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Genetic diversity studies in desi cotton (*Gossypium arboreum* L.)

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Abstract
In any crop breeding program, selection of parents is important on which all other activities depend. Genetic diversity provides opportunities to researchers to develop varieties which accumulate multiple traits. The present research work on genetic diversity of fifty genotypes of *desi* cotton, which were evaluated in Randomized Block Design with two replications at Cotton Research Station, Mahboob Baugh, VNMKV, Parbhani during *Kharif* 2020-21 and observations were recorded on thirteen different traits. The results depicted that ample genetic divergence were present in studied genotypes and the genotypes were divided into nine clusters using Tocher's approach based on D^2 value. In this study, Cluster I has reported the maximum (18) number of genotypes followed by Cluster II (11) genotypes, Cluster V (09) genotypes, Cluster III (04) genotypes, Cluster VIII (3) genotypes and Cluster VII (2) genotypes. For most of the traits inter cluster distance was greater than intra cluster distance which indicates sufficient significant genetic divergence were present for studied traits. From this results it can be suggested that, the genotypes which are present in different clusters could be used in hybridization programme to get recombination with desirable attributes to develop climate smart varieties.

Keywords: Desi cotton, cluster, genetic diversity, genotypes

Introduction
Cotton is an important crop for sustainable economy of India and livelihood of the Indian Cotton Farming Community. Cotton was first cultivated as a fabric in the Indus river valley in 3000 B.C. The word cotton is derived from the Arabic word "quotn" (Lee and Fang 2015) [11] has a place with *Gossypium* variety, which was additionally derived from the Arabic word "goz" (Gledhill 2008) [7] meaning a delicate material. It is grown all over the world, mainly for its fibre. It is referred to as "white gold" primer cash and fibre crop. Cotton is also called as king of fibre crop. It is the world's most important non-food agricultural commodity used for textile purposes, provides basic raw material to cotton textile industries, at present nearly 60 million people depend on cotton cultivation, marketing, processing, and export for their livelihood. It is generating employment for millions of people, farmers and others engaged in activities relating to cotton, processing, transportation, etc.

Due to research and development activities, there have been many fold improvements in production and productivity without a virtual increase in the cultivated area. Now, India holds a prominent position in the global cotton market, with the largest cotton area of 129.57 lakh hectares, 371 lakh bales production and productivity of 487 kg ha^{-1} (Anonymous, 2021) [2]. Maharashtra produces approximately 86.00 lakh bales of cotton lint from 41.84 lakh hectares, with a productivity of 349 kg ha^{-1} (Anonymous, 2021) [3].

Cotton is the leading natural fibre crop. It belongs to the genus *Gossypium* and family Malvaceae which has extensively phenotypic diversity among the approximately 50 species representing this genus (Campbell *et al.* 2010) [6]. Currently, *Gossypium* includes 50 species, among these 44 are diploids, 2 are wild tetraploid and only four species are cultivated (Percival and Kohel, 1990) [15], Out of these four cultivated species *G. hirsutum* and *G. barbadense* commonly known as 'New World Cotton' which are allotetraploids (2n = 2x = 52) whereas *G. arboreum* and *G. herbaceum* are diploid (2n = 2x = 26) are commonly called as 'Old World Cotton'. Most of the global cotton production comes from two allotetraploid species,

G. hirsutum and *G. barbadense* (Wendel *et al*. 1992) [21]. *Gossypium hirsutum* is also called upland cotton, represents 95 percent of global cotton fiber production. *Gossypium barbadense* (also known as Pima cotton) is valued for its higher fiber quality and contributes around 3 percent of global cotton production. (Wendel *et al*. 1992) [21].

Out of four cultivated genus *Gossypium*, only two species i.e., *G. hirsutum and G. arboreum* are being cultivated in Maharashtra. In last two decades, there has been a significant reduction in the area of *Gossypium arboreum* cotton across the country and particularly in Maharashtra, because of lower productivity and inferior fibre properties compared to tetraploid cotton in rainfed ecosystems.

