NEW TECHNOLOGIES IN BREEDING TO MEET CONSUMER DEMANDS

B Crossland[1], M Sweeney[1]
[1]Bayer CropScience Lubbock, TX

Molecular markers are a powerful tool to aid cotton breeders in developing new varieties with improved characteristics. By allowing us to track chromosome segments we can use molecular markers to map the locations of genes that influence agronomic traits. Depending on how many genes control a trait like yield or fiber quality, different techniques can be used to combine favorable genes from different parents into improved cotton plants. Markers can also be used to help recover useful genetic diversity that was lost during domestication and modern breeding bottlenecks.

INTRODUCTION

Cotton Breeding is moving rapidly as the result of DNA sequence information. Traditionally breeders would make crosses between different lines of cotton and test the resulting progeny for plants that combined the best traits from both parents. Now we can associate molecular markers with our traits of interest and precisely design new lines.

USES FOR MOLECULAR MARKERS IN BREEDING

When a few genes control a trait and those genes are tagged with molecular markers, breeders can use those markers to screen through the cotton line collections and find lines that have the trait of interest without having to grow out the lines and measure the trait. Disease resistance to root knot nematode is a good example of a trait that is controlled by a few genes in cotton and those gene locations are well mapped (Figure 1). Using these markers breeders can select plants that will be resistant to root knot nematode without having to grow the plants in soil containing nematodes. This allows breeders to maintain the resistance in years where dry conditions results in low nematode pressure, in winter nursery locations that are not infested and the greenhouse during marker assisted backcrossing programs.

Sometimes traits, like yield, are controlled by many genes with smaller effects. Traditionally to combine a large number of favorable alleles for different parents, breeders needed to test large numbers of progeny. But when markers are used, a smaller subset can be tested to locate the regions contributing to yield and then new crosses made between the progeny lines to combine all the favorable alleles into a single line (Figure 2).

