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INHERITANCE OF SEED COTTON YIELD AND RELATED TRAITS IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

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Abstract

Different genetic parameters and relationships of seed cotton yield with yield related traits were estimated among thirty upland cotton genotypes. Fuzzy seed weight and non fuzzy seed weight showed lesser genetic variability while cotyledonary leaf area, gossypol glands, emergence %, and seed cotton yield exhibited intermediate range of variability. Sufficient genetic variability was observed only for fuzz weight. Heritability values were significant and moderate to high for all the traits. High heritability estimates were found for seed cotton yield followed by cotyledonary leaf area. Fuzzy seed weight, non fuzzy seed weight, leaf area, gossypol glands and emergence % exhibited significant positive genotypic and phenotypic correlations with seed cotton yield. Fuzz weight of single seed showed significant negative genotypic and phenotypic correlations with seed cotton yield. Adequate genetic potential was observed in cotton genotypes under study and information generated here in regarding heritability and other genetic parameters might be useful for establishing selection criteria for improvement of seed yield.

Introduction

Cotton (*Gossypium hirsutum* L.) is an important cash, textile and most premier crop in economic perspective of Pakistan. Cotton being a non-food crop contributes significantly in foreign exchange earning. Besides its textile industry use, it also provides food in form of edible oil and cotton seed cake and its contribution in local edible industry is around 70% (Khan *et al*., 2007; Abid *et al.*, 2011). Cotton accounts for 8.6% of the value added in agriculture and about 1.8% to GDP. During 2009-2010, cotton was sown on an area of 3106 thousand hectares with production of 12.7 million bales, which was 7.4% higher than last year's production (11.8 million bales). However, cotton production was 5% less than the target (13.36 million bales) mainly due to shortage of irrigation water and high temperatures etc. (Anon., 2010). World demand for cotton is growing at a rapid pace, far greater than the world population growth rate. The demand for cotton fiber that is suitable for modern yarn spinning and for high quality textiles is also increasing. Cotton improvement program has responded well to the needs of growers and industry such as combine high yield, early maturity and good fiber quality. Modern cotton breeders and bioengineers have contributed to achieve this goal (Zia *et al*., 2011). Nevertheless, the need for further amplified efforts for continued genetic improvement of cotton is even greater today than before in order to increase productivity per unit area. Therefore, more attention must be paid to the development of such varieties that can meet to the future challenges. Cotton breeders have directed their efforts to improve the architecture of cotton plants and a considerable work in this regard has been carried out but we are still far behind in seed cotton yield as compared to other advanced countries.

Knowledge of genetic variability existing among different genotypes for various parameters is important in crop improvement. Heritability, which measures phenotypic variance and is attributable to genetic causes, is another important consideration for a successful breeding program. Association of heritability with genetic advance helps in understanding the mode of inheritance of quantitative traits (Aqsa *et al.,* 2010). For effective plant improvement genetic correlation of cotton seed with other traits is also important. Correlation coefficients are useful if indirect selection of a secondary trait is to be used for improving the primary trait of interest. Such interrelationships are also helpful to establish effective selection criteria for cotton improvement programs.

Present study was carried out with the objectives, to estimate the genetic components and relationships between seed and yield traits and to find out guidelines for plant selection that can be successfully employed in formulating an effective selection program in cotton breeding.

Materials and Methods

The experimental material was comprised of 30 upland cotton genotypes. The experiment was laid out in a randomized complete block (RCB) design with three replications at Cotton Research Station, Multan, Pakistan. All the varieties were sown by dibbling method in a 3.3 m plot size (having four rows), with 30 and 75 cm plants and rows spacing, respectively. After harvesting and ginning on individual plant basis, the cotton seed was collected. Data for single fuzzy and naked seeds were recorded on electric balance. Fuzz was removed with the help of sharp knife and weighed to get single seed fuzz weight. Seeds were sown in polythene bags and kept under controlled conditions in green house. After 12 days, emergence of plants was recorded and emergence % was calculated. The cotyledonary leaf area was measured with the help of leaf area meter. Twenty seeds were soaked in Petri dishes and then were cut from middle portion with help of sharp knife. The dissected portion was observed under stereoscope to count gossypol glands. The average seed cotton yield was formulated as sum of first and second pickings.

