

Dispersion Analysis studies in Desi Cotton (*Gossypium arboreum* L.) based on Wilk's Criteria and Canonical Vectors

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ABSTRACT

Gossypium arboreum is a native cotton species of India. It is cultivated from extreme north of Punjab to Kanyakumari in the south and Assam in the east to Kutch (Gujarat) in the west of country. *G. arboreum* genotypes matures in 150 to 180 days and is usually having coarse and short fibred and has high degree of resistance to diseases and insect pests and is very valuable germplasm resources and have great export value. The investigation for fifty-eight desi cotton (*Gossypium arboreum* L.) genotypes was undertaken to estimate the degree of divergence among the fifty eight genotypes of desi cotton and thereby to identify potential and diverse genotypes for their utilization in hybridization program based on wilk's criteria and canonical vectors. The analysis of variance revealed significant differences among fifty eight genotypes collected from different cotton growing states in respect of all the twelve morphological characters under study indicating the presence of substantial degree of variability. The canonical root analysis revealed about 80.19 per cent of the total variation was accounted by the first six canonical roots. In root I seed cotton yield per plant, in root II initial plant stand, in root III lint index, in root IV boll weight, in root V number of monopodia per plant and in root VI plant height were important sources of divergence. Among twelve characters studied, seed cotton yield per plant (g) contributed maximum towards divergence followed by initial plant stand, ginning percent, seed index and number of bolls per plant, indicating that yield and yield contributing characters contributed maximum towards divergence.

Key words: Canonical roots, D^2 analysis, Desi Cotton, Genetic divergence, *G. arboreum*.

INTRODUCTION

Cotton word derived from Arabic world *KUTON* or *QUTON*, which is belonging to genus *Gossypium* and family Malvaceae. India has the distinction of growing all the four cultivated cotton species viz. *Gossypium arboreum* L., *G. herbaceum* (both diploids), *G. hirsutum* and *G. barbadense* (both tetraploids). Globally, ninety percent cotton area is under *G. hirsutum*, eight per cent is under *G. barbadense* and just two percent is under *G. arboreum* and *G. herbaceum*. To meet the domestic requirement and to exploit the export potential of coarse lint especially due to its surgical use, development of *desi* cotton varieties with higher productivity and ginning out turn is utmost importance.

The traditional *desi* varieties, which occupied as much as eighty *per* cent of the total cotton area at the time of independence, gradually gave way to the American tetraploid cotton. Though the introduction of tetraploid cotton brought significant increase in the total cotton production both in terms of quantity and quality. *G. arboreum* are reputed in trade for their tensile strength and consistent fibre properties. Owing to their wider adaptability and inherent ability to tolerate both sucking pests and bollworms they can be grown successfully with low input management as against the new world cotton which are highly prone to pests and diseases.

The knowledge of nature and magnitude of genetic diversity present in the germplasm is the most important pre-requisite for success of any breeding programme. It is thus necessary to survey the variation present in the germplasm as the hybrids between diverse parents displays a greater heterotic effects than those between the closely related. Genetic diversity of selected parents is not always based on the factors such as geographical diversity or place of release or ploidy level. Hence many statistical procedures viz., D^2 statistics, non-hierarchical euclidean cluster, metroglyph etc., are developed to measure the total diversity present among the genotypes. Hence the study on the assessment of genetic diversity based on morphological traits was taken up in *desi* cotton.

MATERIAL AND METHODS

An experiment was conducted in randomized block design with three replications at Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola with an objective to estimate the magnitude of divergence based on important twelve morphological traits viz., initial plant stand in per cent, plant height (cm), days to 50 per cent flowering, days to 50 per cent boll bursting, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant

(g), seed index (g), lint index and ginning percentage of fifty eight elite desi cotton genotypes (*Gossypium arboreum* L.) from different cotton growing states of India (Table 1).

