
RESEARCH ARTICLE

Genetic variability and morphological characterization of the elite upland cotton germplasm (*Gossypium hirsutum* L.)

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Abstracts

The study was carried out to evaluate the extent of genetic variability in elite germplasm accessions of upland cotton. Highly significant differences recorded for days to flowering, bolls plant⁻¹, boll weight, number of seeds boll⁻¹ and yield plot⁻¹. However the non-significant differences were recorded for plant height and number of monopodial branches plant⁻¹. The *per se* performance of variable range was observed for all studied traits for all the elite cotton accessions. The current study suggests that the PCV was higher than the GCV for all traits. Broad sense heritability was highest for days to flowering and yield per plot demonstrates that these traits could be successfully transferred to offspring, if selection for these characters is performed in the hybridisation programme. Highest genetic advance observed for boll weight and plant height which implies that these characters could be used to select upland elite accession genotypes for a notable improvement in cultivation in changing environments. The morphological characterization based on pollen color,

stigma position and angle of monopodia will help cotton breeder to identify the elite germplasm accessions.

Key words: Heritability, variability, cotton, heritability, genetic advance, morphological characterization

Introduction

In Pakistan, cotton is grown predominantly in the provinces of Punjab and Sindh. Pakistan ranks 4th in cotton production and contribute 1.6% in GDP & 8% to the value added (Khan *et al.*, 2009). The major production constraints include rain showers in the season of cultivation, maximum fluctuation in temperature at the time of flowering and unsuitable technology. In Sindh Sanghar is the most important cotton producing district. In KPK, cotton is grown in D.I.KHAN in an area of about 230 hectares and production is 111 tones with average yield of 483 kg per hectare. Economic Survey of Pakistan (2013-14). The average yield of cotton (571 kg ha⁻¹) in Pakistan is very low as compared to that of the leading cotton producing countries in the world like china USA, India etc. The low

per hectare yield may be attributed to several factors like low land holdings, poverty of farmers, lack of improved and resistant cultivars to diseases and insect pests, weeds and lack of growers know-how about the advanced package of technology concerning crop production and protection. As cotton is very sensitive and care needing crop and the performance of cotton cultivars varies with location and mainly depends upon the environmental conditions. Hence genetic potential and heritability of various genotypes in terms of performance for various morphological parameters is directly desirable for screening of high potential strains for breeding programmes (Khan *et al.*, 2010). Knowledge of genetic potential of different cultivars and their heritability is of prime importance while breeders tackle the problem of low yield (Ahmed *et al.*, 2008). Maximum heritability and genotypic differences suggests that the trait has the improvement opportunity through selection from segregating populations. As the morphological traits of upland cotton cultivars revealed significant variability and seed cotton yield have significant differences for first and last pick (Soomro *et al.*, 2008). Keeping in view the importance of cotton, the study was carried out to estimate heritability and genetic potential in nine different upland cotton cultivars for yield related attributes in the agro-ecological environment of D.I.Khan.

Materials and methods

The experiment was conducted at Cotton Research Station, D. I. Khan during the cotton cropping season 2015-2016 to estimate the quantitative as well as

qualitative attribute in 9 different accessions of cotton i.e. Lalazar, SLH-4, SLH-8, SLH-12, FH-142 CIM-622, CYTO-178, CIM-602 and CEMB-66. The seeds were sown manually on 10 May, 2015 in randomized complete block (RCBD) design having four replications. Each subplot has four rows, 10 meter long with plant to plant and row to row distance of 30 and 75 cm respectively. For single plant hill⁻¹ thinning was performed after 20 days of germination with all the recommended cultural and standard plant protection measures to reduce the environmental variations. Picking was performed on single plant basis in the end of August 2015. The parameters studied during research were days to first flowering, monopodial branches, number of bolls plant⁻¹, number of seed bolls⁻¹, bolls weight (g), plant height (cm) and yield plot⁻¹. All the collected data were subjected to analysis of variance techniques as suggested by Steel and Torrie (1980) and LSD test was utilized when ANOVA showed significant differences among the genotypes. Heritability broad sense (H₂) was estimated according to Burton (1951) on entry mean basis.

Results and discussion

Analysis of variance is presented in Table 1. Highly significant differences manifested ($p \leq 0.01$) for days to flowering, bolls plant⁻¹, boll weight, number of seeds boll⁻¹ and yield plot⁻¹. However the non-significant differences were recorded for plant height and number of monopodial branches plant⁻¹.