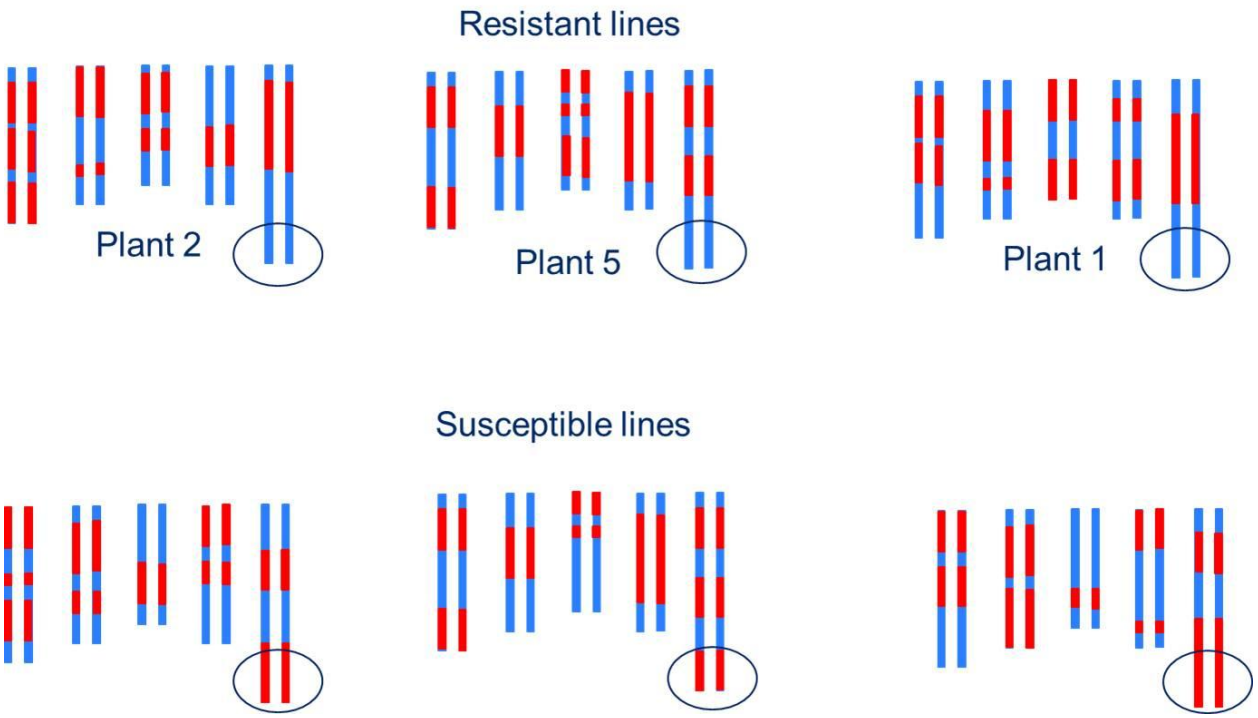

Figure 1. Mapping of simply inherited disease resistance

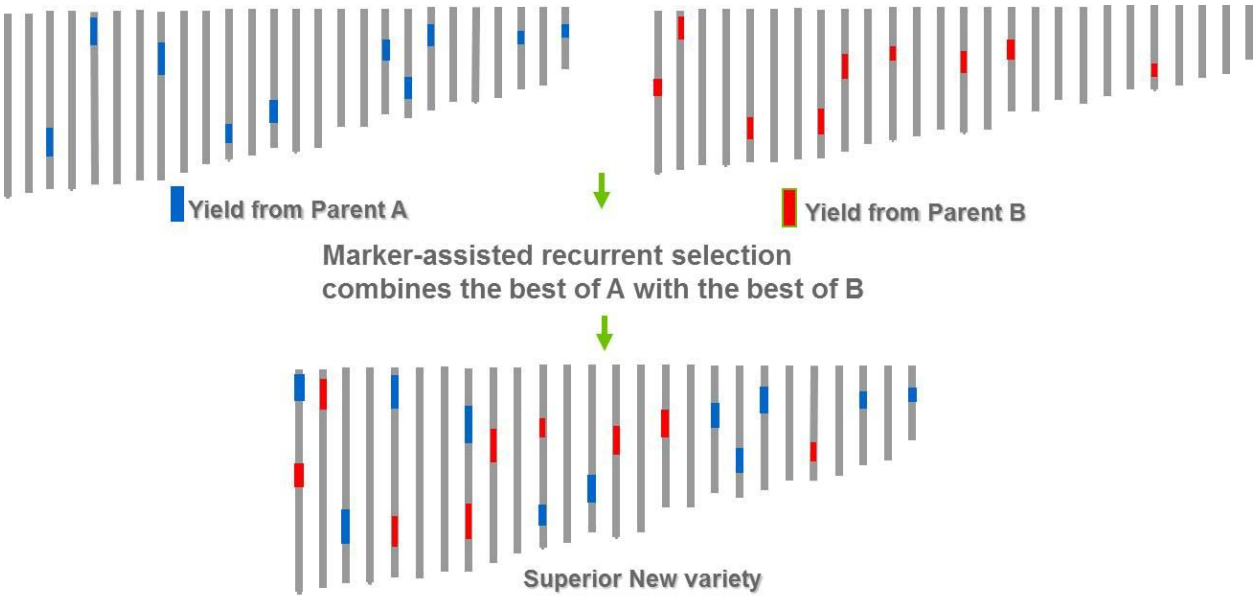

Figure 2. Mapping traits controlled by many genes and using this information to create new lines

Breeders often struggle with negative correlations between traits. They would like cotton lines that are high yielding with long fibers, but strong selection pressure for yield results in plants with shorter fibers and strong selection for fiber length produces lower yielding plants. There are many traits with negative correlations, fiber elongation and fiber maturity, fiber fineness and fiber maturity and disease resistance and yield. By mapping the locations of the genes that affect our traits of interest we can see why we have these negative correlations. There are regions where an allele from one parent improves one trait of interest while that same marker is associated with a decrease for another trait of interest. In these cases markers allow us to measure the magnitude of the competing effects allowing breeders to decide which trait to select, given the tradeoffs. Mapping also reveals regions where these traits are not in competition with other traits and they can be selected without negative associations (Figure3).

