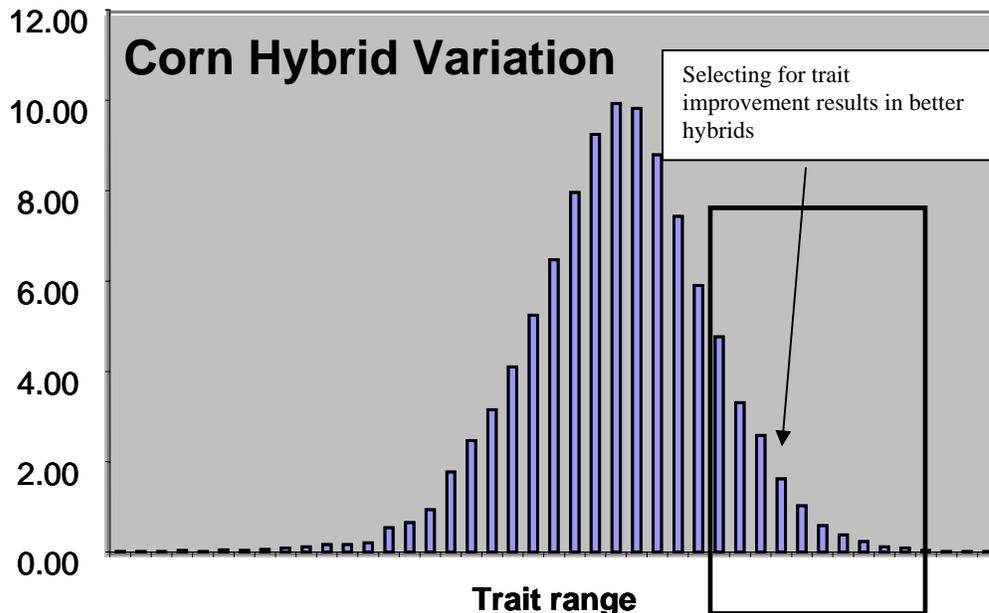


Figure 4. Trait distribution and selection focus for improvement.

SUMMARY

Conventional breeding is the mainstay of inbred and hybrid development. It is based on the theory of heterosis. Advances in technologies have allowed other methods to add efficiencies to modern commercial corn breeding. These include the use of Doubled haploids, transformation, genomics and molecular markers. These technologies have allowed scientists to make more informed decisions around specific genetic combinations to improve genetic gain, and allowed for more rapid identification of lines carrying a particular trait of interest. Utilization of conventional breeding coupled with biotechnology has led to the rapid increase in yield gain in corn. As science continues to move forward, genetic gain for yield and key traits will continue to accelerate.

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