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Genetic divergence studies in upland cotton (*Gossypium hirsutum* L.) germplasm

A B M Sirisha, Lal Ahamed M, S Ratna Kumari and V Srinivasa Rao
Department of Genetics and Plant Breeding, Agricultural College, Bapatla – 522 101

ABSTRACT

The present study was conducted at Agricultural College, Bapatla, Andhra Pradesh, India. 60 cotton genotypes were evaluated for fifteen parameters *viz*., days to 50 % flowering, plant height (cm), No.of monopodia per plant, No.of sympodia per plant, No.of bolls per plant, boll weight (g), Seed index (g), lint index (g), ginning out turn (%), 2.5 % span length (mm), bundle strength (g/tex), fibre elongation (%), uniformity ratio, micronaire (10^{-6} g inch $^{-1}$) and seed cotton yield per plant (g). Analysis of variance showed significant differences among the 60 genotypes for all the fifteen characters showing the presence of genetic variability among the materials studied. Based on Mahalanobis' D^2 statistic, eight clusters were formed and maximum contribution towards genetic divergence was made by uniformity ratio, lint index, boll weight, monopodia per plant, micronaire, bundle strength, 2.5% span length, bolls per plant, days to 50% flowering, fibre elongation, seed index and plant height. Principal component analysis identified six principal components (PCs) which contributed 79.79 % of cumulative variance. The factors, ginning outturn, sympodia per plant, plant height, monopodia per plant, days to 50% flowering, seed cotton yield, fibre elongation, micronaire, seed index, boll weight, bundle strength, bolls per plant, uniformity ratio and lint index contributed positively to the first principal component.

Keywords**:** *Cotton, Clustering, D^2 analysis, Genetic divergence and Principal component analysis.*

Cotton (*Gossypium* spp.) popularly called "White Gold" is the most important renewable natural fibre crop of global importance. It is grown in tropical and subtropical regions of more than 80 countries of the world and enjoys a premier position amongst all commercial crops contributing nearly 65 % of the total raw material needs of the textile industry in our country (Sirisha *et al*., 2019). It is the main stay of India's economy with fascinating history from cultural, economical and scientific perspective. India is the only country in the world growing all the four cultivated species of cotton, *viz*., *G. hirsutum, G. arboreum, G. herbaceum and G. barbadense* (Samuel *et al.*, 2013). Diverse potential germplasm is the basis for any fruitful hybridization programme. Hybridization carried out between diverse parents results in development of high yielding varieties. To identify the diverse parents Mahalanobis D^2 analysis (Mahalanobis 1936) plays a critical role in identification of the diverse parents which can be exploited in the hybridization programme to generate novel and useful varieties. In the present investigation, the germplasm lines under study are analysed with the Mahalanobis D^2 analysis which will result in diverse clusters. The parents from diverse clusters are utilised further in the hybridization programme.

Materials and Methods

Sixty divergent cotton genotypes were evaluated for genetic divergence in a Randomized Block Design with three replications at Agricultural College Farm, Bapatla, Andhra Pradesh. Each plot consisted of two rows each of 6 m length with a spacing of 105 × 60 cm. Observations on days to 50 % flowering, plant height (cm), No.of monopodia per plant, No.of sympodia per plant, No.of bolls per plant, boll weight (g), Seed index (g), lint index (g), ginning out turn (%), 2.5 % span length (mm), bundle strength (g/tex), fibre elongation (%), uniformity ratio, micronaire (10^{-6} g inch^{-1} and seed cotton yield per plant (g) were recorded while Quality parameters were measured at CIRCOT regional Station, Lam, Guntur.

Recommended agronomic practices were followed to raise a good crop. The data were analysed using D^2 statistic (Mahalanobis,1936), heirarchial cluster analysis (Anderberg, 1993) and principal component analysis (Jackson, 1991).

