Study of genetic parameters and clustering on basis of morpho bio traits of cotton genotypes (*Gosyypium arboreum* L.)

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ABSTRACT : The experiment was conducted at Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during 2017-2018 and comprised of 60 *desi* cotton genotypes evaluated for morphological traits. High values of GCV and PCV were observed for gossypol content, lint yield /plant (20.18, 22.03) and seed cotton yield /plant (19.39 and 21.47) thus these traits show high variability. The traits *viz.*, days to first flower (4.09 and 4.95), ginning outturn (6.06 and 6.65), plant height (4.84 and 5.96) and seed index (9.11 and 10.39) had low values, hence these traits does not have any scope for selection. High heritability coupled with high GAM per cent were recorded for oil content (85.96, 19.12%), protein content (89.32, 24.83%) and gossypol content (91.51, 71.59%), lint index (73.3, 18.7), bolls/plant (79.8, 23), seed cotton yield /plant (81.5, 36), lint yield /plant (83.8, 38). These traits exhibit additive gene action and direct selection will be effective. D^2 analysis grouped 60 genotypes into seven clusters which indicate the presence of substantial genetic diversity in the evaluated germplasm lines. In this context, the highest intra-cluster distance was observed in cluster V and lowest in cluster II. The maximum inter cluster distance was showed between clusters II and IV.Thus these genetic parameters help in selection of breeding method and selection intensity to be exerted to develop better varieties for future.

Key words : Cluster analysis, GCV, genetic advance, heritability, PCV

Cotton belongs to genus *Gossypium*, family *Malvaceae*. It has four cultivable species out of which two are diploid (2n=28) *i.e arboreum* and *herbaceum,* other two are tetraploid (2n=52) namely *hirsutum* and *barbadense*. Cotton is known as white gold and it is cultivated in about 70 countries across the world with the planted area of 31.8 million ha. India commands the highest share globally 36 per cent (about 11.3 million ha) followed by USA 14 per cent (about 4.5 million ha) and China 10 per cent (about 3.2 million ha) in term of area under cultivation (ICAC, 2017-2018).India is the largest producer of cotton accounting one-fourth of the global cotton production. However, India's yield is much lower than other top cotton growing countries.

Information about germplasm variability, trait heritability, genetic advance etc is needed so that better selections can be done in the light of developing superior cultivars. The breeder has to assess the magnitude of genetic variability in breeding material for intensity and direction of selection pressure. It has also been well recognized that if genetic variability in any population is higher, greater will be the chances of obtaining desirable gene

combination.Heritability is an effective tool that helps the plant breeder to evaluate the environmental effect for various traits in breeding programmes. It is also current index to determine the extent of trait that is transferred from parents to off springs. Genetic advance gives the information about the gain in the mean value of trait after selection. High heritability and genetics advance shows the existence of additive gene action and direct selection is preferred whereas high heritability or low heritability coupled with low genetic advance leads to non additive gene action and indirect selection may be helpful in such case. Thus, heritability when coupled with genetics advance and genetic variability could be powerful tool for plant researcher to select proper breeding program.

Mahalanobis's D^2 is an active statistics method for measuring the extent of genetic diversity in germplasm collection of various crop plants which would help in better selection of parents, particularly for hybridization purpose and provides a quantitative degree of correlation between genetic divergence and geographic distribution based on comprehensive distances (Mahalanobis, 1928). An estimate of Multivariate analysis and genetic diversity among parents, a breeder can select suitable parents for successful hybridization by utilizing Mahalanobis's D^2 statistics method and the precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes (Ranjan*et al.*, 2014; Nishanth *et al.*, 2015).

Keeping in view, the importance of genetic studies of different quantitative traits, the present investigations was carried out to study genetic variability, PCV, GCV, heritability and genetic advance for seed cotton yield and its contributing traits among 60 diverse *desi* cotton (*Gossypium arboreum* L.) germplasm lines.

The experimental materials comprised of 60 *desi* cotton genotypes taken from cotton germplasm maintained at Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Each genotype was planted in two rows of 2.7m length in randomized block design with three replications. The spacing of 67.5cm between row to row and 30cm between plant to plant was maintained. Normal cultural practices recommended for *desi* cotton were adopted throughout the crop seasons. The morphological data were recorded on days to first flower, plant height (cm), monopods, sympods and bolls /plant, boll weight (g), seed cotton yield /plant (g), Lint yield /plant (g), seed index (g), Lint index (g) and ginning outturn (%).

