

ASSESSMENT OF GENETIC DIVERGENCE AND CHARACTER ASSOCIATION IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) GENOTYPES

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ABSTRACT

The current field experiment was conducted to estimate the genetic divergence between different upland cotton genotypes and also to know the extent of correlation of seed cotton yield with its associated and fiber characters at Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam in Kharif season during year of 2017-2018. The experimental design was laid out in randomized complete block design with four replications for nine genotypes of upland cotton were Bakhtawar, Mehran, Koonj, Sindh-1, NIAB-78, FH-901, BH-160, Chandi-95 and BT-3701. The following observations were recorded. The mean squares from analysis of variance revealed highly significant differences for majority of the traits among the tested genotypes, indicating that used materials can be evaluated for further experiments. Based on mean performance, the genotype NIAB-78 exhibited desirable performance for a wide range of traits, exhibiting its importance in cotton breeding programs. Considering genetic distance, the greater distance was found between Koonj and NIAB-78, followed by Bakhtawar and NIAB-78, NIAB-78 and BT-3701, NIAB-78 and FH-901 and NIAB-78 and Chandi-95, signifying their importance for upcoming hybridization programs in cotton crop. The results also showed that sympodial branches plant⁻¹, bolls plant⁻¹, boll weight and seed index established positive and significant associations with seed cotton yield plant⁻¹, revealing that genotypes having higher extent of these traits may be preferred in selection for evolving high yielding cotton genotypes.

Keywords: Genetic divergence, Correlation, Upland cotton, Genotypes

INTRODUCTION

Cotton, in the form of raw cotton, cotton thread, cloth and manufactured goods, plays a crucial role within our national economy. The upland cotton is recognised as one of the four cultivated species for its high yield ability, large adaptation, variable seeds, and high lint percentage and makes 95% of global output of cotton with the maximum number of released varieties and hybrids (Usharani, 2015). Cotton fiber is the most important raw material for the textile industry. Both yield and quality of fiber are equally important in cotton. Fibre quality parameters should be given due importance in any cotton improvement programme. Since independence of Pakistan genetic improvement of cotton has led to the evolution of large number of cotton varieties with improved productivity by using both indigenous and exotic germplasm. At present all the breeding material and released varieties are susceptible to CLCV-Burewala strain and scientists are in search of resistant sources to develop the resistant or highly tolerant germplasm (Farooq *et al.*, 2014).

High-profile parents cannot actually pass on their dominance in crosses to their progenies. In any systematic breeding program, the elite parents for hybridization and top crosses must be identified (Lingaraja *et al.*, 2017). Therefore, the choice of parents is the most important decision in future cotton breeding programs (van Esbroeck and Bowman, 2015) and interest in genetic heterogeneity is helpful to limit pests or disease vulnerability. It also contains a large amount of allelic diversity, which can be used to generate novel gene variations that are beneficial (Ranal *et al.*, 2015). The requirements of the current spinning method have forced the breeders to create viable genotypes with the optimal strength of the fibre that matches the length and the number of yarns. The present investigation is conducted to estimate industrial heterosis of fibre content characteristics in cotton in rainfed conditions in order to satisfy textile industry needs (Kumar *et al.*, 2017).

Crop improvement primarily refers to the evolution and development of resistant and high yielding crop varieties. The breeding programs are executed generally with the intension to develop varieties with superior qualitative and quantitative traits. However, selection is the most powerful tool for considering a particular trait, which entirely depends on the extent of correlation between yield traits and seed yield (Frasat *et al.*, 2014). Crop genetic diversity is a critical component in crop improvement to identify conservation-oriented breeding programs. Hence, it is essential to know the relationships among crop varieties and genetic diversity in order to recognize complexity of gene pool and also to identify the gaps in the genotype collections (Baloch *et al.*, 2014). It has become necessary to exploit the germplasm properly and also to add new germplasm in the existing genetic pool.

The intensity of a relationship between two variables is defined by the term correlation. A good or high correlation indicates that two or more variables are closely related, while weak or low correlations indicate that the variables are not. The correlation coefficient thus deals with the degree to which multiple plant features are interdependent and identifies the component features which can be used as selection criteria for the improvement of fibre quality and performance (Baloch *et al.*, 2015).

