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Genetic diversity analysis in cotton using morphological traits (*Gossypium hirsutum* L.)

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Abstract

A study “Genetic diversity analysis in cotton using morphological traits (*G. hirsutum* L.)” was undertaken to estimate the degree of divergence among the 50 genotypes of upland cotton using multivariate Mahalanobis D^2 statistics on the field of SDMVM’s college of agriculture, Paithan road, Aurangabad (MH). The analysis of variance revealed significant differences among 50 genotypes for all fourteen characters. This is also confirmed by Wilk’s criterion. The canonical analysis revealed that about 85.96 per cent of the total variation was accounted by the first six canonical roots. In vector I, number of monopodia per plant was important sources of variation. Whereas 2.5 per cent span length was important sources of variation in vector II. In vector III, number of bolls per plant, in vector IV seed index, in vector V, fibre strength and in vector VI, number of bolls per plant played important role in variation. Plant height, seed index and number of bolls per plant were contributing towards genetic divergence. By using Tocher’s method, all 50 genotypes were grouped into seven clusters. Cluster I had highest number of genotypes (19) followed by cluster III (14), cluster IV (8), cluster II (6) and cluster V, VI and VII represented by single genotypes. The maximum genetic distance was recorded between cluster V and cluster VII ($D=9.66$). By considering the mean statistical distance as a guideline to select the divergent genotypes, 18 cluster combinations were identified. The divergent parents selected from these combinations may yield better segregants in hybridization programme. However, when divergent parents are crossed, heterosis is not always found to occur. Therefore, while selecting the divergent parents from a particular cluster, the information on mean and standard deviation of the genetic variance among the divergent parents should be taken into consideration as practically suggested by Arunachalam and Bandyopadhyay (1984). Hence, on the basis of mean and standard deviation of parental divergence, 41 cross combinations out of 192 parental combinations have been finally suggested which are expected to yield desirable genetic gain in breeding programmes.

Keywords: Indian mustard, path coefficient analysis

Introduction

Cotton is one of the most important sources of natural fibre. Its fibre is universally preferred for clothing. In India, it is rightly called as “white gold” as it occupies vital position in Indian agriculture and economy. It is country’s leading cash crop. Cotton forms backbone of textile industry. It is one of the important source of providing employment to millions of people. Simpson (1954) [8] classified cotton as predominantly self-pollinated and often cross pollinated crop. The word cotton is derived from Arabic word KUTON or QUTON (Brown). Cotton belongs to genus *Gossypium* and family Malvaceae.

Cotton comprises of approximately 45 diploid and five allotetraploid species that occur naturally through the semiarid and arid region of Africa, Australia Central and South Africa, the Indian subcontinent, Arabia, Galapagos, and Hawaii (Fryxell 1992) [5]. During the course of evolution and domestication man has selected four species for cultivation whose seed fibers were long and spinnable. *G. arboreum* L. and *G. herbaceum* both are diploid ($2n=26$) from the four cultivated species, and popularly called as Asiatic cotton whereas, *G. hirsutum* L. and *G. barbadense* are allotetraploid ($2n=52$) and known as American upland and Egyptian cotton, respectively.

During 2022-23, area under cotton was 121.91 lakh ha, with production of 345 lacks bales and productivity 481.23 lint Kg ha⁻¹ in India. In Maharashtra, area and production were 40.95 lakh ha and 69 lakh bales respectively whereas productivity 280 lint kg/ha. In Vidharbha, area was 15.6 lakh ha with production of 35.5 lakh bales and productivity 228 lint Kg/ ha.

Genetical improvement in the crop plant depends on variability present in that crop and thereafter the selection of parental lines for breeding programme. There is presence of enough variability in cotton germplasm.

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Which can be used for development of new genotype with higher yield and better quality (Grewal *et al.* 1994) [6]. Genetic diversity plays an important role in adaptability of a species. A species that has a large degree of genetic diversity among its population will have more variation. The genetic diversity is a crucial factor in determining the success of hybridization programme. The importance of genetic diversity in crop improvement has long been appreciated by breeder but the basic difficulty was of recognizing and estimating such diversity. The basis of plant breeding is produced due to inherent genetic difference in plant species and is the major interest of plant breeder is known as genetic diversity. The more diverse the parents within overall limits of fitness, the greater are the chances of heterotic F₁'s and broad spectrum of variability in segregating generation. (Arunachalam 1981; Falconer 1989) [1, 4]. Therefore, the first step to initiate a hybridization programme is to assess genetic diversity and thereby identify genetically diverse parents.

Materials and Method

The study on genetic diversity analysis in cotton using morphological traits (*G. hirsutum* L.) was conducted during *Kharif* 2022-23 on the field of SDMVM's college of agriculture, Paithan road, Aurangabad (MH) using 50 genotypes with three replications. The experimental material of the present investigation comprised of 50 genotypes of cotton (*G. hirsutum* L.) obtained from Cotton Research Unit, Vasantrao Naik Marathwada Krishi Vidhyapeeth, Parabhani (MH). The genotypes of material are given in Table 1.