Results and Discussion

Analysis of variance showed highly significant differences among the 60 cotton genotypes indicating the presence of sufficient genetic variability for the entire characters under study (Table 1) (Sirisha *et al*., 2019). The per cent contribution towards genetic divergence by all the 15 contributing characters is presented in Table 1A and the maximum contribution towards genetic divergence was by uniformity ratio (38.08) followed by lint index (13.28), boll weight (11.81), monopodia per plant (8.19), micronaire (7.85), bundle strength (7.40), 2.5% span length (4.29), no.of bolls per plant (3.95), days to 50% flowering (2.26), fibre elongation (1.69), seed index (0.73) and plant height (0.34), respectively.

Based on Mahalanobis D^2 analysis all the genotypes were grouped into eight (8) clusters. The distribution of sixty genotypes into (Table-2) eight clusters was at random with maximum number of genotypes in clusters IV (16 genotypes) and minimum in the clusters VI, VII and VIII with one genotype each 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 are represented diagrammatically by taking average intra and inter cluster D^2 values. The tree like structure called dendrogram was constructed based on clustering by Tocher's method (Fig.1). The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chaudhary (1985) and are presented in the Table 3. The maximum intra-cluster distance was 56.09 in cluster V, followed by 45.54 in cluster IV, 27.43 in cluster III, 21.49 in cluster II and 14.59 in cluster I. The intra cluster distance was zero for clusters VI, VII and VIII as they were solitary clusters. The inter-cluster distances ranged from 30.41 (between clusters I and II) to 134.79 (between clusters V and VIII). The inter-cluster distance was maximum between clusters V and VIII (134.79) and minimum for cluster I and II (30.41). The genotypes from clusters I, V, VI and VIII may be adopted in the hybridization program which will result in transgressive segregating population. The results are in accordance with Nagaraj *et al*. (2011), Punitha *et al.* (2012), Tulasi *et al.* (2014), Araujo *et al*. (2014) and Ameer Hussain *et al*. (2019).

Principal component analysis

In the present investigation, principal component analysis identified six principal components (PCs), which contributed 79.79 **%** of cumulative variance (Table-4). The first four principal components with eigen values more than one contributed maximum towards the total variability. The principal component with eigen values less than one were considered as non-significant. The first principal component contributed maximum towards variability (25.41%). The characters, ginning outturn (0.38), sympodia per plant (0.36), plant height (0.36), monopodia per plant (0.34), days to 50% flowering (0.33), seed cotton yield (0.27), fibre elongation (0.24), micronaire (0.22), seed index (0.20), boll weight (0.20), bundle strength (0.18), no.of bolls per plant (0.16), uniformity ratio (0.10) and lint index (0.04) had positive loading while negative loading was observed with 2.5% span length (-0.08) in explaining the divergence among the genotypes in $PC_{1.}$ The second principal component (PC_2) described 15.71 **%** of total variance and it was reflected by significant positive loading of plant height (0.28), fibre elongation (0.21), bolls per plant (0.20), monopodia per plant (0.20), days to 50% flowering (0.12), ginning out turn (0.01) while negative loading was observed with 2.5% span length (-0.44), bundle strength (-0.41), boll weight (-0.35), seed cotton yield (-0.33), uniformity ratio (-0.33), seed index (-0.180), micronaire (-0.11), lint index (-0.10) and sympodia per plant (-0.01). The third principal component (PC_3) was characterized by 15.13 % contribution towards the total variability. Characters *viz.*, seed index (0.49), lint index (0.34), monopodia per plant (0.28), ginning out turn (0.25), 2.5% span length (0.17), boll weight (0.07) and plant height (0.05) and number of sympodia per plant (0.02) were positively loaded while, seed cotton yield per plant (-0.36), fibre elongation (-0.32), number of bolls per plant (-0.30), uniformity ratio (-0.23), micronaire (-0.22), bundle strength (-0.13) and days to 50% flowering (-0.0.02) were negatively loaded. The fourth principal component (PC_4) was characterized by 11.36 %

