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Variability, correlation and path coefficient analysis of seedling traits and yield in cotton (*Gossypium hirsutum* L.)

Aziz Irum¹, Aqsa Tabasum² and M. Zaffar Iqbal³

¹College of Agriculture, D. G. Khan, Sub-campus University of Agriculture Faisalabad, Pakistan.

²Nuclear Institute for Agriculture and Biotechnology, Faisalabad, Pakistan.

³Ayub Agriculture Research Institute Faisalabad, Pakistan.

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Indirect selection is a useful means for improving yield in cotton crop. The objective of the present study was to determine the genetic variability, broad sense heritability, genetic advance and correlation among the six seedling traits and their direct and indirect effects on cotton yield by using path coefficient analysis. Thirty cotton genotypes were studied in green house using randomized complete block design with 3 replications at Cotton Research Station Multan, Pakistan. The genotypes exhibited a wide range of variability for all the traits except shoot length. Moderate to high heritability estimates were found for all traits. All the seedling traits showed positive and significant correlation with cotton yield both at genotypic and phenotypic level. Path coefficient analysis showed that root length had the highest and positive direct effect on cotton yield. Positive direct effects were produced by shoot length, root length, shoot/root length ratio, shoot weight and root weight, while shoot/root weight ratio had negative direct effects. The information obtained from the current studies will be utilized in successful cotton breeding program.

Key words: Genetic parameters, seedling traits, selection criteria, cotton.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is an important cash crop in commerce of many countries including Pakistan. It is mainly cultivated for fiber. Development of new cotton varieties with high yield is the primary objective of all cotton breeders (AshokKumar et al., 2010). The improvement in yield is possible using existing genetic resources, which depends on nature and magnitude of genetic variation present in population. An estimate of genetic variation is a pre-requisite for initializing a breeding procedure. An insight into the magnitude of variability in crop species is also of utmost importance as it provides the basis for effective selection. High heritability appraisal shows the presence of fixable additive factors which gives an indication that selection can play a promising role in the improvement of such traits. The

major function of heritability estimates is to provide information on transmission of traits from the parents to the progeny. Such estimates facilitate the evaluation of genetic and environmental effects, thereby aiding in selection. Estimates of heritability can be used to predict genetic advance under selection, so that the breeder can anticipate improvement from different types and intensities of selection. Thus, information on genetic variation, heritability and genetic advance to improve cotton crop is crucial.

For effective selection, identification of various yield attributes is desirable. Correlation of characters is a measure of strength of relationship between various traits. Knowledge of correlation between different traits is necessary in plant breeding. If two traits are positively correlated, then one trait can be improved indirectly by improving the other trait. Correlation coefficients are useful if indirect selection of a secondary trait is to be used for improving the primary trait of interest (Hussain et

*Corresponding author. E-mail: aziz.irum@gmail.com.

Table 1. The varieties and strains used in study.

S/N	Variety	Year of release	S/N	Variety	Year of release
1	FH-901	2000	16	L.S.S	1933
2	MNH635	STRAIN	17	362-F	1946
3	MNH636	STRAIN	18	L-11	1959
4	AC-134	1959	19	199-F	1946
5	BS-1	1962	20	K68-9	1977
6	MS-40	1970	21	CIM-70	1986
7	D-9	1971	22	CIM473	2001
8	NIAB KRISHMA	1996	23	FH-1000	2003
9	S-14	1995	24	GR-156	STRAIN
10	FH-634	STRAIN	25	MNH129	1985
11	MS-39	1970	26	124-F	1945
12	4-F	1914	27	SLS-1	1995
13	B-557	1975	28	CIM446	1998
14	NIAB-78	1983	29	MNH417	1992
15	268-F		30	QALANDRI	1974

al., 2010). Estimation of correlation coefficient is necessary for developing a selection index. To make sense of correlations, Wright (1921) developed the method of path coefficients which have been used to develop selection criteria for complex traits in several crop species (Dewey and Lu, 1959; Diz et al., 1994; Fonseca and Patterson, 1968; Gravois et al., 1991; Ivanovic and Rosic, 1985; Kang et al., 1983; Pandey and Torrie, 1973). Path coefficient analysis provides an effective means of finding the direct and indirect causes of association (Kale et al., 2007). Very little knowledge is available on variability, correlation and path coefficient analysis of seedling traits and yield in cotton (*Gossypium hirsutum* L.).