Data were subjected to the analysis of variance following Steel *et al*., (1997). Genetic and phenotypic components of variance were computed as described by Cochran & Cox (1957). Estimates of broad sense heritability and coefficients of variability were calculated following Hanson *et al*., (1956), Burton (1952) and Johnson *et al.,* (1955). Genetic advance at different selection intensities (5, 10, 15 & 20%) and relative expected genetic advance (at 5% selection intensity) was calculated following Falconer, (1989). Different selection intensities used are;

I = 2.06(5%), 1.755(10%), 1.554(15%), 1.40(20%)

Phenotypic and genotypic correlation coefficients were calculated as outlined by Kwon & Torrie (1964). Significance of genotypic correlation was tested following Reeve (1955) and Robertson (1959).

Results and Discussion

Highly significant ($p \leq 0.01$) differences were observed among genotypes for all the traits (Table 1). Perusal of the mean data (Table 2) revealed that maximum fuzzy seed weight was observed for genotype CIM-70 (108.3 mg/seed) followed by 268-F whereas minimum fuzzy seed weight was recorded for D-9 (55 mg/seed). Non fuzzy seed weight ranged between 50.0 to 98.3 mg for D-9 and CIM-70, respectively. Maximum values for single seed fuzz weight was recorded for varieties, MNH-147, GR-156 and MNH-129 (36.7 mg/seed) while minimum values were noted for D-9 and L-11 (5mg/seed). MNH-635 possessed maximum leaf area (9.9 cm^2) followed by S-14. However, SLS-1 was found to have minimum value (3.04 cm^2). Highest number of gossypol glands was recorded in MNH-147 and NIAB-78 whereas D-9 had the lowest number of gossypol glands. Emergence was found to be 100% in MNH-636, MNH-635, NIAB-78, 199-f, 268-F, 362-F and CIM-446, while BS-1 had lowest emergence %. NIAB-78 gave maximum seed cotton yield per hectare followed by MNH-636 and 124-F.

Table 1. Mean squares of different plant traits among cotton genotypes.

S.O.V.	d.f.	Single fuzzy seed weight	Single naked seed weight	Single seed fuzz weight	Cotyledonary leaf area	Gossypol glands/ seed	Emergence percentage	Seed cotton yield
Reps	2	330.83^{NS}	435.28^{NS}	75.28^{NS}	0.73^{NS}	40.83^{NS}	259.24^{NS}	527.94^{NS}
Genotypes	29	462.16**	384.69**	239.47**	7.80**	376.95**	954.18**	6929.97**
Error	58	172.21	165.36	95.68	1.86	133.91	450.91	3077.97

** = Highly significant, NS= non-significant

Table 2. Mean phenotypic values of different plant traits of cotton genotypes.

Genotypes	Single fuzzy seed weight (mg)	Single naked seed weight (mg)	Single seed fuzz weight (mg)	Cotyledonary leaf area (cm^{-2})	Gossypol glands/ seed	Emergence percentage	Seed cotton yield (kg/ha)
FH-634	66.7	56.7	10.0	7.70	62.7	77.8	1845
BS-1	75.0	63.3	11.7	4.97	44.7	10.0	2306
FH-901	93.3	83.3	10.0	7.32	68.7	55.5	2229
MNH-636	78.3	70.0	8.3	6.86	46.0	100.0	2383
MNH-635	85.0	71.7	13.3	9.97	33.0	100.0	2056
D-9	55.0	50.0	5.0	5.22	23.3	55.5	231
MS-40	70.0	60.0	10.0	3.90	40.7	77.8	2230
S-14	85.0	78.3	6.7	8.10	59.7	88.9	1775
NIAB Krishma	93.3	80.0	13.3	3.94	54.3	77.8	1768
AC-134	81.7	73.3	10.0	3.15	51.7	44.4	1845
MS-39	101.7	85.0	16.7	7.20	50.7	77.8	1384
4-F	78.3	73.3	8.3	4.81	59.0	66.6	1768
NIAB-78	96.7	88.3	8.3	7.70	72.3	100.0	2691
199-F	90.0	78.7	11.7	7.53	59.7	100.0	1845
L-11	88.3	83.7	5.0	6.65	70.66	88.9	1384
268-F	105.0	91.7	13.3	6.17	49.0	100.0	1768
B-557	88.3	81.7	6.7	5.35	55.0	77.7	1768
LSS	88.3	81.3	10.0	6.12	56.3	33.3	1845
K68-9	100.0	88.7	11.7	6.57	59.0	66.7	1076
362-F	81.7	71.7	10.0	7.09	47.3	100.0	2306
CIM-478	85.0	68.3	16.7	6.65	57.3	88.9	1744
CIM-70	108.3	98.3	25.0	4.90	64.7	66.7	1768
FH-1000	88.3	78.3	25.0	4.32	49.0	77.8	1614
GR-156	90.0	88.3	36.7	4.77	54.7	66.7	1768
MNH-129	65.0	58.3	36.7	5.19	50.7	66.7	1153
124-F	95.0	83.3	10.0	6.36	45.0	77.8	2383
SLS-1	90.0	76.7	13.3	3.04	53.7	66.7	2229
CIM-446	91.7	81.7	10.0	4.84	47.7	100.0	2360
Qalandri	100.0	88.3	11.7	4.65	68.3	77.8	1614
MNH-147	70.0	63.3	36.7	4.89	72.3	88.9	1999
Mean ± SD	86.16 ± 12.41	76.52 ± 11.47	14.06 ± 8.94	5.86 ± 1.59	54.24 ± 11.21	75.89 ± 21.38	1837.33±482.54

