



Genetic Divergence in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Genetic diversity in sixty three genotypes of cotton (*Gossypium hirsutum* L.) assessed using Mahalanobis D^2 statistic. The genotypes were grouped into eight clusters. Fiber length, fiber strength, boll weight and uniformity ratio contributed maximum towards genetic divergence. The genotypes of clusters V and II can be utilized in the breeding programme to develop heterotic hybrids. All the five principal components showed eigen values more than 1 and they together explained 93.91% of the variability.

Key words : Cluster analysis, Cotton, Genetic Diversity, Mahalanobis' D^2 statistic, Principal Component analysis.

Cotton is a major fiber-yielding crop of global significance and enjoys special place in cash crops of India which is grown in about 9.53 million hectares with 31 million bales production and productivity of 599 kg/ha (Anonymous, 2008). The basic requirement of any crop improvement programme is genetic diversity present in the material. Multivariate analysis based on Mahalanobis D^2 statistic and quantification of the degree of divergence among biological population helps the plant breeders in selecting the genetically diverse parents for purposeful hybridization programme. Therefore, expecting relative genetic potential difference, an attempt has been made to group sixty three genotypes of American Cotton (*Gossypium hirsutum* L.) on the basis of their degree of total divergence as measured by multivariate analysis.

MATERIAL AND METHODS

The experimental material comprises 63 genotypes of *Gossypium hirsutum* L. laid out in a randomized block design with three replications during kharif 2005-06. Each plot consisted four rows of 6m length. The inter- and intra – row spacing was 120 cm and 60cm, respectively. Observation on five randomly selected plants of each genotype or plot basis were recorded for plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), 2.5% span length (mm), micronaire (10^{-6} g/in), uniformity ratio, bundle strength (g/tex) and seed cotton yield per plant (kg/ha). The data were analyzed using Mahalanobis D^2 statistic as per Rao (1952), principal component analysis (PCA) as per Morrison (1976) and cluster analysis as per Anderberg (1993).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences for all the characters studied revealing that the existence of considerable amount of variability among genotypes. Hence, further analysis was done to estimate D^2 values and on the basis of relative magnitude of D^2 values, all the 63 genotypes were grouped into 8 clusters (Table 1). Distribution of genotypes into different clusters on geographical area is not only a single factor but depends upon genetic diversity (Rajarithnam and Nandaraja, 1993). Cluster I, II, III, IV & V consists of 6, 8, 10, 2, 2 genotypes, respectively. Thus, genotypes originated at different agro-climatic situations were grouped into one cluster and vice versa. This indicates that there is no parallelism between genetic and geographic diversity as also reported by Altaher and Singh (2003) and Samba Murthy *et al.*, (2004).

Based on the Ward's minimum variance dendrogram clustering, cluster III comprised of 17 genotypes followed by cluster VII with 14 genotypes. Cluster IV and V comprised of only two genotypes each as shown in the dendrogram (Figure 1).

The contribution of different characters to the total divergence in Table 2 shows that 2.5% span length (24.53%) contributed maximum followed by bundle strength (21.10%), boll weight (17.77%), uniformity ratio (16.85%) and seed cotton yield per plant (15.57%). Similar results were also reported by Murthy *et al.*, (1995b) and Kumar *et al.*, (2000)

The intra- and inter - cluster distance represent the index of genetic diversity among clusters (Table 3). The intra - cluster distance was maximum in cluster I (102.26) followed by cluster V (92.31) indicating the extent of genetic diversity

