

TOWARDS THE INTERNATIONAL COLLABORATION ON COTTON STRUCTURAL GENOMICS

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Abstract

In the last century, genetic manipulations of the cotton plant were essential to improvement of cotton productivity. While many easy improvements have been accomplished, cotton yields and quality have not reached their full genetic potential. In fact, current cotton yields and quality are static if not declining. In this new century, emerging genomic technologies are revolutionizing our approach to making otherwise difficult genetic improvements, as evidenced in several other crop species. For cotton, there is an urgent need to develop open resources and tools essential to the advancement of basic and applied genome research, which presently lag behind other major crops. Understanding and manipulating the cotton genome will progress only if resources are readily available to characterize the structure of the cotton genome, decipher its functions, and parse its evolutionary history. Cotton structural genomics would provide a foundation and platform for elucidating the function of many thousand genes and their applications in cotton improvement. Recently, the International Cotton Genome Initiative (ICGI) proposed short-term objectives on structural genomics that include (1) development of large numbers of portable DNA markers; (2) integration of cotton genetic and physical mapping information; (3) identification and localization of important agronomic traits (QTLs); (4) better understanding of cotton genome structural organization; and (5) preparation for genome sequencing of the cultivated cotton. The ICGI promotes global communication, collaboration, coordination on cotton genomic research, and education. Improvements in these activities among national and international cotton researchers will advance cotton genomic research and its amenability to genetic manipulation. Time and resources can be saved if participating members of the ICGI complement one another on cotton genomic research and share results. One of the recent examples of such efforts was resulted from the discussion at the Plant Molecular Biology and Biotechnology Research Roundtable of the China-U.S. Relation Conference that was held at the George Bush Presidential Library in College Station, Texas, November 2003. Participating Chinese and American cotton researchers agreed to collaboratively develop open genomic platforms and resources for cotton improvement. A base mapping population, DNA markers, and large insert BAC clones are shared among the cotton researchers. Many other cotton producing countries including Australia, France, India, and Uzbekistan also have been actively involved in related formal and/or informal international collaborations on development and applications of cotton DNA markers, genome mapping, and QTL discovery. These coordinated activities reduce the redundancy and improve the efficiency of cotton structural genomic research for the benefits of the global cotton community.