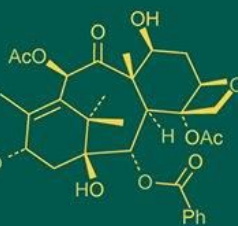
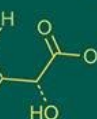


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(4): 149-152
www.biochemjournal.com
Received: 13-01-2026
Accepted: 16-02-2026

Jyoti Sankhala
Ph.D. Research Scholar,
Department of Genetics &
Plant Breeding, RCA,
Maharana Pratap University
of Agriculture & Technology,
Udaipur, Rajasthan, India

Sapovadiya MH
Associate Research Scientist,
Department of Genetics &
Plant Breeding, COA,
Junagadh Agricultural
University, Junagadh,
Gujarat, India

Tilakraj S Bhuva
M.Sc. (Agri.) Research Scholar,
Department of Entomology,
COA, Junagadh Agricultural
University, Junagadh,
Gujarat, India

Corresponding Author:
Jyoti Sankhala
Ph.D. Research Scholar,
Department of Genetics &
Plant Breeding, RCA,
Maharana Pratap University
of Agriculture & Technology,
Udaipur, Rajasthan, India

Evaluation of genetic diversity in cotton germplasm (*Gossypium hirsutum* L.)

Jyoti Sankhala, Sapovadiya MH and Tilakraj S Bhuva

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i4Sb.8082>

Abstract

Genetic divergence among 36 genotypes of cotton (*Gossypium hirsutum* L.) was studied using Mahalanobis D^2 statistics. The genotypes were grouped into six clusters, indicating considerable genetic diversity. Maximum divergence was observed between cluster V and VI, followed by cluster II and IV, and cluster III and VI. The characters contributing most to divergence were days to boll opening, seed index, oil content, fiber strength, and number of monopodia. Cluster VI showed desirable performance for earliness and yield-related traits, while cluster V and IV exhibited superiority for seed index, boll weight, and fiber quality traits. Therefore, the selection of parents from divergent clusters based on these key traits could be effective for heterosis breeding in cotton.

Keywords: Genetic divergence, D^2 statistic, clusters, *Gossypium hirsutum* L.

1. Introduction

Cotton (*Gossypium hirsutum* L.) is a crop of global importance as a major source of natural fiber and is often referred to as “white gold” or the “king of fibers” due to its significant contribution to the textile industry. In India, cotton plays a vital role in the agricultural economy and contributes substantially to foreign exchange earnings through the export of lint and value-added products. Despite achieving self-sufficiency in production, the area under cotton cultivation is declining, and productivity remains low compared to other cotton-growing countries.

Therefore, there is a need to develop high-yielding cultivars with superior fiber quality traits to enhance productivity. Genetic diversity is a prerequisite for effective selection and successful breeding programs. The identification of diverse genotypes facilitates the selection of suitable parents for hybridization and recombination breeding.

Among various methods, Mahalanobis D^2 statistics is a reliable and widely used technique for assessing genetic divergence based on multiple traits simultaneously. Hence, the present study was undertaken to evaluate genetic divergence among 36 genotypes of American cotton using Mahalanobis D^2 statistics, with the aim of identifying suitable parents for hybrid breeding programs.

2. Materials and Methods

Thirty-six genotypes of cotton (*Gossypium hirsutum* L.) were evaluated during *kharif* 2021 at Cotton Research Station, Junagadh Agricultural University, Junagadh. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in a single-row plot of 6.3 m length, with row spacing of 120 cm and plant spacing of 45 cm.

Observations were recorded on five randomly selected plants from each genotype in each replication for fifteen characters, namely: days to 50% flowering, days to boll opening, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), ginning percentage (%), seed index (g), lint index (g), oil content (%), 2.5% span length (mm), fiber strength (g/tex), and fiber fineness (micronaire value). T), RARS, Lam, Guntur, Andhra Pradesh. The data were statistically analyzed to study diversity by Mahalanobis D^2 statistic as per Rao (1952) [2] and principal component analysis (PCA) as described by Jackson (1991).

Results and Discussion

Thirty-six genotypes of cotton were grouped into six clusters based on relative magnitude of D2 values following Tocher's method (Rao, 1952)^[2]. (Table 1). The dendrogram showing the contribution of the 36 genotypes among 6 clusters by using complete linkage and Euclidean distance is shown in Fig 1.

