

*Full Length Research Paper*

## Genetic basis of variation for seedling traits in *Gossypium hirsutum* L.

Waqas Malik<sup>1\*</sup>, M. Zaffar Iqbal<sup>3</sup>, Asif Ali Khan<sup>2</sup>, Etrat Noor<sup>1</sup>, Abdul Qayyum<sup>1</sup> and Mamoona Hanif<sup>4</sup>

<sup>1</sup>Department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakariya University, Multan, Pakistan.

<sup>2</sup>Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.

<sup>3</sup>Agricultural Biotechnology Research Institute, AARI, Faisalabad, Pakistan.

<sup>4</sup>Cotton Research Station, Multan, Pakistan.

Accepted 3 January, 2011

**A 6 × 6 complete diallel analysis was performed to study the inheritance of seedling traits in cotton. Significant differences among genotypes showed the genetic variation and formal analysis predicted the presence of both additive and non-additive genetic variation for inheritance of seedling traits. Further, the estimates of genetic components D, H<sub>1</sub> and H<sub>2</sub> confirmed the presence of both additive and non-additive genetic effects for all the characteristics. Dominant genes were responsible for the increase of seedling shoot length, root length, shoot weight and root weight. However, recessive genes were accountable for the increase of shoot root ratio by length and by weight. Seedling shoot length, root length and root weight can be improved through heterosis breeding. The magnitude of broad sense heritability was greater than narrow sense for all the six traits under study hence diminished the scope of selection in the early segregating generation therefore pedigree breeding method is suggested for the improvement of these traits.**

**Key words:** Additive dominance model, gene action, *Gossypium hirsutum* L, heritability, seedling traits.

### INTRODUCTION

Seedling parameters play important role in obtaining desirable crop stand. In cotton, healthy seedlings provide escape from early infection of insect pests and diseases at early stages of plant development. Robust seedling rooting systems in cotton have shown to be highly heritable, and progeny of crossing two robust seedling-rooting genotypes showed increased robustness, suggesting the opportunity for selection. Hence the endeavors of increasing cotton production have been made through developing improved seedling traits. Seedling traits also influence seed rate use for raising commercial crop. Lower seed rate play a vital role in economical cultivation of crop after the increasing use of seed treatment (for sucking insects), hybrid and transgenic seed. Knowledge of nature of gene action for seedling

related traits would aid in the choice of effective and efficient breeding method and this accelerate the pace of improvement in these traits. For the proper accomplishment of this task, genetic analysis is a prerequisite for innovation in breeding. These analyses not only provide the information about genetic architecture of the character that help in formulating an appropriate selection programme but also predict progress through selection. The selection of cotton genotypes for plant parameters at the seedling stage would help in predicting their performance at the maturity stage. The process of selection in breeding material is facilitated with basic information about the genetic components of variation. The diallel analysis technique developed by Hayman (1954) and Jinks (1954) provides information about heritability and genetic components of variation for various plant traits and thus facilitates the selection process. Very little work on inherent pattern of seedling traits of cotton has already been done. El-Zik et al. (1990), Singh (1992) and Kassianenko (2003) studied inheritance in cotton and

\*Corresponding author. E-mail: waqasmalik@bzu.edu.pk. Tel: 0092619210073-75, Ext. 4032. Fax: 0092619210068.

**Table 1.** Mean squares for analysis of variance of different seedling traits in *Gossypium hirsutum* L.

S.O.V.	D.f	Root length	Shoot length	S/R ratio length	Root weight	Shoot weight	S/R ratio weight
Repeats	2	0.005 <sup>NS</sup>	0.025 <sup>NS</sup>	0.002 <sup>NS</sup>	3.231 <sup>NS</sup>	25.148 <sup>NS</sup>	0.046 <sup>NS</sup>
Genotypes	35	5.425 <sup>**</sup>	0.853 <sup>**</sup>	0.167 <sup>**</sup>	1388.435 <sup>**</sup>	8993.25 <sup>**</sup>	0.806 <sup>**</sup>
Error	70	0.075	0.038	0.004	33.174	29.729	0.034

