Chromosomal Location of RFLP Markers Linked to QTL in Cotton

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ABSTRACT

Plant breeders are primarily involved in improving complex quantitative traits (QTL) that are controlled by many genes. Molecular markers linked to QTL will help breeders to monitor the hereditary materials associated with the QTL. Recently, our research unit reported a linkage map of a class of molecular markers called Restriction Fragment Length Polymorphism (RFLP) and QTL using a second-generation (F_2) population of improved upland cotton cultivars. The objective of this paper is to identify the chromosomal location of some of the RFLP and QTL linkage map that our unit reported.

Introduction

Recently the first report in an intraspecific F_2 population of upland cotton on Restriction Fragment Length Polymorphism (RFLP) markers linked to important Quantitative Trait Loci (QTL) was released (Shappley *et al.*, 1998a, 1998b). The polyploid nature of cotton leads to compensation between the homoeologous loci, which accounts for the tolerance of deletions and deficiencies at whole chromosomes or subchromosomal regions, permitting the derivation of various hypoaneuploids. These have been used for developing partial series of monosomic and monotelodisomic chromosomal substitution lines. These lines provide a tool to develop chromosome-specific genetic markers based on deletion analysis. The overall objective of this paper is to identify the chromosomal location of some of the QTLs and RFLP linkage groups previously discovered (Shappley *et al.*, 1998).

Materials and Methods

The comparative analysis of the cytogenetic deficient interspecific chromosomal substituion lines using probes specific to the QTL linkage groups provided an opportunity to identify the QTL linkage groups to specific chromosomes. Saha and Stelly (1994) reported the chromosomal location of the first biochemical marker in cotton using a similar strategy. The genomic DNAs from an inbred *G. hirsutum* cv. Texas Marker (TM1) and inbred *G. barbadense* cv. Pima 3-79 were used as standards for comparison with the genomic DNAs of monosomic F_1 and monotelodisomic F_1 chromosome substitution lines developed from interspecific crosses between TM1 and Pima 3-79. The overall methods of RFLP analysis were described by Shappeley *et al.* (1998a, 1998b).

Results and Discussion

Chromosomal location of several RFLP and QTL linkage groups were identified using aneuploid chromosomal substitution lines. We observed that about 25 QTL, associated with economically important fiber characteristics were located on A genome-specific chromosomes and 13 fiber-related QTL genes were located on D genome-specific chromosomes. Our results also showed that 5 of the 13 A genome-specific chromosome and 2 of the 13 D genome-specific chromosomes of upland cotton (AD genome) were associated with fiber-specific QTLs. Our results indicate that A genome diploid species may be a useful source for improving some of the QTLs in upland cotton. Some of the RFLP and QTL linkage groups showed that several important QTLs related to fiber characteristics are present on the same position of a chromosome. This might be due to several reasons including a master QTL gene controlling several traits or the same genetic effect of a QTL measured in different ways. The molecular map linked to QTL of specific chromosome regions will be useful in germplasm introgression and map based cloning of important genes.

The deletion analysis of the cytogenetic deficient F_1 stocks indicated that the Ccot52E2RV and Ccot107B2R1A RFLP loci of the RFLP-QTL linkage group (LG) 15 were located on the long arm of chromosome 26. The Ccot13B1RV locus of the RFLP-QTL LG 26 and the Ccot61A6RV locus of the RFLP and QTL LG 30 were also located on the short arm of chromosome 26. The deletion analysis also showed that F3F7R1 RFLP locus of the RFLP-QTL LG 20 were located on chromosome 4. The Ccot78C3R1 locus of the RFLP LG 12 was located on chromosome 12. The F6D4RV RFLP locus of RFLP-QTL LG 21 was located on chromosome 10. The F211RV RFLP locus of the RFLP-QTL LG 17 was assigned to chromosome 9. Results also indicated that the

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Ccot117C5RV and F2E6R1 loci of the RFLP-QTL LG 14, F9D3RV locus of the RFLP-QTL LG 19, the C18A4RV locus of RFLP-QTL LG 18 and the C119F6R1 locus of RFLP LG29 were located on chromosome 3. We observed that about 25 QTL loci associated with fiber characteristics, including elongation, maturity, fiber wall thickness and seed index were located on A genome-specific chromosomes and 13 fiber-related QTL loci were located on D genome-specific chromosomes. Our results also showed that 5 of the 13 A genome-specific chromosomes and 2 of the 13 D genome-specific chromosomes of the tetraploid species (AD genome) were associated with fiber specific QTLs. Diploid members of the D subgenome species, an ancestor of the current tetraploid species, does not produce spinnable fibers, whereas representatives of the A subgenome species, also ancestral to the tetraploid species, produce spinnable fibers and are cultivated in the Asiatic countries. Our results showing more number of A genome specific chromosomal association with fiber related QTL support the theory that tetraploid cotton is of recent origin resembling more their diploid ancestors.

The large influence of the A genome subgroup on fiber properties clearly indicates that investigation and introgression of A genome species germplasm will be very important for improving fiber properties in upland cotton. However, our results are based on only 7 of the total 26 pair of chromosomes in the tetraploid cotton genome. Locating the QTL linkage groups for other unidentified chromosomes, using similar strategy, will help in further dissection and manipulation of the cotton genome. Some of the RFLP and QTL linkage groups showed that several important QTLs related to fiber characteristics (e.g. seed index, micronaire, elongation, weight fineness or linear density, the external surface of a given volume of fibrous materials under standard pressure) are located on the same position of a chromosome. This might be due to several reasons including a master QTL gene controlling several traits or the same genetic effect (QTL) measured in different ways. The high-density genetic map of defined chromosome regions will be very helpful in the future in transferring useful orthologous QTL loci among the tetraploid cultivated species.

The merit of our report is primarily based on the following factors:

1) there are very few reports on the chromosomal localization of RFLP markers linked to important QTLs in cotton;

2) this report includes new information on the association of DNA markers specific with some chromosomes (chromosome 3, 12 and 26) to which linkage groups have not been previously assigned;

3) the probes utilized in this research were cDNAs, thus provide possible information about functional genes and their locations;

4) interspecific chromosomal substitution lines, with identified important QTLs can be used to enhance the germplasm of upland cotton by breeding and

5) our methods demonstrate the portability and strength of the RFLP markers for use between two different intra- and inter-specific cotton populations.

References

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