Although, Indian cotton has a very wide quality spectrum, the right combination of fibre length, micronaire, and desirable fibre strength are however absent in many of the popular varieties and hybrids. The deficiency was particularly discernible in the staple length range of 27 to 30 mm combined with a micronair value of 4.0 to 4.5 ug/inch and strength of 22 to 25 g/tex. Indian cotton confirming to long and extra-long staple group are too fine coupled with weak strength. There is an urgent need to promote those cotton that could come closer in quality to the most sought by modern textile mills. Therefore, more emphasis should be given to increase the seed cotton yield per unit area of *desi* cotton, by developing varieties with short stature, big boll size and medium to long staple length with sustained yield in multiple environments. To achieve such desirable characteristics in a new variety, proper breeding strategies should be followed.

Genetic diversity is one of the levels of biodiversity that refers to the variability present in different individuals of the same species, more genetic diversity in a species or population means a greater ability for some of the individuals to adapt to change in the environment. For genetic improvement of any crop species, there is need to study the variability present in the given material. Because any plant breeding program starts from selectin of parents. Selection of parents is very crucial as it decides further plant breeding processes (Swarup *et al.* 2021) [20]. Genetic diversity in plant breeding provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmers preferred traits (yield potential and large seeds *etc*.) and breeder preferred traits (pest and disease resistance and photosensitivity) (Govindaraj *et al*. 2015) [8].

Cotton breeders aim to create varieties and hybrids with desirable fiber traits and high seed cotton yield. To achieve this, measuring genetic diversity among genotypes is essential for selecting elite parents for hybridization programs. Genetic diversity is crucial for generating heterosis in hybrids between genotypes. Mahalanobis' D2 statistics is an effective tool for determining the degree of genetic divergence at the genotypic level. It also measures the relationship between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928) [12].

In light of the foregoing, the current study was conducted to investigate the genetic diversity of yield, yield-contributing traits, and fiber traits.

Materials and Methods

The present investigation of genetic diversity was conducted during *Kharif* 2020-2021 at Cotton Research Station, Mahboob Baugh Farm, VNMKV, Parbhani. The experiment was carried out with 50 genotypes (Table 1) including six checks *viz.*, AKA 7, AKA 8, JLA 794, JLA 505, PA 255 and PA 402 of *desi* cotton in Randomized Block Design with two replications. Each genotype was sown with a 45 cm row spacing and 22.5 cm between plants. Each genotype was represented by two rows of 6 m length. To raise a healthy crop, recommended agronomical and plant protection practices were followed throughout the crop season. For recording of observations five competitive plants at random, excluding border plants, were chosen at random from each plot in each replication. The 13 characters such as days to 50 percent flowering, plant height, number of sympodia per plant, number of bolls per plant, boll weight (gm), seed cotton yield per plant (gm), seed index, lint index, ginning percentage, upper half mean length (mm), Fiber fineness/micronaire value (µg/in), fibre strength (g /tex) and uniformity ratio were recorded in the field and in the lab, with the mean values being analysed statistically. The fiber quality traits were analysed at CIRCOT, Mumbai.

The D^2 statistic of Mahalnobis (1928, 1936) was used to analyse divergence, as reported by Rao (1952) [16]. As described by Rao (1952), all the D^2 values were clustered using Tocher's method. The intra and inter cluster distances were calculated according to formulae given by Singh and Chaudhari (1977) [18].

Results and Discussion

In any crop improvement programme, Genetic diversity plays an important role the choice of parents each generally done on the basis *per se* performance. The assessment of genetic diversity can be made on the basis of morphological, yield contributing and fibre traits. However, several methods of multivariate analysis have been found to be useful in selecting of parents for hybridization. Among these methods, Mahalnobis (1936) D^2 statistics has been one of reasonable test in estimation of genetic diversity and selection of parents for any breeding objective.

Grouping of genotypes into different clusters

The analysis of variance revealed highly significance difference among 50 genotypes for 13 traits and infers existence of considerable genetic diversity among genotypes it is confirmed by Wilk's criterion. Fifty cotton genotypes were divided into nine clusters using Tocher's approach based on D^2 value, with genotypes belonging to the same cluster having a lower D^2 value on average than genotypes belonging to separate clusters. Table 2 shows the distribution of 50 genotypes into nine clusters.

