J. Cotton Res. Dev. **37**(2), 187-193 (July, 2023) **ISSN No. 0972-8619**

Genetic diversity analysis for seed quality and yield in upland cotton (*Gossypium hirsutum* L.) genotypes

MINAKSHI JATTAN, SANDEEP KUMAR*, OMENDER SANGWAN, SOMVEER NIMBAL, KARMAL SINGH, DEEPAK KUMAR, SUMAN DEVI AND MANUJ SAINI

Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar,-125004

**Email : sjangra.07@gmail.com*

Abstract : Presence of genetic variability is the pre requisite for any crop improvement programme. Hence, present study was conducted to evaluate upland cotton (*Gossypium hirsutum* L.) genotypes for genetic diversity. Forty upland cotton genotypes were sown in randomized block design with two replications at the Research Area, Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif*, 2021. These were evaluated for seed cotton yield and seed quality traits. The analysis of variance revealed that sufficient variability was present in the germplasm for all traits *viz.*, seed cotton yield, crude protein, oil and gossypol content. The phenotypic coefficient of variance (PCV) was slightly greater than genotypic coefficient of variance (GCV) indicating less influence of environment on the trait expression. High GCV and PCV (22.3 and 24.6%, respectively) were recorded for seed cotton yield (SCY) coupled with high heritability (82.1%) and high genetic advance as per cent mean (41.6%) indicating better scope for advancement through direct selection. The biplot analysis revealed that first two principal components explained 55.6 per cent variability among 40 genotypes. The cluster analysis grouped the genotypes in to four clusters and the genotypes in the cluster I and III were the most diverse based on the studied traits.

Keywords: Diversity, fibre quality, genotypes, quality, yield, seed cotton yield, traits

Cotton is majorly grown worldwide for its natural fibre, edible oil and the cotton seed meal is used as feed for ruminant livestock. Hence, it plays an important role in country's economy (Komala *et al.*, 2018). The area under cotton cultivation is decreasing day by day due to various reasons and climate change is one of them. Improving cotton seed and fibre quality along with lint yield is a challenging task for cotton breeders. Therefore, it is essential to develop high yielding cultivars with good quality to meet the present day requirements. The success of any breeding programme depends on the spectrum of genetic variability present in the populations. However, cotton cultivars grown worldwide have narrow genetic base (McCarty and Jenkins, 2005). For instance, continuous incorporation of genes and selection from same breeding material of cultivated species has resulted in narrow genetic base for most of the elite types which is a major bottleneck for cotton breeding, cultivation and production. There is an urgent requirement to screen available germplasm so that it can serve as a valuable source material for broadening the genetic base. Genetic variability studies have been done earlier by different researchers for yield and quality traits in cotton. Study of genetic variability, heritability and genetic advance in the germplasm will help to determine the real potential of a genotype and selection leads to changes in the genetic structure of population due to preservation of superior alleles eliminating undesirable ones (Budak *et al.*, 2004). The biplot and cluster analysis help the researchers to place/group the genotypes based on their similarities or divergence for different traits so that the diverse genotypes can be utilized in hybrid breeding programmes. Hence, the primary objective of this study was to

determine the genetic variability, heritability and genetic advance in upland cotton. Second objective was to perform diversity analysis for successful inclusion of diverse and desirable genotypes in different clusters for the hybrid breeding programmes.

Forty genotypes of cotton (*Gossypium hirsutum* L.) were planted in two replications at the Research Area of Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agriculture University, Hisar during *kharif*, 2021 (Table 1). Two rows of each genotype were sown with a row to row distance of 67.5 cm and plant to plant distance of 30 cm. All the recommended agronomic practices and plant protection measures were performed. The observations were recorded for the traits *viz*. crude protein (%), gossypol (%), oil (%) and seed cotton yield (g/plant). Data were recorded on five randomly selected plants in each replication for seed cotton yield. The average of five plants was taken to get the seed cotton yield/plant. The seed quality in terms of crude protein, gossypol (Bell, 1967) and oil content was analyzed as per standard protocols. The data on these traits were subjected to analysis of variance as suggested by Fisher (1925) and genotypic and phenotypic coefficients of variation as per Burton and Devane (1953). Heritability in broad sense (Falconer, 1981) and genetic advance were also calculated. D^2 analysis (Mahalanobis, 1936; Rao, 1960) was used for assessing the genetic divergence among the genotypes for different traits. The biplot analysis and hierarchial clustering were done using R studio software. For hierarchial clustering, Ward's method was utilized as it minimizes the total within-cluster variance and no outliers (Ketchen and Christopher, 1996).