The primary objective of this study was to determine the genetic variability, broad sense heritability, genetic advance and association of different seedling traits of cotton and their direct and indirect effects on yield. Such information can be useful in articulating efficient selection program for development of new promising cotton varieties with improved yield.

MATERIALS AND METHODS

The experimental material comprised of thirty cotton genotypes (Table 1). The experiment was laid out in a randomized complete block design with 3 replications at cotton research station Multan Pakistan during 2003. Seeds were sown in polythene bags 6" x 4" filled with pure sand pre-washed with water having pH value 7.0 and kept under controlled conditions in green house. After 12 days, data for seedling traits which include shoot length, root length, shoot root ratio, shoot weight, root weight, shoot root weight ratio was measured. Shoot length was measured from the first cotyledonary leaf node to junction point of root and shoot. Root length was also measured from the same point of where shoot length was taken but to downward root side with measuring rod. Shoot root length ratio

was computed by dividing shoot length over root length. The seedling plants were dissected and root and shoot weights were measured on electrical balance and shoot root ratio by weight was also calculated. Seed cotton yield was taken from previous crop obtained by making two picks. The mature and effective bolls in each pick were picked and seed cotton was collected in Kraft paper bags. Picking was done when the dew evaporated and harvest was weighed by triple-beam balance.

Statistical analysis

The data were subjected to analysis of variance given by Steel et al. (1997). Heritability estimates (broad-sense), phenotypic and genotypic coefficients of variability and genetic advance (at 5% selection intensity) were calculated following Burton (1951) and Johnson et al. (1955). Phenotypic and genotypic correlation coefficients were calculated as outlined by Kwon and Torrie (1964). Path coefficient analysis was also performed according to the method of Dewey and Lu (1959) by solving simultaneous equations using genotypic correlations. Seed yield per plant was kept as resultant variable and other characters as causal variables.

RESULTS

The data presented in Table 2 divulged that all the characters under study showed highly significant differences among all genotypes except shoot length. Maximum value for root length (13.7 cm) was noted in Ms-39 followed by statistically similar value (13.5 cm) observed in 268-F. However, the lowest root length (2.667 cm) was recorded in CIM-473. Maximum value for shoot root length ratio (3.83) was observed in FH-634, whereas 4-F had the lowest ratio. Maximum value for root weight (185 mg) was observed in 268-F and minimum (60 mg) in CIM-79. CIM-473 gave highest shoot weight (443.3 mg) at seedling stage followed by (375 mg) in FH-

Table 2. Mean squares for different traits of study in cotton.

SOV	DF	SL	RL	SL/RL	RW	SW	SW/RW	Yield
Replications	2	0.4 ^{ns}	7.9 ^{ns}	1.8 ^{ns}	206.5 ^{ns}	22276.0 ^{ns}	1.2 ^{ns}	861.6 ^{ns}
Genotypes	29	5.1 ^{ns}	38.9 ^{**}	2.9 ^{**}	3553.3 ^{**}	13248.3 ^{**}	3.7 [*]	702400.9 ^{**}
Error	58	3.7	7.3	7.2	727.8	3679.62	1.9	2998.3

* Significant < 0.05; **significant <0.01; ns, non-significant. SOV, Source of variation; Df, degree of freedom; SL, shoot length; RL, root length; SL/RL, ratio of shoot to root length; RW, root weight; SW, shoot weight; SW/RW, ratio between shoot and root weight.

634, while D-9 produced minimum shoot weight (145.0 mg). The varieties S-14 and F-901 were at the top for seedling shoot root ratio by weight (5.8) followed by 124-F and MNH129 (5.2). The 4F was at the bottom for this ratio. The highest yield was recorded in Niab-78 (2691 kg/h). However, D9T (desi cotton) and K689 upland cotton were the lowest yielder for seed cotton.