Fig 1. Ward's minimum variance dendrogram

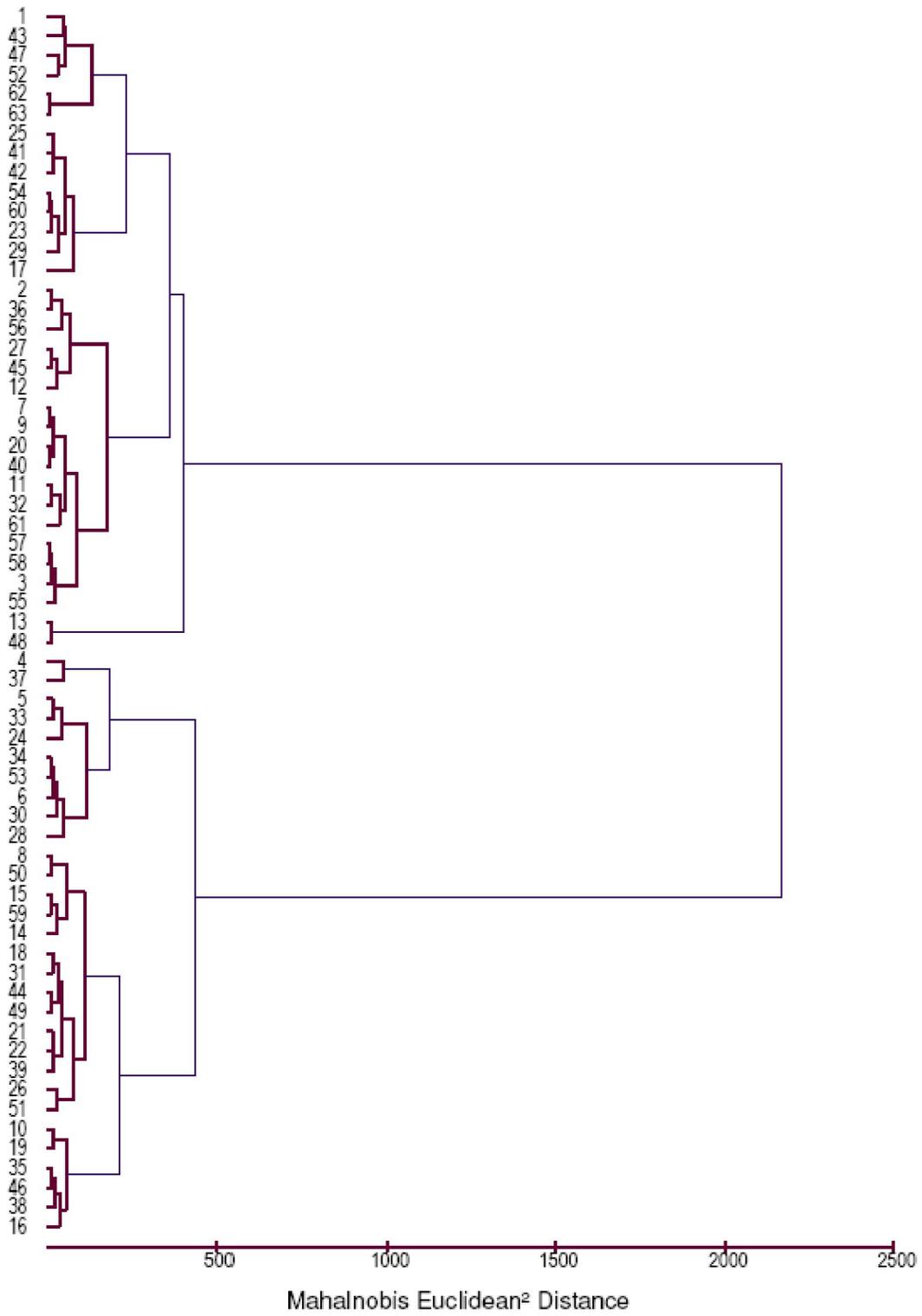


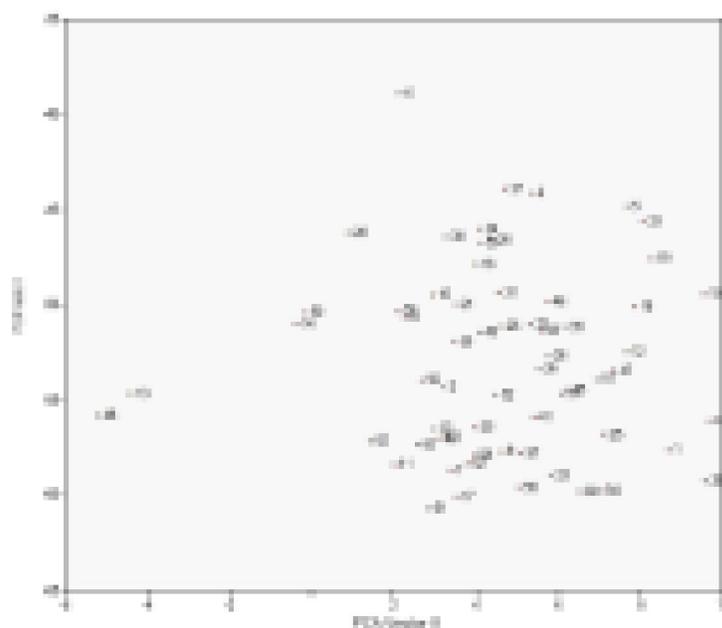
Table 4. Cluster means estimated based on D² analysis in cotton

