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GENETIC VARIABILITY AND HERITIBILITY ESTIMATES OF SOME POLYGENIC TRAITS IN UPLAND COTTON

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Plant breeders are more interested in genetic variance rather than phenotypic variance because it is amenable to selection and bring further improvement in the character. Twentyeight F_2 progenies were tested in two environments so as to predict genetic variances, heritability estimates and genetic gains. Mean squares for locations were significant for all the five traits suggesting that genotypes performed differently under varying environments. Genetic variances, in most cases, however, were about equal to that of phenotypic variances consequently giving high heritability estimates and significant genetic gains. The broad sense heritability estimates were; 94.2, 92.9, 33.6, 81.9 and 86.9% and genetic gains were; 30.19, 10.55, 0.20, 0.89 and 1.76 in seed cotton yield, bolls per plant, lint %, fibre length and fibre uniformity ratio, respectively. Substantial genetic variances and high heritability estimates implied that these characters could be improved through selection from segregating populations.

Key words**:** Genetic variability, Heritability estimates, Upland cotton.

Introduction

Plant breeders can easily observe and measure phenotypic variation in plant populations, which is conditioned by the joint action of both genetic and environmental factors. However, breeders are more interested in determining the proportion of genetic variation from available total phenotypic variance, whereas environmental effect is considered unimportant and hence is neglected.

The success of any breeding venture, therefore, depends mainly on the presence of abundant genetic variability for a trait i.e. is amenable to selection. Thus, the knowledge of degree of genetic variability that is transferable to the progeny referred to as heritability is also of great importance in improving any quantitative trait.

From total genetic variability, it is again additive variance and additive gene action, which play an important role in selecting and improving multigenic traits. Though, lot of work on genetic variability and heritability estimates have already been carried out, yet the differences always existed due to either material and methodology used and environments in which the material is tested (Meredith 1984; Efe and Jancer 1998; Khadi *et al* 1998; Moser *et al* 1999; Baloch and Bhutto 2003). The main objectives of present study were to determine heritability and genetic variances and to predict genetic responses to polygenic traits.

Materials and Methods

Twenty eight F_2 progenies were developed from 28 different cross combinations so as to determine genetic variability and heritability estimates for five quantitative traits of upland cotton. Ten plants from each genotype were randomly tagged for recording on seed cotton yield per plant in g, number of bolls per plant, lint percent, fibre length measured in mm and uniformity ratio. The experiment was carried out in randomized complete block design with four replications at two locations, one at Sakrand and other at Ghotki during the crop year 2002. The combined analysis of variance was done according to Gomez and Gomez (1984) with MSTAT-C software. The row-to-row and plant-to-plant distances were 2.5 feet and 9.0 inches, respectively. All the inputs like fertilizer (150 kg/ha Nitrogen in three split doses), irrigation (eight irrigations with 15 days intervals) and insecticides (two sprays for sucking and two for bollworsm pests) were applied as recommended for our local conditions. Broad sense heritability estimates on entry mean basis were calculated as the proportions of genetic variance (σ^2g) over phenotypic variance (σ^2p) by Fehr (1987). The genetic gain was calculated according to Falconer (1989) with little modification as: $G = h^2D$

Where h^2 is broad sense heritability and D is the selection differential. Broad sense heritability is defined as the proportion of total genetic variance over the phenotypic variance as: $h^2 = \sigma^2g/\sigma^2p$, Where $D = k\sigma p$ and k is selection differential in standard units at 10% = 1.76 and σp is the square root of phenotypic variance.

Results and Discussion

Genetic variability and heritability estimates are considered as very important parameters for the improvement of any quantitative trait. The mean performance, genetic variances, correlation coefficients, heritability estimates and genetic gains were obtained from 28 upland cotton crosses in F_2. The results depicted in (Table 1) indicated significant differences in the mean performance of genotypes for five quantitative traits, seed cotton yield per plant, number of bolls per plant, lint percent, fibre length and uniformity ratio. The seed cotton yield varied from 60.6 to 135.5 gm, bolls per plant from 21.8 to 48.5; lint % from 35.1 to 36.4; fibre length from 25.4 to 28.7 mm and uniformity ratio from 44.1 to 49.9 %.

