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Multivariate analysis in upland cotton (*Gossypium hirsutum* L)

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ABSTRACT: An experiment was conducted to analyze the genetic diversity among 40 genotypes for 15 quantitative characters in upland cotton at Agricultural College Farm, Bapatla. The 40 genotypes were grouped into 7 clusters based on Mahalanobis D^2 analysis with cluster I and II being largest each with 13 genotypes followed by 9 genotypes in cluster III. Based on Hierarchial cluster analysis all the genotypes were grouped into 7 clusters with cluster IV and V being largest each with 9 genotypes followed by 8 genotypes in cluster I. This random distribution of genotypes indicated absence of parallelism between geographical and genetic diversity. In principal component analysis first 5 principal components with eigen value more than one contributed 78.35 per cent towards the total variability with PC_1 alone showing maximum of 38.73 per cent variability.

Key words: Cotton, hierarchial cluster analysis , mahalanobis D^2 analysis, , principal component analysis

Cotton (*Gossypium* spp.) is an important cash crop. It plays a key role in terms of contribution in trade, industrial activities, employment and foreign exchange earnings in India. With the development of social demand, the cotton industry is confronted with problems in how to meet the expanding demands by increasing the quantity with low cost of production besides superior quality. Successful breeding requires genetic diversity to maximize improvement and to minimize the inherient field genetic vulnerability. Hence it is imperative to develop hybrids between genotypes of diverse origin than those involving closely related parents so as to exploit maximum heterosis. So, quantification of genetic variability could direct the breeders for genetic upgrading of cotton genotypes. Multivariate analysis helps to compare and assess genetic diversity among the genotypes which may help in choosing parents for a successful breeding goal.

The experiment was conducted during *kharif* 2010-2011 in randomized block design with 40 genotypes obtained from all over India with three replications following 120 x 60 cm spacing at Agricultural College Farm, Bapatla. The soils are black cotton type with clay texture. Recommended doses of fertilizers were applied in split doses. Each plot consisted of two rows of 6m length and observations were recorded on 5 randomly selected plants from each genotype/ replication for 15 characters *viz.,* plant height (cm), monopodia/plant, sympodia/plant, bolls/ plant, boll weight (g), seed index (g), lint index (g), ginning outturn (%).The data on days to 50 per cent flowering, ginning outturn (%), bundle strength (g/tex), uniformity ratio, 2.5 per cent span length (mm), micronaire (10^{-6}g/in), uniformity ratio and fibre elongation (%) were recorded on plot basis. Mahalanobis D^2 anlysis (Tochers method) was worked out. Agglomerative heirarchial clustering technique (Ward's minimum variance) was followed for cluster analysis and PCA was also performed.

The analysis of variance revealed highly significant differences among 40 genotypes for 15 quantitative traits indicated the existence of variability among genotypes for characters studied. The per cent contribution towards genetic divergence by all the 15 characters is presented in Table 1. Based on D^2 statistic all the 40 genotypes were grouped into 7 clusters (Table 2) using Tocher's method with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values. The distribution of 40 genotypes into VII clusters was at random with maximum genotypes in clusters I and II (13 genotypes each). Cluster III (9 genotypes) was the second largest followed by cluster IV (2 genotypes). The clusters V, VI and VII were solitary and the formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes. The mutual relationships between the clusters were

Table 1. Contribution of different characters towards genetic divergence in 40 genotypes of cotton (*Gossypium hirsutum* L.)

Source	Times ranked first	Contribution per cent towards divergence
Fibre elongation (%)	491	62.95
Seed index (g)	83	10.64
Monopodia/ plant	65	8.33
Boll weight (g)	28	3.59
Lint index (g)	19	2.44
Micronaire (10^{-6} g/in)	17	2.18
Ginning outturn (%)	16	2.05
2.5 per cent span length (mm)	14	1.79
Seed cotton yield/ plant (g)	12	1.54
Uniformity ratio	11	1.41
Bundle strength (g/tex)	10	1.28
Bolls/ plant	9	1.15
Days to 50 per cent flowering	3	0.38
Sympodia/ plant	2	0.26
Plant height (cm)	0	0.00

represented diagrammatically by taking average intra and inter cluster D values. This was in accordance with the results of Eswara Rao *et al.,* (2009), Gopinath *et al.,* (2009), Venkateswarulu *et al.,* (2010) and Srinivasulu *et al.*, (2010). The average intra and inter cluster D and D^2 values are presented in Table 3. The inter cluster distance was maximum between clusters IV and VII followed by clusters V and IV, III and VII , IV and VI , I and VII and II and IV. Based on the inter cluster distances among the groups, crosses after confirming the general combining ability of the genotypes from clusters VII and IV may yield better and desirable segregants. Cluster IV also showed high mean values for most important characters like monopodia/plant, sympodia/plant and bolls/plant, boll weight, seed index, lint index thereby increasing seed cotton yield/plant.