Genetic components

The data represented in Table 4 showed that the values of phenotypic co-efficient of variability (PCV) were higher than genotypic co-efficient of variability (GCV) for all the parameters under investigation except yield. The heritability estimates were significant at 5% probability level for all traits except seedling shoot length. The highest h^2 (0.987) was observed in seed cotton yield and followed by root length (0.592). Moreover, seed cotton yield ha^{-1} , root length, root weight, shoot weight and shoot root length ratio recorded high genetic advance.

Phenotypic and genotypic correlations

The perusal of results revealed that genotypic correlation coefficients were generally higher in magnitude than their corresponding phenotypic correlation coefficients (Table 5). The shoot length had negative statistically non significant genotypic relationship with root length at seedling stage, whereas the phenotypic relationship between these two traits was positive. Shoot length had positive statistically significant genotypic and phenotypic correlations with shoot root length ratio. Correlation between shoot length and shoot weight, as well as root weight at genotypic and phenotypic level was positive and statistically significant. The both correlations between shoot length and S/R weight ratio were positive and statistically non-significant. Shoot length was significantly and positively correlated with yield. The association between root length and shoot root ratio by length was negative and statistically significant.

The genotypic as well as phenotypic correlation coefficient showed statistically significant relationship between root length and root weight shoot root ratio by weight and length. However, root length was positively and significantly correlated with shoot weight and seed

cotton yield at genotypic and phenotypic levels. Shoot / root ratio by length was negatively significantly correlated with shoot weight at genotypic and phenotypic levels. However, it had positive significant genotypic and phenotypic correlations with root weight. Positive but non-significant relationships existed between seedling shoot root ratio by length and seedling shoot root ratio by weight. The value of correlations was positive and significant between seedling shoot root ratio by length and yield of seed cotton ha^{-1} . The phenotypic correlation coefficient between these two traits was also positive but very small.

Furthermore, there was negative and non significant genotypic and phenotypic correlation between shoot weight and root weight, whereas genotypic alliance for this trait with SR ratio weight was negative but significant. The genotypic correlation coefficient between shoot weight and yield of seed cotton ha^{-1} was positive and statistically significant.

The phenotypic association among these characteristics was positive but very low. The genotypic and phenotypic relationship between root weight and shoot root ratio by weight was positive and statistically non significant. Root weight had positive and statistically significant relationship with yield of seed cotton at genotypic and phenotypic basis. The genotypic correlation coefficient between shoot root ratio by weight and yield of seed cotton was also positive and statistically significant.

Path analysis

The data show that seedling shoot length had direct positive effect (0.0713) on yield of seed cotton (Table 6). Shoot length positively and indirectly affected the yield of seed cotton through seedling root length (0.042), seedling shoot root ratio by length (0.2526), root weight (0.8447) and seedling shoot weight (0.649). Negative indirect effect was produced by seedling shoot root ratio by weight (-1.118).

Seedling root length had positive direct effect (1.504) on yield and genotypic correlation between these two parameters was also positive (0.021). Indirect positive effect was created by seedling root weight (1.168) and seedling shoot root ratio by weight (1.357). Seedling root length influenced yield indirectly and negatively by

seedling shoot length (-0.002) and seedling shoot root ratio by length (-0.8089). But the positive indirect effect of root weight and shoot root ratio by weight showed that these can be helpful in selection method indirectly. Seedling ratio of shoot root by length influenced on yield of seed cotton positively (0.871). The shoot root ratio by length had positive indirect effect on yield through path viz shoot length (0.02), root length (1.397) and shoot weight (0.287). The negative indirect effects were produced by root weight (-0.965) and shoot root ratio by weight, (-1.507).

The direct effect of root weight on seed cotton yield was positive and high (1.159).

In addition, the direct positive effect was further supported by positive indirect effects of shoot length (0.052) and shoot root ratio by weight (1.139). The indirect negative effect was created by root length (-1.515), shoot root ratio by length (-0.725) and shoot weight (-0.076). Shoot weight had direct positive effect (0.601) on yield. Shoot length (0.077), root length (0.472) and shoot root ratio by length (0.416) also had positive but indirect effect on yield.

The negative indirect effect was contributed by root weight (-0.146) and shoot root ratio by weight (-0.984). S/R weight ratio had very high direct negative effect on yield of seed cotton (-1.459). The results reveal that we should never use this derived parameter as selection criteria. Shoot root ratio by weight influenced indirectly and negatively yield of seed cotton through seedling root weight (-0.905) and played the whole role making high negative direct effect. Hence, using positive genotypic correlation for selection the negative undesirable indirect negative effect must be nullified.