The analysis of variance indicated that mean sum of squares due to genotypes were highly significant for the traits studied among 40 genotypes (Table 2). The significant differences suggested the presence of ample genetic variability among the genotypes. Similar results were reported by Nikhil *et al.*, (2018), Eldessouky *et al.*, (2021) and Gnanasekaran *et al.*, (2022) for different traits in cotton.

The mean, range, genotypic and phenotypic coefficient of variation (GCV and PCV), broad sense heritability and genetic advance as percent mean for different traits were calculated (Table 3). The mean values of different genotypes for different traits have been represented in Table 4. The seed cotton yield ranged from 92.7 to 235.7 g/plant with a mean value of 146.8 g/plant. The crude protein content ranged from 17.5 to 28.9 per cent with a mean value of 22.1 per cent. The gossypol content ranged from 0.18 to 0.38 per cent and mean value was 0.25 per cent. The oil content ranged from 14.2-20.3 per cent with mean oil content of 17.1 per cent. The high genotypic and phenotypic coefficient of variance was recorded for seed cotton yield (22.3 and 24.6%, respectively); moderate for crude protein (12 and 12.5%, respectively) and gossypol content (18.1 and 18.9%, respectively) and low for oil content (8 and 9.6%, respectively). Khan *et al.*, (2010) reported similar findings for crude protein and oil content in cotton. All the traits showed high heritability. Heritability value alone may not provide clear predictability of the breeding value as high heritability does not always indicate a high genetic gain. Therefore, it has to be considered in association with genetic advance to predict the effect of selecting superior genotypes (Larik *et al.*, 2000). The high heritability coupled with high genetic advance as percent mean was reported for seed cotton yield followed by gossypol and crude protein indicating the role of additive gene action for the inheritance of these traits and selection will be rewarding in improving these traits (Panes and Sukhatme, 1995). However, oil content showed high heritability with moderate genetic advance as percent mean indicating the involvement of additive and non additive type of gene action. Reciprocal recurrent selection will

Table 1: List of 40 upland cotton genotypes used in the study

Sr. No.	Name of genotype	Sr. No.	Name of genotype
1	CT 1-421	21	216 F
2	H 1464 (2015)	22	320 F
3	H 1470 (2015)	23	LL 54
4	DC 1-104	24	J 34
5	Deltapine 66	25	H 655 C
6	Dunn	26	HS 167
7	RS 2141	27	HG 1-P 625
8	EC 117	28	IAN 589-5855
9	Dunn 119	29	IAN 9332
10	Fergusan	30	IAN 1327
11	GS 4	31	IAN 40-10-385
12	GS 11	32	ISC 67
13	G 67/ disc	33	ISC 6-1-2
14	GB pale green	34	J 2 P7
15	GRB 6015	35	J 6
16	H 1098-i	36	TCH 1599
17	H 1455	37	JCMB Reba B 50
18	H 1451	38	Locket 4785 cream
19	HS 227	39	Locket 4785 white
20	LSS	40	GTSV 337

Table 2: Analysis of variance (ANOVA) for the seed cotton yield and seed quality traits in upland cotton genotypes

Source of variation	Degree of freedom	Traits			
		Seed cotton yield (SCY)	Crude protein	Gossypol	Oil
Replication	1	75.140	0.259	0.00005	75.140
Treatment	39	2363.68**	14.607**	0.00443**	4.5708**
Error	39	80.89	0.541	0.00020	0.7943

be beneficial for the improvement of oil content.

