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PHENOTYPIC ASSOCIATIONS, REGRESSION COEFFICIENTS AND HERITABILITY ESTIMATES FOR QUANTITATIVE AND FIBER QUALITY TRAITS IN UPLAND COTTON GENOTYPES

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ABSTRACT

A field trial was carried out at the experimental area of the Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam during 2014, to determine the correlations, regression and heritability estimates for quantitative and fiber quality traits in upland cotton genotypes. The experiment was laid out in RCBD (Randomized Complete Block Design) with four replications. The material was consisted of eight varieties viz. CRIS-134, AA-802, Neelum-121, CIM-598, MNH-886, FH-113, BT-142 and CRIS-342. The observations were recorded on eight plant traits. The ANOVA revealed that there is a significant difference for all the traits except for seed index. Based on mean performance, variety CRIS-342 produced desirable medium taller plants, ginned maximum lint%, formed more sympodia plant^{-1}, set higher bolls plant^{-1}, measured longer fiber and produced higher yield plant^{-1}, yet next good performing genotype was FH-113. However, bigger bolls were weighed by Neelum-121. The phenotypic correlations and regression results revealed significantly positive associations of sympodial branches plant^{-1} with number of bolls plant^{-1} (r=0.931**) and the r^2 revealed that approximately 86.67% of variability in bolls plant^{-1} was attributable to its relationship with sympodia plant^{-1}. The number of bolls plant^{-1} revealed positive association with yield (r=0.985**) and the r^2 revealed that 97.02% of variation in seed-cotton yield was attributable to its correlation with bolls plant^{-1}. On the contrary, number of bolls plant^{-1} demonstrated highly significant but negative correlation with boll weight (r=-0.803**), yet r^2 suggested that 64.48% of variability in boll weight occurred owing to its relationship with bolls plant^{-1}. The present findings suggested that raising bolls plant^{-1} caused a significant decrease in boll weight. Results generally pointed out that sympodial branches plant^{-1}, bolls plant^{-1} and lint% were considered to obtain higher seed-cotton yield. Higher heritability estimates ranging from 36.69 to 99.50% revealed that most of the traits studied were under genetic control, most likely by additive genes, hence significant improvement can be expected through hybridization and selection from segregating populations.

Keywords: fiber traits, heritability, phenotypic relationship, seed-cotton yield, upland cotton genotypes

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INTRODUCTION

The end product of yield components is the seed-cotton yield with good fiber quality traits. Therefore, developmental relationship of plant traits can play a key role in the selection of desirable traits. Thus, superiority of cotton varieties and the association of seed-cotton yield with fiber quality and yield traits are indispensable (Baloch *et al*., 2014). Sustainable cotton productivity in coming years also depends on the development of cotton cultivars with higher seed-cotton yield, good fibre and better tolerance to biotic and abiotic stresses. Breeders have used only a fraction of the available germplasm for cultivar development and most of the modern cultivars are developed by reselections from existing cultivars rendering a drastic reduction in genetic variability (Lewis, 2000). In order to bring genetic improvement in fiber quality parameters, it is important to investigate the relationship between different yield and fiber traits and their mode of inheritance (Aziz *et al*., 2014). Quantitative trait like yield being polygenic is a total sum of genetic illustration of all the yield components (Khan *et al*., 2009). Overall performance of a genotype may vary due to changes in environment and the magnitude of relationship between various characters (Larik *et al*., 1997). The yield of seed-cotton is the product of many component traits like, number of sympodia, fruits plant^{-1}, boll size, lint%, etc. Hence, it is worth that cotton breeders should know the magnitude of association between yield and its associated traits, which may help in the selection of desirable traits.