Phenotypic coefficients of variation were higher than their respective genotypic coefficients of variation for all the traits under study (Table 3). Single seed fuzz weight exhibited maximum genotypic coefficient of variation (GCV = 49.25%) followed by seed cotton yield (26.10%) suggesting substantial amount of genetic variability for these traits. Results suggested that sufficient amount of genetic variability among genotypes may be helpful for improvement of yield through selection. Results were in line with those of Batool *et al*., (2010); Ulloa (2006); Pahlavani *et al*., (2008); Romano & Scheffler (2008); Hussain *et al*., (2009); Khan *et al*., (2009a, 2009b); Efrem *et al.,* (2010) and Bolek *et al*., (2010) who reported significant genetic variability among cultivars for fiber quality traits, gossypol glands, fuzz weight and for seed cotton yield. Selection becomes most viable and stable when it is based on reliable genetic parameters. Presence of high GCV values as an indicator of genetic variability for seed cotton yield and overall great influence of environment on traits under study were in accordance with findings of Asad *et al*., (2002); Khan (2003); Killi *et al.,* (2005) and Ganensan & Reveendran (2007).

Heritability estimates of different traits (Table 3) ranged from moderate to high (0.53 to 0.99). However, heritability estimates were significant for all the traits except gossypol glands/seed. Seed cotton yield and cotyledonary leaf area exhibited highest magnitude of heritability i.e., 0.99 and 0.76, respectively which indicated greater genetic variation among cotton genotypes for these traits. Moreover, it is also evident that these traits could be further improved through simple selection. All other traits showed moderate heritability. Seed cotton yield being highly heritable trait was expected to remain stable under varied environmental conditions as environment is less influential on highly heritable traits. Similarly, Killi *et al.,* (2005); Mahros *et al*., (2008) and Khan *et al*., (2010) also reported high heritability estimates for seed cotton yield. Results indicated that yield was controlled by additive genes having an opportunity for further improvement by mass selection and can be easily transferred to succeeding generations.

Table 3. Coefficients of variation and estimates of broad sense heritability of different plant traits in cotton genotypes.

Genetic components	Traits						
	Single fuzzy seed weight	Single naked seed weight	Single seed fuzz weight	Cotyledonary leaf area	Emergence percentage	Gossypol glands/ seed	Seed cotton yield
GCV %	11.41	11.17	49.24	24.01	16.59	17.07	26.10
PCV %	14.41	14.80	63.54	27.52	20.67	23.50	26.16
$h^2 \pm$ SE	$0.63^{+} \pm 0.523$	$0.57^{+} \pm 0.529$	$0.60^{+} \pm 0.525$	$0.76^{+} \pm 0.513$	$0.64^{+} \pm 0.522$	0.53 ± 0.533	$0.99^{+} \pm 0.506$

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 = Broad sense heritability

± = Standard Error

$^{+}$ = The estimate of broad sense heritability differs significantly from zero as its absolute magnitude exceeded twice its respective standard error

The estimates of genetic advance (GA) and relative expected genetic advance (REGA) for all traits at different selection intensities are presented in Table 4. Generally, the estimates of GA were maximum at 5% selection intensity but there was a decreasing trend with increase in selection intensity. This implies that selection may be feasible at minimum selection intensity. The traits like single seed fuzz weight, cotyledonary leaf area, and seed cotton yield per plant showed great potential for genetic improvement through selection as evident from their heritability and REGA. Selection of two (5% of 30) best cotton genotypes for single seed fuzz weight, cotyledonary leaf area and seed cotton yield per plant may shift their means from 14.06 to 25.76, 5.86 to 8.36 and 1837.33 to 2824.43 in next generation, respectively.