\*Significant ( $p \leq 0.05$ ); \*\*, highly significant ( $p \leq 0.01$ ); NS, non-significant; SOV, source of variability; D.f, degree of freedom.

found variable results. However Crosbie et al. (1980), Hoard and Crosbie (1985) and Andrew (1982) studied seedling trait in maize. Mc Kenzie et al. (1980) and Akram et al. (2007) studied genetic components of seedling traits in rice. Li et al. (1983) worked on sorghum for seedling traits. Present study was conducted to know the gene action of seedling traits in cotton, which will be use for the selection of genetically superior cotton genotypes because vigorous seedling can serve as precursor of healthy plants.

## MATERIALS AND METHODS

### Plant materials

Plant materials comprised of three elite genotypes, MNH-700, VH-142, SLH-279 and three commercial cultivars that is, FH-1000, BH160, MNH-552. The genotype VH-142 are short stature with smaller seedling root weight and length, FH-1000 and BH-160 are medium stature and medium seedling root weight and length. MNH-552 and SLH-279 are tall growing and have longer roots.

### Crossing plan

During the 1<sup>st</sup> year, these genotypes were crossed in a 6 × 6 complete diallel fashion including 15 direct, 15 reciprocals and selfing of six parents at Cotton Research Station, Multan. At the 2<sup>nd</sup> year, these reciprocal and direct crosses (F<sub>1</sub>) and selfed parents were planted in polythene bags 6" × 4" filled with pure sand, prewashed with water having pH value 7.0. Completely randomized design (CRD) with three replications followed for this experimentation.

### Data recording

Sowing was done in June and seedling data was recorded after twelve days. During growth period, seedling plants were irrigated when needed and temperature was maintained at 25°C. The data of seedling plants were collected for shoot length (cm), root length (cm), shoot/ root ratio by length, root weight (mg), shoot weight (mg) and shoot/ root ratio by weight.

### Data analysis and fulfillment of diallel assumptions

Before diallel analysis, the data were subjected to analysis of variance following Steel et al. (1997) using MSTATC software in order to determine the genotypic differences for all the recorded plant performance traits. Only those parameters were evaluated to fit the simple additive-dominance model for genetic analysis that showed significant genotypic differences ( $P \leq 0.05$ ). Moreover, the genotype

sums of squares were partitioned into male, female and male × female interaction as described by Mather and Jinks (1977). The diallel crossing depends upon the following assumptions (Hayman, 1954): Homozygous parents, diploid segregation, no reciprocal effect, independent action of non-allelic genes, absence of multiple alleles and independent distribution of genes among the parents. The parental material was taken from the gene pool maintained in the Cotton Research Station Multan through induced selfing for many years. Therefore, the parents involved in crossing were assumed to be homozygous. *Gossypium hirsutum* L. is a naturally amphidiploid evolved by the combination of A and D genomes. Kimber (1961) and Endrizzi (1962) reported that the chromosomes segregation occur in diploid fashion. Reciprocal differences were removed by taking the means of direct and reciprocal crosses for all the traits.