Genetic divergence of the individual genotypes was computed using the analytical approach of Mahalanobis, 1928. Pivotal condensation method was utilized to calculate opposite matrix of the error dispersion matrix. The generalized distance function (D^2) between two genotypes for example i^{th} and j^{th} genotypes is essentially the sum of square of differences in Y's for example.

$$D^2 = \sum_{t=1}^{p} \left(Y_{it} - Y_{jt} \right)^2$$

Where,

Y_{it} is uncorrelated mean value of ith genotypes for 't' characters

Y_{jt} is uncorrelated mean value of jth genotypes for 't'characters

Genotypic and phenotypic coefficients of variation were estimated using formula suggested by Burton (1952) for each character, as given below:

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\text{Mean}} \times 100$$

Where;

ó2g = Genotypic variance

ó2p = Phenotypic variance

GCV was classified as low (<10%), moderate (10-20%) and high (>20%) and PCV was classified as low (<20%), moderate (20-30%) and high (>30%).

The broad sense heritability (h^2) was estimated for all the characters. It is the ratio of genotypic variance to the total or phenotypic variance as suggested by Burton and Devane*et al.* (1953).The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al.*, (1955):

$GA = h^2 \times s_{p \times}$ K

Where,

h2 = Heritability estimate in broad sense

s_p = Phenotypic standard deviation of the trait

K = Standard selection differential which is 2.06 at 5 per cent selection intensity.

The Genetic advance as per cent of mean was computed by using the following formula:

$$\text{Genetic Advance as \% of mean} = \frac{\text{Genetic Advance}}{\text{Grand Mean}} \times 100$$

Genetic advance was classified as low (<30%), moderate (30-50%) and high (>50%).

All these parameters *viz.* Genetic diversity and heritability, genetic advance, GCV and PCV was done by using OPSTAT software, available online on www.hau.ernet.in

Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The present study is an effort in the same direction by estimating genetic variability, heritability and genetic advance

Table 1. Showing PCV GCV, heritabilty and genetics advance of 11 traits in 60 genotypes of *desi* cotton

Characters	Co-efficient of variation		Heritability (%)	Genetic advance	
	Genotypic	Phenotypic	(broad sense)	Standard	As *per cent* of mean
Days to first flower	4.09	4.95	68.14	5.00	6.95
Plant height (cm)	4.84	5.96	65.99	16.22	8.10
Monopods /plant	9.43	21.09	20.00	0.09	8.69
Sympods /plant	8.53	11.28	57.13	4.35	13.28
Bolls /plant	12.51	14.00	79.80	7.31	23.02
Boll weight (g)	11.93	14.62	66.67	0.53	20.07
Seed cotton yield /plant (g)	19.39	21.47	81.58	30.04	36.08
Lint yield /plant (g)	20.18	22.03	83.91	13.01	38.08
Seed index (g)	9.11	10.39	76.92	0.74	16.46
Lint index (g)	10.63	12.41	73.33	0.59	18.75
Ginning outturn (%)	6.06	6.65	83.21	4.68	11.39

Genotypic and phenotypic co efficient of variation : High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. The estimation of genotypic and phenotypic components of variance reflects the amount of variability present in the population for different traits. However, such estimation cannot be utilized for comparing relative degree of variability for various characters as these estimates are associated with squared unit of measurement for certain characters. Thus, reliable variation can be achieved by estimating phenotypic co-efficient of variation (PCV %) and genotypic co-efficient of variation (GCV %). Present study showed high GCV and PCV values for gossypol content (36.33 and 37.98%), lint yield /plant (20.18 and 22.03) and seed cotton yield / plant (19.39 and 21.47). Khokhar, *et al.*, (2017) and Joshi and Patil (2018) had showed contrasting reports but the results were in agreement with earlier findings of Kumari *et al.*, (2010) and Patnaik and Sial (2010).