The acquaintance of correlation between different yield and fiber traits has been profitably explored in cotton improvement programmes (Erande *et al*., 2014; Farooq *et al*., 2014; Gul *et al*., 2014). It also happens that due to characters association, improvement in one character may bring simultaneous and positive change in another or vice versa (Ahmed *et al*., 2008; Baloch *et al*., 2014). Farooq *et al*. (2014) observed that seed-cotton yield plant^{-1} was positively associated with bolls plant^{-1}, plant height, boll size, fibre length and GOT%. Erande *et al*. (2014) studied different cotton species and reported that lint yield plant^{-1}, bolls plant^{-1}, GOT%, lint index, sympodial branches plant^{-1} and plant height were positively associated with seed-cotton yield plant^{-1}. The relationships among these characters are not well documented in cotton and most of the times the results are highly controversial and variable, mitigating the importance of current research. The understanding of such associations allows determining the degree of the relationship between several characters of the plants and determines the trait which can be used as selection criteria to improve the yield, earliness and fiber traits (Iqbal *et al*., 2003). Salahuddin *et al*. (2010) gave the considerable emphasis upon the interrelationship between yield and its related traits in cotton. Studies on heritability estimates and inherited ability of various cultivars in terms of their expression for various morphological and yield characters are intently needed for the development of potential parents for breeding purpose (Khan *et al*., 2010). The seed-cotton yield being multigenic trait is greatly affected by different morphological and yield contributing characters (Khan *et al*., 2009). The knowledge on the inheritance pattern of morpho-yield and fiber characters are very important for the breeders to improve the plant traits and considerable genetic variability and greater estimates of heritability entail that such traits may be enhanced via selections from segregating generations (Baloch, 2004; Khan *et al*., 2009; Baloch *et al*., 2010). Broad and narrow sense heritability estimates were by and large were establish high in magnitudes in intra-specific crosses of *Gossypium hirsutum* L. as compared to inter-specific crosses of *Gossypium barbadense* L. crosses (Esmail, 2007; Khan *et al*., 2010). Heritability measures portion of genetic variance from its total phenotypic variance, hence is an important genetic parameter for launching successful breeding programme. Connection of heritability with genetic progress helps to know the form of inheritance of quantitative traits (Aqsa *et al*., 2010). Heritability and genetic gain also provide useful information with regard to improving polygenic traits (Batool *et al*., 2010; Khan *et al*., 2010). The current study was staged to determine the association between quantity and quality traits and also heritability estimates of such characters in *Gossypium hirsutum* L. cotton genotypes.

MATERIALS AND METHODS

The experiment was laid out in the field of the Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam. The soil was sandy loam in texture with 7.8 pH. The seed of 8 parental lines (CRIS-134, AA-802, Neelum-121, CIM-598, MNH-886, FH-113, BT-142 and CRIS-342) was sown during 2014. Seed was hand dibbled at the rate of three seeds per hill. The trial was conducted in a RCBD with four replications. Seedlings were thinned to one plant per dibble before first irrigation so as to maintain standardized plant stand to reduce plant competition and favourable plant growth or development. The space between plants was 30 cm, whereas row to row distance was 75 cm. All the cultural practices were carried-out at appropriate time and inputs were applied at recommended rates (fertilizers nitrogen and phosphorous were applied @ 125 N and 75 kg P_2O_5 ha^{-1}). Ten randomly tagged index plants from each cultivar and repeat were picked and ginned individually on roller ginning machine for taking the observations on yield and fiber traits. The significance level was determined by ANOVA (Gomez and Gomez, 1984). LSD (Least significant difference) test was applied to determine significance difference between two means. The correlation coefficients (r) and regression analysis were carried out according to statistical method developed by Raghavrao (1983) with computer software Statistix 8.1 Version. The broad sense heritability estimates were determined from variance components by using statistical procedures as proposed by Baloch *et al*. (2010). The data were collected on plant height (cm), sympodial branches $plant^{-1}$, bolls $plant^{-1}$, boll heaviness (g), seed-cotton yield $plant^{-1}$ (g), lint (%), seed index and fibre length (mm).