In the present investigation the cluster I having largest number of genotypes (28) followed by cluster II (3) and cluster V (2). On the other hand, cluster III, IV and VI are solitary clusters with single genotypes in each cluster.

Intra and inter cluster distance (D) between all possible pairs of three clusters were computed with the help of method given by Singh and Chaudhary (1977)^[3]. Intra and inter cluster average (D) values are summarized in Table 2.

The intra cluster distance ranged from 0.00 to 12.81. Cluster V exhibited maximum intra cluster distance (D = 12.81) followed by the cluster II (D = 11.24), cluster I (D = 10.86). Three clusters, cluster III, IV and VI are found solitary.

The maximum inter cluster distance was observed between cluster V and cluster VI (D = 29.19) followed by cluster II and cluster IV (D = 26.70) and cluster III and cluster VI (D = 24.63). Whereas, minimum inter cluster distance was observed between I and III (D = 14.36).

3.1 Cluster means for various characters

Cluster mean for the 15 characters are presented in Table 2. The results clearly revealed appreciable differences among cluster means for most of the traits.

Wide range of mean values among the clusters was recorded for different traits. Desirable rating in respect to earliness i.e., days to flowering (59.00) was observed in cluster VI, along with high mean value for seed cotton yield per plant (162.07 g), number of bolls per plant (67.60 g), number of sympodia per plant (24.00), oil content (18.16%) and number of monopodia (4.47).

Cluster V exhibited high mean value for the characters viz., seed index (8.88 g), lint index (5.18 g) and boll weight (5.15 g).

Cluster IV exhibited desirable value for days to boll opening (97.00), plant height (119.53 cm), fiber strength (33.47 g/tex) and 2.5% span length (31.40 mm), while Cluster III exhibited a high mean value for ginning percentage (38.30%) and fiber fineness (5.13 mv).

The contribution of each character to genetic divergence was estimated by ranking the D² components in descending order, with rank I assigned to the highest value. The percentage contribution of different characters is presented in Table 4 and Fig. 2. Among the traits, days to boll opening (19.84%), seed index (14.13%), oil content (13.97%), fibre strength (8.89%) and number of monopodia per plant (8.41%) contributed the most to total genetic divergence. Other characters such as fibre fineness (7.14%), number of sympodia per plant and number of bolls per plant (6.67%), boll weight (3.97%), 2.5% span length (3.81%) and days to flowering (3.33%) showed moderate contribution, while seed cotton yield per plant (1.75%), ginning percentage (0.79%) and plant height (0.63%) contributed negligibly. Lint index showed no contribution.

Table 1: Grouping of 36 genotypes of cotton in various clusters on the basis of D2 statistic

Cluster	No. of genotypes	Name of genotypes
I	28	G. P. Hir.-146, G. P. Hir.- 158, G. P. Hir.- 164, G. P. Hir.-144, G. P. Hir.-172, G. P. Hir.-150, G. P. Hir.-149, G. P. Hir.-145, G. P. Hir.-148, G. P. Hir.-165, G. P. Hir.-166, G. P. Hir.-152, G. P. Hir.-163, G. P. Hir.-143, G. P. Hir.-147, G. P. Hir.-154, G. P. Hir.-151, G. P. Hir.-141, G. P. Hir.-137, G. P. Hir.-140, G. P. Hir.-160, G. P. Hir.-139, G. P. Hir.-162, G. P. Hir.-171, G. P. Hir.-169, G. P. Hir.- 161, G. P. Hir.-142, G. P. Hir.-159
II	3	G. P. Hir. -157, G. P. Hir. -170, G. P. Hir. -167
III	1	G. P. Hir. -168
IV	1	G. P. Hir. -153
V	2	G. P. Hir. -155, G. P. Hir. -156
VI	1	G.P. Hir. -138