The traits *viz.,* bolls/plant (12.51 and 14.00), boll weight (11.93 and 14.62), lint index (10.63 and 12.41)), protein content (12.75 and 13.49%) and oil content (10.01 and 10.80%)observed moderate level of GCV (%) and PCV (%) whereas traits like days to first flower (4.09 and 4.95), ginning outturn (6.06 and 6.65%), plant height (4.84 and 5.96) and seed index (9.11 and 10.39) observed low GCV (%) and PCV (%). Similar results for boll weight and lint index were found by Khan *et al.*, (2009), Butool *et al.,* (2010), Patnaikand Sial (2010) and Kulkarni *et al.*, (2011). Low PCV and GCV for ginning outturn and seed index are supported by Vinodhana *et al.*, (2013). Plant breeders always encouraged the genetic variability in breeding populations and considered it as the initial requirement to screen the genetic material for different biotic and abiotic stresses. Traits with high PCV and GCV show abundant variation for selection, also less difference between the two values indicates lesser effect of environment on the trait thus selection will be effective. These results can provide a picture of how much variation is present in the material and forming conclusion
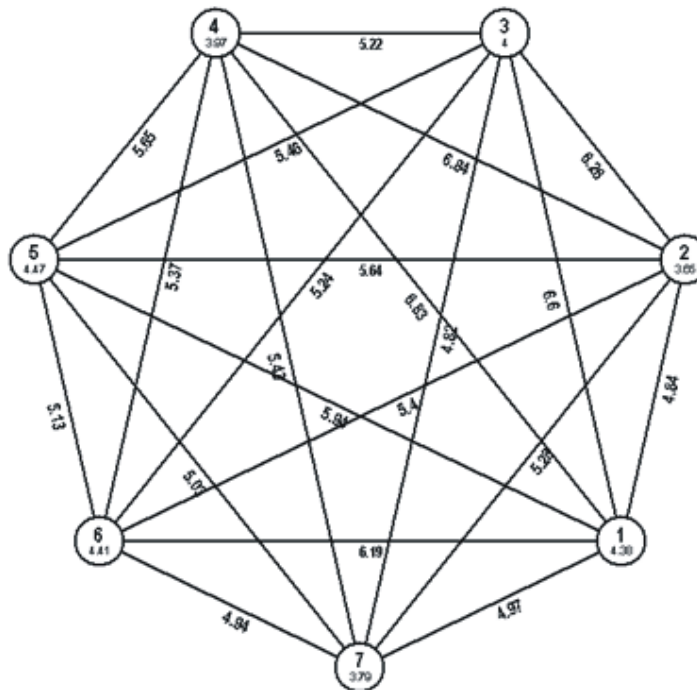
Fig. 1. Seven groups of sixty *desi* cotton genotypes represent inter and intra cluster distance.

whether to go for selection or need to create variation.

Heritability (Broad sense) and genetic advance (GA) : The traits like boll weight (66.67 and 20.08%), lint index (73.33 and 18.75%), bolls /plant (79.80 and 23.03%), seed cotton yield / plant (81.58 and 36.08%), lint yield /plant (83.89 and 38.08%),oil content (85.96 and 19.12%), protein content (89.32 and 24.83%) and gossypol content (91.51 and 71.59%) possess high heritability coupled with high genetic advance which indicates the operation and preponderance of additive gene action and directional selection may be rewarding. Patnaik and Sial (2010) and Pujer *et al.*, (2014) also found additive gene action for boll weight. High heritability with high GAM (%) for seed cotton yield/plant is supported by Kumari *et al.*, (2010)

was in agreement with lint yield/plant and Kulkarni *et al.,* (2011) were supporting lint index exhibiting additive gene action and thus recommending direct selection for these traits.

High heritability was also recorded forginning outturn (83.21 %), seed index (76.92%), plant height (65.99%) and days to first flower (68.14%) but GAM per cent was moderate or low for these traits thus indicates presence of non additive component of gene action which is not fixable. In such cases breeder cannot go for direct selection method, indirect selection may be more helpful. Vinodhana *et al.*, (2013) assists the results for GOT per cent and seed index carrying both additive and non additive gene action. Presence of high heritability in both the traits indicates the possibility of improving this trait through selections.

Moderate estimate of heritability with

Table 2. Distribution of sixty genotypes of *desi* cotton in different clusters

Clusters	Genotypes	Number of genotypes
Cluster I	HD 302, HD 479-2, HD 404, FFS-5, PL 735-1, H 52 -519, FFS-8, BH 30, FFS-6, FFS-7	10
Cluster II	BH 92, DC-93, HD 5278, FFS-9, BH 102, AC 33, HD 351, HD 372	8
Cluster III	FFS-1, Garovilli, H 476-5, HD 10, HD 3, HD 20	6
Cluster IV	HD 392, N-W-1, BH 41, G 20, G 23	5
Cluster V	HD 514, HD 2204, Gao-16 LB VI, Y-1, HD 6, PL 735-2, HD 479-1	7
Cluster VI	BPS, DC 108, D 48-154-1, GOV 6, D 43-21, EB 31-1, D 462-1-1, DS 1, FFS-3	9
Cluster VII	HD 408, FFS-2, HD 524, Arlano, B 2-16-2, FFS-4, RA 1, AC-8, HD 2446, BHO 5 VIII, DS 5, H 1, 35/5 B, B-4, DS-5	15

moderate GAM per cent were observed for sympods/plant (57.13, 13.28%) whereas, low values were recorded for monopods /plant (20, 8.69%). Thus there are low chances of improving these traits with the help of morphological selection.