RESULTS AND DISCUSSION

In general, cotton plant contains the most complex arrangements among major field crops; therefore the yield of this crop may be disturbed by multidirectional interactions of genetic and environmental issues. Study of the true relationship of yield and yield components related with fiber traits will help to reveal their importance in cotton breeding program. Seed-cotton yield is the resultant product of component characters, which are not under the direct control of any single or fewer genes (Baloch *et al.,* 2014). Thus upgrading of yield traits may bring about subsequent increase in seed-cotton yield. Therefore, information about the correlation between different traits helps in the development of appropriate selection criteria so as to achieve the significant improvement in yield and fiber quality characters.

The present research work was conducted on yield and fiber traits so as to evaluate the mean performance of eight cotton genotypes. The correlation and regression analysis of yield and fiber traits were also determined for setting up reliable selection criteria to improve seed-cotton yield per plant. The heritability was also calculated so as to estimate the degree of transmissibility of traits from parents to their progenies.

Analysis of variance and mean performance of cotton genotypes

The eight important yield and fiber traits were studied. The analysis of variance showed significant differences among the genotypes for all the traits studied except seed index. These results indicated that significant variability is present in the cotton varieties for various yield and fiber traits. Significant differences for yield and fiber traits were also reported by some earlier workers like, Aziz *et al*. (2014); Baloch *et al*. (2014) and Gul *et al*. (2014) whose findings are in agreement with ours. The mean performance revealed that medium taller plants were attained by CRIS-342 and CRIS-134, while parent MNH-886 recorded shorter plants; maximum number of sympodial branches were produced by CRIS-342, followed by FH-113, whereas minimum sympodial branches were obtained in Neelum-121. Among all the varieties studied, CRIS-342 and FH-113 produced maximum bolls plant^{-1}, yet lowest bolls plant^{-1} was obtained from Neelum-121 (28.50). Bigger bolls, weighing 3.20 g were recorded by Neelum-121 and longer staple length (29.57 mm) was recorded by CRIS-342. Highest seed-cotton yield per plant was produced by CRIS-342. The variety CRIS-342 ginned the highest GOT% whereas Neelum-121 recorded the lowest GOT%. The highest seed index was recorded by variety FH-113, whereas the lowest seed index was observed by MNH-886. In general, varieties CRIS-342 and FH-113 recorded better performance in terms of seed-cotton yield plant^{-1}, bolls plant^{-1}, sympodial branches plant^{-1} and longer staple length.

Table 1. Mean squares for yield and fiber characters in *Gossypium hirsutum* L. cultivars

Traits	**Mean squares**		
	Replication D.F.= 3	**Varieties D.F.= 7**	**Error D.F.= 21**
Plant height	2.952	592.632**	2.955
Sympodia plant^{-1}	4.4746	82.8655**	1.3584
Bolls plant^{-1}	0.530	308.769**	1.699
Boll weight	0.0002	0.06341**	0.00812
Seed-cotton yield plant^{-1}	4.57	1871.90**	24.52
Ginning outturn%	2.577	129.208**	2.234
Staple length	0.4388	3.4784**	0.90933
Seed index	0.0963	0.4394	0.27792

** = Significant at 1% probability level.

Table 2. Average results of eight cotton genotypes for yield and fiber traits

Characters	**Varieties**								
	CRIS-134	**AA-802**	**Neelum-121**	**CIM-598**	**MNH-886**	**FH-113**	**BT-142**	**CRIS-342**	**L.S.D. (5%)**
Plant height (cm)	113.10	97.95	85.53	95.45	84.10	107.50	100.65	117.95	2.52
Sympodial Branches (plant^{-1})	19.95	22.10	18.05	19.55	22.35	28.50	25.55	30.90	1.71
No. of bolls (plant^{-1})	38.15	41.90	28.50	34.45	38.80	52.60	43.20	54.80	1.91
Boll weight (g)	3.09	2.97	3.20	3.12	3.12	2.83	3.05	2.89	0.13
Seed-cotton yield plant^{-1} (g)	118.00	124.72	91.15	107.42	121.24	148.85	131.90	158.79	7.28
Ginning out turn %	43.45	41.90	34.31	47.69	50.44	45.22	39.21	50.94	2.19
Staple length (mm)	27.27	29.27	28.28	29.03	29.10	27.11	28.02	29.57	1.40
Seed index (100-seed weight, g)	7.97	7.40	7.27	7.51	7.05	8.02	7.67	7.51	ns

ns = non-significant.