All the other parameters in this study had positive indirect effect on yield of seed cotton viz seedling shoot length (0.0549), root length (1.1398), shoot root ratio by length (0.899) and shoot weight (0.405).

DISCUSSION

Genetic variability in plant material is necessary for the development of an effective plant breeding program and selection because it is pre-requisite to find out nature and extent of association among various yield and seedling traits. Therefore, to investigate significant differences among genotypes, analysis of variance was used. The data divulged that all the characters under study showed significant differences among all genotypes at 5 % probability level except shoot length. It suggested that sufficient genetic variability existed in this set of material under study for all traits except for shoot length that can be further utilized for crop improvement (Hussain et al., 2010). The inference drawn from the statistics of shoot length are, however, less reliable.

The data represented in Table 3 showed that the values of phenotypic co-efficient of variability (PCV) were

higher than genotypic co-efficient of variability (GCV) for all the parameters under investigation except yield. This indicated that these traits were influenced by the environment, although yield was relatively less influenced by environment in this investigation. Heritability provides information on the relative practicability of selection. The heritability estimates were significant at 5% probability level for all traits except seedling shoot length, which maybe due to low genetic variability for this trait in the material under study. Heritability is a measure of the phenotypic variance attributable to genetic causes (Songsri et al., 2008). It estimates genetic advance for selection under certain environment. When heritability estimates are higher, selection procedures are simpler (Khan et al., 2008). The high heritability does not necessarily, means that the character would show high genetic gain but such associations accrued, the additive gene effects were most important (Sardana et al., 2007). High h^2 coupled with high genetic advances for yield of seed cotton ha^{-1} , root length and shoot weight indicated the presence of more additive genetic variance for these traits under this study. Similar results were also found by Soomro et al. (2010) who stated that seed cotton yield showed 81.14% broad sense heritability coupled with high genetic advance 60.18%. Moderate heritability with moderate genetic advance for shoot length / root length indicates the presence of non-additive genetic component, which is dominance and epistasis for the controlling of this parameter. Similar results were reported by Idahosa et al. (2010) who found moderate heritability estimate for 100-seed weight under combined locations.

The variances and co-variances were used to find out the direction and extent of relationship between the parameters. The perusal of results revealed that genotypic correlation coefficients were generally higher in magnitude than their corresponding phenotypic correlation coefficients. This suggested that genetic causes were more important to effect genotypic association and also the masking effect of environment on association of these traits. An early application of correlation coefficients and path analysis in plant breeding was made by Dewey and Lu (1959) in the study of crested wheat grass. Since then it is being used widely to improve different plants character that requires basic information about yield inter-relationship among the characters with some objective. This technique was used in segregating cotton plant material so that the strategy with respect to selection of desirable plant may be made. The genetic correlations were further portioned to their direct and indirect effects to know the importance of different traits for yield. The highest direct effect on yield of seed cotton was exhibited by root weight followed by root length. Root shoot weight ratio had highest indirect effect on yield of seed cotton through root length (1.3979) followed by root shoot length ratio (1.3969) through root length.

Table 3. Mean values of different traits under investigation in cotton.

