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GENETIC DIVERSITY STUDIES FOR SEED COTTON YIELD AND FIBER QUALITY PARAMETERS IN DIVERSE COTTON GENOTYPES

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ABSTRACT

Genetic diversity plays a vital role in crop improvement programmes, offering researchers the opportunity to develop new and improved varieties with desirable traits that meet the preferences of both farmers and breeders. The present study aimed to characterize the genetic diversity among 53 cotton genotypes. These genotypes were evaluated using an augmented block design during the *kharif* season of 2024–25 at the Regional Agricultural Research Station, Lam Farm, Guntur. Cluster analysis revealed significant genetic divergence among the genotypes. Based on Tocher's method of D^2 analysis, the genotypes were grouped into four distinct clusters. Cluster II contained maximum genotypes, followed by Cluster III. cluster I exhibited the maximum intra cluster distance (38.42) while the minimum intra cluster distance was observed by cluster IV (19.64). The cluster I recorded the largest distance from cluster IV (49.64). Crossing between genotypes of the cluster I (Suvin and CCB 29) and cluster IV (L 2384, L 2275, L 2385 and L 2383) can be made based on these studies to create suitable transgressive segregants. Seed index contributed the most to genetic divergence, followed by upper half mean length, micronaire and seed cotton yield per plant. It can be concluded that selecting genetically divergent parents based on these attributes would be beneficial for maximizing genetic diversity in breeding programs.

Key words : Cotton, Genetic diversity, D^2 statistic, Seed cotton yield.

Introduction

Cotton (*Gossypium* spp.) is one of the oldest cultivated crops and it is grown as the main source of raw materials for the textile industries. It is a vital commercial cash crop in India, contributing about 20.67% of global cotton production (ICAR-AICRP (Cotton)–Annual Report 2024–25). Cotton is mainly cultivated in tropical as well as sub-tropical regions and is mainly grown for fibre and oil purpose. It is crucial for increasing the country's economy and is popularly known as "white gold" (Komala *et al*., 2018). It belongs to the genus *Gossypium* and the family malvaceae. There is an extensive genetic variation present in this genus distributed among 50 species, of which four are cultivated, 44 are wild diploids and two are wild tetraploids (Percival and Kohel, 1990).

India is the only country where all the four species of cotton are cultivated that include *Gossypium arboreum* L. and *Gossypium herbaceum* L. (Asian cotton) which are diploid species (2n=2x=26) and are known as old world cottons; *Gossypium barbadense* L. (Egyptian cotton) and *Gossypium hirsutum* L. (American upland cotton) which are tetraploid species (2n=4x=52) and are known as new world cottons.

The extent and nature of available genetic variation within germplasm offer significant potential for use in successful breeding programs. This can lead to

improvements in various characteristics related to seed cotton yield and fibre quality (Chapara *et al*., 2022). Genetically diverse germplasm forms the foundation of any successful hybridization programme. Crosses between genetically divergent parents often lead to the development of high-yielding varieties. Mahalanobis D^2 analysis (Mahalanobis, 1936) plays a crucial role in identifying such diverse parents, which can be effectively utilized in hybridization programmes to generate novel and useful varieties.

The importance of Mahalanobis D^2 analysis in quantifying genetic divergence was also studied by Gauswami Jyoti *et al*. (2021), Satish (2021), Sirisha *et al*. (2022), Meena *et al*. (2022), Prakash and Suthar (2023) Sagar *et al*. (2023) and Chapara *et al*. (2024).

In the present investigation, 53 cotton genotypes were analyzed using Mahalanobis D^2 analysis, which resulted in the formation of distinct clusters. Genotypes from these diverse clusters can be effectively utilized in hybridization programmes to enhance genetic variability and develop improved varieties.

Materials and Methods

Plant Material and Site characteristics

50 cotton genotypes along with three checks (NDLH 2051-1, Sivanandhi and CICR 23 Bt) varieties were evaluated during *kharif* season 2024-2025 at experimental area of Regional Agricultural Research Station, Lam farm, Guntur, Andhra Pradesh which was present at 160 20' North latitude and 800 26' East longitude and an altitude of 31.5 m above mean sea level. The experiment was sown on 1st August to evaluate genotypes for yield and fibre parameters. The list of the genotypes was presented in Table 1.