The analysis of variance presented in (Table 2) indicates significant effect of the environment on all the five polygenic traits. The interactions between genotype x environment were also significant, further suggesting that the genotypes' performance have changed over the test environments. In other words, genotypes were not consistent in their performance over testing sites. However, the genotypes' mean squares for all the traits were greater than genotype x environment components, which also demonstrated that environment though largely affected genotype's performance, yet substantial improvement is possible in the traits studied. Correlation studies help plant breeders in two ways, i) to bring simultaneous improvement in two or more traits if they are positively correlated, ii) to improve the traits through indirect selection if the targeted trait is difficult to select. Correlation coefficients between yield and other traits were therefore workedout (Table 2) which suggested significant positive correlations with bolls per plant (r = 0.999), positive but non-significant with lint % (r = 0.450), negative and non-signifi-

Table 1

Means of 28 F_2 progenies for various polygenic traits in upland cotton evaluated in two locations

S. no.	F_2 progenies	Seed cotton yield/plant (g)	Boll per plant	Lint (%)	Fibre length (mm)	Uniformity ratio (%)
1.	VH-137 x FH-1000	127.80	46.00	35.30	26.60	46.60
2.	FH-901 x FH-1000	102.60	36.60	35.30	27.30	46.80
3.	CRIS-476 x FH-1000	116.30	41.10	35.70	27.30	46.40
4.	Cyto-51 x FH-1000	107.00	38.30	35.60	26.50	46.90
5.	CRIS-468 x FH-1000	60.60	21.80	35.60	26.60	45.60
6.	CRIS-467 x FH-945	70.70	25.50	35.10	26.90	48.00
7.	Cyto-9/91 x FH-945	91.00	32.60	36.10	27.20	47.30
8.	Cyto-51 x FH-945	76.10	27.30	35.40	26.60	46.40
9.	CIM-473 x FH-945	85.10	30.50	35.30	27.40	47.10
10.	VH-137 x FH-945	109.70	39.30	35.80	27.10	47.40
11.	FH-901 x CIM-707	91.10	32.60	36.20	27.30	44.30
12.	VH-137 x CIM-707	85.70	30.70	36.00	28.70	46.00
13.	Cyto-9/91 x CIM-707	86.90	31.10	35.50	26.70	45.80
14.	Cyto-51 x CIM-707	86.90	31.30	35.20	27.40	48.20
15.	CRIS-468 x CIM-707	69.70	25.00	35.40	26.80	46.00
16.	Cyto-9/91 x CIM-473	83.30	29.90	36.40	26.60	45.60
17.	Cyto-51 x CIM-473	110.70	39.60	35.70	25.40	46.50
18.	CRIS-468 x CIM-473	80.30	28.70	35.70	26.80	46.30
19.	CRIS-467 x CIM-473	95.60	34.20	35.70	26.40	47.10
20.	FH-901 x CIM-473	107.00	38.30	35.50	26.70	46.40
21.	Cyto-9/91 x CRIS-468	135.50	48.50	36.00	25.90	47.70
22.	FH-901 x Cyto-51	84.60	30.30	36.10	26.90	46.40
23.	Cyto-51 x CRIS-467	121.40	42.90	35.40	26.80	47.00
24.	CRIS-468 x Cyto-51	91.20	32.60	35.60	27.00	49.90
25.	CRIS-468 x Cyto-9/91	117.80	42.20	35.10	28.00	45.80
26.	VH-137 x CRIS-467	102.60	36.70	35.60	26.10	46.30
27.	CRIS-467 x Cyto-9/91	87.80	31.40	35.70	26.90	44.10
28.	CRIS-467 x CIM-707	84.60	30.30	36.10	26.60	45.30
	Population mean	**95.30**	**34.10**	**35.70**	**26.90**	**46.50**
	LSD (5%)	**5.18**	**1.88**	**0.40**	**0.62**	**0.79**