contribution towards the total variability. Characters *viz.*, days to 50% flowering (0.37), boll weight (0.37), seed cotton yield (0.13), monopodia per plant (0.09) and plant height (0.06) were positively loaded while, lint index (-0.54), bolls per plant (-0.46), micronaire (-0.29), sympodia per plant (-0.22), 2.5% span length (-0.13), bundle strength (-0.06), uniformity ratio (-0.05), ginning out turn (-0.05), fibre elongation (-0.04) and seed index (-0.02) were negatively loaded. The results are in accordance with Chapara *et al.* (2022), Abdel *et al.* (2022), , Kulkarni *et al.* (2011), Asha *et al.* (2013) and Haritha *et al.* (2014).

Based on the dendrogram based on Mahalanobis D^2 (Fig-1) and the PCA scores of 60 genotypes were plotted on graph with three dimensional scatter diagrams (Fig. 2). These graphs showed wide divergence between the genotypes, BBGH-77, BGH-23, BGH-94, BL-7, L-603 and HAG 812, signifying their usefulness in cotton improvement programmes.

Table 1. Analysis of variance for seed cotton yield and yield components in cotton (*Gossypium hirsutum* L.)**.**

Source	d.f.	Plant height (cm)	Days to 50% flowering	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	Seed index (g)	Lint index (g)
		Mean Squares							
Replications	2	1.0344	1.0167	0.0009	3.056	5.0549	0.0296	0.1297	0.0146
Treatments	59	293.6790***	13.7494***	0.2873***	12.8108***	48.8241***	0.6529***	1.4518***	0.4568***
Error	118	34.739	0.8924	0.0156	2.9919	3.4476	0.0256	0.1874	0.0168

Source	d.f.	Ginning out-turn (%)	2.5% span length (mm)	Bundle strength (g/Tex)	Fibre elongation (%)	Uniformity ratio	Micronaire (10^{-6} g $Inch^{-1}$)	Seed cotton yield per plant (g)
		Mean Squares						
Replications	2	1.1418	0.6393	0.4788	0.0259	0.683	0.0401	130.7326
Treatments	59	6.7849***	7.7248***	5.5428***	0.2221***	21.8352***	0.5858***	667.4988***
Error	118	1.6414	0.5072	0.3128	0.0282	0.3235	0.0296	63.5781

**** = Significance at 1% level**

CONCLUSION:

The present investigation was carried out for studying the divergence in 60 diverse cotton genotypes. The results of multivariate analysis indicated the presence of considerable genetic divergence among the 60 genotypes and grouping of genotypes into eight clusters using D^2 analysis and cluster analysis. In Mahalanobis' D^2 statistic, maximum contribution towards genetic divergence was made by uniformity ratio, lint index, boll weight, monopodia per plant, micronaire, bundle strength, 2.5% span length, bolls per plant, days to 50% flowering, fibre elongation, seed index and plant height. Principal component analysis identified six principal components (PCs) which contributed 79.79 % of cumulative variance. The factors, ginning outturn, sympodia per plant, plant height, monopodia per plant, days to 50% flowering, seed cotton yield, fibre elongation, micronaire, seed index, boll weight, bundle strength, bolls per plant, uniformity ratio and lint index contributed positively in the first principal component. Diverse genotypes from clusters I, V, VI and VIII may be selected and adopted in the hybridization program for development of desirable varieties. The diverse genotypes, BBGH-77, BGH-23, BGH-94, BL-7, L-603 and HAG 812 may be utilized in cotton improvement programmes.

Table 1 A. Contribution of different characters towards genetic divergence in 60 genotypes of cotton (*Gossypium hirsutum* L.)