Table 1: List of genotypes of cotton

Sr. No	Genotypes	Sr. No	Genotypes	Sr. No	Genotypes
1	H×R-1	19	H×R-19	37	H×R-37
2	H×R-2	20	H×R-20	38	H×R-38
3	H×R-3	21	H×R-21	39	H×R-39
4	H×R-4	22	H×R-22	40	H×R-40
5	H×R-5	23	H×R-23	41	H×R-41
6	H×R-6	24	H×R-24	42	H×R-42
7	H×R-7	25	H×R-25	43	H×R-43
8	H×R-8	26	H×R-26	44	H×R-44
9	H×R-9	27	H×R-27	45	H×R-45
10	H×R-10	28	H×R-28	46	H×R-46
11	H×R-11	29	H×R-29	47	H×R-47
12	H×R-12	30	H×R-30	48	H×R-48
13	H×R-13	31	H×R-31	49	H×R-49
14	H×R-14	32	H×R-32	50	H×R-50
15	H×R-15	33	H×R-33		
16	H×R-16	34	H×R-34		
17	H×R-17	35	H×R-35		
18	H×R-18	36	H×R-36		

Data were recorded on five randomly selected competitive plants from each treatment per replication and observation recorded for the following characters except the observations for days to 50% boll bursting and days to 50% flowering.

A) On plant Basis

a) Plant height (cm)

At the time of maturity the main stem height (i.e. plant height) was recorded in centimeters from the cotyledonary node up to the growing point and the averages were worked out.

b) Number of monopodia per plant

Total numbers of vegetative branches were counted on main stem of each selected plant at maturity and average numbers of monopodia per plant were calculated

c) Number of sympodia per plant

At the time of maturity total number of boll bearing branches were recorded and average number of sympodia per plant were worked out.

d) Number of bolls per plant

Number of bolls per plant from which seed cotton was chosen during each picking was recorded and from this average number of bolls per plant was calculated.

e) Boll weight (g)

At the time of second picking seed cotton from five well opened bolls, from each genotype was collected and weighted. Average value was calculated and recorded.

f) Seed cotton yield per plant (g)

Seed cotton weight acquired from five randomly selected plants was taken separately with calculated mean seed cotton yield per plant.

B) On plot basis

g) Days to 50 per cent flowering

Number of days required from sowing to the date on which fifty per cent of the plants were flowered was recorded and average number of days to 50 per cent flowering was calculated.

h) Days to 50 per cent boll bursting

Number of days required from sowing to the date on which fifty per cent of the plants which showing open bolls were noted with average number of days to 50 per cent boll bursting was calculated.

C) On post-harvest basis

i) Ginning percentage (%)

The ratio of lint weight to that of seed cotton is stated as ginning percentage. The seed cotton was according to ginned treatment and ginning percentage was calculated by using the following formula

$$\text{Ginning percentage} = \frac{\text{Weight of lint (g)}}{\text{Weight of seed cotton (g)}} \times 100$$

j) Seed index (g)

The seed index was recorded by weighing 100 seeds in gram.

D) Fibre quality parameters

The lint samples per genotype per replication were analyzed for fibre quality at Ginning Training Centre, CIRCOT, Nagpur.

k) 2.5 per cent span length (mm)

2.5 per cent span length is the distance from the test specimen clamp line up to which 2.5 per cent fibres extended in the test beard of equipment.

l) Fiber strength (g/tex)

Force required for the breaking of fibre of unit linear density.

It was expressed in grams per tex.

m) Fibre fineness ($\mu\text{g}/\text{inch}$)

The average weight per unit length of fibre is known as fibre fitness. Linear density of fibre is expressed in micrograms per inch and due to this fiber fitness also calculated.

n) Uniformity ratio

The ratio of 50 per cent span length to 2.5 per cent span length is known as uniformity ratio.

Grouping of genotypes into different clusters

The grouping of genotypes was done by Tocher's method as described by Rao (1952) [7]. The criterion used in clustering was that any two varieties belonging to the same cluster should have at least on an average smaller D^2 values than belonging to different clusters.

Canonical analysis

Canonical root method suggested by Rao (1952) [7] was followed. The matrix of variance and covariance (matrix A) was obtained by calculating the difference between group of sum of squares and sum of products from transformed variables (Y_1, Y_2, \dots, Y_{14}). Determination of the canonical variants was done by iteration starting with trial vector (1,-1) each row of the matrix was multiplied and a derived vector which was better approximation was obtained. Same procedure was repeated until stable values of the vector were obtained. The highest value used in the last stage of division to obtain the final vector should be λ_1 , the first canonical root. The vector was standardized by dividing each element, by the square root of the sum of squares of all elements. From the ($i^{\text{th}}, j^{\text{th}}$) element of the matrix A, the product, $\lambda_1 X_i^{\text{th}}$ element, X_j^{th} element of the first vector was subtracted to obtain the reduced matrix (matrix B). The procedure followed in the case of matrix A was repeated to obtain second, third, fourth and fifth canonical roots.

Average intra and inter-cluster distance and cluster means

The average intra-cluster distance was obtained by using following formula.

$$\text{Average intra-cluster distance } D^2 = \frac{\sum_{i=1}^n D_i^2}{n}$$

Where,

$\sum D_i^2$ = the sum of square of distance between all possible combinations (n) of genotypes involved in a cluster.

The average inter-cluster distance was calculated using all possible D^2 values between genotypes included in any two clusters. Cluster means were calculated for individual character on the basis of mean performance of the genotype included in that cluster.