Table 2. Clustering of 40 cotton (*Gossypium hirsutum* L.) genotypes by Ward's minimum variance method (top) and by Tocher's method (bottom)

Cluster number	Genotypes number	Name of genotype(s)
I	8	BWR 39, AKOLA 2, SA 1104, IH 07, CPD 420, LAXMI, RAH 8794, RAH 100
	13	**SA 53 1, NA 1568, BWR 61, CPD 478, VIKRAM, ARB 9009, L 725, 4085, PEE DEE 0113, CPD 431, RAH 8794, BWR 39, CPD 420**
II	4	D.S 26, MCU 11, NA 1678, G 204 13
	13	**CNH 120MB, KHANDWA, JK 276 10 5, CCH 05 2, NA 1584, CSH 3167, NH 577, NA 1588, CCH 1071, AC 88, L 766, CPD 755, D.S 56**
III	2	KH 11, RAH 101
	9	**NA 1678, G 204 13, D.S 26, RAH 100, AKOLA 2, SA 1104, IH 07, MCU 11, LAXMI**
IV	9	ARB 9009, CPD 478, D.S 56, BWR 61, VIKRAM, L 725, 4085, SA 53 1, NA 1568
	2	**KH 11, RAH 101**
V	9	L 766, CSH 3167, CNH 120MB, KHANDWA, JK 276 10 5, NH 577, PEE DEE 0113, CPD 431, AC 88
	1	**BADANWAR**
VI	7	NA 1584, CCH 05 2, BADANWAR, NA 1588, CCH 1071, CPD 755, CNH 301
	1	**CNH 301**
VII	1	COP 420
	1	**COP 420**

Note: underlined genotypes common for both methods

In hierarchial clustering (Ward's minimum variance) method 40 genotypes were grouped into VII clusters. Among all the clusters, cluster IV and V were largest containing 9 genotypes each followed by cluster I with 8 genotypes, cluster VI with 7 genotypes, cluster II with 4 genotypes, cluster III with 2 genotypes and cluster VII with I genotype (Table 2). The average intra and inter cluster distances are presented in Table 3. Maximum inter cluster distance was observed between clusters VII and III; clusters VII and II; clusters VI and III. Cluster III also showed high mean values for most important characters like sympodia/plant, bolls/ plant, boll weight, seed index, lint index and ginning outturn thereby increasing seed cotton yield/plant.

The first 4 principal components with eigen values more than one contributed 78.34 per cent towards the total variability (Table 4).