The other assumptions of the model that is, no epistasis, absence of multiple alleles in governing the expression of different traits and independent distribution of genes were tested by conducting the formal analysis of variance of diallel tables. The adequacy of simple additive-dominance model was assessed using two scaling tests. The first test consisted of joint regression analysis of variance ( $V_r$ ) and co-variance ( $W_r$ ). The assumptions of the genetic model were considered adequate if the regression coefficient ( $b$ ) deviated significantly from zero, but not from unity (Mather and Jinks, 1982). The second test for the adequacy of the model comprised of analysis of variance of ( $W_r + V_r$ ) and ( $W_r - V_r$ ). In the presence of dominance,  $W_r + V_r$  must changes from array to array at the same time if there is epistasis  $W_r - V_r$  will vary between arrays, although if only dominance is present  $W_r - V_r$  will not vary more than expected from error variation (Mather and Jinks, 1977). However the analysis was continued for those traits having partial adequacy of additive dominance model, but according to Hayman (1954) the estimates were less reliable, when all the assumptions have been fulfilled. In direct components,  $h^2$  reveal the contribution of dominance due to heterogeneity of loci and  $F_r$ ,  $H_{1r}$  indicated relative frequencies of dominance and recessive alleles in breeding material. These direct (D,  $H_1$ ,  $H_2$ ,  $h^2$ , F and E) and derived genetic components ( $H_1/D$ )<sup>1/2</sup>,  $H_2/4H_1$ ,  $H_1 - H_2$ ,  $1/2F/[D(H_1-H_2)]$ <sup>1/2</sup>,  $h^2/H_2$ ,  $r$  = correlation between  $W_r + V_r$  and parental value,  $h^2$  NS = (heritability narrow sense),  $h^2$  BS = (heritability broad sense) were calculated according to Hayman (1954) and used by Singh and Chaudhry (1985). Heritabilities in narrow and broad sense were computed following Mather and Jinks (1977).

## RESULTS

### Analysis of variance and test of gene action

The data revealed that genotypes under observation were significantly different from each other at  $p \leq 0.01$  probability level for all the traits under study (Table 1). This indicated that there was ample scope for continuing the analysis for determination of genetic parameter.

**Table 2.** Mean squares of formal analysis of variance\test of gene action of different seedling traits in *Gossypium hirsutum* L.

Components	D.F	Mean square		Retested C	Mean square			
		Root length	Shoot length		Shoot/root by length	Root weight	Shoot weight	Shoo/root by weight
a	5	27.4023**	3.7880**	23.6002**	0.8181**	7097.31**	45299.5**	3.8647**
b	15	3.4730**	0.6149*		0.1220**	854.71**	5463.7**	0.5278**
b <sub>1</sub>	1	33.1031**	5.8698**		0.7420**	7135.87 <sup>NS</sup>	41378.8**	0.4995 <sup>NS</sup>
b <sub>2</sub>	5	0.8864 <sup>NS</sup>	0.2002 <sup>NS</sup>		0.0813*	343.28 <sup>NS</sup>	2639.8**	0.7757 <sup>NS</sup>
b <sub>3</sub>	9	1.6178*	0.2613**		0.0757**	440.93 <sup>NS</sup>	3042.06**	0.4099 <sup>NS</sup>
c	5	0.0466 <sup>NS</sup>	0.1601*		0.0015 <sup>NS</sup>	16.40 <sup>NS</sup>	129.0 <sup>NS</sup>	0.0175 <sup>NS</sup>
d	10	0.0674 <sup>NS</sup>	0.0341 <sup>NS</sup>		0.0011 <sup>NS</sup>	20.60 <sup>NS</sup>	202.9 <sup>NS</sup>	0.0144 <sup>NS</sup>
Block	35	5.4281	0.8373		0.1697	1388.43	8889.3	0.7892
B x a	10	0.1814	0.0520		0.0093	75.15	302.4	0.1415
B x b	30	0.0962	0.0441		0.0054	91.02	374.8	0.1038
B x b <sub>1</sub>	2	0.0134	0.0869		0.0014	69.79	437.0	1.1069
B x b <sub>2</sub>	10	0.2440	0.0619		0.0140	73.05	207.0	0.1413
B x b <sub>3</sub>	18	0.0234	0.0294		0.0014	103.37	461.1	0.0826
B x c	10	0.0171	0.0302		0.0008	69.92	492.8	0.0605
B x d	20	0.0196	0.0335		0.0009	54.29	337.8	0.0588
Block interaction	70	0.0752	0.0402		0.0040	75.25	370.8	0.0901

\*, Significant ( $p \leq 0.05$ ); \*\*, highly significant ( $p \leq 0.01$ ); NS, non-significant.