Observations recorded

Data was collected from ten randomly selected plants on various seed cotton yield contributing traits like days to fifty per cent flowering (plot basis), plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), lint index (g), seed index (g), ginning out turn (%), seed cotton yield per plant (g) and for fibre quality traits like Upper Half Mean Length (UHML) (mm), uniformity index (%), micronaire (µg/inch) and tenacity (g/tex) data was recorded on plot basis.

Experimental design

The experiment was conducted using Augmented Block Design (Federer, 1956) in six blocks. In first five blocks, 12 entries (nine genotypes + three checks) and in the last block eight entries (five genotypes + three checks) were planted randomly in the blocks. Each entry was sown in two rows with a row length of 6.3 m each with a spacing of 105 × 60 cm.

Table 1 : Details of the cotton genotypes studied in the present investigation.

S. no.	Genotypes	Entries	S. no.	Genotypes	Entries
1	GP 1	LHBT 2203	28	GP 28	L 2273
2	GP 2	LHBT 24	29	GP 29	Yaganti
3	GP 3	LHBT 8	30	GP 30	Srinandi
4	GP 4	NDLH 3104-4	31	GP 31	NDLA 3116-4
5	GP 5	LHBT 9	32	GP 32	Suvin
6	GP 6	NDLH 2985	33	GP 33	CCB 29
7	GP 7	LHBT 26	34	GP 34	L 2396
8	GP 8	NDLH 3116-4	35	GP 35	L 2384
9	GP 9	LHBT 6	36	GP 36	L 2274
10	GP 10	LHBT 22	37	GP 37	L 2275
11	GP 11	LHBT 7	38	GP 38	L 2277
12	GP 12	ARCV 111	39	GP 39	L 2278
13	GP 13	WGCV Bt 26	40	GP 40	L 2281
14	GP 14	LHBT 2390	41	GP 41	L 2265
15	GP 15	LHBT 2392	42	GP 42	L 2386
16	GP 16	LHBT 2385	43	GP 43	L 2389
17	GP 17	LHBT 2383	44	GP 44	L 2390
18	GP 18	LHBT 2395	45	GP 45	L 2385
19	GP 19	Lam Bt 2208	46	GP 46	L 2395
20	GP 20	ARCV 99	47	GP 47	L 2388
21	GP 21	LHBT 3	48	GP 48	L 2383
22	GP 22	Lam Bt 2209	49	GP 49	L 2387
23	GP 23	LHBT 4	50	GP 50	L2382
24	GP 24	L 2381	51	Check 1	CICR 23 Bt
25	GP 25	L 2267	52	Check 2	NDLH 2051-1
26	GP 26	L 2268	53	Check 3	Sivan-andhi
27	GP 27	L 2270			

Statistical analysis

The means of 14 traits were subjected to Analysis of Variance (ANOVA) following the statistical procedure outlined by Falconer (1964). Subsequently, the data were analyzed using Mahalanobis D^2 statistics (Mahalanobis, 1936) to assess genetic divergence. Genotypic clustering

was performed based on the minimum generalized distance using Tocher's method, as described by Rao (1952).

Intra-cluster distances were calculated as the sum of D^2 values between all possible pairs of genotypes within a cluster, divided by the number of such combinations. For inter-cluster distances, each cluster was compared with all others by computing the average D^2 distance between all genotype pairs from the two clusters. This was obtained by summing the D^2 values for all combinations between members of the two clusters and dividing by the product of the number of genotypes in each cluster. Based on the inter-cluster D^2 values, the classification scale proposed by Rao (1952) was used to interpret the extent of genetic divergence and a cluster diagram was constructed accordingly. The mean data was used to perform Principal Component Analysis (PCA) using '*factoextra*', '*factoextra*' package in R studio version R.4.4.2.