***Per se* performance of the elite cotton germplasm accessions**

The plant height ranged from 110 to 134.33 cm among the cotton cultivars (Table 2). Maximum height (134.33 cm) was recorded in Lalazar followed by CIM-602 (126.67 cm). Minimum plant height was recorded in Cyto-178. Although dwarf plants are desired on account of threat due to lodging, but it has also been investigated in various studies that in the absence of lodging plant height are positively associated along with number of bolls plant⁻¹ and yield. Days to maturity ranged from 49.33-56.33, which showed that early flowering was observed in Lalazar and CIM-622 (49.33) reflecting early maturing cultivars, followed by SLH-12 and FH-142 (50.66), while late maturity was observed in SLH-8 (56.33). The data ranged from 1.33-1.83, with maximum number of monopodial branches was found in Lalazar (1.83) which was statistically at par with SLH-8 (1.80), while minimum value was observed in CEMB-66 (1.33). Bolls plant⁻¹ ranged from 16.33 to 30.13. Highest bolls plant⁻¹ (30.13) was recorded in FH-142 which was statistically at par with Lalazar. Minimum bolls plant⁻¹ was recorded in genotype SLH-8. Ahmed *et al.*, (2008) also obtained similar results for boll number. also investigated various *G. hirsutum* cultivars for yield parameters and recorded significant differences for bolls number and weight and contributed significant variation and direct relation with seed cotton yield. The highest boll weight was recorded in Lalazar. Minimum boll weight (2.77 g) was recorded in CIM-622. The remaining genotypes showed intermediate boll weight also observed the same proportion and variation regarding boll weight in association with seed cotton yield in various genotypes of

cotton. Seeds boll⁻¹ ranged from 18.55 to 27.11. Highest seeds boll⁻¹ (27.11) was recorded in SLH-12 which was statistically at par with Lalazar (table 6). Minimum seeds boll⁻¹ were recorded in genotype CIM-622. Ahmed *et al.*, (2008) also obtained similar results for seeds boll⁻¹. The data regarding yield plot⁻¹ indicated highly significant differences among various cotton genotypes. It ranges from 6.56-8.23, which showed that maximum yield was observed in FH-142 and while Minimum was observed in CENB 6.56. Hence, it is seen from the mean performance that variable range was present among all the elite cotton accessions.

Variability parameters

For plant height genetic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) recorded in between 4.18 and 11.16 but from analysis in variance the value of genetic variance (GV) and phenotypic variance (pv) ranged between 26.19 and 186 respectively (Table 3). The values of phenotypic coefficients of variability (PCV) were larger than genotypic coefficient of variability (GCV) which means the interaction of environment with plant height. Similarly results were reported by Suinaga *et al.*, (2006) and Meena *et al.*, (2007). From ANOVAs the value of heritability for plant height is 15 but the value of genetic advance is 40. The variation among low heritability and high genetic advance depicts that there is a more role of additive gene. For days to first flowering the coefficient of variability in the genetic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) the value are 3.73 and 4.68 but from

analysis in variance the value of genetic variance (GV) and phenotypic variance (pv) are 3.68 and 5.79 respectively. The value phenotypic coefficients of variability (PCV) were larger than genotypic coefficient of variability (GCV) showed the interaction of environment for days to first flowering. Similar results were reported by Reddy and Sarama (2014), Dhamayanathi *et al.*, (2010). From ANOVA the value of heritability for days to first flowering is 63 but the value of genetic advance is 3. The variation among high heritability and low genetic advance depicts that there is a more role of additive gene. Similar result is recorded by earlier researchers viz., Reddy and Sarama (2014) and Dhamayanathi *et al.*, (2010). For bolls plant⁻¹ the coefficient of variability in the genetic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) the value ranged in between 10.98 and 59.02 from analysis in variance it is observed that the value of genetic variance (GV) and phenotypic variance (pv) ranged between 14.33 and 33.09 respectively. The value phenotypic coefficients of variability (PCV) were larger than genotypic coefficient of variability (GCV) showed the interaction of weather for bolls plant⁻¹. Earlier Ahmed *et al.*, (2008), Khan (2003) reported similar reports. The values of heritability for bolls plant⁻¹ is 18.60 but the value of genetic advance is 30. The variation among high heritability and low genetic advance depicts that there is a greater role of additive gene. Similar results were reported by Khurram *et al.*, (2009). For seeds boll⁻¹ the coefficient of variability in the genetic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) the value reported as 9.83

