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Exploring Variability and Genetic Diversity in Desi Cotton (*Gossypium arboreum*) for Yield and Fibre Traits

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Abstract

The present study was executed with 20 desi cotton genotypes to unravel the extent of magnitude of genetic variance, heritability (broad sense) and genetic advance as *percent* of mean for yield and fiber traits. The analysis of variance revealed the existence of significant differences among the entries for all the traits studied. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied revealed that the characters were highly influenced by the environmental effects. High PCV, GCV and high heritability coupled with high genetic Advance (>20%) as per cent of mean was displayed by traits seed cotton yield and lint yield. High heritability (>60%) was noted for all traits studied indicating that these characters were under the control of additive gene effects. Selection based on these characters would be effective in designing future desi cotton breeding strategy. All the 20 genotypes were partitioned into seven distinct clusters based on Tocher's method implying the substantial genetic diversity among the genotypes. Cluster II was the largest with eight genotypes followed by cluster I comprised of seven genotypes and the rest were monogenotypic clusters consisting of single genotype in each cluster indicating that high degree of heterogeneity among the genotypes. Clusters VI and VII showed maximum inter-cluster distance (13.64) between them implying these genotypes with high degree of genetic diversity may be utilized in inter-varietal hybridization programme. The trait, halo length followed by seed cotton yield contributed maximum towards total divergence implying feasibility of crop improvement through those characters.

Key words : *Desi cotton, genetic diversity, genetic advance, heritability and variability.*

Introduction

Cotton, king of fiber crops also called as the "White gold" is the main economic and industrial crop of many countries supplying a prime raw material for textile mills. China, India, United States and Pakistan arethe leading cotton producing nations accounting for morethan 70% of the world production. There are more than 50different species belonging to the genus Gossypium. The cultivated species of cotton comprises of two AD genome tetraploids (2n=4x=52) namely *G. hirsutum* and *G. barbadense*, and two A genome diploid (2n=2x=26) namely *G. arboretum* and *G. herbaceum*. Although *G. hirsutum* cultivars contributed about 95% of current world production of 118 million bales and produce superior quality fiber with higher lint yield, yet they are susceptible for many biotic and abiotic stresses (1). In this context, diploid cotton such as *G. arboreum* is the better choice for cotton breeders as it exhibits desirable traits even in low input management practices, tolerates drought and salinity, resistant to pests and diseases. The fiber of desi cotton is suited for medical and surgical purposes as it produces short stable unlike upland cotton produces superior fiber quality for textile industry. Besides desi cotton can generate similar economic benefits to Bt cotton under rain-fed conditions (2). Hence there is need for breeders to focus on desi cotton for their exploitation in breeding programmes by the involvement of genetically diversified desi cotton genotypes identified through diversity and variability studies (3,4).

The findings of this study attribute useful information to implement desi cotton breeding programs. Promising genotypes with desirable traits were identified for further selection and hybridization efforts and also laid a foundation for the development of improved desi cotton varieties with enhanced yields and agronomic performance. The documented genetic variability and associated insights pave a way for future research and breeding strategies aimed at addressing the challenges of sustainable cotton production.

Knowledge on heritability and genetic advance of the character indicate the scope for the importance of a trait through selection. Heritability estimates along with genetic advance are also helpful in predicting the yield under selection. Seed cotton yield and Lint Yield being a complex character is very difficult to improve by selecting the genotypes for yield *per se*, hence identifying the characters which are closely related and have contributed to yield becomes highly essential. The present investigation was conducted to study the genetic parameters like variability, heritability and genetic advance to formulate selection indices for crop improvement.

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Assessment of the genetic diversity of genotpyes is a prerequisite to select appropriate lines for making crosses. Information on the genetic diversity and distance among the breeding lines are important for determining breeding strategies, classifying the parental lines and defining heterotic groups. For assessing genetic diversity, D^2analysis is the potential biometric tool to quantify the degree of divergence (5).