Results and Discussion

ANOVA revealed significant differences among the 53 genotypes for all the traits studied, indicating the presence of substantial genetic variability and diversity within the material. Based on Tocher's method (Rao, 1952), the genotypes were grouped into four distinct clusters, ensuring that the average intra-cluster D^2 values were lower than the inter-cluster D^2 values. The distribution of genotypes across the four clusters was presented in Table 2 and illustrated diagrammatically in Fig. 1. Similar finding was reported by Sarwar *et al*. (2021).

The analysis showed that cluster I contained the fewest genotypes, with only two genotypes both belonging to the *Gossypium barbadense* L. species. Cluster II showed the highest number of genotypes, totaling of 29 genotypes, which included both *Gossypium arboreum* L. and *Gossypium hirsutum* L. Cluster III comprised of 18 genotypes. Lastly, cluster IV included four genotypes. The observed pattern of clustering indicated that genetic diversity is not necessarily correlated with geographical origin. Instead, it may result from various factors such as natural selection, exchange of breeding material, genetic drift, and environmental variation. Therefore, the selection of genotypes for hybridization should be based on genetic diversity rather than geographical distribution (Arunachalam and Ram, 1967).

The intra-cluster average D^2 values ranged from 19.64 to 38.42. Among the four clusters, Cluster I exhibited the highest intra-cluster distance (38.42), indicating greater genetic variability among its genotypes, while Cluster IV showed the lowest intra-cluster distance (19.64). The maximum inter-cluster distance was observed between Cluster I and Cluster IV (49.64), followed by Cluster I and Cluster II (47.46) and Cluster I and Cluster III (47.00), suggesting a high degree of genetic divergence between these groups.

These results highlight the importance of carefully selecting both the appropriate clusters and specific genotypes within them when planning a crossing programme. Crosses between genotypes from divergent clusters are more likely to exhibit high heterosis and generate useful transgressive segregants. For further genetic studies, such as diallel or line × tester analysis, one or two genotypes from each cluster may be selected

Table 2 : Clustering pattern using Tocher's method for seed cotton yield attributing traits and fibre quality traits in 53 cotton genotypes.

Cluster No.	Number of genotypes	Name of genotype(s)
I	2	Suvin and CCB 29
II	29	Yaganti, Srinandi, NDLA 3116-4, L 2395, L 2388, L 2277, L 2390, L 2389, LHBT 22, LHBT 7, ARCV 111, WGCV Bt 26, LHBT 2390, LHBT 2392, LHBT 2385, LHBT 2395, Lam Bt 2208, LHBT 3, LHBT 24, LHBT 8, NDLH34104-4, LHBT 9, NDLH 2985, LHBT 26, NDLH 3116-4, LHBT 6, CICR 23 Bt, Sivanandhi and NDLH 2051-1
III	18	L 2387, L 2274, L 2281, L 2386, L 2396, L 2278, L 2382, L 2265, LHBT 2203, LHBT 2383, ARCV 99, Lam Bt 2209, LHBT 4, L 2267, L 2273, L 2381, L 2268 and L 2270
IV	4	L 2384, L 2275, L 2385 and L 2383

Table 3 : Average intra (bold) and inter-cluster D^2 values among the four clusters for seed cotton yield attributing and fibre quality traits in 53 cotton genotypes.

Clusters	I	II	III	IV
I	**38.42**	47.46	47.00	49.64
II		**25.00**	27.00	30.51
III			**23.52**	30.56
IV				**19.64**