Table 1. Details of experimental material

State	No. of genotypes	Genotypes	State	No. of genotypes	Genotypes
Maharashtra	29	JLA-0804	Karnataka	6	ARBa-1502
		PA-785			ARBa -1501
		PA 801			DWDa -1501
		JLA-0614			DWDa - 1502
		CNA-2023			DLSA-17
		AKA-2005-3			RAAS-601
		CNA 2019	Andhra Pradesh	6	NDLA-3020
		AKA-9703			GAM-231
		AKA-2007			NDLA-3068
		AKA-5			NDLA - 3089
		AKA-7			NDLA – 3094
		AKA-8401			GAM - 235
		PA-255	Haryana	6	CSA 1028
		PA-402			CSA 2043
		PA-528			CISA-6-2
		PA 812			CISA-6-256
		PA-08			CISA 6 – 123
		PA-760			HD 524
		CNA 1003(Roja)	Punjab	5	FDK 260
		AKA - 209			PBD 6
		Phule Dhanvantari			FDK 259
		AKA - 8			PBD-20
		PA-828			PBD 17
		CNA-2030	Rajasthan	3	RG 784
		CNA-1031			RG 778
		CNA-1032			RG-801
		JLA - 0906	Tamil Nadu	2	CCA – 2003
		JLA-0603			TKA-9102/3
		AKA-2013-21	Gujarat	1	G COT – 15

Statistical analysis: The inverse matrix of original genotypic variance covariance matrix was computed to derive the relationship by which the original character mean ($X_i - X_j$) will be transformed to an uncorrelated set of variables $Y_i - Y_j$. In term of variance and covariance, the D^2 values were obtained as follows (Mahalanobis 1936) whereas, the Canonical root method was followed as suggested by Rao (1952).

RESULT AND DISCUSSION

Analysis of Variance: The analysis of variance was undertaken for all the twelve characters which were furnished in Table 2. The analysis of variance revealed significant differences by genotypes for all the twelve characters studied. The differences due to replication were found non-significant. Analysis of variance revealed that, mean squares due to genotypes were highly significant indicating that genotypes differ significantly for all the characters studied indicating the existence of considerable amount of genetic variability among the genotypes under study. These results coincide with the findings of [3,4,5,9,11]

Table 2. Analysis of variance for twelve characters

Sr No.	Name of character	Replications (df-2)	Treatments (df-57)	Error (df-114)
1	Initial Plant Stand	6.65	105.40**	3.86
2	Plant Height	14.00	122.84**	76.01
3	Days to 50 percent Flowering	0.25	24.52**	2.31
4	Days to 50 percent Boll Bursting	2.93	18.38**	2.53
5	Number of Monopodia per plant	0.13	0.74**	0.09
6	Number of Sympodia per plant	14.74	17.86**	6.60
7	Number of Bolls per plant	2.49	15.89**	1.21
8	Boll weight(g)	0.01	0.10**	0.01
9	Seed cotton yield per plant	0.01	3.87**	0.01
10	Seed index	0.18	1.22**	0.09
11	Lint index	0.16	1.26**	0.13
12	Ginning percent	0.21	7.28**	0.37

*, ** significant at 5% and 1% level of degrees of freedom

Analysis of dispersion and Wilk's criterion: Analysis of dispersion presented in Table 3 The analysis of dispersion and the simultaneous test of significance based on Wilk's criterion for the pooled effect of thirteen characters showed highly significant differences among fifty eight genotypes studied in the present investigation ($X^2 = 3020.99$ at d.f. = 741).

Table 3 Analysis of dispersion

Source of variation	Degrees of freedom	Mean squares
Genotypes	57	2.9617E13

Error	113	2.6283E03
Total	170	9.9304E12

The concept of genetic diversity is very important in differentiating a population. It is a prerequisite for initiating a hybridization program because the choice of potent and diverse parents determines the success of such program. Selection of diverse parents for crossing program serves the purpose of combining desirable genes to obtain superior recombinants.