Selection of parents for hybridization programme

Selection of parents for hybridization from different clusters was done on the basis of mean statistical distance suggested by Bhatt (1970) [3].

$$\bar{D} = \frac{\sum d_i}{n(n+1)/2}$$

Where,

$$\begin{aligned} \bar{D} &= \text{Mean statistical distance} \\ \sum d_i &= \text{Sum of all } D^2 \text{ values between all inter-clusters} \\ n &= \text{Number of clusters} \end{aligned}$$

However, the divergent parents selected from these cluster combinations are not always bound to give high heterotic effect. Therefore, on the basis of mean and standard deviation of parental divergence, the selection of divergent genotypes from a particular cluster was carried out as suggested by Arunachalam and Bandopadhyay (1984) [2].

Results and Discussion

Mean performance of genotypes

The mean performance of genotypes for fourteen quantitative characters under study is presented in Table 2.

1. Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 57 to 66 days with mean value of 62.19 days. Among the genotypes tested seventeen genotypes took less than 60 days for 50 per cent flowering than general mean. The genotypes namely HXR-13 (57days) and HXR-31 (58 days) show superiority over general mean. The genotype HXR-10 (66 days) recorded maximum number of days to 50 percent flowering.

2. Plant height (cm)

Plant height ranged from 60 cm to 111 cm, out of 50 genotypes twenty four genotypes showed plant height more than 77.70 cm. Among these HXR-16 (60cm) was found to be dwarfest and HXR-5 (111cm) observed tallest.

3. Number of Monopodia per plant

In case of number of monopodia per plant HXR-20 (1.2) had least number of monopodia per plant and genotype HXR-6 (3.2) had more number of monopodia per plant and the ranged for these characters was 1.2 to 3.2.

4. Number of Sympodia per plant

Amongst fifty genotypes eighty genotypes showed significantly more number of sympodia per plant than general mean (12.93). The genotype HXR-49 (12.93) had more number of sympodia followed by genotype H X R-34 (12.87), H X R-33 (12.73) and genotype H X R-41 (8) showed least number of sympodia per plant. The ranged for this character was 8 to 12.93 sympodia per plant.

5. Number of bolls per plant

Mean value ranged for the number of bolls per plant was from 12.7 to 23.6. The highest number of bolls per plant were recorded by genotypes HXR-18 (23.6) followed by HXR-20 (23), HXR-21 (22.5). The lowest number of bolls per plant were produced by HXR-25 (12.7) followed by HXR-10 (13.8) and HXR-6 (13.8). Amongst 50 genotypes forty one genotypes showed maximum number of bolls per plant than general mean (14.22).

6. Days to 50 per cent boll bursting

The range for the days to 50 % boll bursting was from 104 to 117. Among fifty genotypes thirty three genotypes showed maximum number of days to 50 % boll bursting than general mean (113). The earliest genotype was HXR-17(104days) and HXR-22 (104.67days). The genotype HXR-39 (117.67 days)

was late followed by HXR-42 (117 days).

7. Boll weight (g)

The boll weight ranged from 2.6 to 3.9. Among fifty genotypes twenty two genotypes showed high boll weight

than general mean (3.43g). The highest boll weight was observed in genotype HXR-13 (3.97g) followed by HXR-12(3.83g) and the lowest boll weight was recorded in HXR-41 (2.63 g).

Table 2: Mean performance of 50 genotypes of cotton (*G.hirsutum* L.)

Sr. No.	Genotypes	Days to 50% flowering	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Days to 50% boll bursting	Boll weight (g)	Ginning percentage (%)	Seed index (g)	2.5% Span length (mm)	Uniformity ratio	Fineness (µg/inch)	Strength (g/tex)	Seed cotton yield per plant (g)
1	H X R-1	65.0	61.0	2.33	10.67	23.0	114.67	3.57	32.97	6.37	27.23	54.33	3.37	20.77	69.67
2	H X R-2	64.0	73.7	2.87	10.27	19.9	112.67	3.17	36.10	6.50	26.70	54.00	3.40	20.43	60.67
3	H X R-3	62.0	93.7	2.93	9.93	20.8	112.67	3.27	38.07	7.17	27.10	54.00	3.33	20.40	74.00
4	H X R-4	63.7	73.0	2.87	9.87	18.9	116.00	3.43	31.33	7.67	26.47	52.00	3.40	19.50	69.67
5	H X R-5	61.7	111.3	2.07	12.33	22.4	114.67	3.67	33.77	7.00	27.63	54.00	3.80	21.17	70.33
6	H X R-6	62.7	63.3	3.27	10.87	13.8	114.00	3.33	36.30	6.17	28.43	51.67	3.60	20.43	46.00
7	H X R-7	62.7	105.3	2.10	12.40	21.6	114.00	3.60	39.60	7.33	27.33	54.67	3.63	20.33	78.00
8	H X R-8	60.7	73.0	1.87	11.40	15.6	112.67	3.57	35.50	6.67	26.93	54.00	3.20	20.73	55.67
9	H X R-9	61.0	65.0	2.60	11.13	16.0	113.67	3.50	38.00	7.67	27.63	53.00	3.63	19.03	56.00
10	H X R-10	66.3	66.7	2.73	10.60	13.8	114.33	3.47	41.27	7.17	26.27	53.00	3.20	20.30	47.67
11	H X R-11	60.3	88.3	3.07	10.07	19.8	113.67	3.53	29.60	7.67	26.80	52.00	3.53	20.97	69.33
12	H X R-12	63.0	99.0	2.40	9.27	20.4	112.33	3.83	33.23	7.67	26.97	55.00	3.67	20.93	75.33
13	H X R-13	57.0	104.0	2.40	10.80	21.7	116.33	3.97	38.30	7.67	25.50	52.33	3.73	18.13	69.67
14	H X R-14	59.7	110.0	2.13	11.47	18.8	114.33	3.67	34.87	7.17	25.60	50.67	3.60	18.30	68.67
15	H X R-15	64.7	63.3	2.87	9.40	19.6	116.67	3.53	35.20	7.17	25.60	50.67	3.53	20.00	69.33
16	H X R-16	63.7	60.7	2.07	12.67	16.2	113.33	3.33	39.07	8.00	26.43	51.33	3.33	19.70	54.67
17	H X R-17	65.7	91.3	1.33	11.60	21.2	104.00	3.73	35.97	6.67	25.13	50.33	3.37	18.20	78.67
18	H X R-18	65.3	66.0	1.33	11.40	23.6	114.67	3.53	35.13	7.83	26.07	51.33	3.70	19.20	80.67
19	H X R-19	65.7	61.7	1.33	11.43	21.8	114.00	3.30	33.50	7.67	24.90	51.67	3.50	18.60	67.33
20	H X R-20	62.0	64.0	1.20	12.43	23.0	110.67	3.63	34.73	7.50	25.13	52.00	3.40	18.67	83.67
21	H X R-21	60.3	78.3	1.33	11.73	22.5	114.00	3.80	33.57	7.67	25.07	51.33	3.67	19.53	79.00
22	H X R-22	60.0	101.0	1.60	12.47	19.2	104.67	3.17	31.10	7.50	26.40	51.33	3.27	19.73	60.67
23	H X R-23	65.7	82.7	1.60	9.87	14.6	111.00	3.43	34.87	7.67	27.13	51.33	3.43	19.27	50.00
24	H X R-24	62.7	104.3	2.27	12.40	15.8	113.67	3.43	34.87	7.00	25.63	51.00	3.47	18.77	66.00
25	H X R-25	63.0	77.3	2.27	11.93	12.7	113.67	3.70	33.20	6.17	26.83	50.00	3.30	18.53	60.00