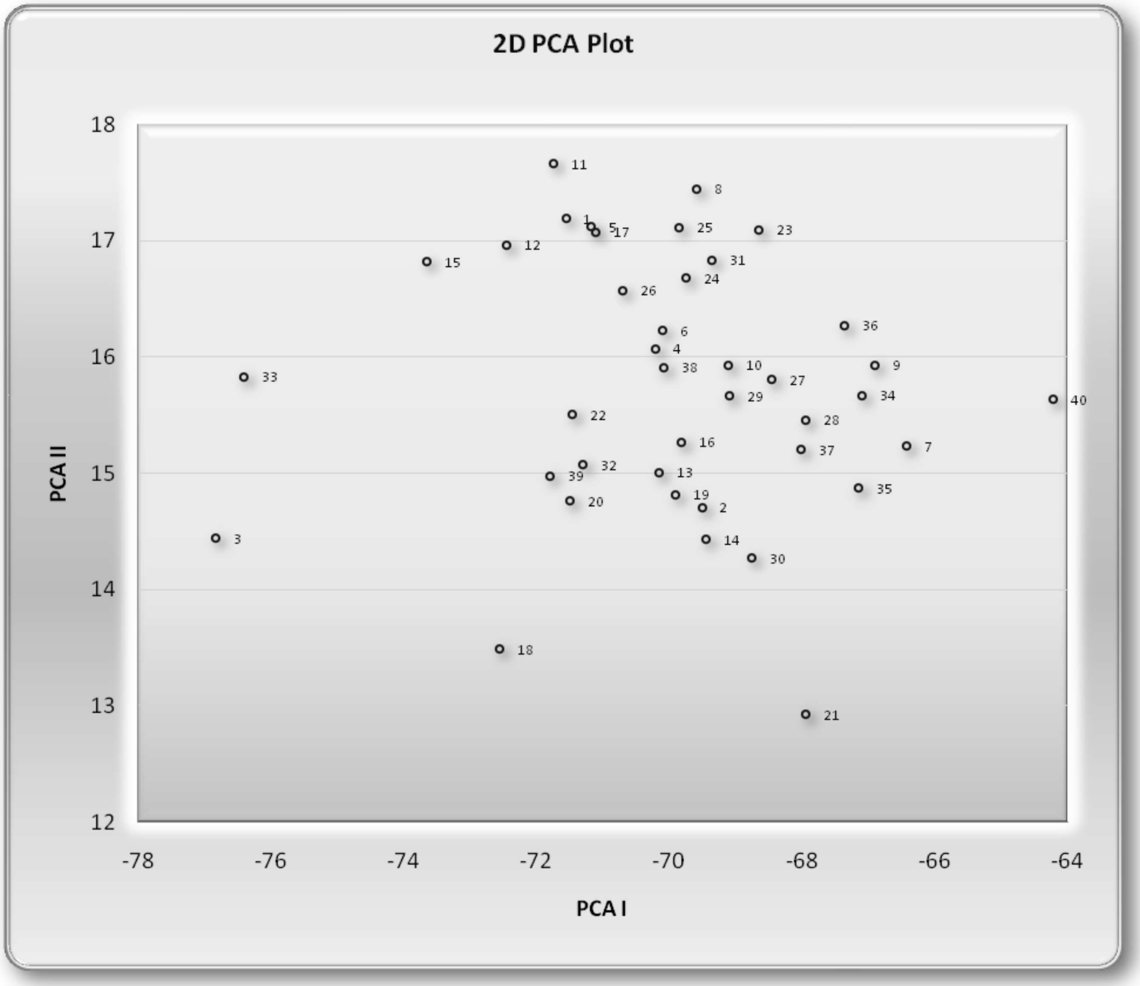

Fig. 1. Two dimensional graph showing relative position of 40 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores

Table 3. Average intra and inter cluster Euclidean^2 values (top) and D^2 values (bottom) among the VII clusters in 40 cotton genotypes (*Gossypium hirsutum* L.)

Cluster No	I	II	III	IV	V	VI	VII
I	**43.43**	60.93	121.00	58.05	93.51	172.65	467.06
	13.50(3.67)	25.44(5.04)	22.39(4.73)	61.38(7.83)	66.61(8.16)	40.13(6.33)	119.18(10.91)
II		**38.24**	124.75	82.68	145.12	270.57	619.56
		17.60(4.19)	51.71(7.19)	105.76(10.28)	31.78(5.63)	24.23(4.92)	63.25(7.95)
III			**38.68**	200.39	279.66	395.05	830.52
			17.91(4.23)	40.13(6.33)	116.64(10.80)	73.08(8.54)	182.40(13.50)
IV				**35.36**	57.14	112.59	349.18
				12.89(3.59)	190.65(13.80)	126.05(11.22)	276.84(16.63)
V					**41.37**	68.26	217.66
					0.00(0.00)	27.27(5.22)	20.87(4.56)
VI						**54.37**	132.48
						0.00(0.00)	47.00(6.855)
VII							**0.000**
							0.00(0.00)

Note: Bold and diagonal values indicate intra cluster distance; figures in parentheses are D values

Table 4. Eigen values, proportion of the total variance represented by first five principal components, cumulative per cent variance and component loading of different characters in cotton (*Gossypium hirsutum* L.).

	PC_1	PC_2	PC_3	PC_4	PC_5
Eigene Value (Root)	5.810	2.055	1.744	1.228	0.916
Percent Var. Exp.	38.731	13.698	11.624	8.187	6.107
Cum. Var. Exp.	38.731	52.429	64.053	72.240	**78.346**

The hierarchial cluster analysis and PCA confirmed findings of each other. The 2D scattered diagram showed genotypes in the same cluster closer to each other (Fig.1). The above results are supported by Vijaya Lakshmi *et al.,* (2009), Srinivasulu *et al.,* (2010) and Altaher and Singh (2003).

All the 3 methods of grouping revealed a single concept of non correspondence of genetic divergence and geographic diversity. The genotypes, KH 11 and RAH 101, and COP 420 showed maximum inter-cluster distance in the multivariate analysis and can be exploited for the development of heterotic hybrids after testing their combining ability.

REFERENCES

Altaher, A. F. and Singh, R. P. 2003. Genetic diversity studies in upland cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Imp.* **28**: 158-63.

Eswara Rao, G., Chenga Reddy, V., Lal Ahamed, M., Srinivasa Rao, V., Panduranga Rao, C and Bali Reddy, V. 2009. Genetic divergence in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agril. J.* **56** : 309-14.

Gopinath, M., Rajamani, S., Naik, R. K and Rao, C. M. 2009. Genetic divergence for lint characters in upland cotton (*Gossypium hirsutum* L.). *J.Cotton Res. Dev.* **23**: 46-48.

Srinivasulu, P., Samba Murthy, J.S.V., Rama Kumar, P.V and Srinivasa Rao, V. 2010. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agril. J.* **57** : 148-55.

Venkateswarulu, K., Chenga Reddy, V., Samba Murthy, J. S. V., Srinivasa Rao, V., Panduranga Rao, C., Siva Reddy, K. V. and Sateesh Babu, J. 2010. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agril. J.* **57** : 240-47.

Vijaya Lakshmi, G., Chenga Reddy, V., Panduranga Rao, C., Satish Babu, J and Srinivasulu, R. 2009. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agril. J.* **56**: 8-15.

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