

Genetic Diversity Analysis in Cotton (*Gossypium hirsutum* L.) Based on Morphological Traits and Microsatellite Markers

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ABSTRACT

One hundred and fifty six cotton genotypes representing different plant types were studied for genetic diversity on the basis of quantitative and qualitative traits using Mahalanobis D² statistic and SSR marker analysis. Out of ten clusters obtained, cluster I was the largest with fifty nine genotypes, cluster II had fifty five genotypes, cluster III had ten genotypes, cluster V had 13 genotypes, cluster VI had twelve genotypes, cluster VII had three genotypes while the remaining four clusters had single genotype each. Cluster X exhibited the maximum mean values for seed cotton yield, number of bolls per plant and number of sympodia per plant. Two distinct groups resulted from SSR marker data analysis. Among the 49 primers, BNVB-37421, CIR081, CIR081, CIR005, CIR182, CIR238, CIR413, JESPR29, NAU1278, NAU3561, NAU1262, NAU992, NAU1037 produced maximum number of alleles. All the robust lines were clustered in cluster I (fifty nine) and all the compact lines (fifty five) were clustered in cluster II and also confirmed by molecular study. The highest contribution towards genetic divergence was recorded by boll weight (gm), in 6917 cases out of 19506 combinations, accounting for 35.46 per cent followed by number of bolls per plant and seed cotton yield. Hence, these traits may be used as selection parameters in the hybridisation programme.

Keywords: Plant types, Genetic diversity, SSR marker.