S.No.	Source	Times Ranked First	Contribution %
1	Plant height (cm)	6	0.34
2	Days to 50% flowering	40	2.26
3	No. of monopodia per plant	145	8.19
4	No.of sympodia per plant	0	0
5	No. of bolls per plant	70	3.95
6	Boll weight (g)	209	11.81
7	Seed index (g)	13	0.73
8	Lint index (g)	235	13.28
9	Ginning out-turn (%)	2	0.11
10	2.5 % span length (mm)	76	4.29
11	Bundle strength (g/Tex)	131	7.4
12	Fibre elongation (%)	30	1.69
13	Uniformity ratio	674	38.08
14	Micronaire (10^{-6} g $Inch^{-1}$)	139	7.85
15	Seed cotton yield per plant (g)	0.01	0

Table 2. Clustering of 60 genotypes of cotton *(Gossypium hirsutum* L.*)* by Tocher's method

Cluster number	No. of genotypes	Cluster members
1	5	L 766, AC-88, G.AGETI, ACOLA-2, ICMF-23.
2	14	G COT-16, SA-1104, ICMF-86, LH-1566, G COT-12, CNH-7-947, TX LAMA, HLS-323, 117-60-30, NA-1584, GJHV-302, CPD-431, GSHY-01/1338, ARB-815.
3	9	SA 53-1, CNH-120MB, KHANDWA, CSH 3167, CCH-16, TSH-33, CCH-727, NA1568, BANDWAR.
4	16	L 603, NA 1290 BP, RAH-100, COP-420, H492, ARB-8901, NISC 40, KH-121, AET-5, NA 1588, NARASIMHA, NA-1650, SFA-5, HAG-812, ARB 9009, BGH-23
5	13	BBGH-26, BBGH-1, BGH-94, BL-7, BBGH-3, GHL-5, JK-206-6, JK-276-4, CSH-17,PEE DEE-0113,KD CKAD, , BBGH-77, TSH-9974.
6	1	GJHV-338
7	1	GHL-8
8	1	BBGH-33

Table 3. Average intra-and inter-cluster D^2 values among eight clusters in 60 cotton genotypes (*Gossypium hirsutum* L.)

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	**14.59 (3.82)**	30.41	33.50	72.52	60.68	63.80	111.46	66.82
2 Cluster		**21.49 (4.64)**	33.03	46.37	64.67	50.72	74.23	79.30
3 Cluster			**27.43 (5.24)**	62.92	62.92	57.80	103.65	83.09
4 Cluster				**45.54 (6.75)**	107.60	73.71	66.89	87.20
5 Cluster					**56.090 (7.49)**	100.25	125.18	134.79
6 Cluster						**0.000 (0.00)**	134.50	88.52
7 Cluster							**0.000 (0.00)**	112.07
8 Cluster								**0.00 (0.00)**

Note: Bold and diagonal values indicate intra-cluster D square distance: figures in parantheses are D Values

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

	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector
Eigen Value (Root)	**3.81**	**2.35**	**2.27**	**1.7**	**0.99**	**0.82**
% Var. Exp.	**25.41**	**15.71**	**15.13**	**11.36**	**6.64**	**5.52**
Cum. Var. Exp. %	**25.41**	**41.12**	**56.26**	**67.62**	**74.27**	**79.79**
Plant height (cm)	0.36	0.28	0.05	0.06	0.26	0.14
Days to 50% flowering	0.33	0.12	-0.02	0.37	0.07	0.02
No. of monopodia per plant	0.34	0.2	0.28	0.09	0.12	0.25
No.of sympodia per plant	0.36	-0.01	0.01	-0.22	0.32	-0.04
No. of bolls per plant	0.16	0.2	-0.3	-0.46	0.11	-0.02
Boll weight (g)	0.2	-0.35	0.07	0.37	-0.35	-0.11
Seed index (g)	0.2	-0.18	0.49	-0.02	-0.04	-0.28
Lint index (g)	0.04	-0.1	0.34	-0.54	-0.24	-0.03
Ginning out-turn (%)	0.38	0.01	0.25	-0.05	-0.25	0.14
2.5 % span length (mm)	-0.08	-0.44	0.17	-0.13	0.44	-0.04
Bundle strength (g/Tex)	0.18	-0.41	-0.13	-0.06	0.34	-0.19
Fibre elongation (%)	0.24	0.21	-0.32	-0.04	-0.1	-0.44
Uniformity ratio	0.1	-0.33	-0.23	-0.05	-0.04	0.73
Micronaire (10^{-6} g $Inch^{-1}$)	0.22	-0.11	-0.22	-0.29	-0.45	0.03
Seed cotton yield per plant (g)	0.27	-0.33	-0.36	0.13	-0.02	-0.15

