

# Conference Summary Cotton Breeding and Biotechnology

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This conference covered broad areas of cotton breeding and biotechnology. There were several themes that emerged:

1. Genetic diversity and germplasm
2. Breeding for biotic and abiotic stress resistance
3. DNA marker applications in cotton
4. Biotechnology

The critical role of germplasm in the "Era of Biotechnology" was mentioned often in this conference. The products of biotechnology have limited benefits if they are in unadapted and poor performing genetic backgrounds. There is a rationale for deploying transgenes in regional pools of germplasm that optimize crop performance, stability, and fiber quality. This will require strategic alliances between technology providers, seed companies and research organizations.

Sustained genetic gain for lint yield has been hindered in some regions of the world by a narrowing genetic base. There were several papers on exploiting genetic variation both in intra- and interspecific breeding populations. Gains can be achieved in intraspecific populations with large numbers of crosses and adequate population sizes and selection pressure. Mutation breeding has also been successfully utilized to enhance intraspecific genetic variation.

Cotton is fortunate to have a germplasm base spanning over 50 species. With a few exceptions, these have not contributed to cotton improvements. Extensive breeding programs involving hybridization with secondary and tertiary gene pools are underway at the University of Arkansas in USA, CIRAD in France, and University of Gembloux in Belgium. These numerous interspecific populations are problematic due to extensive linkage drag and restricted recombination in some genomic regions. This is evident in the *G. australe* introgressed germplasm selected for glandless seed/glanded plant traits and HLT trispecies hybrid using *longicalyx* & *thurberi* for resistance to reniform nematode. These are under development in Belgium.

The use of DNA markers to tag the trait of interest and reduce linkage drag will accelerate progress in these areas. In fact, DNA markers are most useful in facilitating interspecific introgression.

Chromosome engineering of *Gossypium hirsutum* via neuploid stocks is progressing well. A set of *G. barbadense* chromosomes substitution lines in *G. hirsutum* have been developed by USDA and other university collaborators. This will facilitate assignment of genes controlling fiber quality to individual cotton chromosomes. The stocks will be useful as a vehicle for introgressing useful traits from *G. barbadense* into *G. hirsutum*. Other programs are underway to introgress chromosomes from other tetraploid species.

DNA marker assisted selection still remains an elusive goal in cotton improvement. Many economic traits in cotton exhibit quantitative inheritance. Special

genetic populations are required to associate DNA markers with Quantitative Trait Loci (QTL). Recombinant inbred lines (RIL) have been developed in several programs. RIL populations can be grown in replicated experiments and across diverse environments. This should accelerate the discovery of QTLs in cotton. Framework DNA markers are being identified for many cotton chromosomes. This will facilitate consensus linkage map construction from the various genetic maps around the world.

There were many good presentations on cotton biotechnology. Dr. Kater Hake presented a thorough review of biotechnology. There is great potential from this technology as important output traits are enhanced. Developments in cotton biotechnology force high regulatory costs and uncertain intellectual property protection in some countries. This will drive where institutes and companies focus their investments. Cotton biotechnology programs are emerging in China, Egypt, India, and Pakistan. GM cotton is likely forthcoming from these programs. Dr. Randy Deaton also projected a future array of biotech products, for example: abiotic stress tolerance, improved fiber properties, and non-lepidopteron insect control. He stated that regulatory processes need to be established where they do not already exist, and these must be based on sound science. Public concerns must be addressed without creating unnecessary hurdles for technology development.

Progress in model genomes, such as *Arabidopsis*, will accelerate candidate gene discovery in cotton. This was illustrated clearly by Dr. Giband with the *CesA* gene family in cotton. Orthologous genes are being studied that derive from mutants in *Arabidopsis* for hypocotyl and root elongation. The genes are being used to develop DNA markers for genetic mapping of fiber quality QTLs and genetic diversity studies. Furthermore, this information can be utilized to genetically modify cotton fiber quality.

In summary, it is my opinion that sustained cotton genetic improvements are limited by the lack of international collaboration and coordination. This is partly attributable to no International CGIAR-type center in cotton. The financial situation of the entire CGIAR system and donor countries make this unlikely in the short term. However, I would not discourage anyone, ICAC or otherwise, from vigorously pursuing international resources. I have experienced this first-hand with the International Cotton Genome Initiative (ICGI). It has taken over three years to mobilize and organize international scientists. There are still significant barriers to scientific collaboration and reduction of duplication in research. Yet, I am optimistic we can optimize the use of available resources for productive research at the international level.

The WCRC has and must continue to foster scientific exchange and collaboration. The daunting challenges facing the cotton industry demands no less.