S/N	Variety	Traits						Yield (kg/h)
		Shoot length (cm)	Root length (cm)	Ratio of Root length to shoot length	Root Weight (mg)	Shoot Weight (mg)	Ratio of root weight to shoot weight	
1	CIM473	10.3	23.7 ^h	3.8 ^{ab}	73.3 ^{fgh}	443.3 ^a	3.4 ^{bcdefgh}	1744.0 ^g
2	CIM70	10.5	5.5 ^{efgh}	2.0 ^{efghijk}	60.0 ^h	220.0 ^{ghij}	3.7 ^{abcdefgh}	1768 ^{efg}
3	FH 1000	12.0	4.5 ^{fgh}	2.7 ^{efghi}	72.3 ^{fgh}	305 ^{bcdef}	4.8 ^{abcdefg}	1614 ^h
4	GR 156	11.7	6.5 ^{defgh}	2.6 ^{bcdefg}	136.7 ^{bc}	298.3 ^{cdefgh}	2.4 ^{efgh}	2153 ^d
5	MNH129	11.5	3.7 ^{gh}	3.7 ^{abc}	63.3 ^h	285.0 ^{bcdefghi}	3.2 ^{cdefgh}	1153 ⁱ
6	124 F	10.5	7.3 ^{cdefg}	1.5 ^{ghijk}	65.0 ^{gh}	341.3 ^{bcdef}	5.2 ^{abs}	2383 ^b
7	SLS 1	11.0	4.5 ^{fgh}	2.6 ^{bcdefg}	68.3 ^{fgh}	336.3 ^{bcdef}	4.9 ^{abcd}	2229 ^{cd}
8	CIM 446	13.3	7.5 ^{cdefg}	2.9 ^{abcdef}	90.0 ^{defgh}	340.0 ^{bcdef}	3.5 ^{cdefgh}	2306 ^{bc}
9	MNH 147	12.0	12.7 ^{ab}	1.7 ^{fghijk}	125.0 ^{bcd}	245.0 ^{efghi}	3.5 ^{cdefgh}	1614 ^h
10	QALANDRI	13.0	4.0 ^{fgh}	3.4 ^{abcd}	76.7 ^{efgh}	328.3 ^{bcdef}	4.6 ^{abcde}	1999 ^e
11	MS39	12.7	13.7 ^a	0.88 ^k	162.3 ^{ab}	322.3 ^{bcdef}	2.8 ^{defgh}	1384 ^l
12	4F	10.2	12.3 ^{ab}	0.84 ^k	110.7 ^{cdef}	198.3 ^{ij}	1.8 ^h	1768 ^{efg}
13	B557	11.2	12.3 ^{ab}	0.9 ^{jk}	125.0 ^{bcd}	225.0 ^{defghi}	2.1 ^{gh}	1768 ^{efg}
14	NIAB 78	13.2	11.7 ^{abc}	1.14 ^{ijk}	163.3 ^{ab}	351.7 ^{abcd}	2.1 ^{gh}	2691 ^a
15	268 F	11.5	13.5 ^a	0.96 ^{jk}	185.0 ^a	210.0 ^{ghij}	2.3 ^{fgh}	1768 ^{efg}
16	L.S.S	11.6	11.7 ^{abc}	1.05 ^{ijk}	72.3 ^{fgh}	326.7 ^{bcdef}	3.9 ^{abcdefgh}	1845 ^f
17	362 F	11.8	9.83 ^{abcde}	1.2 ^{ijk}	108.3 ^{cdefg}	270.0 ^{cdefghi}	3.6 ^{bcdefgh}	2306 ^{bc}
18	L11	13.7	8.17 ^{bcdef}	1.31 ^{hijk}	131.7 ^{bcd}	366.7 ^{abc}	2.8 ^{defgh}	1384 ^l
19	199 F	11.8	10.5 ^{abcd}	1.15 ^{ijk}	120.0 ^{bcde}	273.3 ^{cdefgghi}	2.4 ^{efgh}	1845 ^f
20	K 68 9	11.8	8.15 ^{bcdef}	1.7 ^{fghijkl}	135.0 ^{bc}	367.3 ^{abcd}	2.8 ^{defgh}	1076 ^j
21	FH 901	11.8	3.57 ^{gh}	3.5 ^{abc}	78.3 ^{efgh}	343.3 ^{bcde}	5.8 ^a	2229 ^{cd}
22	MNH635	12.8	4.10 ^{fgh}	3.2 ^{abcde}	93.3 ^{cdefgh}	350.0 ^{abcd}	3.8 ^{abcdefgh}	21056 ^e
23	MNH636	13.9	5.03 ^{fgh}	3.05 ^{abcde}	80.0 ^{efgh}	353.3 ^{abcd}	4.5 ^{abcdef}	2383 ^b
24	AC 134	9.3	3.8 ^{fgh}	2.48 ^{cdefgh}	90.0 ^{defgh}	210.7 ^{hij}	2.5 ^{efgh}	1845 ^f
25	BS 1	12.7	4.3 ^{fgh}	3.11 ^{abcde}	107.7 ^{cdefg}	353.3 ^{abcd}	3.3 ^{cdefgh}	2306 ^{bc}
26	MS 40	11.3	4.6 ^{fgh}	2.58 ^{bcdefg}	70.0 ^{fgh}	258.3 ^{defghi}	3.8 ^{abcdefgh}	2230 ^{cd}
27	D 9	8.8	4.2 ^{fgh}	2.13 ^{defghij}	63.3 ^h	145.0 ^j	2.6 ^{efgh}	231 ^k
28	N.KRISHMA	8.9	3.97 ^{fgh}	2.28 ^{defghi}	76.7 ^{efgh}	243.3 ^{ghij}	3.2 ^{cdefgh}	1768 ^{efg}
29	S 14	12.5	3.5 ^{gh}	2.27 ^{defghi}	61.7 ^h	360.0 ^{abc}	5.8 ^a	1774.7 ^{efg}
30	FH634	13.3	3.6 ^{gh}	3.83 ^a	76.7 ^{efgh}	375.0 ^{ab}	5.2 ^{abc}	1845 ^f
CD 0.05		N.S	4.41	1.237	4.077	99.1	2.226	89.462
CD0.01		N.S	5.877	1.650	58.813	132.241	2.969	119.372