Cluster I has reported the maximum (18) number of genotypes followed by Cluster II (11) genotypes, Cluster V (09) genotypes, Cluster III (04) genotypes, Cluster VIII (3) genotypes and Cluster VII (2) genotypes. Only one genotype was found in the remaining clusters IV, VI, and IX. Solitary clusters may arise as a result of absolute isolation of extensive gene flow or natural/human selection for rigorous varied adaptive complexes. These genotypes could be one-of-a-kind and important in breeding programme. Similar findings reported by Bhimate *et al.* (2019) [5] grouped 36 genotype into nine clusters, Naik *et al*. (2016) [14] grouped 50 genotypes into eight clusters. Sing *et al.* (2009) grouped 68 genotypes into ten clusters. Gopinath *et al.* (2009) 60 genotypes grouped into eight clusters.

Average intra and inter cluster D^2 values

The average intra and inter cluster D^2 value is estimated as per the procedure. The values are presented in the Table 3 The mean D^2 value of cluster elements were used as measure of intra and inter cluster distance. Intra cluster D^2 values ranged from 0.00 to 252.59. The maximum intra cluster D^2 value was observed (252.89) for cluster V followed by cluster VIII had 226.1, cluster II (182.16), cluster I (144.95), cluster III (108.34) and cluster

VII (75.57). While intra clusters D^2 value was zero for cluster IV, VI and IX. The intra cluster indicates the diversity among the genotypes grouped in that clusters. Genotypes grouped into same clusters presumably differ little from one another as the aggregate of character measured. In the study it was also revealed that, the inter cluster values varies from 137.15 to 2134.45. The maximum inter cluster distance (D= 2134.45) was observed between cluster VII and cluster VIII, followed by cluster V and IX (D= 1795.34), cluster VI and VIII (1692.65), cluster I and IX (D= 1513.31) and cluster VI and IX (D= 1140.29). The minimum inter cluster distance (D= 137.15) was noticed between cluster VI and cluster VII.

The highest statistical distance was found between cluster VI and cluster VIII, followed by cluster V and cluster IX for yield contributing and fibre traits. The maximum inter cluster distance suggests that the genotypes belonging to these clusters were genetically most divergent, if chosen for further breeding programme, they are likely to give higher performances. Similarly, Amla *et al.* (2011) observed inter cluster distances were higher than the intra cluster distances showing the presence of wider genetic diversity among the clusters.

Cluster mean for different characters

Mean performance of clusters for thirteen characters were represented in table 4. The cluster mean for most of the characters were high in cluster VIII, which consisted of three genotypes and differed significantly from those of other clusters, indicating that the genotypes included in this cluster have a different genetic makeup than those other clusters.

It is concluded that, for each character contribution differs from cluster to cluster. So, for improvement of such particular character, the genotypes were selected from different clusters having highest mean value for it. Boll weight cluster mean was ranged from 2.16 to 2.96. Highest cluster mean for boll weight was found in cluster IX (2.96 g) followed by cluster VIII (2.89 g) and cluster III (2.75 g). For this trait, improvement could be done by selecting genotypes from different clusters.

Using cluster means as a guide, promising clusters and genotypes for selecting ideal parents for a hybridization programme to improve certain characters was shown in table 5.

Percent contribution of each character towards genetic divergence

Table 6. Shows the percent contribution to diversity of all thirteen morphological, yield contributing, and fibre traits in 50 cotton genotypes. It was observed that upper half mean length contributed maximum (44.49%) followed by number of sympodia per plant (26.12%), fibre strength (20.57%), plant height (12.29%), days to 50% flowering (3.51%) and fibre fineness (1.39%) toward the genetic divergence. While, lint index (0.98%), number of bolls per plant (0.24%), seed index (0.16%), boll weight (0.08%), uniformity ratio (0.08%), seed cotton yield per plant (0.08%) minimum contributes towards genetic divergence and the character ginning percent (0.00%) indicate negligible contribute towards genetic divergence. Similar result findings were reported by Handi *et al.* (2016) [10], Basavaraddi *et al.* (2011) [4], Sanjaya (2006) [17].

