

Estimation of genetic distance based on RAPDs between 11 cotton accessions varying in heat tolerance

A.I. Khan¹, I.A. Khan², F.S. Awan¹, H.A. Sadaqat² and S. Bahadur³

¹Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture, Faisalabad, Pakistan ²Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan ³Nursery Division, Desert Group, Dubai, U.A.E.

Corresponding author: A.I. Khan E-mail: azeemiqbalkhan@yahoo.com

Genet. Mol. Res. 10 (1): 96-101 (2011) Received April 9, 2010 Accepted October 28, 2010 Published January 25, 2011 DOI 10.4238/vol10-1gmr835

ABSTRACT. The genetic distance of 11 cotton genotypes varying in heat tolerance was studied using RAPD markers. Fifty-three random decamer primers were used for the estimation of genetic distance. Among the 53 RAPD primers, which were custom synthesized by GeneLink Inc., UK, 32 were polymorphic and 21 were monomorphic. The 32 polymorphic primers produced 273 fragments, with a mean of 8.3 fragments per primer. The number of polymorphic bands produced in the 11 cotton accessions ranged from 1 to 31. Primer GLC-20 produced 31 polymorphic bands, while two primers, GLB-5 and GLC-12, produced one polymorphic band each. A range of 88.89 to 42.48% genetic similarity was observed among the 11 cotton accessions. The highest genetic similarity was observed between FH-945 and BH-160 (88.89%), whereas the lowest value was found between NIAB-801/2 and FH-945 (42.48%). Unique amplification profiles were produced by most of the cultivars; the differences were sufficient to distinguish them from other genotypes. This confirms the efficacy of RAPD markers for the identification of plant genotypes. An accumulative analysis of amplified products generated by RAPDs was sufficient to assess the genetic diversity among the genotypes. This information should be helpful for formulating breeding and genome mapping programs.

Key words: Genetic distance; Random-amplified polymorphic DNA; Cotton