UPDATE OF THE COTTON GENOME MAPPING

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Abstract

Modern cottons are grown as industrial raw materials for the textile and oil seed industries. Genetic improvement of the cotton plant has been a major activity to its continued productivity. Cotton has a gametic chromosome number of 26, more than any of the other major crops. While the application of DNA markers has offered a valuable tool for revealing the genetic basis of both simple and complex traits in crop plants, cotton genome mapping lags behind other major crops as well. A few research programs in cotton-belt states have been devoted to the molecular mapping of this large, complex genome. We will report molecular mapping and characterization of genes controlling fiber quality properties in both extra long staple (ELS) cotton (*G. barbadense* L.) and Upland cotton (*G. hirsutum* L.). QTLs for fiber quality properties in two Upland cottons, Acala accession HS427-10 and Pee Dee accession PD6992, will be compared with those of ELS cotton 3-79, with regard to their locations and gene effects. A total of thirteen QTLs have been identified, four for fiber strength, three for fiber length, and six for fiber fineness. They are located on different chromosomes or linkage groups of our molecular maps comprised of 355 DNA markers covering 4,766 cM (Haldane function) of the cotton genome in 50 linkage groups. These QTLs explain 30% to 60% of phenotypic variance for each fiber quality property in the F_2 population. Both A and D sub-genomes contain fiber quality genes. Most of them are recessive in TM-1 genetic background, making marker-assisted selection (MAS) more desirable. Molecular mapping of simple inherited traits includes Gl_e^2 for glandless cotton, *Se* for photoperiod sensitivity, *im* for immature fiber, *Li* for lintless cotton, and *Lc* for lint color. Among these major genes, Gl_e^2 is currently targeted for high-resolution mapping and positional cloning. An introgressed fragment of about 20 cM was estimated on chromosome 12. This fragment contains the Gl_e^2 gene, and two linked DNA markers. The closer one is about 5.6 cM away from the Gl_e^2 gene. Regional saturation of this locus is underway using a pair of NILs and bulks. Molecular characterization of *Gossypium* germplasm with DNA markers is another area of our genome programs. An initial set of 155 land races and cultivars have been examined with 60 DNA markers selected from different chromosomes or linkage groups of the cotton genome. Recommendation to further utilization of *Gossypium* germplasm resources will be made according to the level of uniqueness of the DNA marker profiles. In collaboration with other labs, we have initiated a possibility of integrative physical mapping, and linkage between *Arabidopsis* and cotton genomes. Although cotton genome is large and complex, its physical size of a cM is only 50% larger than that of *Arabidopsis*. A high level of homology between *Arabidopsis* and *Gossypium* genomes and abundant polymorphism among *Gossypium* germplasm were detected using conserved cDNAs from the *Arabidopsis* genome. Integration of plant genes and DNA markers with large genomic clones such as BACs would move cotton genome mapping to a new phase of broader applications. Bioinformatics tools are being developed to interface with CottonDB, a plant genome database maintained in our research unit.

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