The variability in the germplasm is responsible to induce resistance against abiotic and biotic stresses. To attain desirable genetic variability, various strategies such as hybridization, exotic germplasm and the polyploidy have been practiced in plant breeding. Genetic distance is a measure of the genetic divergence between species or individuals in populations or within species (Liaquat *et al.*, 2015). The populations with similar alleles have low genetic distance, which indicate that they are closely related and have acquired common ancestors. To overcome the threat of this uniformity, it is very important that genetic diversity, available in both the cultivated and its wild progenitors may be thoroughly utilized to create new genetic complexes for higher yield and tolerance to various biotic and abiotic stresses in cotton (Sanghera *et al.*, 2014).

The current study was, therefore, designed to assess genetic distance between the commercial genotypes of cotton and also to shed the light on interrelationships between the traits.

MATERIALS AND METHODS

Experimental Site and Plant Material

The current field experiment was conducted at the experimental farm of Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, during Kharif season, 2017-2018. The experimental design was laid out in randomized complete block design with four replications. Row to row space 75cm and plant to plant distance was kept at 30 cm. All the recommended agronomic practices and plant protection measures were applied to obtain healthy plants. In total, ten plants of each genotype per replication were tagged at random to record the data. The nine genotypes of upland cotton such as Bakhtawar, Mehran, Koonj, Sindh-1, NIAB-78, FH-901, BH-160, Chandi-95 and BT-3701 were studied for different cotton characters like plant height (cm), sympodial branches plant⁻¹, bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹ (g), GOT%, staple length (mm) and seed index (g).

Statistical analysis

Data collected from the experiment were subjected to the analysis of variance according to the method given by Gomez and Gomez (1984), the means of genotypes for all the traits were compared by using the least significant difference (LSD) at 5% probability level as suggested by Steel and Torrie (1980) and correlation coefficient analysis between different traits was applied following Raghavrao (1983). All these data were computed through the software Statistix 8.1. Genetic distance among the genotypes was computed under the procedure of (Murty and Arunachalam, 1966) with the help of SPSS software.

RESULTS AND DISCUSSION

Analysis of variance

Results revealed that traits were significantly differences ($P < 0.05$) for plant height, sympodial branches plant⁻¹, bolls plant⁻¹, boll weight, seed cotton yield plant⁻¹, ginning outturn percentage and seed index, while mean squares for staple length remained non-significant (Table 1). This demonstrates that used genetic resources tend to have useful genetic variations, which may be exploited for further breeding programs so as upland cotton genotypes may

be improved for variety of traits. Genetic variability due to the differences in cotton genotypes was also observed by Pujer *et al.* (2014). Similar to our findings, other researchers including Makhdoom *et al.* (2010), Mugheri (2015), Jatoi (2015) and Mirjat (2018).

Table 1. Mean squares of various yield and yield related characters of upland cotton genotypes.

SOV	d.f.	PH (cm)	SBPP	BPP	BW (g)	SCYPP (g)	GOT (%)	SL (mm)	SI (g)
Replication	2	8.55	4.86	3.78	0.02	24.03	0.01	0.23	0.00
Genotypes	8	261.07**	17.67*	407.32**	0.1**	4063.65**	13.55**	0.88 ^{ns}	0.29**
Error	16	8.41	3.61	11.04	0.02	317.7	0.31	0.67	0.03

SOV, Source of Variation; df, Degree of Freedom; PH, Plant Height; SBPP, Sympodial Branches Plant⁻¹; BPP, Bolls Plant⁻¹; BW, Boll Weight; SCYPP, Seed Cotton Yield Plant⁻¹; GOT, Ginning Outturn; SL, Staple Length; SI, Seed Index