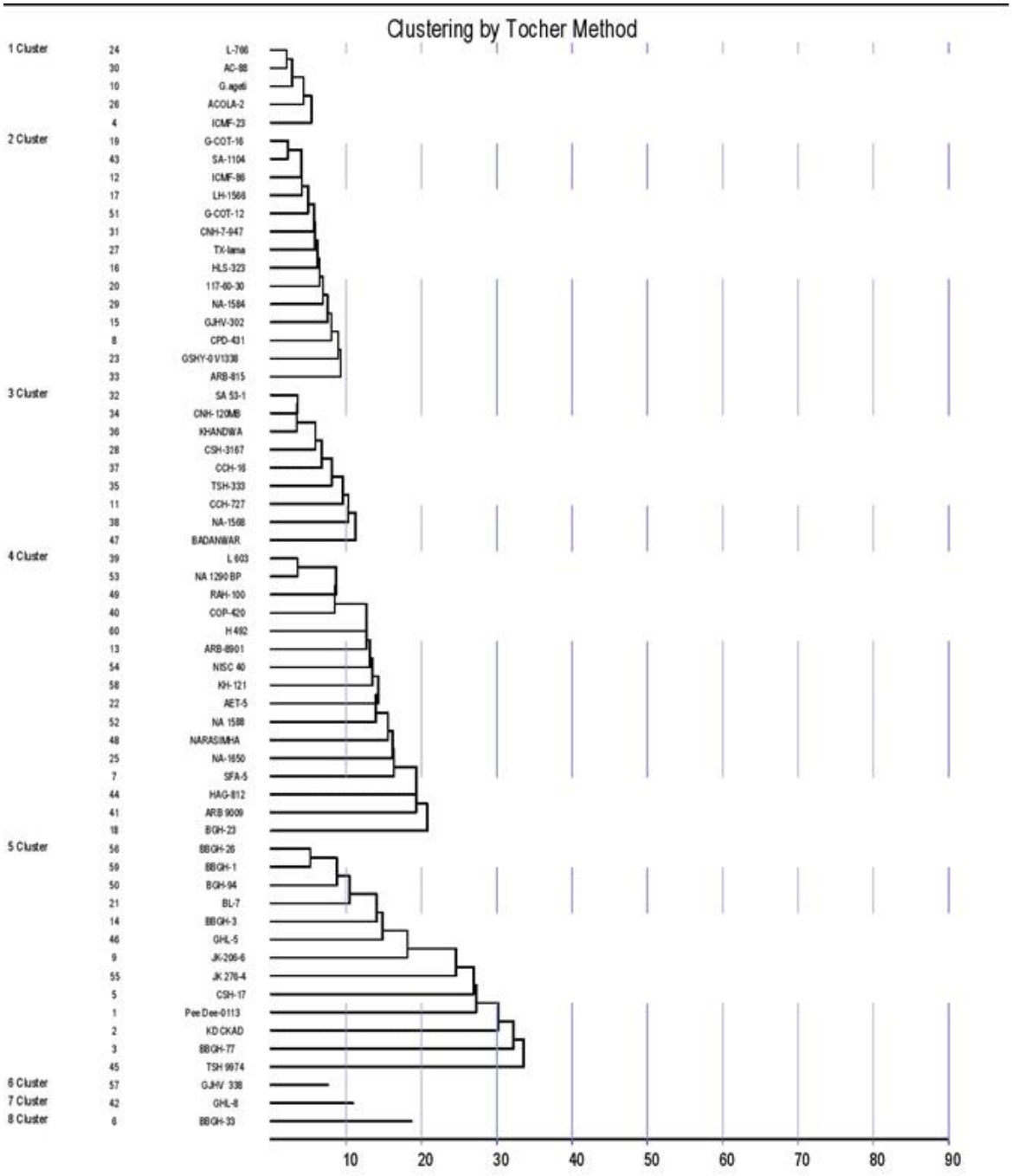

Fig. 1: Dendrogram showing relationship of 60 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis' D^2 values

