MOLECULAR MAPPING OF THE COTTON GENOME: QTL ANALYSIS OF FIBER QUALITY PROPERTIES John Yu, Yong-Ha Park, Gerard R. Lazo and Russell J. Kohel USDA-ARS, Crop Germplasm Research Unit College Station, TX

Abstract

We have constructed a molecular map in cotton and have identified locations of QTLs for fiber quality properties, by use of F₂ progeny from an interspecific cross between two improved cottons, G. hirsutum L. acc. TM-1, and G. barbadense L. acc. 3-79. The unique high quality fiber characteristics of 3-79 and the high productivity and wide adaptability of TM-1 led to our choice of these parents for a polymorphic mapping population. Presented here is a framework map consisting primarily of RFLP and RAPD markers, with some SSR markers, among 171 F₂ individuals of TM-1 X 3-79. These 219 loci are assembled into 40 linkage groups and cover 3,855 cM of the cotton genome. More than one half of the linkage groups have been assigned to their respective genomic origin (A vs. D) or chromosomal identity (1 through 26) by use of diploid and aneuploid cottons.

As bundle fiber strength, fiber length, and other fiber properties have been observed to display quantitative inheritance, the differences between TM-1 and 3-79 (18.4 vs. 27.4 cN/tex for strength. 1.17 vs. 1.38 inches for length. and 4.49 vs. 3.63 micronaire units for fineness, respectively) facilitates QTL mapping by use of the same 171 F₂ individuals. With both MapMaker/QTL and SAS program, we have detected three QTLs for bundle fiber strength, three QTLs for fiber length, and five QTLs for fiber fineness in different linkage groups. These OTLs, together with other minor ones, explain about 35% to 50% of the total genetic variance for fiber characteristics in the F_2 population. Further characterization of these QTLs is underway by use of recombinant inbred lines of the same mapping individuals, and also in the intraspecific G. hirsutum crosses.

Information on the mapped DNA markers and their map locations will be available to the cotton community through the plant genome database, CottonDB, maintained by our research unit.

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