MOLECULAR MARKERS ASSOCIATED WITH COTTON CYTOPLASMIC MALE STERILITY RESTORER GENE Rf_1

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Abstract

Molecular marker assisted selection (MAS) can accelerate the process of plant breeding. Sequence tagged site (STS) markers are more suitable than most types of molecular markers for MAS. The objective of this research is to develop STS markers tightly linked with *Rf_1*, the fertility-restoring gene for cytoplasmic male sterility in cotton. Bulked segregate analysis (BAS) was conducted to screen for *Rf_1*-linked RAPD markers with 300 10-mer random primers on a 114-individual backcross population (B416R X Ark8518) X Ark 8518. Four RAPD markers were found, among which three markers co-segregated with *Rf_1* and one co-dominant marker segregated 4.5cM from *Rf_1*. The two homologous bands from this last primer demonstrated repulsion linkage. A previously reported marker was 2.7cM from *Rf_1* and 1.8 cM from the co-dominant marker. Three pairs of STS primers were designed based on the sequences of the three co-segregating RAPD markers. Both *Rf_1*STS-1400 and *Rf_1*STS-500 primer pairs amplified a single band present in fertile plants and absent in sterile plants. The *Rf_1*STS-700 primer pair amplified a band from fertile plants that was derived from *G. harknessii*, and a monomorphic band from all plants that was derived from the A subgenome. These two bands were homologs. The three *Rf_1* STS markers were present in *G. harknessii*, the donor species of *Rf_1*. *G. trilobum* also contained three STS fragments but the fragment amplified by the *Rf_1*STS-1400 primers was larger than that from *G. harknessii*. Some species of the D genome yielded only two fragments with the primer pairs. Sequence analysis suggested that *Rf_1*STS-1400 contains an initial exon, *Rf_1*STS-500 contains an internal exon, and *Rf_1*STS-700 contains a terminal exon. These STS markers will be useful in breeding parental R lines for cotton CMS fertility restoration.