and 14.47 but from analysis in variance the value of genetic variance (GV) and phenotypic variance (pv) recorded as 5.82 and 12.60 respectively. The value phenotypic coefficients of variability (PCV) were larger than genotypic coefficient of variability (GCV) showed the interaction of environment with seeds per boll similar result were reported by earlier researchers such as Khurram *et al.*, 2009. From the value of heritability for a seed per boll reported as 46.19 but the value of genetic advance is 34. The variation among high heritability and low genetic advance depicts that there is a great role of additive gene. Similar result recorded by Khurram *et al.*, 2009. From the table (3) for yield plot⁻¹ the coefficient of variability in the form of genetic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) ranged in between 20.36 and 26 but from analysis in variance the value of genetic variance (GV) and phenotypic variance (pv) recorded as 2.19 and 3.45 respectively. The value phenotypic coefficients of variability (PCV) were larger than genotypic coefficient of variability (GCV) showed the interaction of weather for yield plot⁻¹. Similar results were reported by earlier researchers Reddy and Sarama (2014). From Anova the value of heritability for yield plot⁻¹ is 63 but the value of genetic advance is 24. The variation among high heritability and low genetic advance depicts that there is a great role of additive gene. Similar result is recorded by Dhamayanathi *et al.*, 2010.

Morphological characterization

All the elite genotypes were evaluated for morphological variations like pollen color,

stigma position and angle of monopodia (Table 4). The cultivar lalazar have light yellow color pollen, exerted stigma and their monopodia were at an angle to the main stem. SLH-4 have deep pollen color, embedded stigma and their monopodia were at an angle to the main stem. SLH-8 have deep pollen color, Exerted stigma and their monopodia were at an angle to the main stem. SLH-12 have deep pollen color, embedded stigma and their monopodia were at an angle to the main stem. FH-142 have deep pollen color, embedded stigma and their monopodia were at an Straight to the main stem. CIM-622 142 have light pollen color, exerted stigma and their monopodia were at straight to the main stem. CYTO-178 have deep pollen color, exerted stigma and their monopodia were at straight to the main stem. CIM-602 have light pollen color, Embedded stigma and their monopodia were at straight to the main stem. CEMB-66 have light pollen color, embedded stigma and their monopodia were at straight to the main stem. The identified morphological traits may serve morphological markers in the identification the elite germplasm. Earlier Ramesh (2017) characterized pigeonpea germplasm based on morphological characteristics, which supports our findings. The characterization will help cotton breeder to identify the elight germplasm accessions.

References

1. Ahmad, W., N.U. Khan, M.R. Khalil, A. Parveen, U. Aiman, M. Saeed, Samiullah and Shah, S.A. 2011. Genetic variability and correlation analysis in upland cotton. *Sarhad. J. Agril.*, 24: 195-201.
2. Burton, G.W. 1951. Quantitative inheritance in pearl millet (*Pennisetum glaucum*). *Agron. J.*, 43:409–417.
3. Dhamayanathi K. P., M.S. Manickam and K. Rathinavel, K. 2010. Genetic variability studies in *Gossypium barbadense* L. genotypes for seed cotton yield and its yield components. *Electronic J. Plant Breed.*, 1(4): 961-965.
4. Economic Survey of Pakistan 2013-14. Economic advisors Wing, Finance Division, Government of Pakistan, Islamabad.
5. Khan, N.U. 2003. Genetic analysis, combining ability and heterotic studies for yield, its components, fibre and oil quality traits in upland cotton (*G. hirsutum* L.). Ph.D Dissertation, Sindh Agril. Univ. Tandojam, Pakistan.
6. Khurram, Tausif and Patil S.S. 2009. Genetic studies on improving productivity and quality traits Involving interspecific (H x B) crosses and barbadense genotypes. *Karnataka J. Agric. Sci.*, 22(5).
7. Khan, N.U., Basal, H. and Hassan ,G. 2010. Cotton seed oil and yield assessment via economic heterosisand heritability in intra-specific cotton populations. *African J. Biotechnol.* 9(44): 7418-7428.
8. Meena, R., Monga, A.D. and Kumar, R. 2007. Undisruptive cotton cultivars of north zone: an evaluation. *J. Cotton Res. Dev.*, 21: 21-23.
9. Ramesh, M. 2017. Genetic diversity and characterization of pigeonpea germplasm., *J. Genet, Genomics, Plant Breed.*, 1(1) 32-35.
10. Reddy, R.Y. and Sarma, A..S.R. 2014. Genetic variability for yield components and fibred characters in cotton (*Gossypium arboreum* L.). *Plant Archives*, 14 (1): 417-419.
11. Soomro, A.R., Kaskar, R.G., Ali, H. and Abid, S.A. 2008. Comparison of yield and

its components in some commercial cottons varieties. *Indus J. Plant Sci.*, 4: 545-552.

