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Genetic diversity analysis in some elite desi cotton cultivars of *Gossypium herbaceum* and *G. arboreum* and genetic purity testing of their hybrids through microsatellite markers

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SUMMARY

Microsatellite markers were employed to analyse the extent of genetic diversity present in parents and genetic purity testing of inter-specific (*Gossypium herbaceum* and *Gossypium arboreum*) hybrids of desi cotton**.** The SSR analysis with 10 microsatellite markers produced 14 alleles. The average number of alleles per locus were found to be 1.40. The most informative primers were JESPR-223, JESPR-231, JESPR-296 and JESPR-298. No primer amplified two loci in a cultivar. The PIC values varied from 0.00 to 0.80 with an average of 0.30. The repeat markers amplified by a particular JESPR microsatellite primer were compared with the repeats amplified in 'A' genome standard line CMD 09. All ten JESPR series microsatellite primers used in the present study amplified the repeats which were quite near or same in the size to that of amplified repeats in 'A' genome standard line CMD 09. Jaccard's coefficients of similarity revealed that genetic similarities ranged from 0.25 to 1.00. Average genetic similarity among these 16 genotypes was found to be 0.62. Among seven *G. herbaceum* cultivars, range of genetic similarity was found to be between 0.91 to 1.00 with an average of 0.96 and among nine G. *arboreum* cultivars; range of genetic similarities was between 0.50 to 1.00 with an average of 0.75. Dendrogram generated by UPGMA cluster analysis based on jaccard's similarity coefficients grouped the cotton genotypes into two main clusters each cluster including genotypes from respective species only. A total of fourteen loci were amplified by 10 JESPR primers out of which nine were heteroallelic and five homoallelic. Heteroallelic loci were produced by primers JESPR-223, JESPR-231, JESPR-296, JESPR-298 and JESPR-300. These five primers were useful to confirm the hybridity of genotypes.

Key words : Desi cotton, Microsatellite, Genetic diversity

Many cotton (*Gossypium hirsutum* L.) varieties have been developed from crosses between closely related ancestors but so far only limited increase in productivity has been obtained. Pressure for higher productivity in cotton farming has stimulated the search for more exotic germplasm, but although breeding methods have increased the efficiency of transferring alleles from exotic germplasm sources to cotton breeding gene pools but many germplasm sources still remain underused. Van Esbroeck and Bowman (1998) have pointed out that genetic diversity ensures protection procedures against diseases and pests and thus provides a basis for future genetic gains. Molecular markers have been widely used in genetic analyses, breeding studies and investigations of genetic diversity and the relationship between cultivated species and their wild parents because they have several advantages as compared with morphological markers, including high polymorphism and independence from effects related to environmental conditions and the physiological stage of the plant.

Simple sequence repeat (SSR) markers (microsatellites) have been successfully employed in many genetic diversity studies (Liu *et al.*, 2000a; Gutiérrez *et al.*, 2002) and are useful for a variety of applications in plant genetics and breeding because of their reproducibility, multiallelic nature, codominant inheritance, relative abundance and good genome coverage (Powel *et al.*, 1996). The availability and abundance of microsatellite markers throughout the cotton genome coupled with the fact that they are polymorphic, codominant and are based on the polymerase chain reaction (PCR) make them particularly useful in genetic diversity studies of cotton (Reddy *et al.*, 2001), within excess of 1000 microsatellite primers having already been isolated from cotton DNA genome libraries (Nguyen *et al.*, 2004).

The success of hybrid cotton technology depends on the timely production and adequate supply of genetically pure hybrid seed to the farmers. Thus, seed testing or genotype identification is of prime importance for assuring good quality seed. In order to determine the genetic purity,

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