

1853 Lessons Learned and Challenges ahead of the Cotton Genome Mapping

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Abstract

The fundamental goal of genetic linkage mapping is gene discovery. The identification of genes conditioning a trait, their mode of expression, and how genes interact, provide us with leverage in manipulating a given trait to the desired effect. The process of manipulating the cotton genome is complex because the cotton fibers (lint) used in textiles are derived from the seed trichomes (hairs) of four *Gossypium* species: two Old World diploid species, *G. arboreum* L. and *G. herbaceum* L. (A genome), and two New World allotetraploid species, *G. barbadense* L., and *G. hirsutum* L. (AD genomes). The New World D genome diploid species have also served as important sources of genes for lint quality. In just over a decade, our understanding of the structure of the cotton genome has expanded tremendously. Before 1994, genetic linkage mapping in cotton was limited to linkage detection among morphological markers and the placement of those markers on chromosomes using cytological stocks. Since then, approximately 27 major mapping efforts in *Gossypium* have emerged. Twenty of those efforts have addressed mapping of the tetraploid genome, while only five have addressed diploid maps. In addition, PCR-based markers, such as microsatellites, have been placed on 26 cotton chromosomes. Over the past decade new gene discovery tools have emerged (e.g., BAC physical mapping, differential display, microarrays, and SNPs), providing new avenues for gene discovery that circumvent some of the limitations of genetic linkage mapping. A global research environment has also provided the opportunity for wide collaboration in efforts to saturate and expand genetic maps by merging marker data on consensus or join maps. However, difficulties have risen from the use of different electrophoresis systems (RFLP, agarose, acrylamide, SSCP gels, and labeled primer-markers) for calling alleles on mapping populations. In addition, the need for standard nomenclature in naming molecular markers, as well as in identifying quantitative trait loci (QTL) in the cotton genome still exists. The challenge facing cotton improvement for the next decade involves characterization of morphologically complex traits controlled by many interacting genes. Real gains in cotton improvement will require an unprecedented understanding of the molecular genetics of these complex traits, and expanded genetic linkage maps that can be used to manipulate the cotton genome in ways that were previously inconceivable.

Note: The complete paper for the presentation at the ICGI symposium (No. 1163) entitled "Lessons learned and challenges ahead of the cotton genome mapping (No. 1853)" by Ulloa M and co-authors can be found at the Breakout session Plant Breeding and Genetics 2 (No. 1128) under the presentation by Ulloa and co-authors entitled "The Future of cotton breeding in the Western United States (No. 1798)". The complete paper of the presentation No. 1798 was not included in this Proceedings, and it will be published some place else.