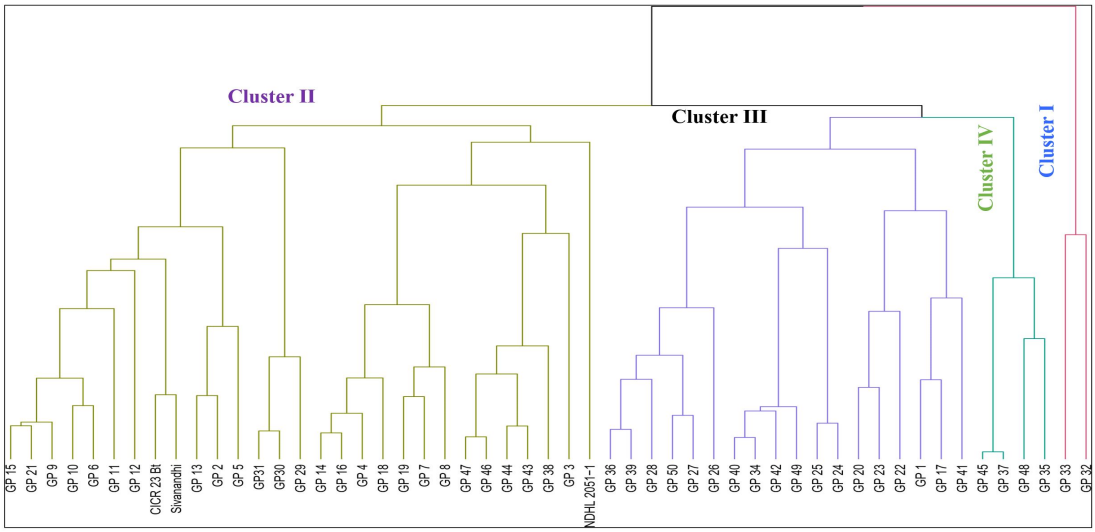

Fig. 1 : Dendrogram showing relationship among 53 cotton genotypes in four clusters based on Mahalanobis D^2 values by Torcher's Method.

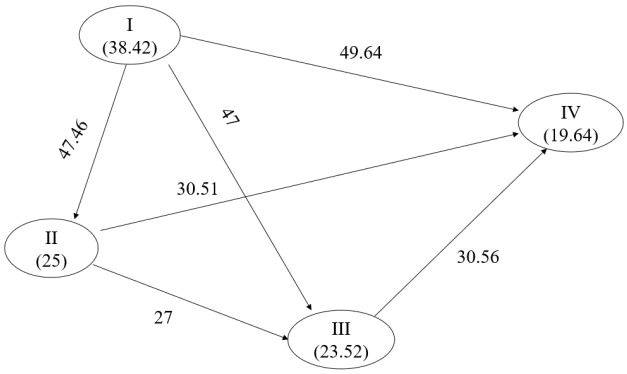

Fig. 2 : Intra and inter-cluster distances in four clusters based on Tocher's method in 53 cotton genotypes.

strategically. Notably, crosses between genotypes from Cluster I (Suvin and CCB 29) and Cluster IV (L 2384, L 2275, L 2385, and L 2383) are expected to produce desirable transgressive segregants and could be promising for future breeding efforts. The intra- and inter-cluster D^2 values among the four clusters are presented in Table 3 and illustrated in Fig. 2.

Cluster means for yield and fibre quality traits in 53 genotypes were presented in Table 4. Cluster means reflect the average performance of all genotypes within a specific cluster. These estimates were useful for identifying potential donor genotypes that could be used to enhance particular traits.

The cluster mean analysis revealed considerable variation across the studied traits. Among all clusters, Cluster III recorded the highest and most desirable mean values for key yield-related traits, including number of sympodia per plant, number of bolls per plant, seed index, lint index, ginning out turn and seed cotton yield per plant. In contrast, Cluster I exhibited the highest mean values for important fibre quality traits such as upper half mean length and uniformity index. Based on these findings, the selection of genotypes from Clusters I and III could be recommended for future crop improvement programmes aimed at developing high-yielding cotton genotypes with superior fibre quality.

A perusal of the results on per cent contribution of 53 genotypes for 14 characters towards genetic divergence were presented in Fig. 3 and Table 5. The results revealed that maximum contribution towards genetic divergence was observed by seed index (10.89%), followed by upper half mean length (10.11%), micronaire (10.10%), seed cotton yield per plant (9.01%), lint index (8.62%), tenacity (8.55%), days to fifty per cent flowering (7.94%), boll weight (7.79%), uniformity index (7.77%), plant height (6.39%), number of sympodia per plant (5.64%), number of bolls per plant (3.82%) and number of monopodia per plant (2.09%). The lowest contribution

