TMC MM 1.5: Molecular characterization of cotton germplasm using DNA markers

Introduction:

Germplasm which represents the entire variability available in crop species is the basic material with which plant breeder has to initiate crop improvement programme. Effective breeding and selection strategies could be adopted once molecular markers linked to specific trait/s are identified. Modern technologies such as gene tagging and marker aided selection are additional tools for crop improvement specialists. Molecular markers have gained more significance with globalization and introduction of Plant Variety protection. With this in view it is essential to document and catalogue our existing germplasm using molecular markers which are also environmentally stable and reliable. In addition, molecular cataloguing helps in avoiding conservation of duplicates if any in the germplasm.

Objectives:

Molecular characterization of Cotton germplasm using PCRbased markers and known molecular tags for economic traits.

Salient findings:

A total of 236 STMS primer pairs were screened to find out the polymorphic primers for molecular characterization of cotton germplasm. Ninety, 99 and 100 accessions of G. *hirsutum*, G. *arboreum* and G. *herbaceum*, respectively were used for characterization. In G. *arboreum* 15 STMS primer pairs were used which amplified a total of 55 bands out of which 54 were found to be polymorphic. Cluster analysis of G. *arboreum* accessions revealed two major clusters with minor sub-clusters. In G. *herbaceum* 10 STMS primer pairs produced 25 polymorphic bands. In G. *hirsutum* ninety cotton germplasm lines were used for characterization. A total of thirty-seven primer-pairs giving sharp and scorable amplification were identified in these 90 G. *hirsl.!tum* germplasm lines. On an average 3 bands per primer were observed. Neighbor-Joining clustering for the Jaccard's similarity coefficient divided the ninety lines into two major groups. Overall the results indicated that all the lines could be discriminated from one another in G. *arboreum* and G. *hirsutum*, however, 10 STMS primers were not sufficient in case of G. *herbaceum* for uniquely identifying each accession and we need to search more STMS markers.
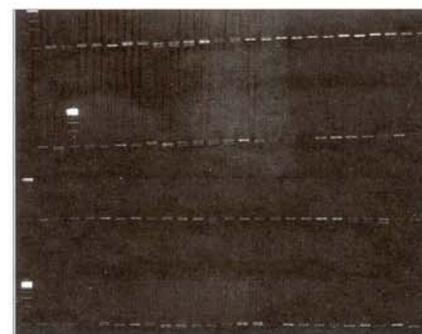
STMS profile of G. *arboreum* germplasm lines using primers for the locus **BNL** 1694
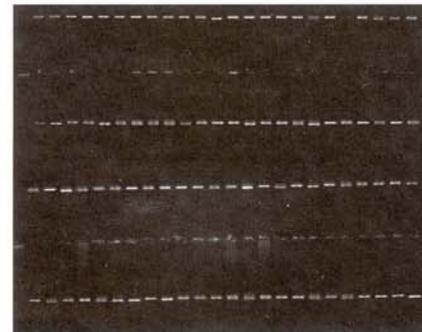
STMS profile of G. *herbaceum* germplasm lines using primers for the locus MGHES 16