Table 2
Mean squares for five polygenic traits in studied 28 F_2 progenies of upland cotton

Source of variation	Degrees of freedom	Mean squares				
		Seed cotton yield	Bolls per plant	Lint %	Fibre length	Uniformity ratio
Location	1.0	366.18**	62.16**	208.090**	44.286**	158.458**
Rep/Loc.	6.0	29.47	3.75	0.657	0.143	0.795
Genotypes	27.0	2668.55**	335.23**	0.906**	3.075**	10.646**
Loc. X Geno.	27.0	155.39**	23.69**	0.602**	0.556	1.374**
Pooled error	162.0	27.49	3.54	0.159	0.389	0.624

Correlatios: Yield with bolls r, 0.999; Yield with lint % r, 0.450; Yield with fibre length r, -0.070; and yield with uniformity ratio r, 0.131
**Significantly different at 1%probability level

cant with fibre length (r = -0.070) and small but positive with uniformity ratio (r = 0.131). Moser *et al* (1999) also observed significant and positive correlations between lint yield and boll numbers (r = 0.98) and lint yield with lint per seed (r = 0.85).

Genetic variances (σ^2g), heritability estimates (h^2) and predicted genetic gains (G) were calculated (Table 3) so as to predict genetic advance that could be made through selection in segregating populations. The genetic variance (σ^2g = 314.145) for yield being about equal to its phenotypic variance (σ^2p = 333.568) and high heritability estimates (h^2 = 94.2 %) indicated that yield, though is influenced by the environment, yet significant improvement is possible in cotton yield. High heritability estimates of h^2 = 92.9% coupled with significant portion of genetic variance (σ^2g = 38.943) connoted that environment had rather smaller impact on the number of bolls, therefore selection in segregating generations can be very effective to improve this trait (Baloch and Bhutto 2003). Large portions of genetic variances, high heritability estimates for bolls per plant and its significant positive correlations with yield (r = 0.999), all suggested that indirect selection through bolls per plant could also make considerable improvement in yield. Khadi *et al* (1998) noted that in characters like yield and bolls per plant, phenotypic coefficient of variability was almost equal to that of genotypic coefficient of variability, thus these characters had high heritability estimates of 82.9 and 94.3%, respectively. Efe and Jancer (1998) also observed 59 and 47% broad sense heritability estimates in seed cotton yield and bolls per plant respectively from half-diallel hybrids.

Table 3
Genetic and phenotypic variances, heritability estimates and genetic gains for some polygenic traits in upland cotton

Traits	σ^2g	σ^2p	h^2	G
Yield / pl. (g)	314.145	333.568	94.2	30.19
Bolls per plant	38.943	41.904	92.9	10.55
Lint (%)	0.038	0.113	33.6	0.20
Fibre length (mm)	0.315	0.385	81.8	0.89
Fibre uniformity (%)	1.159	1.333	86.9	1.76

Lint percent in cotton was significantly affected by the environmental factors because genetic variance (σ^2g = 0.038) was smaller than its phenotypic variance (σ^2p = 0.113). Moderate heritability estimates (h^2 = 33.6%) and small but still comparable genetic variance to phenotypic variance further suggested that improvement with more efforts is also possible in lint percent. Similar to our results, Efe and Jancer (1998) also reported moderate heritability estimate of 63%, whereas, Lancon (1998) observed on an average of 72% heritability in lint % over two spacings i.e. crop spacing (normal spacing) and nursery spacing (narrow spacing). Regarding fibre length, about equal portions of genetic (σ^2g = 0.315) and phenotypic variances (σ^2p = 0.385) resulting high heritability estimates (h^2 = 81.8%), demonstrated that fibre length is significantly controlled by genetic factors, therefore, higher responses to selection from segregating populations could be obtained for this trait. Contrary to our results, Efe and Jancer (1998) reported moderate broad sense heritability estimate of 38% in fibre length. However, variable heritability estimates, ranging from 23.0 to 81.0 % were also reported by Meredith (1984) for fibre length. About equal genetic (σ^2g = 1.159) and phenotypic (σ^2p = 1.333) variances, consequently high heritability estimates (h^2= 86.9%) revealed that environment had little influence on uniformity ratio in cotton, implied that significant improvement can be expected from selection in segregating generations.

