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MOLECULAR CHARACTERIZATION OF ASIATIC COTTON *G. HERBACEUM* AND *G. ARBOREUM* GENOTYPES USING SSR MARKERS LINKED FOR FIBER QUALITY TRAITS

MISHRA KUNDAN K[1], FOUGAT RS[1]*, BALLANI A[2], SASIDHARAN N[2]

1: Centre of Excellence in Biotechnology, B. A. College of Agriculture, Anand Agricultural University, Anand – 388 110, Gujarat, India

2: Department of Agricultural Botany, B. A. College of Agriculture, Anand Agricultural University, Anand – 388 110, Gujarat, India

***Corresponding Author: E Mail: kkmbt@yahoo.co.in, aau@gmail.com; Ph.: 02692-261134; (O), 02692-263003 (R); Fax: 02692-261134 (O)**

ABSTRACT

Advances in molecular marker technologies have generated large number of Simple Sequence Repeat (SSR) markers for different traits. These SSR markers can be used for estimation of diversity in genome and may be useful for comparative mapping, for tagging important QTL traits for fibre quality and for map based cloning of other important traits. Two diploid cotton species viz, *G. arboreum* (A2) 7 genotypes and *G. herbaceum* (A1) 11 genotypes are included for comparative analysis. PCR assay for simple sequence repeat (SSR) marker separation using agarose gel electrophoresis was done. Of a total of 41 QTL SSR primers, 75.75% amplified in both diploids species, indicating that flanking primer sequences are conserved in the both diploid genome of cotton. Out of 41 primers 33 primers showed amplification and produced a total of 345 bands. Average number of bands amplified by each primer was 10.45. Statistical analysis for SSR data was conducted using software programme NTSYS pc version 2.02e and GeneAlEx The genetic distance (GD) among the cotton genotypes ranged from 0.06 to 0.69. The highest GD (0.69) was detected between Gvhv 235 and lintless DDK while the lowest GD (0.06) was observed between V-797 and G.cot 23.

Keywords: Simple Sequence Repeat (SSR), *G. arboreum*, *G. herbaceum*, Cotton, Diploids