Materials and Methods

The present investigation was carried out during *Kharif*, 2021-22 with 20 desi cotton genotypes to examine the nature and magnitude of heritable variation for nine yield and fiber traits. The field experiment was conducted at an altitude of 211.3 m above mean sea level, latitude of 18.29°N and longitude of 78.29° East ANGRAU, Regional Agricultural Research Station, Nandyal, Andhra Pradesh. Standard crop protection and production practices were followed to raise a healthy crop. The experimental material sown in line with a row length of 5 m in randomized block design (RBD) with 3 replications and a spacing of 60 x 30 cm is followed. Observations were taken for the nine yield and fiber traits *viz.,* days to 50% flowering, days to maturity, plant height, boll number per plant, boll weight, seed cotton yield, ginning percentage, halo length and lint yield which were recorded in five randomly selected plants per accession in each replication.

The mean for each trait under each replication was subjected to statistical analysis. The data for various characters were statistically analyzed for significance by using analysis of variance technique (6). The components of variances were used to estimate the genotypic and phenotypic coefficient of variance (7). Heritability in broad sense was estimated as per the method described by (8) and traits were classified as high (<60%), moderate (30-60%) and low (0-30%) and expressed as percentage of mean. Traits were classified as high (>20%), moderate (10-20%) or low (0-10%) genetic advance as per the method suggested by (9). The data analysis was carried out by using INDOSTAT 9.2 version software.

Results and Discussion

The analysis of variance for the nine yield and fiber traits revealed that the mean sum of squares due to genotypes were highly significant for all the traits studied indicating that adequate variability was present in the material studied Table-1. The outcomes related to general mean, range and genetic parameters of variation, broad sense heritability and genetic advance as per cent mean for all the characters presented in Table-2.

The estimates of genotypic and phenotypic coefficient of variation were observed high for seed cotton yield and lint yield indicating the presence of huge amount of variability amongst all the genotypes and these characters contributed markedly to the total variability. The results are in concordance with the findings of (10,11,12) for lint yield.

High heritability (>60%) coupled with high genetic advance (>20%) reveals that most likely the heritability is due to additive gene effects and simple selection may be rewarding for improving a particular trait. Heritability along with high genetic advance provide the plant breeder with efficient choices of selection. At selection pressure, the extent of genetic gain changes according to the available heritability (13). In this context, high heritability estimates coupled with high genetic advance as per cent of mean were observed for traits seed cotton yield and lint yield suggesting that these traits were governed largely through additive effect of genes and improvement in these characters may be achieved through simple phenotypic selection. In contrast, days to 50% flowering, days to maturity and ginning percentage recorded high heritability with low genetic advance implying that less genetic gains expected through selection in characters depicting high heritability estimates with low genetic advance. These results are in conformity with the findings of (12,13) for trait seed cotton yield and (10,14) for days to 50% flowering and ginning percentage.

The mean values of 20 genotypes were tested for significance by univariate ANOVA and wilk's statistic. Significance of these statistics suggested the existence of considerable divergence and justified further calculation of D^2 clustering which resulted in the grouping of 20 genotypes into seven clusters. The squares of the distance (D^2 value) between any two entries calculated as sum of the difference between the mean values of all 20 genotypes were obtained for further analysis. Group constellation was carried out following Tocher's method (5) which utilizes the D^2 value. The 20 genotypes were grouped into seven clusters. The composition of different clusters is given Table 3 and Fig-1. Among these seven clusters, maximum number of genotypes were grouped in cluster II (8 genotypes) followed by cluster I (7 genotypes) and remaining clusters namely cluster III, cluster IV, cluster V, cluster VI and cluster VII had one genotype each *i.e* they are monogenotypic clusters. Solitary clusters were also reported by (15). High yielder Yaganti falls under cluster VI. The study revealed D^2 values from 0.00 to 15.10 indicating significant divergence in the genotypes (Table-4). The inter cluster distances were greater than intra cluster distances similar to the work of (15). In contrary, (16) recorded higher intra cluster distance. Maximum intra-cluster D^2 value of 15.83 was observed for cluster II (5.75) followed by cluster I (5.47) as remaining clusters exhibited zero intra cluster distance

Table-1 : ANOVA for nine yield and fiber traits in 20 desi cotton genotypes.