Characters	I	II	III	IV	V	VI	VII	VIII
Plant height (cm)	136.75	148.44	149.24	146.50	187.00	150.69	142.32	168.00
No.of monopodia per plant	3.00	2.18	2.15	1.98	2.50	2.28	2.17	2.23
No.of sympodia per plant	20.25	17.25	19.27	19.75	23.50	19.69	18.75	20.17
No.of bolls per plant	55.08	40.75	46.68	40.25	58.25	44.00	47.39	53.58
Boll weight (g)	4.57	5.03	4.67	2.48	3.88	4.54	4.34	4.92
2.5% span length (mm)	29.33	30.08	29.66	30.12	22.99	24.15	26.77	26.22
Micronaire (10 ⁻⁶ g/in)	3.57	4.01	3.71	4.33	4.46	4.12	3.91	3.98
Uniformity ratio	42.86	44.48	49.20	45.28	53.28	51.75	49.25	47.28
Bundle strength (g/tex)	23.91	23.81	23.74	22.77	19.03	20.28	21.67	26.22
Seed cotton yield per plant (kg/ha)	1729	1238	1438	1194	2007	1298	1140	1654

Table 5. Main principal components for 10 characters in 63 genotypes of cotton

Principal component	Prin 1	Prin 2	Prin 3	Prin 4	Prin 5
Eigene value (root)	1512.21	492.79	378.31	302.55	92.22
Variation proportion	51.12	16.66	12.79	10.23	3.12
Cumulative	51.12	67.78	80.57	90.79	93.91

Fig 2. 2 D plots based on PCA values.



between the cultivars of the same cluster. The maximum inter - cluster distance of 732.89 was noticed between cluster II (BWR 58, L 389, BWR 25, HYPS 152-6-SP4, TCH 1706, H 96, HSC 1-132 and F6-98-2-3) and cluster V (BS 33-1 and CCH 4) followed by 567.49 between cluster IV (HSC 1-427 and BN) and cluster V revealing the magnitude of genetic divergence between these clusters. Inter-crossing the genotypes from these clusters might result in a wide array of variability for exercising effective selection of these traits.

The genotypes of cluster V can be used for direct adoption for hybridization for improving yield with regard to number of bolls per plant, number of sympodia, number of monopodia and plant height (Table 4). Cluster II recorded highest mean values for boll weight (5.02 g), fiber strength (30.07 mm) and bundle strength (23.81 g/tex) and can be used to improve boll weight and fiber properties to generate heterotic hybrid combinations. Arunachalam and Bhandopadhyay (1984) have proved that more number of heterotic combinations with high level of heterosis were from the parents grouped into moderate divergent groups. Hence, selection of parents for hybridization should be more based on genetic diversity rather than geographic diversity.

In the present investigation, all the Principal Components were found to be >1 which were retained as they are found to be significant (Legendre and Legendre, 1984). The PCA technique has been applied in cotton by Brown (1991). The fifth PC's showed eigen values more than one and they altogether explained 93.91% of the variability (Table 5). The fourth PC explained 90.79% of the total variability in the set of all variables and remaining ones accounted for progressively lesser and lesser amount of variations. The principal factor scores for all the 63 genotypes were estimated in all the 5 PC's and utilized to construct precise 2D plot (Figure 2). All the genotypes were plotted for PC1, PC2, PC3 PC4 and PC5 which cumulatively explained 93.91% variability and accounted for all the characters.

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