Sr. No.	Genotypes	Days to 50% flowering	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Days to 50% boll bursting.	Boll weight (g)	Ginning percentage (%)	Seed index (g)	2.5 % Span length (mm)	Uniformity ratio	Fibre Fineness (µg/inch)	Fibre Strength (g/tex)	Seedcotton yield per plant (g)
26	H X R-26	60.0	69.7	1.60	12.13	17.2	115.33	3.67	31.83	7.33	25.03	50.67	3.10	18.87	55.67
27	H X R-27	60.0	65.3	2.67	12.00	17.8	110.00	3.37	34.43	6.67	26.80	50.33	3.20	18.07	39.33
28	H X R-28	62.7	78.7	2.60	11.27	17.6	115.67	3.33	31.20	7.17	24.53	53.33	3.70	18.90	56.33
29	H X R-29	61.7	66.0	2.33	11.47	19.6	109.00	3.20	36.90	7.17	25.73	52.00	3.40	18.67	60.67
30	H X R-30	60.0	100.0	2.20	12.67	20.4	116.67	3.67	34.17	8.00	26.53	49.60	3.60	18.00	69.67
31	H X R-31	58.0	65.3	3.13	11.00	17.6	113.33	3.47	38.03	6.67	24.60	51.00	3.10	18.07	63.00
32	H X R-32	61.7	73.3	2.33	11.47	17.6	112.00	3.03	30.93	7.83	25.67	50.33	3.00	18.87	53.33
33	H X R-33	62.3	70.0	2.33	12.73	16.4	115.33	3.37	32.33	7.67	26.07	50.33	3.67	19.73	53.67
34	H X R-34	61.7	85.7	2.40	12.87	14.4	114.33	3.53	33.10	7.83	25.50	51.00	3.43	18.70	51.67
35	H X R-35	59.7	73.0	2.13	12.53	12.7	112.67	3.20	31.77	8.50	26.53	51.00	3.07	17.70	36.67
36	H X R-36	60.3	85.7	2.60	11.80	15.9	115.33	3.53	33.03	7.83	25.53	51.00	3.47	19.30	58.00
37	H X R-37	60.7	101.7	2.07	12.53	19.9	115.33	3.50	34.57	8.67	26.83	52.33	3.20	19.97	68.67
38	H X R-38	62.7	77.7	2.47	10.13	14.6	112.33	3.30	32.33	7.33	25.93	53.00	3.23	20.77	56.00
39	H X R-39	62.7	86.7	2.33	11.00	18.6	117.67	3.53	36.07	7.67	26.17	53.33	3.17	19.77	65.67
40	H X R-40	64.7	76.3	2.27	11.27	18.0	115.00	3.63	32.53	7.17	25.87	52.00	3.17	19.00	60.67
41	H X R-41	62.7	68.3	1.60	8.07	13.6	113.00	2.63	36.13	7.17	26.50	51.33	3.37	18.97	32.33
42	H X R-42	62.7	66.7	2.33	11.13	17.4	117.00	3.07	31.67	8.00	26.53	50.33	3.57	19.13	53.33
43	H X R-43	60.3	97.0	2.07	11.73	20.9	115.00	3.63	31.67	6.67	26.40	52.33	3.10	18.90	67.67
44	H X R-44	65.3	104.7	2.07	12.47	20.4	114.00	3.60	33.43	7.83	25.63	51.67	3.33	19.50	74.00
45	H X R-45	60.7	82.3	2.27	9.87	16.0	114.67	3.47	36.73	7.67	26.37	53.67	3.17	22.07	42.00
46	H X R-46	60.3	72.3	2.60	12.55	18.6	114.33	3.27	34.40	7.50	26.73	53.00	3.03	19.27	60.67
47	H X R-47	64.3	109.7	2.33	11.93	16.4	114.67	3.53	32.07	7.67	27.67	54.00	3.80	20.77	58.00
48	H X R-48	63.3	82.0	1.87	12.13	18.6	114.33	3.27	40.47	7.50	27.27	54.67	3.63	21.00	32.67
49	H X R-49	61.3	69.0	2.00	12.93	20.8	115.33	3.73	36.30	7.67	26.87	54.33	3.63	21.37	68.67
50	H X R-50	61.7	78.3	2.00	11.27	21.0	115.33	3.70	35.13	7.17	27.23	53.00	3.60	20.03	71.00
	Range	57-66	60-111	1.2-3.2	8.07-12.9	12.7-23.6	104-117	2.6-3.9	29.6-41.2	6.1-8.6	24.5-28.4	49.6-55	3-3.8	17-22	32-83
	GM	62.19	77.70	2.09	11.32	14.22	113.68	3.43	34.61	7.3	26.30	52.13	3.41	19.53	68.88
	SE(mean)	1.3719	5.1748	0.3408	0.775	1.1584	1.9471	0.1743	1.2916	0.1882	0.3825	0.8652	0.1065	0.5615	5.8693
	C.D at 5%	3.8503	14.5227	0.9563	2.1749	3.2509	5.4643	0.4893	3.6249	0.5281	1.0734	2.4282	0.2989	1.5759	16.4718