Table 4. Genetic advance of plant traits at different selection intensities in cotton genotypes.

Genetic advance	Single fuzzy seed weight (mg)	Single naked seed weight (mg)	Single seed fuzz weight (mg)	Cotyledonary leaf area (cm^{-2})	Emergence percentage	Gossypol glands/ seed	Seed cotton yield (Kg/ha)
5%	16.1	13.3	11.1	2.5	14.9	19.4	987.1
10%	13.7	11.3	9.4	2.2	12.7	16.5	839.7
15%	12.1	10.0	8.3	1.9	11.2	14.6	743.6
20%	10.9	9.0	7.5	1.7	10.1	13.2	669.9
REGA (5%)	19	17	79	43	27	26	54

REGA = Relative expected genetic advance

Results suggested that genotypic correlations were higher in magnitude than their corresponding phenotypic correlations (Table 5). Single fuzzy seed weight had significant positive genetic correlation with single naked (non fuzzy) and seed weight (r_g = 0.98) which is an indicator of strong genetic association between them. Single naked seed weight also showed significant positive genetic correlation with emergence % (r_g = 0.87). In all other traits, the genotypic correlations were non-significant. At phenotypic level, highest magnitude of significant positive correlation was observed between single fuzzy seed weight and single naked seed weight (r_p = 0.97). Emergence % showed significant positive phenotypic correlations with single fuzzy seed weight and single naked seed weight. Similarly, gossypol glands/seed were observed to be positively and significantly correlated with cotyledonary leaf area and seed cotton yield. Seed cotton yield had positive association with all other traits except single seed fuzz weight which was negatively correlated at both genetic and phenotypic levels. Single seed fuzz weight exhibited negative correlations with cotyledonary leaf area, gossypol glands/seed and seed cotton yield at genetic and phenotypic levels. Cotyledonary leaf area was found to be in positive genetic and phenotypic association with all traits except single seed fuzz weight. Correlations of gossypol glands/seed were positive with all traits except single seed fuzz weight and emergence % at both levels. Higher genotypic correlation for various morpho-yield traits in cotton had been previously reported (Asad *et al*., 2002; Elsiddig. *et al*., 2004; Hussain *et al*., 2010; Efrem *et al*., 2010). Positive correlations of different traits with seed cotton yield pointed towards indirect improvement in yield through other traits. For example, more seed weight gives more vigorous seedling which may lead to the production of high yield as depicted in our results. In earlier studies (Afiah & Ghoneim, 2000; Badr, 2003; Khan, 2003; Khan *et al*., 2007; Ahmad *et al*., 2008; Soomro *et al*., 2008; Khan *et al*., 2010) significant variations were observed for seed traits and seed cotton yield had strong positive association with seed traits which indicated that any improvement in seed traits would have a positive impact on seed cotton yield.

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different traits of cotton genotypes.

Traits	Single fuzzy seed weight	Single naked seed weight	Single seed fuzz weight	Cotyledonary leaf area	Emergence percentage	Gossypol glands/ seed	Seed cotton yield
Single fuzzy seed weight (mg)	1	0.98$^+$	0.09	0.14	0.69	0.15	0.27
Single naked seed weight (mg)	0.97**	1	0.09	0.12	0.87$^+$	0.04	0.24
Single seed fuzz weight (mg)	-0.05	-0.05	1	-0.05	0.29	-0.16	-0.13
Cotyledonary leaf area (cm^{-2})	0.10	0.07	-0.03	1	0.004	0.62	0.12
Emergence percentage (%)	0.39**	0.46**	0.15	0.05	1	-0.04	0.25
Gossypol glands/ seed	0.09	0.02	-0.09	0.41**	-0.02	1	0.57
Seed cotton yield (Kg/ha)	0.23	0.19	-0.12	0.10	0.21	0.41**	1

**= Significant at 0.01% probability level

$^+$ = The estimate of genetic correlation coefficient differs significantly from zero as its absolute magnitude exceeded twice its respective standard error