S. No.	Character	Mean squares		
		Replications (df : 2)	Genotypes (df : 19)	Error (df : 38)
1.	Days to 50% flowering	0.116	7.890**	2.853
2.	Days to maturity	9.216	37.013**	8.655
3.	Plant height (cm)	134.216	291.851**	46.332
4.	Bolls per plant	0.618	13.496**	5.063
5.	Boll weight (g)	0.006	0.169**	0.037
6.	Seed cotton yield (Kg)	4269.927	177335.996**	7322.606
7.	Ginning Percentage	0.653	4.445**	1.093
8.	Halo Length (Cm)	0.802	9.825**	0.410
9.	Lint yield (Kg)	280.740	22563.868**	867.739

Table-2 : Mean, Variability, Heritability, Genetic advance as per cent of mean in 20 desi cotton genotypes.

Characters	General mean	PCV %	GCV %	Heritability (%)	Genetic advance	Genetic Advance as % of mean
Days to 50% flowering	64	2.53	2.02	63.8	2.13	3.33
Days to maturity	117	2.99	2.61	76.6	5.54	4.72
Plant height (cm)	111.57	8.83	8.10	84.1	17.08	15.31
Bolls per plant	22.14	9.30	7.35	62.5	2.73	11.97
Boll weight (g)	2.08	11.41	10.07	77.9	0.38	18.31
Seed cotton yield (Kg)	459.70	52.88	51.78	95.9	480.16	104.45
Ginning Percentage	37.84	3.21	2.79	75.4	1.89	4.99
Halo Length (Cm)	23.06	7.84	7.67	95.8	3.57	15.48
Lint yield (Kg)	172.19	50.36	49.38	96.2	171.78	99.76

Table-3 : Cluster composition of 20 desi cotton genotypesbased on Tocher's method.

Clusters	Total No. of genotypes	Genotypes
I	7	3156,3167-3,3146-2,3163,3167-1,3148-2
II	8	3151-1,3152-1,3161-2,3166-2,3154-3,3162-1,3161-1,3161-3
III	1	3147-2
IV	1	3169-2
V	1	3166-3
VI	1	Yaganti
VII	1	3147-1

Table-4 : Average Intra and inter-cluster average of cluster distances.

Clusters	I	II	III	IV	V	VI	VII
I	5.47	9.75	9.20	7.84	6.78	9.53	13.36
II		5.75	7.90	10.43	10.09	8.80	8.68
III			0.00	11.06	9.37	11.72	6.71
IV				0.00	7.43	6.27	15.10
V					0.00	9.28	13.38
VI						0.00	13.64
VII							0.00

since they were represented by a single genotype. Maximum inter-cluster D^2 was observed between IV and VII (15.10) followed by cluster VI and VII (13.64), V and VII (13.38) and clusters I and VII (13.36). Since these clusters have higher inter-cluster distance among them, crossing between these clusters will result in heterotic hybrids with high yield and fibre quality and also the resultant segregants from these crosses would be of promising nature. The inter-cluster D^2 value was found to be minimum between III and VII (6.71) suggesting a close relationship between them and a low degree of diversity among the lines.

The cluster mean values for yield and fiber traits are presented in Table-5. A perusal of these results revealed character wise contribution differs from cluster to cluster, so far improvement of a particular character can be carried out by utilizing genotypes from the respective

Table-5 : Cluster means for nine yield and fiber traits in desi cotton.

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Bolls per plant	Boll weight (g)	Seed cotton yield (Kg)	Ginning Percentage	Halo Length (Cm)	Lint yield (Kg)
I	64.43	121.43	115.74	24.13	2.09	339.64	38.93	21.24	132.54
II	63.00	116.88	112.90	23.26	1.91	586.05	37.48	24.08	218.68
III	64.50	115.50	117.70	20.00	2.00	706.50	37.33	21.89	277.02
IV	64.50	114.50	94.70	19.00	1.80	202.00	38.18	20.99	77.13
V	64.50	116.00	104.40	24.40	2.70	353.00	36.17	20.64	127.57
VI	64.00	115.00	97.30	19.50	2.10	349.00	40.04	23.17	127.04
VII	63.50	116.50	128.50	19.90	2.10	1035.50	36.49	23.52	362.34

Table-6 : Contribution of nine yield and fiber characters towards genetic divergence.