9. Seed index (g)

The seed index ranged from 6.1 to 8.6 g. Among fifty genotypes twenty six genotypes showed highest seed index than general mean (7.3 g). The highest seed index values were recorded in genotype HXR-37 (8.67g) and HXR-35 (8.50 gm). The lowest seed index value showed by genotype HXR-25 (6.17g) followed by HXR-17 (6.67g).

10. 2.5 per cent span length (mm)

The 2.5% span length ranged from 24.5 to 28.43 mm. Among fifty genotypes thirty eight genotypes had more span length over general mean (26.30mm). The highest span length observed in genotype HXR-6 (28.43mm) followed by HXR-46 (27.73mm). The lowest span length showed by genotype HXR-28 (24.53mm).

11. Uniformity ratio

The uniformity ratio ranges from 49.6 to 55. Among fifty genotypes twenty one genotypes had more span length over general mean (52.13). The lowest uniformity ratio recorded in genotype HXR-30 (49.60) followed by HXR-25 (50). The highest uniformity ratio showed by genotype HXR-12 (55) followed by HXR-7 and HXR-48 (54.64).

12. Fibre strength (g/tex)

The range of fibre strength was observed 17 to 22 g/tex. Among fifty genotypes twenty two genotypes showed maximum fibre strength (19.53g/tex) over general mean. The highest value of fire strength was exhibited by HXR-45

(22g/tex) and HXR-49 (21.37g/tex). The lowest value recorded for genotype HXR-35 (17.70g/tex).

13. Fibre fineness ($\mu\text{g}/\text{inch}$)

The fibre fineness ranged of 3 to 3.8 $\mu\text{g}/\text{inch}$. Among fifty genotypes twenty four genotypes showed more fineness than general mean (3.41 $\mu\text{g}/\text{inch}$). The lowest value recorded by genotype HXR-32 (3.00 $\mu\text{g}/\text{inch}$).

14. Seed cotton Yield per plant (g)

Average for seed cotton Yield per plant ranged from 32g to 83g. Among fifty genotypes twenty two genotypes showed more seed cotton yield per plant than general mean (68.88g). The highest seed cotton yield per plant recorded in genotypes HXR-20 (83.67g) followed by HXR-18 (80.67g), HXR-21 (79.00g). The lowest value recorded in genotype HXR-48 (32.67g) followed by HXR-41 (32.33g).

Contribution of each character towards genetic divergence

The contribution of each character towards genetic divergence had been presented in Table 3. The character plant height had highest contribution towards genetic divergence (22.29%) followed by seed index (18.78%), number of bolls per plant (14.04%), 2.5% span length (12.41%), fibre fineness (9.06%), ginning percentage (7.35%), seed cotton yield per plant (3.51%), fibre strength (2.69%) and number of sympodia per plant (2.69%).

Table 3: Contribution of various quantitative characters towards genetic divergence

Sr. No.	Characters	Times ranked F ^t	Contribution in percentage
1	Days to 50 per cent flowering	19	1.55
2	Plant height (cm)	273	22.29
3	Number of monopodia per plant	10	0.82
4	Number of sympodia per plant	33	2.69
5	Number of bolls per plant	172	14.04
6	Days to 50% boll bursting	27	2.20
7	Boll weight(g)	4	0.33
8	Ginning percentage (%)	90	7.35
9	Seed index (g)	230	18.78
10	2.5% span length(mm)	152	12.41
11	Uniformity ratio	28	2.29
12	Fibre fineness($\mu\text{g}/\text{inch}$)	111	9.06
13	Fibre strength(g/tex)	33	2.69
14	Seed cotton yield per plant(g)	43	3.51

Relatively less contribution was made by uniformity ratio (2.29%), days to 50% boll bursting (2.20%), days to 50% flowering (1.55%), number of monopodia per plant (0.82%) and boll weight (0.82) towards genetic divergence.

Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was carried out by using Tocher's method and is presented in Table 4. All genotypes were grouped into seven clusters (Fig 1).

Table 4: Distribution of genotypes in different clusters by Tocher's method

Clusters	Total No. of genotypes	Genotypes
I	19	HXR-34,36,33,42,32,4,40,39,46,38,26,28,29,23,15,50,8,45,9.
II	6	HXR-18,19,20,21,49,16.
III	14	HXR-14,24,44,30,22,43,7,3,12,11,47,5,37,13.
IV	8	HXR-1,2,6,27,41,10,25,31.
V	1	HXR-35.
VI	1	HXR-48.
VII	1	HXR-17.

Cluster I was larger containing nineteen genotypes namely (H x R - 34, H x R - 33, H x R- 42, H x R- 32, H x R-4, H x R - 40, H x R-39, H x R-46, H x R-38, H x R-26, H x R-28, H x R-29, H x R-23, H x R-15, H x R-50, H x R-8, H x R-45, H x R-9 H x R-36) Cluster III was comprised fourteen genotypes namely (H x R-14, H x R-24, H x R-44, H x R-30, H x R-22, H x R-43, H x R-7, H x R-3, H x R-12, H x R-11, H x R-47,

H x R-5, H x R-37, H x R-13) Cluster IV consists of eight genotypes viz. (H x R-1, H x R-2, H x R-6, H x R-27, H x R-41, H x R-10, H x R-25, H x R-31).

Cluster II involved six genotypes (H x R-18, H x R-19, H x R-20, H x R-21, H x R-49, H x R-16).

The cluster V, VI and VII consists of only one genotype (H x R-35), (H x R-48) and (H x R-17) respectively.

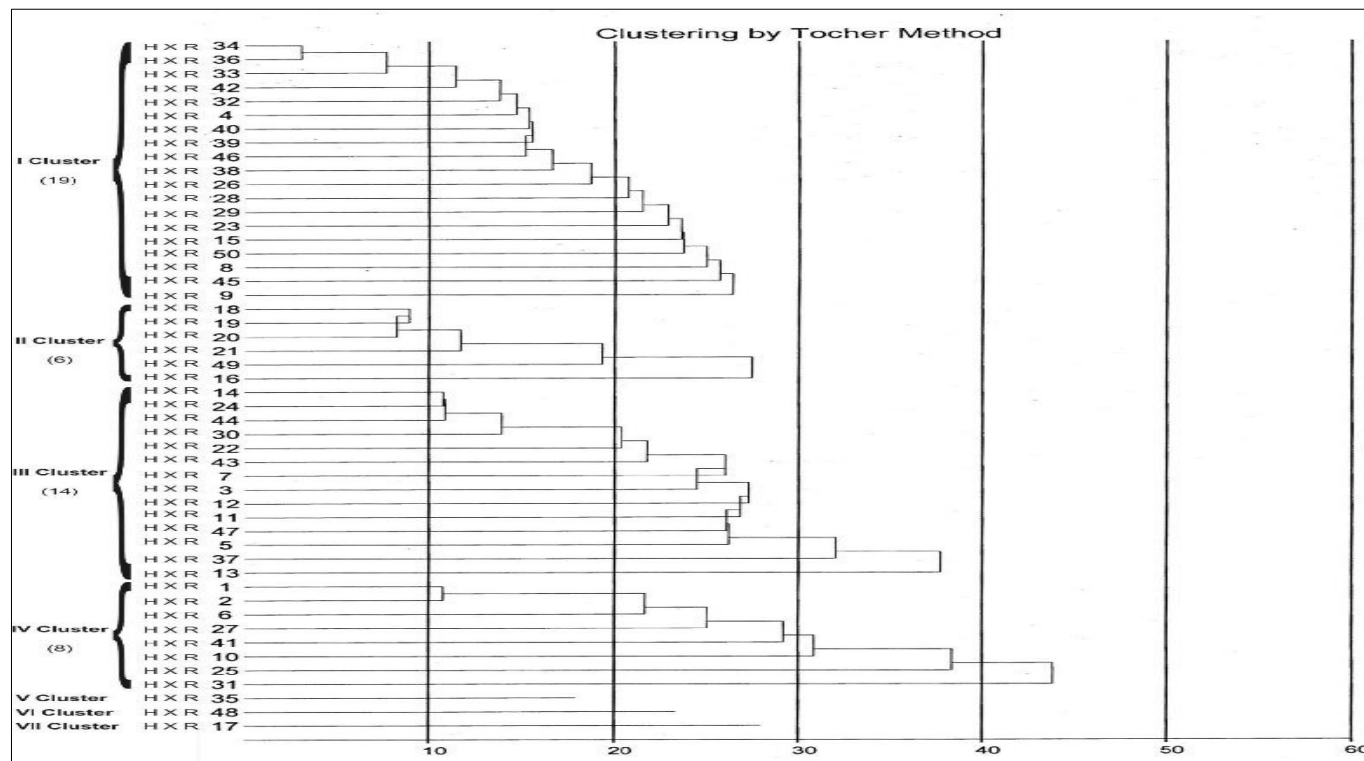


Fig 1: Dendrogram

Canonical analysis

The values of six canonical vectors and canonical roots have been presented in Table 5.