Canonical root analysis for twelve characters: The total 80.19 per cent of diversity for twelve characters under present study was represented by six canonical vectors (Table 4). The first canonical vector accounted 25.45% of the total observed diversity in the material (Table 5). In present investigation, the vector I seed cotton yield per plant (g) (0.49) was found to be the most important source of genetic variation, which was followed by ginning percent (0.38) and boll weight (0.34). In vector II initial plant stand (0.53), number of sympodia per plant (0.21) and boll weight (0.18) were important source of genetic variation. In vector III lint index (0.56) and seed index (0.43) was the important source of genetic variation. In vector IV boll weight (0.23) and seed cotton yield per plant (0.14) found to be the most important source of genetic variation. In vector V number of monopodia per plant (0.70) followed by initial plant stand (0.44) played important role in genetic variation. In vector VI number of bolls per plant (0.40) followed by lint index (0.28) was found to be the most important source of genetic variation.

Table 4: Canonical root analysis for twelve characters

Sr No.	Name of character	Vector I	Vector II	Vector III	Vector IV	Vector V	Vector VI
1	Initial Plant Stand	0.04	0.53	0.08	0.03	0.44	0.11
2	Plant Height	-0.13	-0.51	0.05	0.12	0.08	-0.46
3	Days to 50 percent Flowering	0.26	0.17	-0.05	-0.51	0.38	-0.23
4	Days to 50 percent Boll Bursting	0.19	0.10	-0.31	-0.45	-0.19	-0.43
5	Number of Monopodia per plant	-0.13	-0.34	-0.15	-0.02	0.70	-0.07
6	Number of Sympodia per plant	0.08	0.21	0.49	0.04	-0.10	-0.40
7	Number of Bolls per plant	0.21	-0.19	-0.18	-0.41	-0.16	0.40
8	Boll weight(g)	0.34	0.18	0.13	0.23	0.01	-0.18
9	Seed cotton yield per plant	0.49	-0.18	0.002	0.14	-0.01	-0.08
10	Seed index	-0.24	-0.15	0.43	-0.36	-0.07	-0.12

11	Lint index	0.08	-0.18	0.56	-0.31	0.03	0.28
12	Ginning percent	0.38	-0.17	0.22	0.10	0.24	0.20

Table 5 : Canonical root analysis and its per cent contribution

Sr. No.	Canonical roots	Contribution of each canonical roots (%)
1	$\lambda_1 = 330.92$	$\lambda_1\% = 25.45$
2	$\lambda_2 = 203.81$	$\lambda_2\% = 15.67$
3	$\lambda_3 = 189.99$	$\lambda_3\% = 14.61$
4	$\lambda_4 = 137.70$	$\lambda_4\% = 10.59$
5	$\lambda_5 = 99.39$	$\lambda_5\% = 7.64$
6	$\lambda_6 = 80.68$	$\lambda_6\% = 6.20$
Total		80.19 %