The figures having common letters are statistically similar.

Table 4. Genetic components of different traits under study in cotton.

Trait	GV	PV	(GCV) %	(PCV) %	(h ² BS) %	(GA)
Shoot Length	0.4863	4.164	5.97	17.49	0.1169	3.58
Root Length	10.53	17.8	46.44	60.37	0.5917*	62.68
Ratio between shoot to root length	0.798	1.362	39.6	52.03	0.5793*	52.9
Root Weight	941.84	1669.7	31.29	41.67	0.5641*	41.25
Shoot Weight	3189.6	6869.2	18.67	27.41	0.4643*	22.33
Ratio between root to shoot weight	0.624	2.48	22.43	44.7	0.2518*	19.7
Yield			26.20	26.29	98.7	45.53

Table 5. The upper diagonal genotypic correlation (rg) with their standard error and lower diagonal phenotypic correlation for different seedling traits and yield in cotton.

Traits	Shoot length	Root length	Ratio of shoot length to root length	Shoot weight	Root weight	Ratio of shoot weight to root weight	Yield
Shoot Length	1	-0.2775 ± 0.2934 ^{ns}	0 ± 0.0428	0.7282 ± 0.1982*	1.803 ± 0.068*	0.776 ± 1.066 ns	0.7416 ± 0.0461*
Root Length	0.2393	1	-0.9288 ± 0.5069*	1.0073 ± 0.0289*	-0.3141 ± 0.00098*	-0.9293 ± 0.1614*	0.021 ± 0.0062*
Ratio between shoot to root length	0.1048	-0.8402	1	-0.8321 ± 0.1163*	0.477 ± 0.0653*	1.0327 ± 0.8512 ^{ns}	0.1028 ± 0.0099
Shoot Weight	0.9082	0.4807	-0.3522	1	-0.1257 ± 0.0065 ^{ns}	-0.7806 ± 0.0297*	0.0362 ± 0.005*
Root Weight	0.4429	-0.1838	0.3570	-0.0030	1	0.6741 ± 0.0234 ^{ns}	0.4364 ± 0.0006*
Ratio between shoot and root weight	0.0183	-0.2752	0.2479	-0.5521	0.3343	1	0.3922 ± 0.0044*
Yield	0.2247	0.0007	0.0761	0.0353	0.2930	0.1937	1

Conclusion

High h² coupled with high genetic advances for

yield of seed cotton ha⁻¹, root length and shoot weight indicated that these traits are controlled by additive genetic action, thus suggesting hybrid

breeding for the improvement these traits. Therefore, while making selection for high yielding cotton genotype, seedling root length and weight

Table 6. Direct and indirect effects matrix of traits under study in cotton.