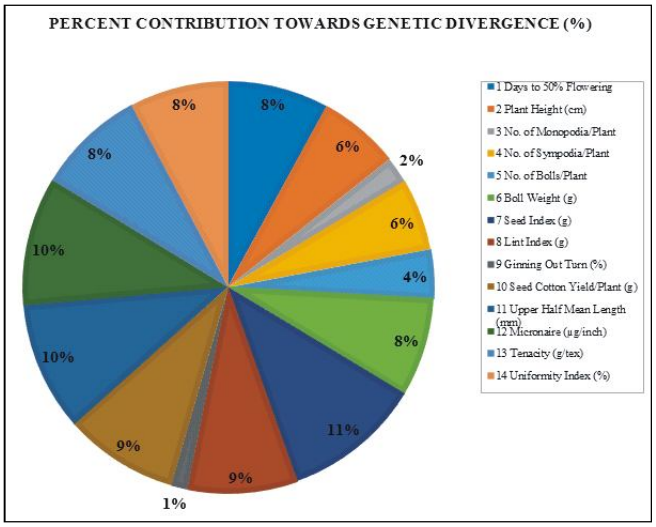

Fig. 3 : Relative contribution of 14 traits towards total genetic divergence in 53 cotton genotypes.

Table 4 : Cluster means for seed cotton yield attributing traits and fibre quality traits by Tocher's method in 53 cotton genotypes.

Characters	Clusters No.			
	I	II	III	IV
Days to fifty per cent flowering	78.11	**59.99**	60.22	61.70
Plant height (cm)	127.22	**157.73**	142.23	123.95
Number of monopodia per plant	2.09	**1.11**	1.29	1.30
Number of sympodia per plant	18.68	18.47	**20.89**	20.36
Number of bolls per plant	32.92	42.67	**55.54**	40.85
Boll weight (g)	2.51	4.66	4.70	**4.95**
Seed index (g)	8.11	9.94	**11.30**	10.76
Lint index (g)	4.32	5.14	**5.59**	4.16
Ginning out turn (%)	33.08	35.03	**35.43**	34.83
Seed cotton yield per plant (g)	63.59	102.96	**135.30**	123.07
Upper half mean length (mm)	**32.41**	28.28	28.81	30.61
Micronaire (µg/inch)	3.25	**4.65**	4.60	4.38
Tenacity (g/tex)	29.23	28.58	28.46	**29.98**
Uniformity Index (%)	**85.67**	81.87	82.42	84.75

Table 5 : Per cent contribution of different characters towards genetic divergence in 53 cotton genotypes.

S. no.	Traits	Contribution (%)
1	Days to fifty per cent flowering	7.94
2	Plant height (cm)	6.39
3	Number of monopodia per plant	2.09
4	Number of sympodia per plant	5.64
5	Number of bolls per plant	3.82
6	Boll weight (g)	7.79
7	Seed index (g)	10.89
8	Lint index (g)	8.62
9	Ginning out turn (%)	1.29
10	Seed cotton yield per plant (g)	9.01
11	Upper half mean length (mm)	10.11
12	Micronaire (µg/inch)	10.10
13	Tenacity (g/tex)	8.55
14	Uniformity Index (%)	7.77

was observed by ginning out turn (1.29%) indicating less towards divergence inferring more homogeneity in the material evaluated. Similar studies were reported by Sagar *et al.* (2023), Satish (2021) and Naik *et al.* (2016).

Principal Component Analysis (PCA)

Mean data of all the 14 studied traits were analyzed by principal component analysis in R Studio to investigate the genetic divergence among 53 cotton genotypes. The results suggested the importance of the first four PCs with eigen values greater than or equal to one in discriminating the germplasm collection. The first two PC' s were considered to represent the biplot as it was capable to explain 49.73 % of the total variation. Hence, the other two PC's (PC_3 and PC_4) were ignored for biplot analysis. The results revealed that four canonical roots accounted for 70.56% of total divergence. The PC_1 contributed maximum towards divergence (26.47%) with eigen value of 3.70. The second, third and fourth canonical vectors contributed 23.25%, 11.54% and 9.28% respectively to total divergence with eigen values of 3.25, 1.61 and 1.30, respectively (Table 6).