Table 2: Average intra and inter cluster distances between 6 clusters in cotton

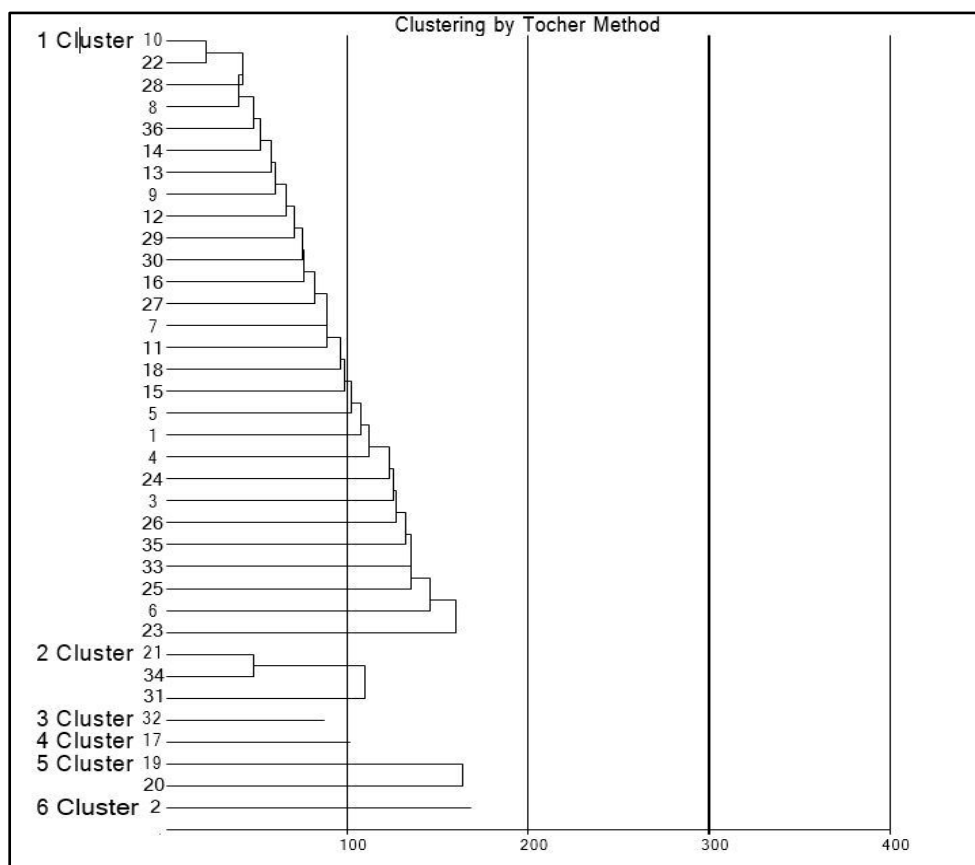
Cluster	I	II	III	IV	V	VI
I	10.86	19.03	14.36	14.55	21.38	16.27
II		11.24	21.18	26.70	18.44	20.17
III			0.00	16.44	18.87	24.63
IV				0.00	24.58	22.88
V					12.81	29.19
VI						0.00

Table 3: Cluster mean values of fifteen characters in 6 clusters in 36 genotypes of cotton

Sr. No	Character	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
1	Days to flowering	61.70	72.44	65.00	56.00	73.50	59.00
2	Days to boll opening	103.87	125.78	107.67	97.00	129.50	102.33
3	Plant height (cm)	118.81	108.67	96.67	132.93	119.53	113.13
4	No. of monopodia per plant	3.20	3.22	1.33	3.27	3.63	4.47
5	No. of sympodia per plant	19.16	21.42	14.07	15.80	15.23	24.00
6	No. of bolls per plant	32.01	41.56	18.30	18.93	20.13	67.60
7	Boll weight (g)	3.36	2.77	3.43	4.30	5.15	2.47
8	Seed cotton yield per plant (g)	102.27	111.24	55.90	76.63	98.82	162.07
9	Seed index (g)	8.76	8.78	7.17	8.50	8.88	8.00
10	Ginning percentage (%)	35.21	34.17	38.30	33.33	37.12	34.27
11	Lint index (g)	4.78	4.54	4.47	4.27	5.18	4.17
12	Oil content (%)	18.25	18.49	17.67	18.30	18.28	18.60
13	2.5% Span length (mm),	27.63	27.51	29.33	31.40	28.35	25.50
14	Fibre strength (g/tex)	29.35	30.36	31.80	33.47	29.05	30.20
15	Fibre fineness (mv)	4.62	4.58	5.13	3.53	4.85	4.20