Table 5 Canonical vectors and roots

Sr. No.	Characters	vectors					
		I	II	III	IV	V	VI
1	Days to 50 per cent flowering	0.069	0.156	0.107	0.009	0.193	0.199
2	Plant height (cm)	-0.667	0.046	-0.455	-0.255	-0.248	-0.148
3	Number of monopodia per plant	0.160	0.144	-0.113	0.087	0.114	-0.059
4	Number of sympodia per plant	0.093	-0.178	0.062	0.063	-0.146	-0.225
5	Number of bolls per plant	-0.385	0.241	0.545	-0.334	0.161	0.405
6	Days to 50% boll bursting	-0.115	0.036	0.092	0.097	0.124	-0.172
7	Boll weight(g)	-0.088	-0.040	-0.062	-0.136	-0.122	-0.264
8	Ginning percentage (%)	0.032	0.071	0.240	0.178	-0.824	0.293
9	Seed index (g)	-0.475	-0.460	0.094	0.675	0.138	0.145
10	2.5 per cent span length(mm)	-0.100	0.627	-0.355	0.308	-0.081	0.050
11	Uniformity ratio	0.113	0.279	0.076	0.232	0.065	0.223
12	Fibre fineness(µg/inch)	-0.241	0.253	0.483	0.033	-0.064	-0.655
13	Fibre strength (g/tex)	-0.148	0.281	-0.076	0.209	0.288	0.030
14	Seed cotton yield per plant(g)	-0.122	-0.164	-0.122	-0.315	0.113	0.218

Values of canonical roots	Contribution of each canonical root
$\lambda_1 = 235.38$	$\lambda_1 \% = 23.00\%$
$\lambda_2 = 166.00$	$\lambda_2 \% = 16.29\%$
$\lambda_3 = 163.99$	$\lambda_3 \% = 16.02\%$
$\lambda_4 = 123.14$	$\lambda_4 \% = 12.03\%$
$\lambda_5 = 73.87$	$\lambda_5 \% = 7.21\%$
$\lambda_6 = 55.46$	$\lambda_6 \% = 5.41\%$
	Total = 85.96

The first canonical vector accounted 23.00% of the total observed variability in the material. The overall contributions by different characters towards total variability depicted by six vectors were 85.96%. In vector I number of monopodia per plant (0.160) was found to be the most important source of genetic variation followed by uniformity ratio (0.113), days to 50% flowering (0.069). In vector II 2.5% span length (0.627) and fibre strength (0.281) were important source of genetic variation. In vector III number of bolls per plant (0.545) and by fibre fineness (0.483) played important source of genetic variation. In vector IV Seed index (0.675) and

2.5% span length (0.308) found to be the most important source of genetic variation. In vector V fibre strength (0.288) followed by days to 50% flowering (0.193) played important role in genetic variation. In vector VI number of bolls per plant (0.405) followed by ginning percentage (0.293) was found to be the most important source of genetic variation.

Average intra and inter cluster D² values

Average intra and inter cluster distance for fourteen characters estimated by Tocher's methods have been presented in Table 6.

Table 6: Average intra (Bold) and inter cluster (Without bold) distance ($D=\sqrt{D^2}$)

Clusters	I	II	III	IV	V	VI	VII
I	4.80	5.91	6.32	6.28	6.32	6.86	6.95
II		4.77	7.22	7.70	8.20	6.80	6.83
III			5.51	8.13	8.19	7.50	7.08
IV				6.34	8.34	7.70	7.60
V					0.00	8.60	9.66
VI						0.00	9.11
VII							0.00

The intra cluster variation ranged from 0 (cluster V, VI and VII) to 6.34 (Cluster IV). The cluster IV exhibited the highest intra cluster distance ($D = 6.34$) which includes eight genotypes (H x R-1, H x R-2, H x R-6, H x R-27, H x R-41, H x R-10, H x R-25, H x R-31). The cluster III ($D = 5.51$) comprised of fourteen genotypes (H x R-14, H x R-24, H x R-44, H x R-30, H x R-22, H x R-43, H x R-7, H x R-12, H x R-11, H x R-47, H x R-5, H x R-3, H x R-37, H x R-13). Cluster I ($D = 4.80$) comprised off nineteen genotypes (H x R-34, H x R-36, H x R-33, H x R-42, H x R-32, H x R-4, H x R-46, H x R-39, H x R-40, H x R-38, H x R-26, H x R-28, H x R-29, H x R-23, H x R-15, H x R-50, H x R-8, H x R-45, H x R-9).

Cluster II ($D = 4.77$) comprised off six genotypes (H x R-18, H x R-19, H x R-20, H x R-21, H x R-49, H x R- 6).

The maximum average inter cluster distance was observed cluster V and cluster VII ($D = 9.66$) followed by cluster VI and cluster VII ($D = 9.11$), cluster V and cluster VI ($D = 8.60$), Cluster IV and V ($D = 8.34$), Cluster II and V ($D = 8.20$), Cluster III and V ($D = 8.19$), cluster III and IV ($D = 8.13$) and last cluster II and IV ($D = 7.70$).

Cluster means

The cluster means for fourteen quantitative characters have been presented in Table 7.