In the first principal component (PC_1), the trait number of bolls per plant made the highest contribution to total genetic divergence, accounting for 14.82% of the variability. This was followed by days to 50% flowering (12.19%), seed cotton yield per plant (11.63%), upper half mean length (10.15%), uniformity index (8.48%), lint index (8.29%), and number of monopodia per plant (7.97%). In the second principal component (PC_2),

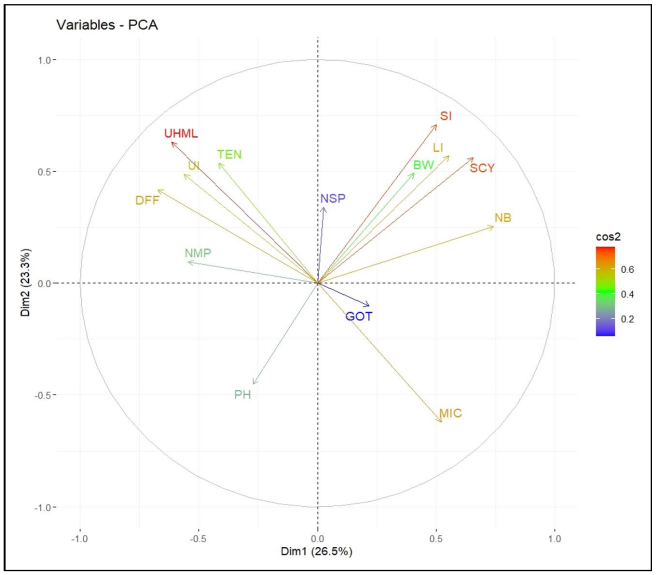

Fig. 4 : PCA biplot representing distribution of 14 variables in 53 cotton genotypes.

seed index emerged as the most influential trait, contributing 15.36% to the total divergence. This was followed by UHML (12.19%), micronaire (11.78%), lint index (9.91%), seed cotton yield per plant (9.66%), tenacity (8.80%), boll weight (7.38%), and uniformity index (7.22%) (Table 6).

The PCA biplot analysis of 53 cotton genotypes in 14 traits identified that the yield contributing variables *i.e.*, number of sympodia per plant number of bolls per plant, boll weight, lint index and seed cotton yield per plant were significantly loaded in PC_1 and contributed more towards variability. The PC_2 contributed for fibre quality traits like UHML, tenacity and micronaire (Fig