Table 1: List of 50 genotypes with their sources

Sr. No.	Genotypes	Source	Sr. No.	Genotypes	Source
1	DWDa 1902	UAS, Dharwad	26	CISA 90	CICR, Sirsa
2	DWDa 1801	UAS, Dharwad	27	CISA 405	CICR, Sirsa
3	NDLA 3116-3	ANGRAU, Nandyal	28	LD 1026	PAU, Ludhiana
4	NDLA 3104-4	ANGRAU, Nandyal	29	LD 1033	PAU, Ludhiana
5	NDLA 3113	ANGRAU, Nandyal	30	RAAS 751	UAS, Raichur
6	MDL 2689	PJTSAU, Mudhol	31	RAAS 701	UAS, Raichur
7	MDL 2679	PJTSAU, Mudhol	32	CCA 710	CICR, Coimbatore
8	GAM 267	JAU, Amreli	33	AKA 14-51	Dr.PDKV, Akola
9	GAM 273	JAU, Amreli	34	AKA 2009-1	Dr.PDKV, Akola
10	GAM 259	JAU, Amreli	35	AKA 2013-8	Dr.PDKV, Akola
11	GAM 261	JAU, Amreli	36	AKA 2013-17	Dr.PDKV, Akola
12	JLA 1102	ARS, Jalgaon	37	PA 796	VNMKV, Parbhani
13	JLA 1313	ARS, Jalgaon	38	PA 760	VNMKV, Parbhani
14	JLA 1207	ARS, Jalgaon	39	PA 806	VNMKV, Parbhani
15	CNA 1054	CICR, Nagpur	40	PA 828	VNMKV, Parbhani
16	CNA 2031	CICR, Nagpur	41	PA 842	VNMKV, Parbhani
17	CNA 2035	CICR, Nagpur	42	PAIG 373	VNMKV, Parbhani
18	RG 846	ARS, Shriganganagar	43	PAIG 379	VNMKV, Parbhani
19	RG 856	ARS, Shriganganagar	44	PAIG 384	VNMKV, Parbhani
20	PBD 35	PAU, Bhatinda	45	AKA 7 ©	Dr.PDKV, Akola
21	PBD 36	PAU, Bhatinda	46	AKA 8 ©	Dr.PDKV, Akola
22	HD 550	CCSHAU, Hisar	47	JLA 505 ©	ARS, Jalgaon
23	HD 551	CCSHAU, Hisar	48	JLA 794 ©	ARS, Jalgaon
24	FDK 286	PAU, Faridkot	49	PA 402 ©	VNMKV, Parbhani
25	FDK 295	PAU, Faridkot	50	PA 255 ©	VNMKV, Parbhani

Table 2: Grouping of 50 genotypes into different clusters

Sr. No.	Clusters	Number of genotypes	Name of genotypes
1	I	18	CCA 710, RAAS 751, HD 551, RG 856, PAIG 379, PAIG 384, PA 796, PAIG 373, DWDa 1801, AKA 2015-17, PA 402, AKA 7, CNA 1054, PA 828, PA 806, GAM 261, AKA 14-51, PA 842.
2	II	11	AKA 2013-8, AKA 8, PA 255, GAM 267, JLA 794, AKA 2009-1, CNA 2031, JLA 1207, NDLA 3113-4, LD 1026.

3	III	04	JLA 1313, GAM 273, MDL 2689, FDK 286.
4	IV	01	RG 846.
5	V	09	CAN 2035, GAM 259, PBD 35, HD 550, PBD 36, CISA 90, CISA 405, MDL 2679, DWDa 1902.
6	VI	01	LD 1033.
7	VII	02	RAAS 701, PA 760.
8	VIII	03	JLA 1102, FDK 295, NDLA 3116-3.
9	IX	01	JLA 505.