Correlation and regression analysis

Correlation studies indicated that plant height revealed significant and positive correlation with sympodia plant^{-1}, bolls plant^{-1}, yield plant^{-1} and lint% which suggested that increase in plant height caused a proportionate increase in these traits also. Ganapathy *et al*. (2006) stated that plant height, sympodia plant^{-1} and bolls per plant were positively associated with seed-cotton yield per plant. Their results thus suggested that, simultaneous selection of plant height, sympodial branches per plant and bolls per plant will increase the seed-cotton yield automatically. Regression (b) indicated that increase of 1.0 cm in plant height will correspondingly increase 0.225 sympodial branches plant^{-1}, 0.514 bolls plant^{-1} and 0.256 g in seed-cotton yield. Coefficient of determination (r^2) indicated that approximately 86.67% of variability in bolls plant^{-1} was due to its association with sympodial branches plant^{-1} and 87.04% of disparity in yield was attributable to its association with sympodia plant^{-1}. Bolls plant^{-1} demonstrated negative correlation with boll weight and r^2 revealed that 64.48% of variability in boll weight was caused by its association with bolls plant^{-1}. These results connoted that rise in bolls plant^{-1} caused decrease in boll weight. Negative correlation between lint% and seed index revealed that increasing 100-seed weight caused parallel decline in lint% whereas r^2 established nearly 29.16% of variabiliy in lint%. Results generally suggested that bolls plant^{-1} and lint% may be improved to obtain higher yields. Baloch *et al.* (2014) while working on regression stated that about 78.49% of total variation in seed-cotton yields was due to its correlation with sympodial branches plant^{-1}. Whereas bolls plant^{-1} demonstrated highly significant negative correlation with boll weight and r^2 revealed that 40.57% of variability in boll weight was owned by its relationship with bolls plant^{-1}. These results revealed that increase in bolls plant^{-1} caused decline in boll weight. Sympodial branch is an important quantitative trait on which the bolls are formed. Thus, plant breeders and researchers recommended that sympodia do serve as good selection measure for selecting cotton varieties producing higher yields. Sympodia plant^{-1} was positively associated with bolls plant^{-1} and significantly but negatively associated with boll weight. Positive association of sympodial branches with bolls plant^{-1} suggested that increase in sympodial branches will equally increase in boll number while negative association with boll weight indicated that increase in sympodial branches causes reduction in boll size. Khan (2011), and Batool and Khan (2012) observed positive associations between sympodial branches plant^{-1} with seed-cotton yield. Bolls plant^{-1} being a major component for seed-cotton yield is generally observed as having strong positive association with seed-cotton yield. Thus an increase in number of bolls plant^{-1} will ultimately raise the seed-cotton yield. Bolls plant^{-1} exhibited positive relationship with seed-cotton yield and seed index, yet expressed negative correlation with boll weight. These associations indicated that increasing bolls per plant will correspondingly add to both seed-cotton yield and seed index while its increase causes negative impact on boll weight by reducing its size.