The biplot is an enhanced scatterplot which utilizes both points and vectors to represent a structure. The biplot analysis depicted that the variables were super imposed on plot as vectors where the relative length of the vector signified the relative proportion of variability in the variable. The genotypes present close to each other were more similar than the

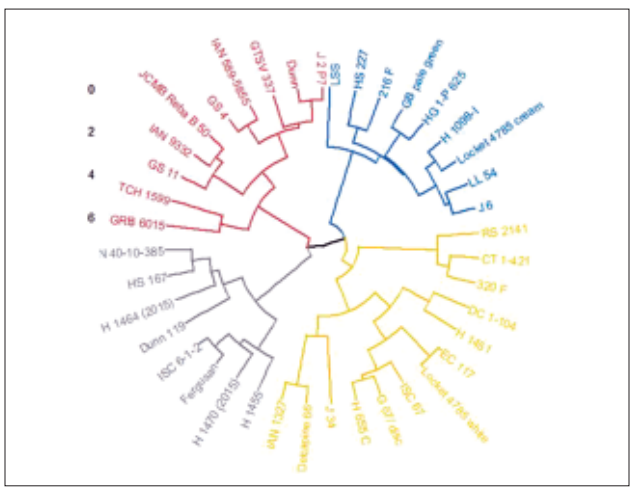

Fig. 2. Hierarchial clustering based on Ward's minimum variance showing grouping of 40 cotton genotypes

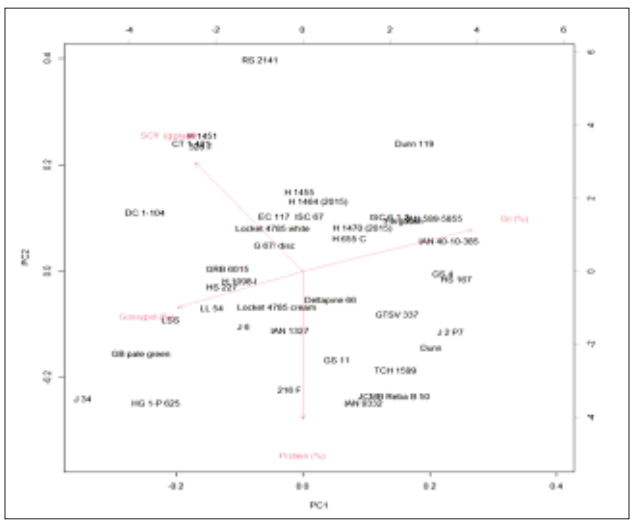

Fig. 1. PC1 & PC 2 Biplot amongst cotton genotypes and studied traits

Table 3: Estimates of genetic variability parameters for different traits in upland cotton genotypes

Traits	Mean ± SE	Range	GCV (%)	PCV (%)	h^2(bs) (%)	Genetic advance as per cent mean
SCY (g/plant)	146.8 ± 6.4	92.7-235.7	22.3	24.6	82.1	41.6
Crude Protein (%)	22.1 ± 0.52	17.5-28.9	12.0	12.5	81.5	23.8
Gossypol (%)	0.25 ± 0.01	0.18-0.38	18.1	18.9	80.0	35.6
Oil (%)	17.1 ± 0.63	14.2-20.3	8.0	9.6	70.4	13.9