Table 3: Intra (diagonal) and inter (above diagonal) cluster distance (D^2) value for thirteen characters in cotton

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	144.95	278.90	466.21	201.94	425.54	195.12	415.41	1025.63	953.90
II		182.16	348.83	242.86	357.25	561.48	881.04	501.02	949.89
III			108.34	725.92	892.64	792.28	884.35	626.98	330.70
IV				0.00	167.72	344.93	746.35	849.38	1513.31
V					252.89	647.83	1140.19	799.80	1795.34
VI						0.00	137.15	1692.65	1140.29
VII							75.57	2134.45	922.80
VIII								226.10	1366.71
IX									0.00

Table 4: Clusters mean for thirteen different morphological, yield contributing and fibre characters in cotton

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX
1	Days to 50% flowering	69.92	70.05	72.38	69.00	70.06	69.00	70.25	71.83	76.50
2	Plant height (cm)	108.78	122.25	140.13	88.00	107.11	91.00	110.50	141.33	134.00
3	No. of sympodia/plant	13.00	14.03	14.58	13.30	12.93	12.30	12.95	15.90	15.75
4	No. of bolls/plant	16.77	20.16	24.43	14.80	18.64	16.40	14.10	24.47	23.60
5	Boll weight (g)	2.44	2.66	2.75	2.17	2.48	2.16	2.41	2.89	2.96
6	Seed index (g)	5.66	6.21	6.91	5.42	5.85	5.68	5.71	6.58	6.79
7	Lint index (g)	4.33	4.51	4.44	4.29	4.38	4.38	3.89	4.62	4.49
8	Ginning percentage (%)	37.00	37.71	38.42	38.75	38.82	37.64	37.31	38.74	37.16
9	Upper half mean length (mm)	27.38	25.66	27.93	25.00	23.90	29.00	30.95	23.07	31.50
10	Fibre strength (g tex^{-1})	25.62	26.75	29.03	24.35	23.75	23.40	22.81	28.84	29.23
11	Fibre fineness (µg/in)	5.13	5.51	4.95	5.20	5.63	5.50	5.08	5.90	5.60
12	Uniformity ratio	81.22	80.36	81.50	79.00	79.22	82.00	83.00	79.33	81.00
13	Seed cotton yield per plant (g)	37.00	42.06	50.83	31.29	39.23	35.33	34.12	51.89	49.40

Table 5: Characters improvement on the basis of source clusters

Sr. No	Characters	Sources of clusters
1	Days to 50% flowering	IV, VI, I
2	Plant height (cm)	VIII, III, IX, II
3	No. of sympodia/plant	VIII, IX, III, II
4	No. of bolls/plant	VIII, III, IX, II, V
5	Boll weight (gm)	IX, VIII, III, II, V
6	Seed index (g)	III, IX, VIII, II,
7	Lint index (g)	VIII, II, IX, III
8	Ginning percentage (%)	V, IV, VIII
9	Upper half mean length (mm)	IX, VII, VI
10	Fibre strength (g tex^{-1})	IX, III, VIII
11	Fibre fineness (µg/in)	VIII, V, IX, IV, II, VI,
12	Uniformity ratio	VII, VI, III, I, IX, II
13	Seed cotton yield per plant (g)	VIII, III, IX, II, V

Table 6: Percent contribution of thirteen different characters toward genetic divergence in cotton

Sr. No.	Characters	No. of times appearing I^{ts} ranking	% Contribution
1	Days to 50% flowering	43	3.51
2	Plant height (cm)	28	12.29
3	No. of sympodia/plant	320	26.12
4	No. of bolls/plant	3	0.24
5	Boll weight (gm)	1	0.08
6	Seed index (g)	2	0.16
7	Lint index (g)	12	0.98
8	Ginning percentage (%)	0	0.00
9	Upper half mean length (mm)	545	44.49

10	Fibre strength (g tex^{-1})	252	20.57
11	Fibre fineness (µg/in)	17	1.39
12	Uniformity ratio (%)	1	0.08
13	Seed cotton yield per plant (g)	1	0.08

Conclusion

D^2 statistical analysis indicates a considerable amount of genetic variation among the genotypes with D^2 values corresponding to the pairs of combination between 50 genotypes. All the genotypes were grouped into nine clusters good amount of genetic diversity was present among the genotypes studied, which can be involved in a hybridization programme to get recombination with desirable attributes. Ultimately, the findings provide valuable insights for improving genetic diversity and developing superior cotton varieties.

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Conflicts of Interest. None.

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