Correlation of boll weight was non-significant but positive with seed-cotton yield yet negative and non-significant with seed index. These correlations indicated that while improving boll weight, seed-cotton yield may slightly increase. In consonance to present results, positive association between boll weight and seed-cotton yield was also reported by Preetha and Reveendran (2007) and Farooq *et al*. (2013). However, the opposite results were obtained by Naveed *et al.* (2004). Yield is considered as the most important character which is required to boost-up the yield production to its maximum level, since it plays positive role in escalation of financial status of the farmers and ultimately the nation. Seed-cotton yield revealed its non-significant and positive association with seed index but non-significant and negative association with staple length. Kumar *et al.* (2012) and Wang *et al*. (2012) observed positive and significant associations of number of bolls per plant, number of sympodial branches per plant and plant height with seed-cotton yield per plant, indicating the importance of these characters for improving seed-cotton yield. Ginning outturn% (GOT) primarily depends on the ratio of lint obtained from seed-cotton sample. The correlations of GOT% with staple length were recorded non-significantly positive; nonetheless it was negatively associated with seed index. These results indicated that increasing lint% will correspondingly increase staple length but may cause decline in seed index. Results from correlation studies revealed that GOT% was non-significantly but positively correlated with staple length, yet significantly and positively associated with bolls plant^{-1} and seed-cotton yield but negatively correlated with seed index. It could be inferred from the present results that significant improvement could be made in improving staple length along with lint% without causing adverse impact on other important traits. These types of results are quite encouraging in cotton breeding programmes. Correlation studies further indicated that seed index exhibited non-significant positive association (Table 3) with only seed-cotton yield while it showed negative and non-significant association with GOT%. These results revealed that increasing seed index will cause associated increase of seed-cotton yield yet it will reduce the lint %. Present studies indicated that traits like sympodia per plant^{-1} and number of bolls were the most essential yield traits to be exploited for further progress in cotton yield.`

Table 3. Correlations analysis for yield and fiber traits in *Gossypium hirsutum* L. genotypes

Character associations	(r)	(b)	(r^2)
Plant height *vs* bolls plant^{-1}	0.713**	0.514	0.5083
Plant height *vs* boll weight	-0.584**	-0.007	0.3410
Plant height *vs* seed-cotton yield plant^{-1}	0.699**	0.256	0.4886
Plant height *vs* sympodial branches plant^{-1}	0.587**	0.225	0.3445
Bolls plant^{-1} *vs* boll weight	-0.803**	-0.013	0.6448
Bolls plant^{-1} *vs* GOT. %	0.506 **	0.334	0.2560
Bolls plant^{-1} *vs* seed-cotton yield plant^{-1}	0.985**	2.454	0.9702
Sympodial branches plant^{-1} *vs* bolls plant^{-1}	0.931**	1.750	0.8667
Sympodial branches plant^{-1} *vs* boll weight	-0.675**	-0.021	0.4556
Sympodial branches plant^{-1} *vs* seed-cotton yield plant^{-1}	0.933**	4.369	0.8704
Boll weight *vs* seed index	-0.081^{ns}	-0.021	0.0065
Boll weight *vs* seed-cotton yield plant^{-1}	0.098^{ns}	6.516	0.0096
Seed-cotton yield plant^{-1} *vs* GOT.%	0.540**	0.143	0.2916
Yield plant^{-1} *vs* staple length	-0.011^{ns}	-6.475	0.0001
Yield plant^{-1} *vs* 100-seed weight	0.290^{ns}	0.007	0.0841
GOT. % *vs* seed index	-0.015^{ns}	-0.001	0.0002
GOT.% *vs* fiber length	0.285^{ns}	0.061	0.0812
Staple length *vs* 100-seed weight	-0.471**	-0.213	0.2218

* = Significant at 1% level of probability, ** = Significant at 5% level of probability.

Table 4. Heritability estimates for various yield and fiber traits in upland cotton

Trait	Genetic variance ($\delta^2 g$)	Phenotypic variance ($\delta^2 p$)	Environ-mental variance ($\delta^2 e$)	Heritability (h^2 %)
Plant height	147.419	148.158	0.7387	99.50
Sympodial branches plant^{-1}	15.250	15.589	0.3396	97.82
No. of bolls plant^{-1}	76.767	77.191	0.4247	99.45
Boll weight	0.013	0.015	0.0020	86.66
Ginning outturn %	31.743	32.301	0.5585	98.27
Seed-cotton yield plant^{-1}	461.845	467.975	6.13	98.69
Staple length	0.642	0.869	0.2273	73.87
Seed index	0.040	0.109	0.0694	36.69