S. No.	Characters	Times ranked 1st	% Contribution
1.	Days to 50% flowering	1	0.53
2.	Days to maturity	8	4.21
3.	Plant height (cm)	17	8.95
4.	Bolls per plant	3	1.58
5.	Boll weight (g)	13	6.84
6.	Seed cotton yield (Kg)	48	25.26
7.	Ginning Percentage	12	6.32
8.	Halo Length (Cm)	76	40.00
9.	Lint yield (Kg)	12	6.32

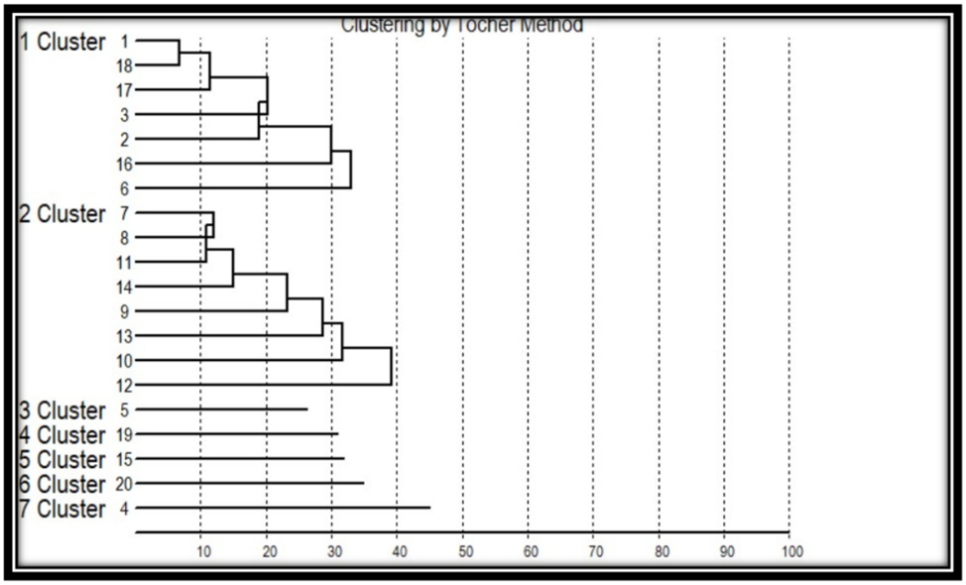

Fig.-1 : Clustering pattern of 20 desi cotton genotypes by Tochers method.

cluster having the highest mean values. Higher mean values for boll number and boll weight were observed in Cluster V while cluster III recorded high mean values for trait seed cotton yield and lint yield. Genotypes in cluster II may be utilized for incorporation of high halo length trait. The results are in accordance with the findings of (17) for boll number and boll weight; (18) for ginning percentage and seed cotton yield.

The contribution of different traits for the diversity was remarkably pronouncing presented in Table 6. The traits halo length and seed cotton yield contributed highest for total genetic divergence. Similar results were observed by (19) for trait seed cotton yield.

Conclusions

The experimental material chosen for present investigation differed in genotypic make up as evidenced for considerable variability and diversity that provides sufficient basis for selection by the breeder. The PCV for all the characters are higher than the GCV indicating that masking effects of environment on the variability. The high PCV, GCV, heritability and genetic advance as per cent of mean was noticed for seed cotton yield and lint yield indicating that selection of these traits would be effective for further cotton improvement programme. The genotypes i.e., NDLA 3169-2 and NDLA 3147-1 present in the clusters IV and VII with maximum inter-cluster distances are exploited in hybridization programme leading to the development of transgressive segregants in desi cotton breeding.

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