Genetic divergence analysis : Sixty genotypes of *desi* cotton were grouped into seven main clusters on the basis of comparative magnitude of cluster distance (Table 2). Pattern of clusters displayed that maximum genotypes (15) present in the largest group of cluster VII followed by 10 genotypes in cluster I, 9 in cluster VI, 8 in cluster II, 7 in cluster V, 6 in cluster III and 5 genotypes in cluster IV. Through ward's minimum variance method of Non-hierarchical

Euclidean cluster analysis pattern of clustering of 60 *desi* cotton genotypes represented in Dendrogram (Fig. 2).The investigation discovered that the genotypes from the distinctive regions of the nation were grouped in similar clusters.The distance between inter and intra cluster are showed in Table 3, Fig. 1. The maximum intra clusters distance of 4.47 was observed in cluster V followed by 4.41 in cluster VI, 4.38 in cluster I, 4.00 in cluster III, 3.97 in cluster IV, 3.79 in cluster VII and 3.65 in cluster II. The range of diversity between clusters was found from 4.82 to 6.84 and cluster II and IV exhibited maximum inter cluster distance (6.84) whereas the minimum inter cluster distance was observed between cluster III and VII (4.82). The farther are the clusters the more is the

Table 3. Inter and Intra cluster distances for sixty *desi* cotton genotypes

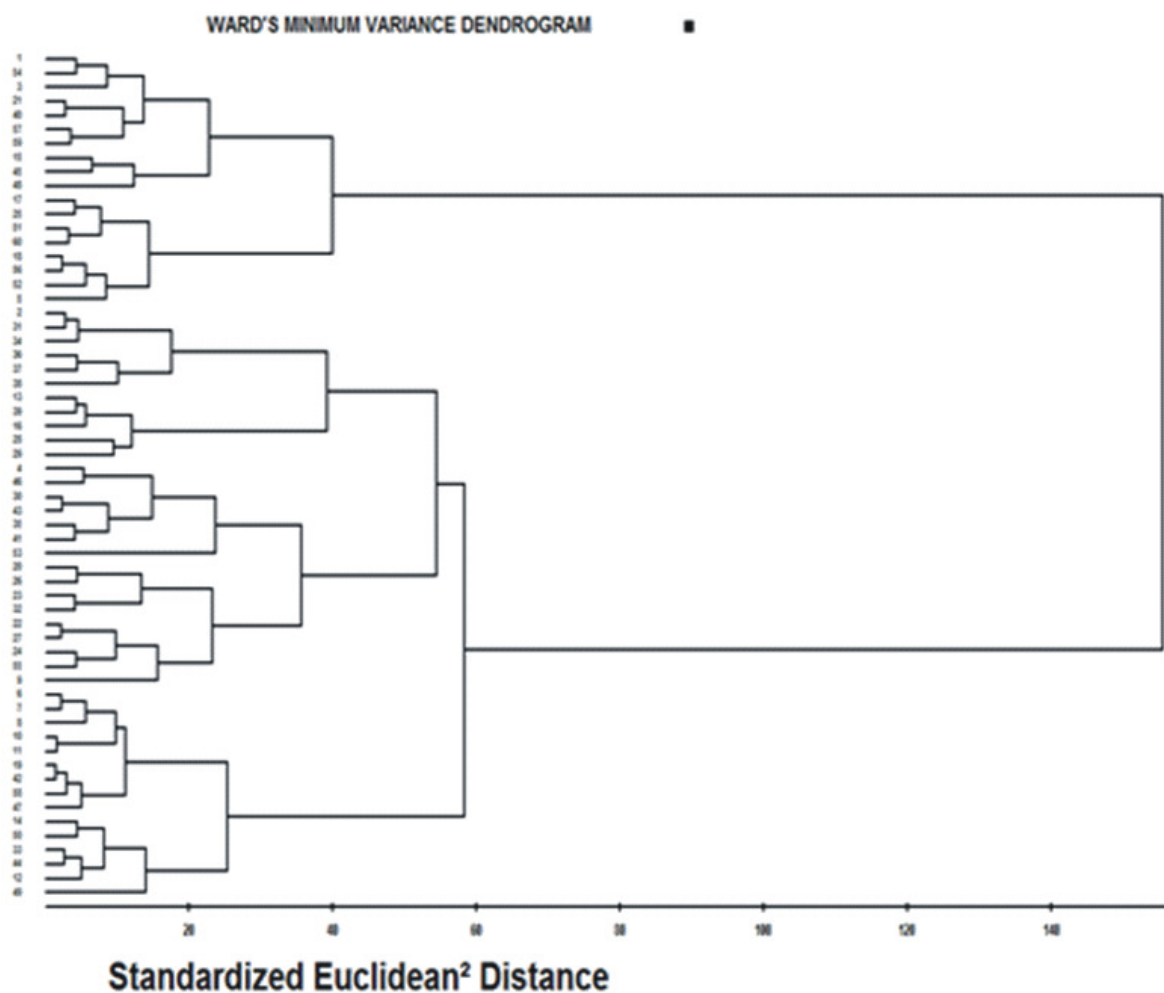|	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**4.38**	4.84	6.60	6.83	5.94	6.19	4.97
Cluster II		**3.65**	6.26	6.84	5.64	5.41	5.28
Cluster III			**4.00**	5.22	5.46	5.24	4.82
Cluster IV				**3.97**	5.65	5.37	5.43
Cluster V					**4.47**	5.13	5.03
Cluster VI						**4.41**	4.94
Cluster VII							**3.79**