Heritability estimates

For effective selections, heritability estimates are deciding factors for crop improvement. The heritability estimates (h^2) in broad sense, genetic variances ($\delta^2 g$), phenotypic variances ($\delta^2 p$) were calculated and presented in Table 4. The genetic variance (δ^2g=147.41) for plant height was slightly lower than its phenotypic variance (δ^2p=148.15), which resulted in higher heritability estimates (h^2=99.50%). Regarding sympodial branches per plant, genetic variance (δ^2g=15.25) was about equal to its phenotypic variance (δ^2p=15.58), thus expressed higher heritability estimates of h^2=97.82%. Bolls per plant expressed almost at par genetic variance (δ^2g=76.76) and phenotypic variances (δ^2p=77.19) which resulted in higher heritability estimates of h^2=99.45% for this character. In case of boll weight, the genetic variance (δ^2g=0.013) which was close to its phenotypic variance (δ^2p=0.015), reflected into higher heritability estimates (h^2=86.66%). For GOT%, genetic variance (δ^2g=31.74), though little bit lower, but it was numerically at par with its phenotypic variance (δ^2p=32.30). So, the higher heritability (h^2=98.27%) was observed for this character. Seed-cotton yield per plant manifested substantial amount of genetic variance (δ^2g=461.84), yet it was numerically at par with its phenotypic variance (δ^2p=467.79), as a consequences, the higher heritability (h^2=98.67%) was achieved for seed-cotton yield per plant. Regarding staple length, the genetic variance (δ^2g=0.642) was slightly lower against its phenotypic variance (δ^2p=0.869), which resulted higher heritability estimates of h^2=73.87% but still lesser than majority of other traits. For seed index, genetic variance (δ^2g=0.04) was considerably less than its phenotypic variance (δ^2p=0.10). These differences in variance components caused significant declines in heritability estimates (h^2=36.69%). Generally, greater broad sense heritability estimates were recorded for the traits studied which revealed that the variations recorded for plant characters were mostly advocated by genes and was less affected by environment factors; this further demonstrates the influence of additive genes for the characters studied. Hence, the improvement in those characters can be brought via visual basis. Present results are in conformity with earlier findings of Abbas *et al*. (2013); Farooq *et al*. (2013) and Ahsan *et al.* (2015). Approximately 80% of broad sense heritability estimates were recorded by Aziz *et al*. (2014) and Farooq *et al.* (2015) for height of plant, sympodia plant^{-1}, boll size, bolls plant^{-1} and seed-cotton yield. It is evident from our and previous results that improvement in above mentioned characters may be achieved via selection from segregating populations.

CONCLUSION

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on mean performance, varieties CRIS-342 and FH-113 performed very well in terms of seed-cotton yield, bolls per plant, lint%, sympodia plant^{-1} and staple length, thus such cultivars may be preferred for hybridization and selection programmes so as to develop new promising cotton varieties. The phenotypic correlations revealed that plant height, sympodial branches, lint% and bolls plant^{-1} were significantly and positively associated with seed-cotton yield, hence these yield traits may be used as dependable criteria for making progress in seed-cotton yield. Significantly negative correlations between number of bolls plant^{-1} and boll size suggested that bolls per plant may be given priority over boll weight when the objective is to improve yield production in cotton crop. Negative non-significant association of lint% with seed index indicated that though, yield could be improved with bolder seeds but higher value of lint may not be too much compromised with seed index. Coefficient of determinations revealed that maximum variations in seed-cotton yield were caused by bolls per plant and sympodial branches per plant. Present results clearly demonstrated that cotton production could be increased by increasing bolls plant^{-1}, sympodia plant^{-1}, lint% and boll weight. All the studied traits revealed high heritability estimates indicating that the genotypes of current research may be dependably used to isolate the rewarding segregants from subsequent generations to improve the multigenic characters studied.

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