Table 4: Contributions of various traits towards genetic divergence in cotton

Sr. No	Characters	Time ranked first	Contribution (%)
1	Days to flowering	21	3.33
2	Days to boll opening	125	19.84
3	Plant height (cm)	4	0.63
4	No. of monopodia per plant	53	8.41
5	No. of sympodia per plant	42	6.67
6	No. of bolls per plant	42	6.67
7	Boll weight (g)	25	3.97
8	Seed cotton yield per plant (g)	11	1.75
9	Ginning percentage (%)	5	0.79
10	Seed index (g)	89	14.13
11	Lint index (g)	0	0.01
12	Oil content (%)	88	13.97
13	2.5% Span length (mm)	24	3.81
14	Fibre strength (g/tex)	56	8.89
15	Fibre fineness (mv)	45	7.14

**Fig 1:** Dendrogram showing the distribution of 36 cotton genotypes into 6 cluster

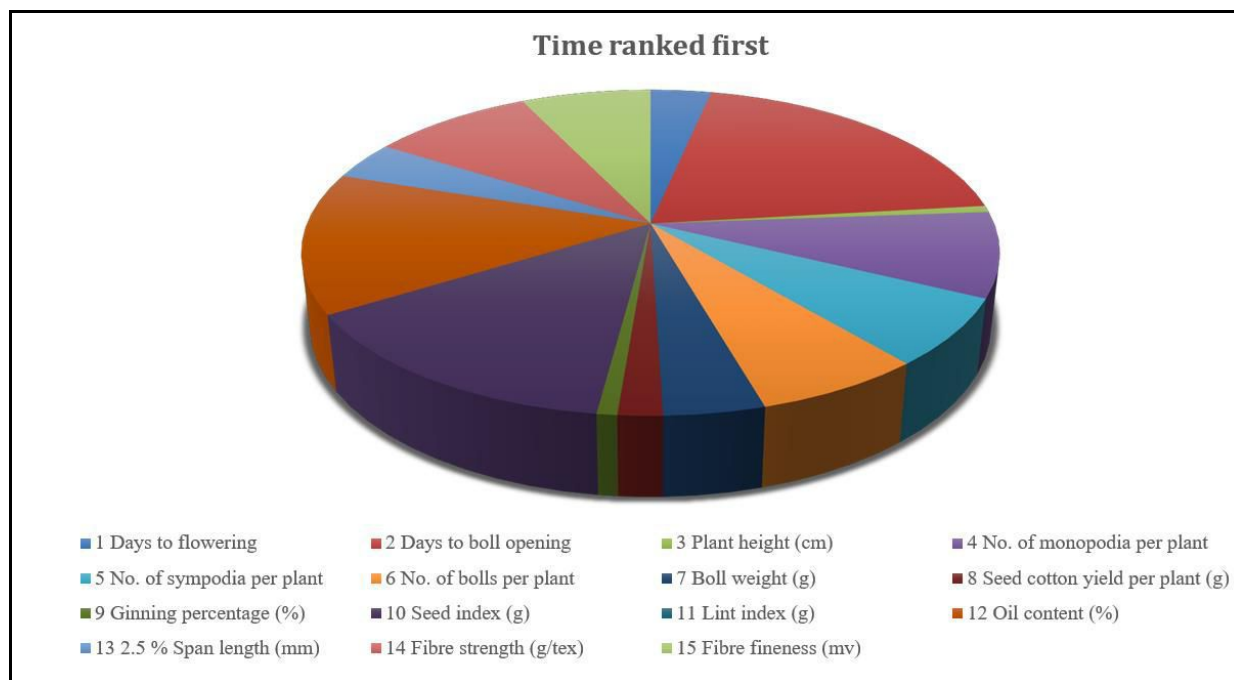


Fig 2: Relative contribution of different characters towards diversity

References

1. Mahalanobis CR. On the generalized distance in statistics. Proc Natl Inst Sci India. 1936;11(1):49-55.
2. Rao CR. Advanced statistical methods in biometrical research. New York: John Wiley and Sons; 1952.
3. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetics analysis. New Delhi: Kalyani Publishers; 1985.
4. Anderberg MR. Cluster analysis for applications. New York: Academic Press; 1973.
5. Arunachalam V. Genetic distance in plant breeding. Indian J Genet Plant Breed. 1981;41:226-236.
6. Allard RW. Principles of plant breeding. New York: John Wiley and Sons; 1960.