

**THE INTERNATIONAL COTTON GENOME INITIATIVE (ICGI)
-PAST, PRESENT AND FUTURE-**

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Abstract

Biotechnology is revolutionizing cotton production and is being adopted at a rapid pace compared to other agronomic crops. The future of biotechnology in cotton is limited by the current state of knowledge of the cotton genome, which is the DNA blueprint of the cotton plant. Many diverse research laboratories around the world are working on various aspects of dissecting the cotton genome. The research to fully understand the cotton genome is demanding and far too costly for any one country to attempt alone. Diverse resources, genetic tools, and technologies are essential to make progress. International cooperation will reduce duplication and maximize research efficiency. The International Cotton Genome Initiative (ICGI) was formed in 2000 to provide a forum for collaboration and cooperation. The initial motivation for ICGI emerged from the frustration a few cotton scientists had with the progress of DNA-marker assisted selection in cotton genetic improvement compared to other agronomic crops. This clearly was a result of limited international cooperation in cotton genetics and genomics compared to other crop systems. The formal document "Developing the International Cotton Genome Initiative" emerged from a workshop at CIRAD in France in 2001 and is published at <http://icgi.tamu.edu> . The true scientific merit of ICGI was demonstrated at the very successful workshop in Nanjing China in 2002 where 225 scientists attended from 17 countries. The 2002 workshop featured 102 technical presentations on all aspects of cotton genomics. With determined and focused ICGI working groups, real progress is being made in several critical research areas. Framework DNA marker development and widespread distribution is underway. ICGI can best facilitate and coordinate the nomenclature issues that emerge with cotton genomics and DNA markers. QTL verification for important traits from population to population and across diverse environments, by its very nature, requires extensive collaboration and sharing of data. Consensus linkage maps are being constructed from diverse genetic maps, along with complete assignment of linkage groups to chromosomes and integration of homeologies. The vast functional genomic resources, such as DNA microarrays, are providing very useful tools for collaborative research to identify cotton genes. ICGI is proving to be the only viable forum for discussion of DNA sequencing of the cotton genome and integration of the genetic and physical maps. How far this lies in the future, depends on the timeframe developed from within ICGI and the international cooperation that can be generated.