Trait	Shoot length	Root length	Ratio of root length to shoot length	Root weight	Shoot weight	Ratio of root weight to shoot weight	Yield (rg)
Shoot Length	(0.0713)	0.0417	0.2526	0.8447	0.6489	-1.1184	0.742
Root Length	-0.0019	(1.5041)	-0.8089	1.1683	-0.1887	1.3566	0.021
Ratio of root length to shoot length	0.0208	1.3969	(0.8710)	-0.9652	0.2867	-1.5074	0.103
Root Weight	0.0522	-1.5150	-0.7248	(1.1599)	-0.0755	1.1394	0.036
Shoot Weight	0.0775	0.4724	0.4155	-0.1458	0.6007	-0.984	0.436
Ratio between root and shoot weight	0.0549	1.3979	0.8995	-0.9054	0.4049	-1.4597	0.392

rg = Genotypic correlation.

must be kept in mind.

REFERENCES

- Ashokkumary K (2010). Combining ability estimates for yield and fiber quality traits in Line \times Tester Crosses of upland cotton, (*Gossypium hirsutum* L.). *Int. J. Biol.* 2(1): 179-189.
- Burton GW (1951). Quantitative inheritance in pearl millet (*Pennisetum glaucum*). *Agron.J.* 43: 409-417.
- Dewey DR, Lu KH (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agron J.* 51: 515-518.
- Diz DA, Wofford DS, Schank SC (1994). Correlation and path-coefficient analyses of seed-yield components in pearl millet \times elephant grass hybrids. *Theor. Appl. Genet.* 89: 112-115.
- Fonseca S, Patterson FL (1968). Yield component heritabilities and interrelationships in winter wheat (*Triticum aestivum* L.). *Crop Sci.* 8: 614-617.
- Gravois KA, Milligan SB, Martin FA (1991). Additive genetic effects for sugarcane components and implications for hybridization. *Trop. Agric.* 68: 376-380.
- Hussain K, Khan IA, Sadaqt HA, Amjad M (2010). Genotypic and phenotypic correlation analysis of yield and fiber quality determining traits in upland cotton (*Gossypim hirsutum*). *Int. J. Agric. Biol.* 12: 348-352.
- Idahosa DO, Alike JE, Omoregie A (2010). Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in Cowpea (*Vigna unguiculata* L.). *Walp. Academia Arena*, 2(5).
- Ivanovic M, Rosic (1985). Path coefficient analysis for three stalk traits and grain yield in maize (*Zea mays* L.). *Maydica.* 30: 233-239.
- Johnson HW, Robinson HF, Comstock R.E (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.* 47: 314-318.
- Kang MS, Miller JD, Tai PYP (1983). Genetic and phenotypic path analysis and heritability in sugarcane. *Crop Sci.* 23: 643-647.
- Khan H, Rahman H, Ahmad H, Ali H (2008). Magnitude of heterosis and heritability in sunflower over environments. *Pak. J. Bot.* 1: 301-308.
- Kwon SH, Torrie JH (1964). Heritability and interrelationship among traits of two soybean populations. *Crop Sci.* 4: 196-198
- Pandey JP, Torrie JH (1973). Path coefficient analysis of seed yield components in soybeans (*Glycine max* L. Merr.). *Crop Sci.* 13: 505-507.
- Sardana S, Mahajan R, Gautam N, Ram B (2007). Genetic variability in pea (*Pisum sativum* L.) germplasm for utilization. *SABRAO J. Breed. Genet.* 39(10): 31-41.
- Songsri P, Jogloy S, Kesmala T, Vorasoot N, Akkasaeng CPA, Holbrook C. (2008). Heritability of drought resistance traits and correlation of drought resistance and agronomic traits in peanut. *Crop Sci.* 48: 2245-2253.
- Soomro ZA, Kumbhar MA, Larik AS, Imran M, Brohi SA (2010). Heritability and selection response in segregating generations of upland cotton. *Pak. J. Agric. Res.* 23(1-2): 25-30.
- Steel RGD, Torrie JH, Dicky DA (1997). *Principles and Procedures of Statistics, A Biometrical Approach*, McGraw Hill Book Co. New York, USA. pp. 204-251.
- Kale UV, Kalpande HV, Annapurve SN, Gite VK. (2007). Yield components analysis in American Cotton (*Gossypium hirsutum* L.). *Madras Agric. J.* 94 (7-12): 156-161.
- Wright S (1921). Correlation and causation. *J. Agric. Res.* 20: 557-585.