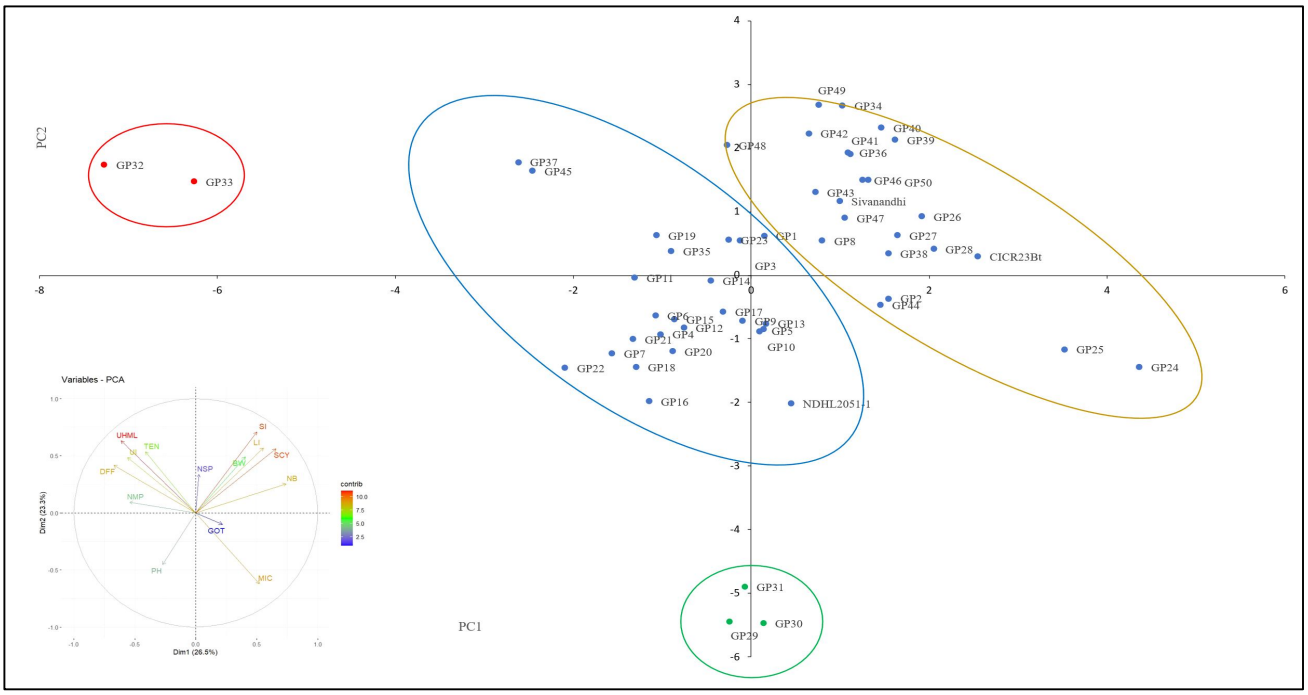

Fig. 5 : PCA biplot representing distribution of 53 cotton genotypes.

Table 6 : Canonical vectors for 14 characters in 53 cotton genotypes.

Parameter	**PC_1**	**PC_2**	**PC_3**	**PC_4**
Eigen Value (Root)	3.70	3.25	1.61	1.30
Variance (%)	26.47	23.25	11.54	9.28
Cumulative Variance (%)	26.47	49.73	61.27	70.56
Characters				
Days to fifty per cent flowering	12.19	5.32	3.12	8.07
Plant height (cm)	1.99	6.30	9.91	28.75
Number of monopodia per plant	7.97	0.27	17.15	5.17
Number of sympodia per plant	0.02	3.51	0.01	49.41
Number of bolls per plant	14.82	1.98	10.37	1.16
Boll weight (g)	4.43	7.38	13.44	1.22
Seed index (g)	6.77	15.36	2.86	0.29
Lint index (g)	8.29	9.91	1.78	0.13
Ginning out turn (%)	1.29	0.32	28.00	3.35
Seed cotton yield per plant (g)	11.63	9.66	0.42	0.05
Upper half mean length (mm)	10.15	12.19	2.29	0.01
Micronaire (µg/inch)	7.33	11.78	2.02	0.91
Tenacity (g/tex)	4.63	8.80	7.79	0.02
Uniformity Index (%)	8.48	7.22	0.85	1.46

4).

The PCA biplot analysis of 53 cotton genotypes revealed that GP 49 (L2387), GP 34 (L 2396), GP 24 (L 2381), GP 25 (L 2267), GP 29 (Yaganti), GP 30 (Srinandi), GP 31 (NDLA 3116-4), GP 32 (Suvin), GP 33 (CCB 29), GP 37 (L 2275) and GP 45 (L 2385) were identified as the most divergent genotypes as they were located far away from the origin. Hence, these genotypes could be effectively used in hybridization programmes for crop improvement (Fig. 5).

Conclusion

Multivariate analysis demonstrated substantial genetic diversity among the 50 cotton genotypes, including three checks. The genotypes were grouped into four clusters using D^2 analysis. Cluster II contained the highest number of genotypes (29), followed by cluster III (18), cluster IV (4) and cluster I (2). Among all the clusters, cluster III recorded the highest desired mean values for most of the yield traits *viz*., plant height, number of sympodia per plant, number of bolls per plant, seed index, lint index and seed cotton yield per plant. Selection of genotypes from clusters III could be therefore suggested for utilization in future crop improvement programs aimed at the development of high yielding cotton genotypes. The seed index contributed the most to genetic divergence (10.89%), followed by UHML (10.11%), micronaire (10.10%) and seed cotton yield per plant (9.01%). Cluster analysis revealed that crossing between genotypes of clusters I (Suvin and CCB 29) and cluster IV (L 2384, L 2275, L 2385 and L 2383) were divergent and should be tested for their combining ability through Line x Tester mating design or diallel analysis and then could be utilized in future crop improvement programs for the exploitation of heterosis.

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All authors have read and agreed to the manuscript.

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Conflicts of interest

The authors declare no competitive or financial conflicts of interest.

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