Substantial genetic variances and high heritability estimates are very important contributing parameters towards genetic gains for a trait. Results in Table 3 revealed 30.19 gm, 10.55

bolls, 0.20 %, 0.89 mm and 1.76 % genetic gains in yield, bolls per plant, lint percent, fibre length and fibre uniformity ratio, respectively. Mustafa *et al* (1995) observed that at 5% selection intensity, on an average of 10.3 and 5.9% genetic gains were obtained in seed cotton yield and bolls per plant. Genetic gains of 16.9 kg/ha per year were also reported by Moser *et al* (1999). Similar studies in upland cotton (*G. hirsutum* L.) showed genetic gains of 4.8-10.5 kg/ha per year (Bassett and Hyer 1985; Culp and Green 1992; Meredith *et al* 1997). Significantly positive correlations between yield and bolls, their higher heritability estimates consequently more genetic gains suggested that improvement in one trait could bring simultaneous improvement in another trait.

References

Baloch M J, Bhutto H U 2003 Design-11 analysis for estimating general and specific combining ability effects of cotton leaf curl virus resistant inbred parents. *Zagazig J Agric Res* **30**(3) 635-649.

Bassett D M, Hyer A H 1985 Acala cotton in California: 60 years of varietal improvement. In: *Proceedings on Beltwide Cotton Conference*, pp 76.

Culp T W, Green C C 1992 Performance of obsolete and current cultivars and Pee Dee germplasm lines of cotton. *Crop Sci* **32** 35-41.

Efe L, Jancer O 1998 Inheritance of important properties in Half-Diallel hybrids of some glandless cotton, (*Gossypium hirsutum* L.) cultivars. In: *Proceedings on World Cotton Research Conference*, September 6-12, Athens, Greece, **1** 239-243.

Falconer D S 1989 *Introduction to Quantitative Genetics.* Longman Scientific & Technical, 3rd (ed), New York, USA, pp, 187-192.

Fehr W R 1987 *Principles of Cultivar Development*, Theory and Techniques. Macmillan Publishing Company, New York, USA, Vol. **1** pp 95-102.

Gomez K A, Gomez A A 1984 *Statistical Procedures for Agricultural Research.* John Wiley & Sons Inc., 2nd (ed), New York, USA.

Khadi B M, Kulkarni V N, Narrajji S S 1998 Achieving multiple pest tolerance through manipulation of morphological features in cotton. In: *Proceedings of World Cotton Research Conference*, September 6-12, Athens, Greece, **1** 201-203.

Lancon J 1998 Evaluating F_3 lines of single crosses for yield improvements in cotton. In: *Proceedings of World Cotton Research Conference*, September 6-12, Athens, Greece, **1** 144-147.

Meredith W R J 1984 *Quantitative Genetics*, Kohel R J and Lewis C F (eds). Cottons ASA, CSSA and SSSA. Agronomy Monograph No.24, Madison, WI, USA, pp 131-150.

Meredith J, Heitholt W R, Pettigrew W T, Rayburn S T J 1997 Comparison of obsolete and modern cotton cultivars at two nitrogen levels. *Crop Sci* **37** 1453-1457.

Moser H S, Maricopa A Z, Percy R G 1999 Genetic improvement of yield, yield components and agronomic characters of Pima Cotton. In: *Proceedings of Beltwide Cotton Conferences*, National Cotton Council, Memphis, *TN* **1** 488-489.

Mustafa F, Awaad M, Awaad H 1995 Evaluation of some strains of long staple cotton hybrids at different locations in Egypt in 1993 season 1. Seed cotton yield and its contributing variables. In: *Proceedings of Beltwide Cotton Conference*, National Cotton Council, Memphis, *TN*, pp 583.