Energy consumption is one of the largest expenses of a cotton gin. Considering the ever increasing cost of energy, all avenues should be exploited to optimize energy use in modern cotton gins. To evolve commercially acceptable varieties, one option is to assess the genetic variability within the available germplasm and to find genotypes that gin faster and require less energy (Efrem *et al*., 2010). In present study, the negative correlation of fuzz weight with seed cotton yield provides the justification that reduction in fuzz weight might be helpful for increased yield due to lowest fuzz (linters), signifying its good ginning efficiency. Gossypol is a toxic polyphenolic compound contained in glands located throughout the plants which helps to protect the plant from pests. Results suggested that yield might increase somehow with increased number of gossypol glands/seed. Glandless varieties have been developed, but were not adopted as these plants are left vulnerable to pests (Bolek *et al*., 2010). Cotton seed is a rich source of high quality protein, but its value as an animal feed is limited by gossypol so a breeding strategy to decrease the toxic levels of gossypol in the seed with optimum yield gain should be set out.

Success in cotton breeding is predominantly based on efficient selection which uses promising genotypes. Information regarding genetic variability among genotypes, heritability and correlation of desirable traits provides reliable basis for crop improvement. Results discussed above indicated that positive correlation of seed cotton yield with other traits suggested the feasibility of indirect selection. The traits like single seed fuzz weight, cotyledonary leaf area and seed cotton yield may be used for making efficient selection of cotton genotypes leading to improvement in cotton germplasm.

References

Abid, M., M. Ashfaq, M. A. Quddus, M. A. Tahir and N. Fatima. 2011. A resource use efficiency analysis of small BT cotton farmers in Punjab, Pakistan. *Pak. J. Agri. Sci*., 48: 75-81.

Afiah, S.A.N. and E.M. Ghoneim. 2000. Correlation, stepwise and path coefficient analysis in Egyptian cotton under saline conditions. *Arab Univ. J. Agric. Sci*., 8: 607-618.

Ahmad, W., N.U. Khan, M.R. Khalil, A. Parveen, U. Aimen, M. Saeed, Samiullah and S.A. Shah. 2008. Genetic variability and correlation analysis in upland cotton. *Sarhad J. Agric*., 24: 573- 580.

Anonymous. 2010. Pakistan Economic Survey 2007-08. Ministry of Finance, Govt. of Pakistan. (http://www.finance.gov.pk).

Aqsa, T., M. Saleem and I. Aziz. 2010. Genetic variability, trait association and path analysis of yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Pak J Botany.,* 42(6): 3915-3924.

Asad, M.A., F.M. Azhar and Z. Iqbal .2002. Association of yield with various economic traits in *Gossypium hirsutum* L. *Intl. J. Agri. Biol.,* 4(1): 105-106.

Badr, S.S.M. 2003. Evaluation of some Egyptian cotton varieties by the yield and seven methods of earliness of crop maturity measurements. *Egyp. J. Agric. Res*., 81: 671-688.

Batool, S., N.U. Khan, K. Makhdoom, Z. Bibi, G. Hassan, K.B. Marwat, F. Mohammad, Raziuddin and I.A. Khan. 2010. Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. *Pak. J. Bot*., 42(2): 1057-1064.

Bolek, Y., M.S. Fidan and M. Oglakci. 2010. Distribution of gossypol glands on cotton (*Gossypium hirsutum* L.) genotypes. *Bot. Hort. Agrobot. Cluj,* 38(1): 81-87.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Sixth Intl. Grassland Conf*., 1: 277-285.

Cochran, W.G. and G.M. Cox. 1957. Experimental designs. John Wiley and Sons. Inc., New York, 661 pp.

Efrem, B., W.R. Meredith and J.C. Boykin. 2010. Varietal variability for cotton ginning efficiency. USDA ARS, crop genetics research unit, Stoneville, MS J.C. Boykin USDA ARS, cotton ginning research unit, Stoneville, MS 2010 Beltwide cotton conferences, New Orleans, Louisiana, January 4-7: 698.

Elsiddig, A.A., A.H. Abdalla and A.S. Fadlalla. 2004. Genotypic and phenotypic correlations between yield and some yield components and fiber characteristics in some cotton (*Gossypium* spp.) genotypes. *J. Agric. Sci.,* 12(1): 1-18.

Falconer, D.S. 1989. Introduction to Quantitative Genetics. 2nd ed., Longman, New York, USA.Ganesan, K.N. and T.S. Raveendran. 2007. Enhancing the breeding value of genotypes through genetic selection in cotton (*G. hirsutum* L.). *Bull. Inst. Trop. Agr. Kushu Univ*., 30: 1-10.