Table 7: Cluster means for 50 genotypes of Cotton

Cluster	Days to 50% flowering	Plant height (cm)	Number of monopodia per plant	Number of of sympodia per plant	Number of bolls per plant	Days to 50% boll bursting	Boll weight(g)	Ginning percentage (%)	Seed index (g)	2.5% span length (mm)	Uniformiy ratio (%)	Fibre fineness (µg/inc)	Fibre strength (g/tex)	Seed cotton yield per plant (g)
I	62.1	75.1	2.33	11.2	17.2	114.3	3.4	33.8	7.48	26.1	52.0	3.3	19.5	57.86
II	63.0	66.1	1.54	12.1	21.3	113.6	3.5	35.3	7.72	25.4	52.0	3.5	19.5	72.33
III	61.4	102.2	2.26	11.6	19.9	113.7	3.5	34.2	7.50	26.5	52.5	3.5	19.7	69.29
IV	62.5	67.6	2.61	10.7	16.5	113.2	3.3	36.0	6.61	26.6	51.9	3.3	19.4	52.33
V	59.6	73.0	2.13	12.5	12.7	112.6	3.2	31.7	8.50	26.5	51.0	3.0	17.7	36.67
VI	63.3	82.0	1.87	12.1	18.6	114.3	3.2	40.4	7.50	27.2	54.6	3.6	21.1	32.67
VII	65.6	91.3	1.33	12.6	21.2	104.0	3.7	35.9	6.60	25.1	50.3	3.3	18.2	78.67
Variance	3.38	173.91	0.21	0.49	9.30	13.57	0.03	7.21	0.43	0.53	1.82	0.04	1.21	313.89

For days to 50% flowering the lowest cluster mean was recorded by cluster V (59.60 days) followed by cluster III (61.40 days) while the cluster VII (65.8 days) recorded highest cluster mean for this character. In case of plant height the lowest cluster mean showed by cluster II (66.10 cm) followed by cluster IV and III (102.20 cm) showed highest cluster mean. In case of number of monopodia per plant cluster VII (1.33) was lowest followed by cluster II (1.54) and cluster IV (2.61) showed highest cluster mean for number of monopodia per plant.

In respect of number of sympodia per plant minimum cluster mean was recorded in cluster IV (10.70) followed by cluster I (11.20). The highest cluster mean was recorded in cluster VII (12.61), Followed by cluster I (11.20).

In case of boll per plant the lowest cluster mean was recorded in cluster V (12.70) followed by cluster IV (16.50). The

highest cluster mean for this character showed by cluster II (21.33).

In case of boll weight the lowest cluster mean was recorded by cluster V (3.2 g) and highest cluster mean for cluster VII (3.7 g). In case of ginning percentage lowest cluster mean was recorded by cluster V (31.7%) followed by cluster I (33.8%) and the highest cluster mean recorded cluster VI (40.4%).

For seed index lowest cluster mean was recorded IV (6.61 g) followed by cluster VII (6.60 g) and the highest cluster V (8.50 g).

In case of 2.5% span length lowest cluster mean was recorded VII (25.10 mm) followed by cluster II (25.40 mm). The highest cluster means VI (27.20 mm).

In case of uniformity ratio lowest cluster mean exhibited by VII (50.30%) followed by cluster V (50.00%). The highest cluster VI (54.60%).

For fibre fineness lowest cluster mean cluster V (3.0 µg/inch) followed by cluster I (3.3). The highest cluster mean for this character in cluster VII (3.6 µg/inch).

In case of fibre strength lowest cluster mean for cluster V (17.70 g/tex) followed by cluster III (18.20 g/tex). The highest cluster mean for this character observed in cluster VI (21.10 g/tex).

For characters seed cotton yield per plant lowest cluster mean observed in cluster VI (32.67 g) followed by cluster V (36.00 g). The highest cluster mean for this character in cluster VII (78.67 g).

Overall study of cluster mean for all characters by Tocher's method indicated that cluster I showed highest cluster mean values for day to 50% flowering (114.39 days). Cluster II showed highest cluster mean values for number of boll per plant (21.30). Cluster IV showed highest cluster mean values for number of monopodia per plant (2.61) and lowest cluster mean values for number of sympodia per plant (10.7) and lowest for seed cotton yield per plant.

Cluster V showed highest cluster mean value for seed index (8.50 g) and lowest cluster mean value for characters days to 50% flowering (59.60), number of bolls per plant (12.70), boll weight (3.2 g), ginning percentage (31.70%), fibre fineness (3.0 kg/inch) and fibre strength (17.79 g/tex).

Cluster VI showed highest cluster mean values for characters ginning percentage (40.40%), 2.5% span length (27.2 mm), boll weight (3.7 g), seed cotton yield per plant (78.67 g) and the lowest cluster mean value for characters number of monopodia per plant (1.33) and days to 50% boll bursting (104.0 days).

Conclusion

Hence taking into consideration the limit of parental divergence for getting good amount of heterosis in F_1 , mean and standard deviation of parental divergence were worked out and 41 genetically diverse parental combinations have been finally identified out of 192 cross combinations, for crossing programme which are expected to produce maximum heterotic effect in F_1 generation and yield desirable segregates in subsequent generations.

Credit authorship contribution statement

Salve Surekha Bhanudas, Minnu Sasi: Conceptualisation; Methodology; Data curation; Writing- original draft.

Manisha Phaugat: Review & editing; Validation; Supervision.

Declaration of Competing Interest

The authors declare no conflict of interest.

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