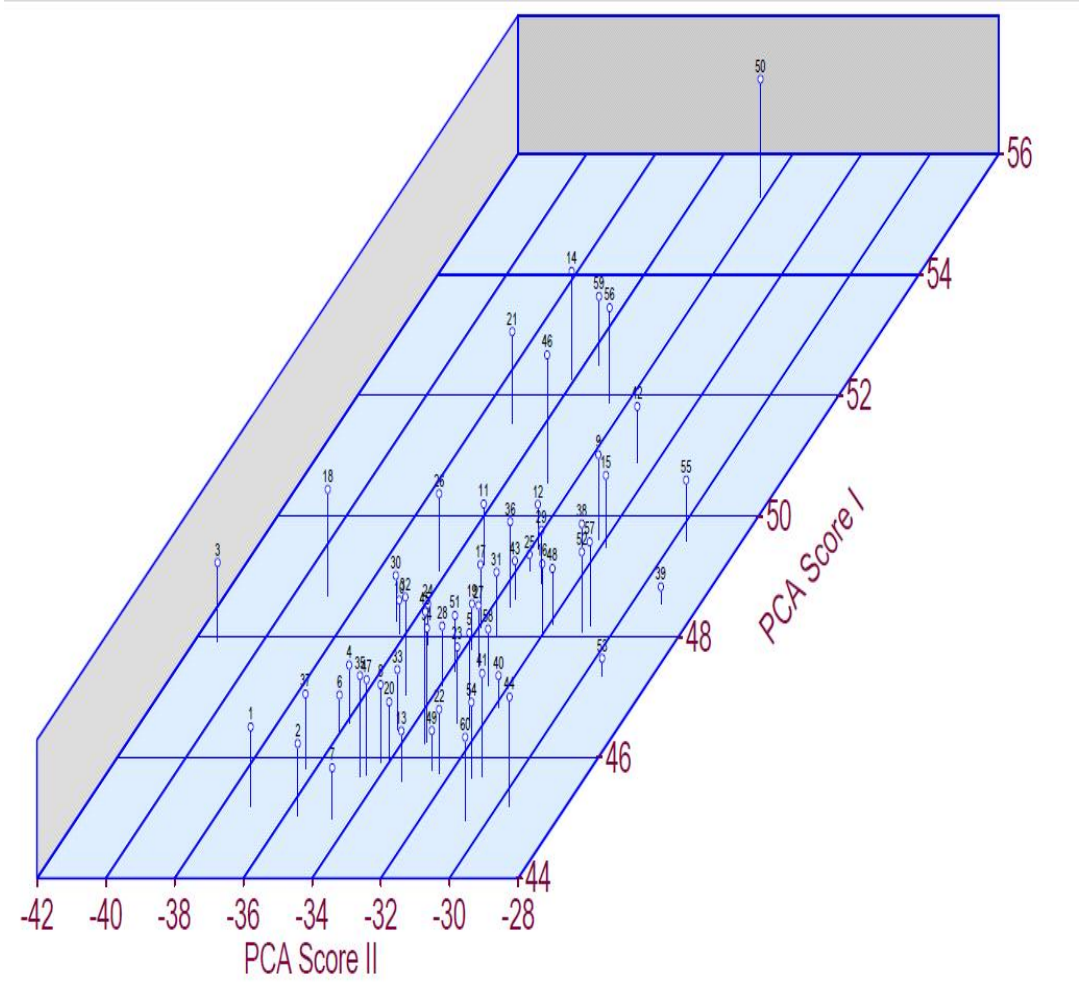

Fig-2: Three dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores

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