* = Significant at 0.05% probability level

** = Highly significant at 0.01% probability level

NS = Non-significant at 0.05% probability level

Mean performance

The data regarding mean performance of cotton genotype revealed that all the genotype performed variably for most of the traits under investigation. Results revealed that maximum plant height (135.46 cm) was attained by FH-901, followed by BT-3701 (131.33 cm), while minimum plant height was recorded in Mehran (110.26 cm). For sympodial branches plant⁻¹, the maximum sympodial branches plant⁻¹ were recorded in NIAB-78 (23.46), followed by Chandi (21.06), and minimum sympodial branches plant⁻¹ were recorded in Koonj (16.4). Regarding bolls plant⁻¹, the maximum bolls plant⁻¹ (58.93) were set by NIAB-78, next in rank was Sindh-1 (41.66); however, minimum bolls plant⁻¹ were set by Bakhtawar (20.06). In relation to parameter boll weight, the maximum boll weight was weighed in Bakhtawar (3.62g), while minimum boll weight was weighted in BT-3701 (3.00g) (Table 2). For seed cotton yield plant⁻¹, maximum seed cotton yield plant⁻¹ was produced by the genotype NIAB-78 (189.49g), followed by Sindh-1 (133.34g), whereas minimum was produced by the cultivar Koonj (70.49g). Taking ginning outturn percentage, the maximum ginning outturn was recorded in Mehran (40.66%), while minimum was reported in Sindh-1 (33.39%). With regard to staple length, the longer fiber length was measured in Bakhtawar (27.33mm), while shorter fiber length was measured in the genotype FH-901 (25.6mm). As far as seed index is concerned, higher seed index was obtained in NIAB-78 (6.80g), while minimum was obtained in Chandi (5.70g) (Table 2). Memon *et al.* (2016) studied genetic diversity and got the best values for performance. Our findings were also supported by previous researchers such as, Islam *et al.* (2013) and Farooq *et al.* (2013) assessed different cotton genotypes found similar results in their experiments. Better performance of cotton genotypes for different characters were also experimented in the research work of Tamilselvam *et al.* (2013) and Talib *et al.* (2015).

Table 2. Mean performance of upland cotton genotypes for different yield and yield related traits

Genotypes	PH (cm)	SBPP	BPP	BW (g)	SCYPP (g)	GOT (%)	SL (mm)	SI (g)
Bakhtawar	114.13	17.33	20.06	3.62	77.6	39.04	27.33	6.26
Mehran	110.26	16.46	29.86	3.34	94.13	40.06	25.87	6.49
Koonj	127.00	16.4	22.00	3.22	70.49	38.676	26.00	6.06
Sindh-1	115.26	21.2	41.66	3.38	133.34	33.39	26.27	6.21
NIAB-78	110.66	23.46	58.93	3.34	189.49	40.66	26.87	6.8
FH-901	135.46	20.86	28.26	3.13	89.63	39.02	25.6	6.18
BH-160	123.93	18.8	32.06	3.15	100.64	40.03	26.53	6.11
Chaandi	114.86	21.06	30.06	3.09	93.35	38.49	25.93	5.7
BT-3701	131.33	19.93	36	3.00	83.49	38.17	26.13	5.97
LSD (5%)	5.02	3.28	5.75	0.25	30.85	1.41	0.92	0.33

PH, Plant Height; SBPP, Sympodial Branches Plant⁻¹; BPP, Bolls Plant⁻¹; BW, Boll Weight; SCYPP, Seed Cotton Yield Plant⁻¹; GOT, Ginning Outturn; SL, Staple Length; SI, Seed Index

Correlation analysis (r)

Phenotypic corrections among the trait were recorded in all nine genotypes. The results about correlation are mentioned below (Table-3). The relationship between plant height and sympodial branches plant⁻¹, bolls plant⁻¹, boll weight, seed cotton yield plant⁻¹, staple length, GOT% and seed index revealed positive, negative, significant and non-significant correlations with the correlation coefficient of $r = 0.02, -0.22, -0.45^*, -0.35, -0.23, -0.29$ and -0.46^* . The association between sympodial branches plant⁻¹ and bolls plant⁻¹, boll weight, seed cotton yield plant⁻¹, staple length, GOT% and seed index revealed positive, negative, significant and non-significant correlations with the correlation coefficient of $r = 0.61^*, -0.23, 0.67^{**}, -0.11, -0.16$ and 0.10 . Positive, negative significant and nonsignificant associations of bolls per plant were observed with boll weight, seed cotton yield plant⁻¹, staple length, GOT% and seed index with the correlation coefficient of $r = -0.18, 0.82^{**}, 0.01^*, -0.04$ and 0.19 . Significant and nonsignificant positive associations of boll weight were discovered with seed cotton yield plant⁻¹, staple length, GOT% and seed index with the correlation coefficient of $r = 0.47^*, 0.17, 0.13$ and 0.37^* . Significant and nonsignificant positive associations of seed cotton yield per plant were observed with boll weight, staple length, GOT% and seed index with the correlation coefficient of $r = 0.01, 0.04$ and 0.30^* . Nonsignificant and positive associations of staple length were observed with GOT% and seed index with the correlation coefficient of $r = 0.24$ and 0.15 . Significant and positive correlation ($r = 0.44^*$) between ginning outturn percentage and seed index was noted.

