

How Molecular Markers Can Help Wheat Breeders and Farmers?

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In the past couple of decades, the advent of molecular markers has immensely improved our understanding about plant genes and genomes. Molecular markers are useful tools to identify the variation in the DNA sequence and eventually the regions of DNA or the genes controlling the qualitative and/or quantitative traits of agronomic importance. Marker-assisted selections are commonly used in breeding programs for screening and selecting desirable biotic and abiotic stress tolerant traits. Application of molecular marker technology in wheat is a relatively complex process compared to other cereal crops given the fact that wheat has one of the largest and most complex genomes. Since the first wheat genetic map using simple sequence repeat markers was published in 1998, numerous studies have used them to locate quantitative trait loci or genes controlling important agronomic traits in wheat.



Identification of markers tightly linked to important genes is a critical process in genetic studies. The complexity of the wheat genome makes it hard to find markers closer to the target genes. However, the affordability and cutting-edge science of high throughput sequencing technologies coupled with advanced cloning techniques provide ample resources and opportunities to study the wheat genome better than ever. These advances in genomics and molecular genetics are assisting in designing perfect markers from gene sequences and in cloning several important genes into wheat.

The high throughput sequencing technologies can detect variation or polymorphism in DNA at a single nucleotide level to design single nucleotide polymorphic (SNP) markers. Several sequencing platforms allow re-sequencing of the target region controlling a trait of interest and the use of SNP markers allow screening several hundred lines simultaneously. Abundant SNP markers have been discovered in wheat and are available for high throughput screening of breeding populations. Wheat research communities in the U.S. and Europe are working together to design a 90,000-SNP database using publicly available sequences and information on diverse germplasm lines.



The Wheat Improvement Genetics group at Texas AgriLife Research in Amarillo, in collaboration with breeding, physiology, entomology and pathology teams, is working to identify molecular markers for drought, greenbug, wheat streak mosaic virus resistance and other important traits. In addition to identifying markers, considerable progress has been made to clone greenbug resistance gene, *Gb3*, in wheat. The Wheat Genetics group is also trying to identify the physiological and molecular mechanisms of widely adapted cultivars. These efforts will accelerate the breeding process and increase the selection efficiency for

traits limiting wheat production in the Southern Great Plains including the Texas High Plains. Considering farming requirements in the Texas Panhandle, the wheat team tries to integrate multiple traits with high yield into cultivar development.

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