Hanson, W.D., H.F. Robinson and R.E. Comstock. 1956. Biometrical studies on yield segregating population of Korean Lespedeza. *Agron*. *J*., 48: 268-272.

Hussain, K., I.A. Khan, H.A. Sadaqat and M. Amjad. 2010. Genotypic and phenotypic correlation analysis of yield and Fiber quality determining traits in upland cotton (*G. hirsutum* L.). *Intl. J. Agric. Biol*., 12(3): 348-352.

Hussain, M., F.M. Azhar and A.A. Khan. 2009. Genetics of inheritance and correlations of some morphological and yield contributing traits in upland cotton. *Pak. J. Bot*., 41(6): 2975-2986.

Johnson, H.W., H.F. Robinson and R.E. Comstock. 1955. Estimation of genetic variability in soybean. *Agron. J*., 47: 314-318.

Khan, N.U. 2003. Genetic analysis, combining ability and heterotic studies for yield, its components, fiber and oil quality traits in upland cotton (*G. hirsutum* L.). Ph.D. Dissertation, Sindh Agri. Univ. Tandojam, Pakistan.

Khan, N.U., G. Hassan, K.B. Marwat, Farhatullah, S. Batool, K. Makhdoom, I. Khan, I.A. Khan and W. Ahmad. 2009a. Genetic variability and heritability in upland cotton. *Pak. J. Bot*., 41(4): 1695-1705.

Khan, N.U., G. Hassan, K.B. Marwat, M.B. Kumbhar, I. Khan, Z.A. Soomro, M.J. Baloch and M.Z. Khan. 2009b. Legacy study of cottonseed traits in upland cotton using Griffin's combining ability model. *Pak. J. Bot.*, 41(1): 131-142.

Khan, N.U., G. Hassan, M.B. Kumbhar, A. Parveen, U. Aiman, W. Ahmad, S.A. Shah and S. Ahmad. 2007. Gene action of seed traits and oil content in upland cotton (*G. hirsutum* L.). *SABRAO J. Breed. Genet*., 39: 17-30.

Khan, N.U., K.B. Marwat, G. Hassan, Farhatullah, S. Batool, K. Makhdoom, W. Ahmad and H.U. Khan. 2010. Genetic variation and heritability for cottonseed, fiber and oil traits in *G. hirsutum* L. *Pak. J. Bot*., 42(1): 615-625.

Killi, F., L. Efe and S. Mustafayev. 2005. Genetic and environmental variability in yield, yield components and lint quality traits of cotton. *Intl. J. Agri. Biol.,* 7 (6): 1007-1010.

Kwon, S.H and J.H. Torrie. 1964. Heritability and inter-relationship of traits of two soybean populations. *Crop Sci.,* 4(1): 196-198.

Mahros, E.H. 2008. Triple test cross analysis in some cotton crosses. M.Sc Thesis, Menofiya Univ. Egypt. Pahlavani, M.H., A.A. Miri and G. Kazemi. 2008. Response of oil and protein content to seed size in cotton. *Intl. J. Agric. Biol.,* 10: 643-647.

Reeve, E.C.R. 1995. Variance of the genetic correlation coefficients. *Biometrics.,* 11: 351-374.Robertson, A. 1959. The sampling variance of genetic correlation coefficients. *Biometrics.*, 15: 469-485.

Romano, G.B. and J.A. Scheffler. (2008). Lowering seed gossypol content in glanded cotton (*G. hirsutum* L.) lines. *Plant Breed*., 127: 619-624.

Soomro, Z.A., A.S. Larik, M.B. Kumbhar, N.U. Khan and N.A. Panhwar. 2008. Correlation and path analysis in hybrid cotton. *SABRAO J. Breed. Genet*., 40: 49-56.

Steel, R.G.D., J.H. Torrie and D.A. Dicky. 1997. Principles and Procedures of Statistics. A biometrical approach. Second Edition. McGraw Hill Book Company. Inc. New York, USA.

Ulloa, M. 2006. Heritability and correlations of agronomic and fiber traits in okra-leaf upland cotton population. *Crop Sci*., 46: 1508-1514.

Zia, K., M. Ashfaq, M.J. Arif and S.T. Sahi. 2011. Effect of physico-morphic characters on population of whitefly (*Bemisia tabaci*) in transgenic cotton. *Pak. J. Agri. Sci*., 48: 63-69.

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