Diagonal values indicates intra cluster distances

Fig. 2. Dendrogram depicting pattern of clustering among sixty *desi* cotton genotypes

Table 4. Cluster means for different morphological

	DTF	PH	NM/P	NS/P	NB/P	BW	SCY/P	LY/P	SI	LI	GOT
Cluster I	73.53	189.37	1.00	30.47	27.17	2.39	62.88	27.39	4.20	3.24	43.59
Cluster II	71.21	194.42	1.00	31.29	28.92	2.37	67.48	25.97	4.10	2.56	38.47
Cluster III	72.67	200.06	1.10	31.78	35.45	3.08	107.59	42.14	4.95	3.16	39.04
Cluster IV	69.86	200.47	1.46	35.13	35.67	2.79	97.53	40.93	4.63	3.34	41.97
Cluster V	69.05	212.81	1.00	35.29	31.52	2.56	79.73	32.41	4.81	3.25	40.40
Cluster VI	68.44	204.15	1.03	34.07	34.44	2.72	91.97	36.27	4.59	2.98	39.43
Cluster VII	75.11	202.27	1.00	32.62	31.98	2.76	87.16	37.18	4.40	3.26	42.56
Mean	71.41	200.50	1.08	32.95	32.16	2.67	84.91	34.61	4.53	3.11	41.78

DTF- Days to first flower, PH- Plant height (cm), NM/P- Number of monopods/plant, NS/P- Number of sympods/ plant, NB/P- Number of bolls/plant, BW- Boll weight (g), SCY/P- Seed cotton yield/Plant (g), LY/P-lint yield/ plant(g), SI- Seed index (g), LI- Lint index (g), GOT- Ginning outturn (%).

genetic divergence. The cluster formation can help in selection of parents for hybridization program as we need diverse parents for exploitation of heterosis. Similar studies were conducted by Kulkarni *et al.*, (2011).

The mean of 14 traits of 60 *desi* cotton genotypes showed considerable difference among clusters as shown in Table 4. Cluster III showed the highest mean value for boll weight (3.08), seed cotton yield /plant (107.59), lint yield /plant (42.14), seed index (4.95), and Cluster V also revealed the highest mean value for plant height (212.81) and sympods /plant (35.29). Cluster IV exhibited the maximum mean value for monopods /plant (1.46) and boll /plant (35.67). For lint index (3.35) and protein content (28.62) the highest mean value indicated in cluster IV. Days to first flower had highest mean value in cluster VII (75.11) and lowest in cluster VI (68.44). For ginning outturn the maximum mean value showed in cluster I (43.59%). Thus specific cluster can be chosen for a particular trait to improve. The high mean value of a trait shows that the cluster can be a potent donor of that character. The above given evaluation showed that cluster III and IV showed the maximum mean value for the four characters hence found most desirable for selecting genotypes.The above generated information was comprehensively in concurrence with the results of Kulkarni *et al.,* (2011).The cross breeding between the genotypes belonging to cluster pairs separated by large inter-cluster distance and acquiring high cluster mean for different traits would be progressively helpful for devising hybridization programmes for future .

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