

New wheat genetic advancements aimed at yield enhancement

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Texas A&M AgriLife Research is making genetic advancements in wheat to increase yields in the future. Credit: Texas A&M AgriLife Communications photo by Kay Ledbetter

Texas A&M AgriLife Research is closing in on specific genetic traits in

wheat that can help increase yields in the future.

The title of a recent paper published in the *Crop Science* journal, "Validation of Chromosomal Locations of 90K Array Single Nucleotide Polymorphisms in US Wheat," may leave some dazed and confused.

But lead scientist, Dr. Shuyu Liu, AgriLife Research small grains geneticist in Amarillo, said it simply means they are narrowing the knowledge gap as to where key traits are in the wheat genome and how to access them.

"Our goal is to develop improved wheat varieties with high yield capability and resilience to a variety of stressors across differing climates and water resource availability," Liu said.

The AgriLife Research study included teams led by Dr. Jackie Rudd and Dr. Amir Ibrahim, wheat breeders in Amarillo and College Station, respectively; Dr. Dirk Hays, plant geneticist in College Station; and Dr. Qingwu Xue, crop stress physiologist in Amarillo.

Their study included three wheat populations derived from two popular AgriLife Research cultivars, TAM 111 and TAM 112, and other diverse wheats.

Rudd said the importance of this research should not be lost in the technical jargon.

"We have talked about using genetic markers for many years now, but this research moves us from 'proof of concept' to actual practice in our TAM wheat germplasm," he said. "To be able to accelerate the movement of greenbug and wheat curl mite resistance from TAM 112 into new varieties is huge."

Single nucleotide polymorphisms, known as SNPs, are the most common type of genetic variation in a plant, animal or human. Each SNP represents a difference in a single DNA building block, called a nucleotide.

Those variations are found throughout the wheat DNA and act as biological markers, helping scientists locate genes that are associated with a certain trait or characteristic.

The international wheat community, including the U.S., has developed an array chip with 90,000 SNP markers, Liu said. Markers are used to tag the trait so it is easily identifiable with new lines of wheat containing the key genes.

The 90,000 SNP array chip has become a common genetic marker method used by wheat breeders and geneticists, but there are limitations. Of the 90,000 markers, only about 40,000 of them had been mapped onto chromosomes, he said.

Mapping SNPs in wheat can help to develop high throughput molecular markers for important traits, Liu said.

Silvano Ocheya, a doctoral student of Liu's who is completing his thesis research, has already mapped 6,000 of the SNPs, including those pinpointing drought tolerance and wheat streak mosaic virus characteristics, in one of the three mapping populations.

Liu's lab has also developed high throughput molecular markers for greenbug and wheat curl mite resistance.

The AgriLife Research study confirmed 13,000 previously mapped SNPs in their three [wheat](#) population crosses, and they newly mapped 2,190 unique SNPs.

Liu said the 15,000 SNPs they have confirmed are being used to study complex agronomic traits such as yield, yield components and heat tolerance, in addition to disease and insect resistance controlled by single dominant genes.

They are also studying the interaction between the genes and the environments.

"For instance, we are working to identify major genes controlling yield under dryland and irrigation conditions," Liu said. "Data is collected from multiple environments so we can focus on how major genes contribute to yield improvement under different climates."

All this information will help breeders incorporate key genes associated with the traits and get the new enhanced varieties to producers sooner, he said.

Provided by Texas A&M University

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