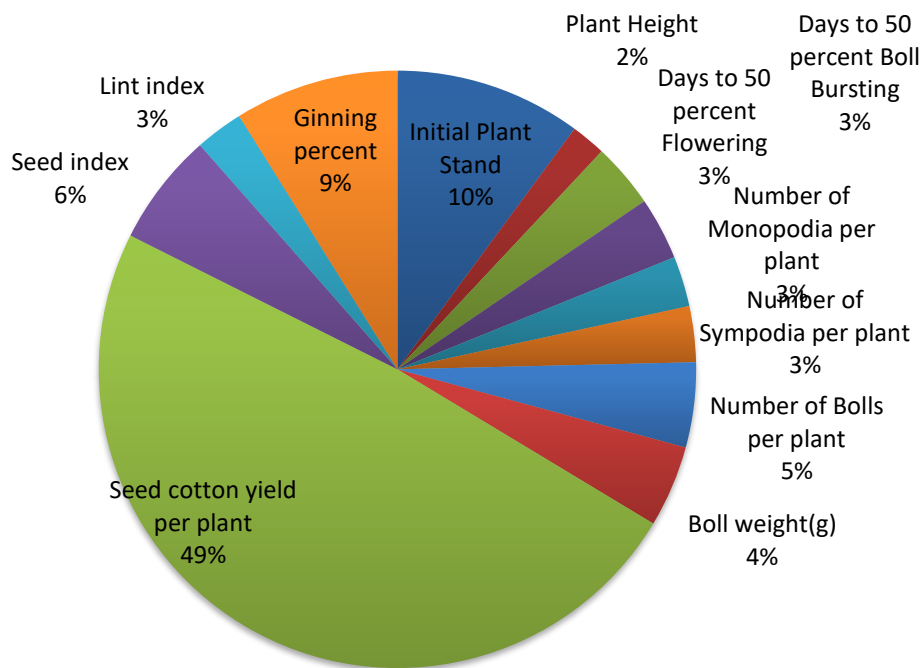
Contribution of Characters towards divergence: The *per cent* contribution of each character towards divergence is presented in Table 6 and Fig.1. It was observed that seed cotton yield per plant (48.76%) contributed maximum towards divergence followed by Initial plant stand (10.10%), Ginning percent (8.89%) whereas lowest contribution to divergence was shown by Plant height (1.88%) followed by Lint index (2.60%) and Number of monopodia per plant (2.72%).

Table 6. Contribution of Twelve characters towards divergence

Sr No.	Name of character	Times ranked first	Percent contribution
1	Initial Plant Stand	167	10.10
2	Plant Height	31	1.88
3	Days to 50 percent Flowering	58	3.51
4	Days to 50 percent Boll Bursting	56	3.39
5	Number of Monopodia per plant	45	2.72
6	Number of Sympodia per plant	50	3.02
7	Number of Bolls per plant	76	4.60
8	Boll weight(g)	73	4.42
9	Seed cotton yield per plant	806	48.76
10	Seed index	101	6.11
11	Lint index	43	2.60
12	Ginning percent	147	8.89
Total		1653	100.00

The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first. This study helps to identify diversity in different proportion which ultimately helps to decide utilization of genetic material for improvement of specific characters. Among the twelve characters studied, the highest contribution to divergence was recorded by seed cotton yield per plant (48.76 per cent), followed by initial plant stand (10.10 per cent), ginning percent (8.89 per cent), seed index (6.11 per cent), number of bolls per plant (4.60 per cent) and boll weight (4.42 per cent). Whereas, the lowest contribution towards divergence was recorded by character plant height (1.88 per cent). The above results suggest that, in order to incorporate diversity among the existing genotypes, the genotypes which are more diverse in respect of the characters like seed cotton yield, initial plant stand, ginning percent, seed index, number of bolls per plant and boll weight which are pre-requisites for higher yield per unit area may be utilised for future breeding program. Similar results were interpreted for number of bolls per plant, boll weight, seed cotton yield per plant and seed index [8]. The highest contribution of seed cotton yield, number of bolls per plant, ginning percent and seed index towards divergence [1]. Same results were also interpreted by cotton workers [7,2,6,12,13]

Fig.1: Contribution of each character towards divergence



CONCLUSION

The data obtained from observations was subjected to analysis of variance revealed that, the mean sum of squares due to genotypes were significant for all the traits indicating the substantial degree of diversity present among the genetic material selected for the present study.

By using Mahalanobis D^2 statistics, 1653 D^2 values were estimated and Wilk's criterion revealed that, these estimated D^2 values were statistically significant. In the canonical root analysis, first six vectors altogether explained 80.19 per cent of variability. All vector populations were characterized by various divergent values for characters. The trait seed cotton yield per plant (g) shown the highest contribution towards divergence followed by characters such as initial plant stand, ginning percent, seed index and number of bolls per plant. This reveals that traits which are related to higher yields showed maximum contribution towards divergence and these traits are pre-requisite to carry out the divergence studies in cotton.

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