

Cotton breeding researchers take giant leap

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Lower branch of a potentially valuable breeding line of cotton with fruiting sites that are numerous and closely spaced. By analyzing variations among lines, like branch length and internode distance between fruiting sites, and dovetailing that with SNP data, scientists can typically figure out which SNPs can be used to select for the desirable genetic combinations. Credit: Texas A&M AgriLife Research photo

Narrow germplasm base and limited technology have made it difficult for cotton researchers to identify specific DNA markers needed to locate genes that confer desirable traits. But that's no longer the case.

Dr. David Stelly, a Texas A&M AgriLife Research [cotton](#) breeder in College Station, said cotton is ready to merge into the breeding fast lane with the expected release of "cotton SNP chips" loaded with single nucleotide polymorphisms, or SNPs (snips). SNPs are variations within

the DNA.

"The new chip will be the first of several quantum steps forward over the next couple of years that will open many doors for cotton breeding research and improvements," Stelly said. "While DNA markers are not a panacea in themselves, they can turbo-charge the breeding process."

Joining Stelly and Amanda Hulse, his Texas A&M University doctoral student, and Dr. Fei Wang, his post-doctoral researcher, on this massive project were researchers from the University of California-Davis, Brigham Young University and the U.S. Department of Agriculture-Agricultural Research Service, all with support from Cotton Incorporated.

Markers differentiating cotton lines are essential to applying genomic technologies in breeding research, he said. For maximum utility, the DNA markers must be numerous, variable among breeding lines and relatively cheap to screen and use. Across all crops, SNPs are the most numerous, widely distributed type of DNA marker. They also are the least expensive to use for most purposes.

"Breeders of cotton and other crops traditionally create genetic advances by hybridizing, inbreeding and selecting," Stelly said. "We hybridize lines with prospectively complementary genetic differences and sift through subsequently inbred generations to find genetically recombined lines with attributes superior to both parents."

A new breeding product must be equal to or better than all other available cultivars to compete well in the marketplace, he said. To enhance the odds of finding excellent genetic recombinants, breeders almost always rely on parents that are themselves elite and, as a result, closely related.

Even so, the breeder's selection process must be comprehensive, Stelly said. Lines must be tested in diverse growing environments and address all important traits, involving multiple genes, many of which are expensive to evaluate. Some processes can be significantly aided by molecular markers, including parental selection, dissection of genetically complex traits and selection for beneficial genes and regions.

This need for high-throughput marker-based capabilities in cotton motivated these researchers to establish large-scale cotton SNP development efforts, he said. They formed a consortium to develop a "cotton SNP chip" for global use by breeders, geneticists and other researchers to enhance cotton.



In this cotton breeding field, the red Upland cotton rows separate different chromosome substitution lines of Upland cotton that each contain a different pair of alien chromosomes from a different wild non-cultivated species. Each line contains about 2,000 new genes not found in cultivated cotton. Credit: Texas A&M AgriLife Research photo

Internationally, the group was joined by the Commonwealth Scientific and Industrial Research Organization in Australia, the Centre for International Cooperation in Agronomic Research for Development in

France, the Council of Scientific and Industrial Research Organization-National Botanical Research Institute in India. Dow AgroSciences is participating as a commercial contributor.

"The launch of the chip marks an important step forward for cotton," Stelly said. "This signals the capturing of genomic technology and our ability to put it into a platform that researchers can use to breed better cotton."

After many years of work, the international cotton community has identified large numbers of SNPs and chosen 70,000 public SNPs as "base content" to be included in every cotton SNP chip, with fully disclosed DNA sequences, he said. In addition, each chip will have capacity for "add-on content" for another 20,000 non-public SNPs, as might be desired by private industry.

Stelly said AgriLife Research worked especially close with University of California, Davis, to develop many of the SNPs in the chip.

"It was great teamwork, our lab working with that of Dr. Allen Van Deynze and his post-doctoral researcher, Dr. Hamid Ashrafi, at UC Davis. There was a lot of cross-talk in all aspects—for years," he said.

Stelly said the Texas A&M group led in development of the inter-specific SNPs, which differentiate between cultivated cottons and closely related species, and Allen's lab was the lead in developing intra-specific SNPs, which differentiate among cultivars and lines of cultivated cotton.

He explained the SNPs are basically a tool "to find your way around the genome. Breeders can use sets of these markers as tools for determining where traits of economic interest are located." For instance, a breeder trying to incorporate longer fiber length will use SNPs to do indirect

selection for that trait, knowing specific SNPs are close to specific genes at different genome locations in different varieties.

"We aim to enable SNP applications that help create superior genetic combinations and foster greater and faster success by breeding programs," Stelly said. "Some of the most immediate applications will be for simply inherited traits for which plant-screening experiments are inaccurate and/or expensive, such as nematode resistance."

The consortium has announced an agreement with Illumina, a genomics technology company, to produce "BeadArray" panels or chips for analysis of cotton SNPs, Stelly said. Each array will include up to 70,000 public SNPs.

With an overall collection of 10,000 different cotton lines available, a researcher may only want to select 300 lines and access the most diversity, he said. By using these markers, they will be able to detect which chromosome segments of their genomes are similar or different. Such knowledge becomes a powerful tool in choosing parent, experimental and breeding goals, as well as strategies for conventional breeding.

"This will open many doors for more effective utilization of naturally occurring wild accessions of cotton and open the door to things we previously could not do feasibly as public researchers," Stelly said. "We want to be able to better use natural biology to enhance and bring genetics to breeding, so producers and other parts of the industry can optimize natural resources, yet maintain economics."

Moving higher and higher on the priority list for breeding are those traits related to natural resource sustainability, he said. Yield will always be important, but land and water conservation have become very important, too.

"Breeding is most successful when you can break down a trait to specifics and get down to relatively small numbers of genes. Otherwise, there is so much 'noise' in the system, you can't see where the important [genes](#) are. But if you can take a complex trait and simplify it, then you have more and more success. SNPs help us do this, as they are a great analytical tool for trait dissection."

Cotton is an economically important crop to the nation, and this tool will better enable breeders to develop the crop to produce more with less, thus making agriculture more sustainable, he said.

"We are all interested in scientific advancement, so having this kind of resource puts cotton in a more competitive position to utilize cutting-edge science," Stelly said.

Provided by Texas A&M University

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