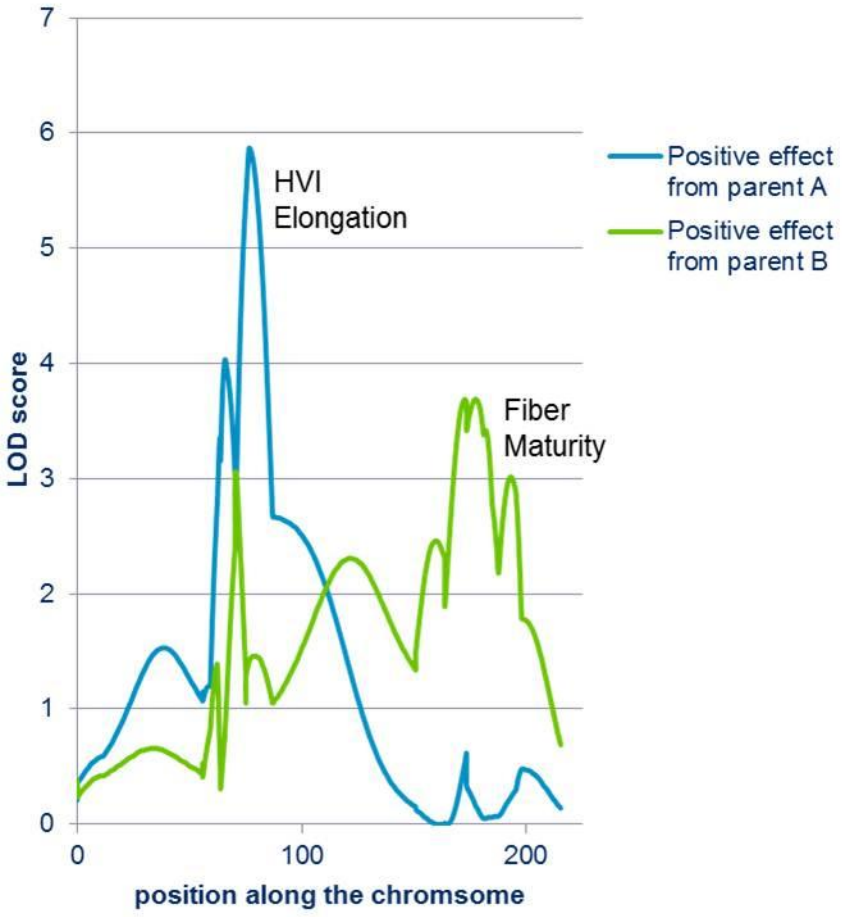

Figure 3. QTL mapping of HVI elongation and Fiber Maturity traits.

Modern breeding has greatly increased the productivity, quality and stability of cotton harvests. In order to continue to make these gains we need to introduce new beneficial alleles to our elite lines. Markers allow us to return to earlier cotton gene pools, the landraces and the wild cotton. These gene pools contain a large diversity of unused alleles, some of which could improve yield and quality traits in cotton.

However breeders have avoided using these lines because they also have a number of negative traits including low yield, plant height and flowering time. Using markers was can locate genes controlling these negative traits, eliminate these regions and find positive alleles that were hidden by the negative alleles (Figure 4).

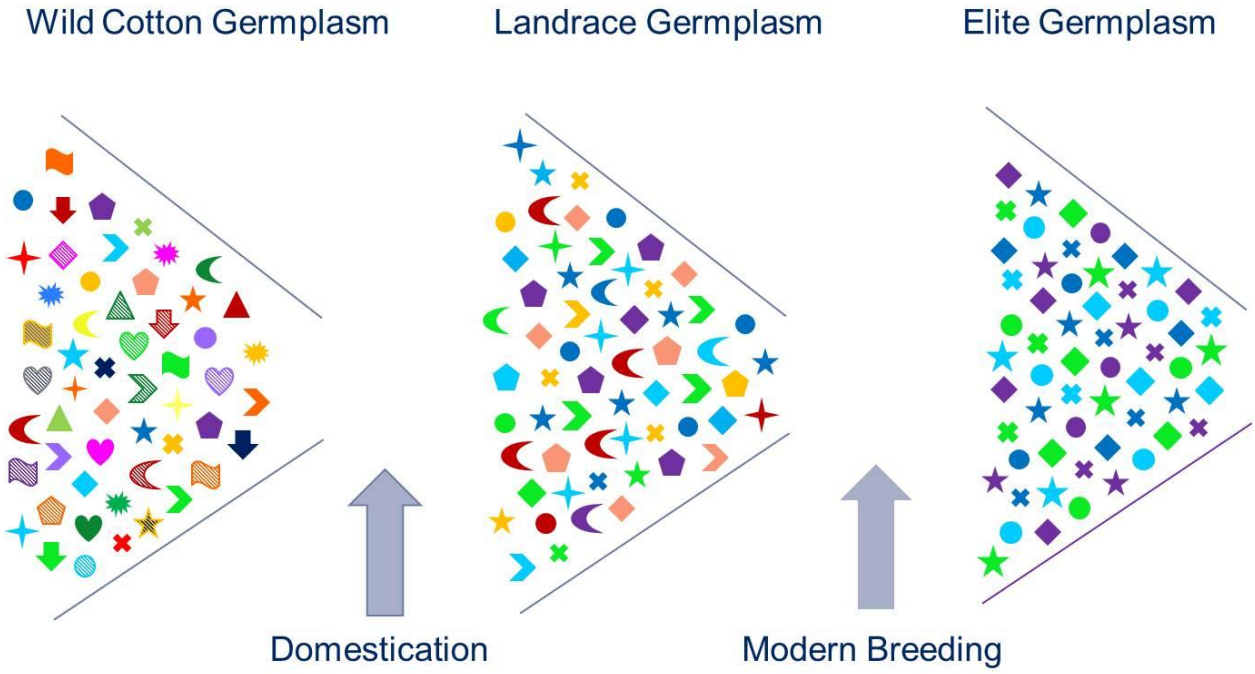

Figure 4. Loss of Genetic Diversity in Cotton Germplasm During Domestication and Modern Breeding