Table 4: Mean values of different traits in 40 upland cotton genotypes

Sr. No.	Name of genotype	SCY (g/lant)	Crude protein (%)	Gossypol (%)	Oil (%)
1	CT 1-421	227.6	21.2	0.20	15.5
2	H 1464 (2015)	123.6	17.5	0.29	17.6
3	H 1470 (2015)	106.3	18.0	0.23	16.7
4	DC 1-104	200.2	21.4	0.35	17.3
5	Deltapine 66	129.6	22.2	0.33	19.1
6	Dunn	118.2	24.9	0.21	18.2
7	RS 2141	235.7	18.9	0.22	17.8
8	EC 117	187.5	22.2	0.28	18.2
9	Dunn 119	157.5	18.6	0.27	20.3
10	Fergusan	127.4	19.8	0.20	17.6
11	GS 4	131.3	22.8	0.19	18.6
12	GS 11	117.2	24.2	0.25	17.0
13	G 67/ disc	152.3	21.0	0.26	16.8
14	GB pale green	138.6	23.1	0.30	14.3
15	GRB 6015	208.0	25.6	0.22	16.3
16	H 1098-i	145.6	21.7	0.24	15.3
17	H 1455	146.9	18.7	0.20	15.7
18	H 1451	182.3	17.5	0.31	17.2
19	HS 227	156.3	22.6	0.21	14.5
20	LSS	108.2	19.8	0.32	14.7
21	216 F	105.8	24.2	0.22	14.9
22	320 F	195.8	19.1	0.23	15.6
23	LL 54	140.5	22.1	0.30	16.0
24	J 34	155.4	25.4	0.38	15.4
25	H 655 C	139.6	20.7	0.25	17.9
26	HS 167	107.5	21.4	0.24	19.2
27	HG 1-P 625	138.0	25.4	0.28	14.2
28	IAN 589-5855	148.7	21.5	0.20	18.8
29	IAN 9332	114.9	26.1	0.28	18.2
30	IAN 1327	122.9	22.6	0.33	17.9
31	IAN 40-10-385	92.7	18.6	0.24	18.6
32	ISC 67	170.6	21.5	0.23	17.4
33	ISC 6-1-2	130.3	19.6	0.22	17.8
34	J 2 P7	107.4	23.6	0.21	18.3
35	J 6	152.6	24.2	0.27	16.3
36	TCH 1599	166.6	28.9	0.22	18.9
37	JCMB Reba B 50	115.2	26.3	0.24	18.0
38	Locket 4785 cream	138.9	22.8	0.25	16.2
39	Locket 4785 white	182.9	22.4	0.28	18.1
40	GTSV 337	147.4	25.2	0.18	17.5
	CD (o=0.05)	20.2	1.5	0.02	1.6
	CV %	6.8	3.3	3.80	4.7

genotypes present away from origin. The genotypes RS 2141 and J 34 lied away from the origin. The biplot between principal component 1 and 2 depicting the extent of variation in upland cotton germplasm has been shown in Fig. 1. The first two principal components explained 28.8 and 26.8 per cent of the variability, accounting for a cumulative value of 55.6 per cent variability among 40 genotypes. Shakeel *et al.*, (2015) studied genetic diversity among 50 upland cotton genotypes for quality and yield related traits. They reported that the variability among traits under study exhibited the divergence among the genotypes. Similar results were also reported by Isong *et al.*, (2017) and Jarwar *et al.*, (2019).

All the 40 genotypes were grouped into four major clusters using Ward's minimum variance dendrogram (Fig. 2). Cluster I was comprised of 13 genotypes, and the largest one. Cluster II was having eight genotypes, cluster III with 10 genotypes and cluster IV with nine genotypes (Table 5). The intra cluster distance was the highest for cluster I (2.473); indicating more variability in the genotypes present within this cluster (Table 6). The inter cluster distance was the highest between cluster I and III (3.05) followed by cluster II and IV (2.914). Hence, genotypes in the cluster I and III were the most diverse. The cross combinations can be made between the genotypes belonging to these clusters to get desirable genetic improvement. The cluster mean value for crude protein was the highest in cluster I (25.2%), cluster IV (18.3%) for oil and cluster III (190.0 g/plant) for SCY (Table 7). The lowest cluster mean for gossypol was found in cluster I (0.22%). These results showed that genotypes in cluster I were good in terms of high crude protein and low gossypol content which can be utilized in hybrid breeding with high yielding genotypes in cluster III.

Kaliyaperumal and Ravikesavan (2011) studied morphological diversity and per se performance in 11 upland cotton genotypes and grouped the genotypes in to four clusters. Similar findings were also reported by Muminov *et al.*, (2020) and Sarwar *et al.*, (2021).

CONCLUSION

The grouping of genotypes in to different clusters will be helpful in deciding breeding priorities for simultaneous improvement of seed quality and seed cotton yield. The genotypes RS 2141, CT-1-421 and DC 1-104 belonging to cluster I and GRB 6015 belonging to cluster III had high seed cotton yield. The genotype TCH 1599 belonging to cluster III, Dunn 119 belonging to cluster II and GSTV 337 and GS 4 belonging to cluster III were found promising for protein, oil and low gossypol, respectively. Also, genotypes in cluster I and III were the most diverse. Hence, the cross combinations between the promising genotypes belonging to these clusters will be effective to get desirable cotton improvement.

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Received for publication : May 16, 2023
Accepted for publication : June 6, 2023