12. Steel, R.D.G. and Torrie, J.H. 1980. Principles and procedures of statistics, a biological approach 2nd ed. McGraw Hill inc, New York, Toronto, London.
13. Suinaga, F.A., C.S. Bastos and Rangel L.E.P. 2006. Phenotype adaptability and stability of cotton cultivars in Mato Grosso State, Brazil. *Pesquisa Agropecuaria Trop.*, 36: 145-150.

Table 1. Mean squares for different yield related traits for elite germplasm accessions

Parameters	Replication	Genotype	Error	CV
Days to first flowering	0.44	13.16**	2.11	2.83
Monopodium branches	0.38	0.17 N.S	0.26	33.89
Number of boll per plant	346.73	80.98**	48.04	29.86
Number of seed par boll	67.52	24.25**	6.78	10.62
Boll weight (g)	0.61	0.65**	0.11	9.54
Plant height (cm)	983.11	133.51 N.S	212.09	11.92
Yield plot ⁻¹	0.48	0.98**	0.07	3.89

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$, N.S. = Non-significant, CV = Coefficient of variation

Table 2: Mean table of elite accessions for various traits

Accessions	Days to first flowering	Monopodial branches plant ⁻¹	Bolls plant ⁻¹	Boll weight	seeds per boll	Plant height	Yield plot ⁻¹
Lalazar	49.33 c	1.83 a	30.13 a	4.55 a	26.21 ab	134.33a	8.00 a
SLH-4	51.0 bc	1.40 a	23.93 ab	3.77 b	27.11 a	117.07 a	7.13 b
SLH-8	56.33 a	1.80 a	16.33 b	3.38 b	23.66 ab	122.20 a	6.60 c
SLH-12	50.66 bc	1.66 a	19.86 ab	3.66 b	27.22 a	121.53 a	6.90 bc
FH-142	50.66 bc	1.46 a	30.80 a	3.49 b	24.55 ab	124.87 a	8.23a
CIM-622	49.33 c	1.20 a	24.06 ab	2.77c	18.55 c	120.0 a	7.33 b
Cyto-178	52.33 b	1.26 a	25.60 ab	3.77 b	27.10 a	110.00 a	7.23 b
CIM-602	51.00 bc	1.73 a	21.46 ab	3.75 b	23.88 ab	126.67 a	7.00 bc
CEMB-66	51.33 bc	1.33a	16.73 b	3.48b	22.44 bc	123.33 a	6.56 c
LSD _{0.05}	2.51	0.89	11.99	0.59	4.50	25.20	0.48

Table 3: Variability parameters for various studied traits

Parameters	Vg	Vp	GCV	PCV	H ² _{BS}	GA
Days to first Flowering	3.68	5.79	3.73	4.68	63.55	3.0
Monopodium Branches	0.03	0.23	11.16	31.50	13.00	15.0
Number of ball per plant	10.98	59.02	14.27	33.09	18.60	30.0
Number of seed par Ball	5.82	12.60	9.83	14.47	46.10	34.0
Boll weight(g)	0.18	0.29	12.0	15.0	62.00	68.0
Plant Height (Cm)	26.19	185.9	4.18	11.16	15.00	40.0
Yield plot ⁻¹	2.19	3.45	20.36	26.0	63.00	24.0

Vg: genotypic variance; Vp: phenotypic variance; GCV: genotypic coefficients of variation; PCV: phenotypic coefficients of variation H²_{BS}: broad sense heritability; GA: genetic advance as percent of mean

Table 4: Morphological characterization of the elite cotton germplasm accessions

Accession	Pollen color	Stigma position	Position of Monopodia
Lalazar	Light yellow	Exerted stigma	Angle
SLH-4	Deep yellow	Embedded	Angle
SLH-8	Deep yellow	Exerted stigma	Angle
SLH-12	Deep yellow	Embedded	Angle
FH-142	Deep yellow	Embedded	Straight
CIM-622	Light yellow	Exerted stigma	Straight
CYTO-178	Deep yellow	Exerted stigma	Straight
CIM-602	Light yellow	Embedded	Straight
CEMb-66	Light yellow	Embedded	Straight