Tang and Yang (2012) and Nizamani *et al.* (2017) studied the crop cotton in which they described significant and nonsignificant and positive association between different characters. Similar results of positive and negative associations between seed cotton yield and its related traits were reported by Kumar and Ravikesavan (2010), Baloch *et al.* (2014) and Kaleri (2015), Sahito *et al.* (2016), Ahmad *et al.* (2016), Tariq *et al.* (2012) and Baloch *et al.* (2014).

Table 3. Correlation coefficient (r) between yield and its components of upland cotton genotypes

Traits	PH (cm)	SBPP	BPP	BW (g)	SCYPP (g)	SL (mm)	GOT (%)
SBPP	0.02						
BPP	-0.22	0.61**					
BW (g)	-0.45*	-0.23	-0.18				
SCYPP (g)	-0.35	0.67**	0.82**	0.47*			
SL (mm)	-0.23	-0.11	0.00	0.17	0.01		
GOT (%)	-0.29	-0.16	-0.04	0.13	0.04	0.24	
SI (g)	-0.46*	0.1	0.19	0.37*	0.30*	0.15	0.44*

PH, Plant Height; SBPP, Sympodial Branches Plant⁻¹; BPP, Bolls Plant⁻¹; BW, Boll Weight; SCYPP, Seed Cotton Yield Plant⁻¹; GOT, Ginning Outturn; SL, Staple Length; SI, Seed Index

Table 4. Estimation of genetic distance between different upland cotton genotypes

Genotypes	Bakhtawar	Mehran	Koonj	Sindh-1	NIAB-78	FH-901	BH-160	Chandi-95
Mehran	19.743	.000						
Koonj	14.927	30.079	.000					
Sindh-1	60.186	42.156	67.268	.000				
NIAB-78	118.662	99.946	125.874	59.352	.000			
FH-901	26.13	26.079	22.306	50.3	107.41	.000		
BH-160	27.833	15.506	32.053	35.868	93.888	16.575	.000	
Chandi-95	19.113	6.956	27.508	41.955	100.52	21.026	12.139	.000
BT-3701	24.368	24.765	19.913	52.912	110.482	10.797	19.215	20.126

Genetic distance

The data matrix of tested characters formed on the basis of Euclidean genetic distance calculation. Genetic distance values for all 36 pair wise comparisons of the 9 upland cotton genotypes are presented in Table 4. The greater distance of 125.87 was found between Koonj and NIAB-78, followed by Bakhtawar and NIAB-78 (118.68), NIAB-78 and BT-3701 (110.482), NIAB-78 and FH-901 (107.410), NIAB-78 and Chandi (100.520) and NIAB-78 and Mehran (99.946). However, the minimum or less genetic distance was observed between Chandi and Mehran (6.956), followed by BT-3701 and FH-901 (10.797), Chandi and BH-160 (12.139), BH-160 and Mehran (15.506), BH-160 and FH-901 (16.675), BT-3701 and BH-160 (19.216) and BT-3701 and FH-901 (20.126). Similar to our findings, Wang *et al.* (2012), Memon (2016), Thiago *et al.* (2017) also distinguished upland cotton genetic resources based on phenotypic assessment and reported a number of combinations of genotypes having greater dissimilarity. Mirjat (2018) also reported the greater genetic distance between CRIS-342 and Lalazar, followed by BT-905 and Lalazar, BT-703 and Lalazar, IR-901 and Lalazar, CRIS-494 and Lalazar, Lalazar and BT-886, Lalazar and Sindh-1 and SI-85 and Lalazar. Such results were also observed Suresh *et al.* (2017) and Rajeev *et al.* (2017).

CONCLUSION

Considering genetic distance, the greatest distance was found between Koonj and NIAB-78, followed by Bakhtawar and NIAB-78 signifying their importance for upcoming hybridization programs in cotton crop.

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