RESEARCH PAPER International Journal of Agricultural Sciences, June to December, 2009, Vol. 5 Issue 2 : 536-539

Genetic diversity analysis in elite cotton cultivars using RAPD markers

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ABSTRACT

Genetic variability and relationship between varieties are of great importance for cotton breeding. RAPD marker system was used for identification and genetic diversity analysis of elite *G. hirsutum*, *G. arboreum* and introgressed lines. 12 cotton genotypes were subjected to RAPD analysis using 20 RAPD primers. PCR products were subjected to agarose gel electrophoresis and the banding patterns were compared among 12 elite cotton varieties of diploid, tetraploid and introgressed cotton. Out of 20 random primers tested, 15 primers produced reproducible results yielding 123 markers with 92 (74%) being polymorphic. The random primer OPA 17 generated the maximum number of polymorphic markers with a specific band of 300bp for variety PA-255. A dendogram constructed from RAPD data classified 12 cotton genotypes into two major clusters, one containing six genotypes belonging to *G. hirsutum* cultivars and the other contained 4 genotypes belonging *G. arboreum* cultivars. Two introgressed cultivars PAIG-8/1 and PAIG-27 showed highest level of genetic similarity with *G. arboretum* varieties. RAPD technique was thus found to be efficient method for detecting DNA polymorphism useful for molecular evaluation in cotton.

Key words : Genetic diversity, Molecular markers, RAPD, Cotton

INTRODUCTION

Cotton 'The white gold' is the world's leading natural fiber crop and it is the corner stone of textile industries world wide. The cultivated cottons include *Gossypium arboreum* (L) *and Gossypium herbacium* (L) (Old World species), both diploid species with an AA genome native to southern Asia, Africa and two allotetraploid species *Gossypium barbadense* (L) and *Gossypium hirsutum (L)* (New World species) with AD genome from Central, North and South America. Although small gains in yield and fiber quality continue to be made by conventional breeding programs, genetic improvement of agronomic traits is beginning to plateau as a result of an increasing narrow germplasm base for selection. Genetic diversity is desirable for long term crop improvement and reduction of vulnerability to important crop pests. Genetic diversity resulting from interspecific introgression can be evaluated with morphological characteristics, seed proteins, isozymes and DNA markers. To have reliable estimates of genetic relationship, a large number of polymorphic markers are required. This limits the use of morphological characteristics and isozymes, which are few, or lack adequate levels of polymorphism in *Gossypium* spp. Therefore there is a need to study polymorphism at the DNA level which can be indicative of genetic diversity in cotton.

DNA markers have proven to be valuable in crop breeding especially in studies of genetic diversity and in cultivar identification. Polymerase chain reaction (PCR) based molecular markers, e.g. ISSR, RAPD, SSR, STS; AFLP etc. are useful for various applications in the plant breeding. RAPD markers involve the amplification of random DNA segments using arbitrary sequences of 10-15 base pairs without any prior knowledge of DNA sequence (Welsh *et al*., 1990). The present molecular diversity analysis was carried out to analyze genetic relationship and genetic diversity of the cultivars using RAPD markers.

MATERIALS AND METHODS

Plant material and DNA extraction:

The list of elite cotton cultivars used in the present study is as below.

Elite *G. hirsutum* cultivars: 1. pH-93 2. pH-325 3. pH-348 4. NH-452 5. NH-545

Elite *G. arboreum* cultivars. 1. PA-402 2. PA-255 3. PA-405

Elite introgressed cultivars: 1. PAIG- 8/1 2. PAIG-27

Parents of introgressed cultivars: 1. PA-140 (*G. arboreum*) 2. Poornima (*G. hirsutum*).

The seeds of the above 12 cotton cultivars were obtained from the Cotton Research Station, Nanded; Cotton Research Station, Mahboob Baugh Farm; and the Cotton Research Scheme, Marathwada Agricultural University, Parbhani. Total genomic DNA was extracted from 4g of bulked leaf sample by a modified procedure of Edwards *et al.*, (1991).

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