Results for the formal analysis of variance/ test of gene action showed the maternal effects 'c' and reciprocal effects 'd' were non significant for all traits except seedling shoot length therefore the significance of 'a' and 'b' items were not retested (Table 2). Significant values of 'a' and 'b' items revealed that variations in these traits were controlled by additive and non additive genes, respectively, while at the same time retested values of 'c' for seedling shoot length also confirmed the presence of additive type of gene action.

#### Test of adequacy and estimation of genetic components

The results of the two tests carried out using  $F_1$

data on six characters revealed that the  $W_r$  and  $V_r$  regressions were all significantly different from zero but not from unity for all traits (Table 3). The  $(W_r + V_r)$  array difference were also significant for all seedling traits but so were the  $(W_r - V_r)$  array difference with the exception of shoot length. For the other traits, there was evidence of inadequacies in the simple additive dominance models and hence possible biases in the estimates of genetic component of variance (Tables 3 and 4).

The estimates of genetic components divulged that both additive (D) and dominance ( $H_1$  and  $H_2$ ) values were significant hence suggested that both additive and non-additive effects were responsible for the variation observed in the diallel cross population for all six traits under study (Table 4). The magnitude of  $H_2$  was lower than  $H_1$  for all

traits, it confirmed the unequal allelic frequencies in parents and this influence was strengthened by the low ratio of  $H_2/4H_1$  than 0.25. The further proof of this unequal distribution of alleles over loci was obtained from positive value of  $H_1 - H_2$ , which indicated that  $\mu \neq \nu$  at all loci. In this context,  $\mu$  refers to frequency of alleles, which increases the mean expression of the character and are situated at loci, which exhibited dominance, on the other hand  $\nu$  correspond to the frequency of alleles at loci that decreases the expression of this character and was recessive. The significant and positive value of net dominance ( $h^2$ ) over all loci in heterozygous phase in the cross indicated that the direction of dominance was towards greater seedling shoot length, seedling root length and seedling shoot weight. The negative signifi-

**Table 3.** Scaling test for the adequacy of additive dominance model for seedling traits in *Gossypium hirsutum* L.

Traits	Test 1			Test 2	
	b+/- SE(b)	b-0 SE (b)	1-b SE (b)	Wr-Vr between array MS	Wr+Vr between array MS
Root length	0.925 ± 0.051	18.238*	1.475 <sup>NS</sup>	0.0275**	0.234901**
Shoot length	0.959 ± 0.092	10.446*	0.445 <sup>NS</sup>	0.003299 <sup>NS</sup>	0.005683**
S/R by length	0.923 ± 0.057	16.182*	1.356 <sup>NS</sup>	0.0000597**	0.0006239**
Root weight	0.919 ± 0.107	8.626*	0.763 <sup>NS</sup>	1329.8**	11756.2**
Shoot weight	0.997 ± 0.101	9.884	0.029 <sup>NS</sup>	4184.56**	45806.6**
S/R by weight	1.203 ± 0.163	7.395*	-1.249 <sup>NS</sup>	0.0024876*	0.025734**

b, Regression coefficient; SE(b), standard error of regression coefficient; NS, non significant; \*\*, highly significant at  $p \leq 0.01$ ; \*, significant at  $p \leq 0.05$ ; Vr, variance; Wr, co-variance; S/R, shoot root ratio.

cant estimate of  $h^2$  showed that dominance occurred toward the parent exhibited lower seedling shoot root ratio by length and a substantial contribution to dominance was due to heterogeneity of loci. As  $h^2$  value was greater than  $H_1$  and  $H_2$ , hence the suggested bi-directional dominance for this character's length in this material. The non-significant value of  $h^2$  for root weight revealed that substantial contribution to dominance was due to homogeneity of loci, while non significant and negative value of  $h^2$  revealed the direction of dominance was towards lower seedling shoot/ root by weight (Table 4). An excess of recessive genes was found in parent for seedling shoot length, seedling root length and seedling root weight as value of F was negative. However its non significance indicated that parents having dominant and recessive alleles were equal in number. This excess of recessive alleles as compared to dominant was confirmed from the value of  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ , which was less than unity. The positive value of F showed the presence of higher number of dominant genes in parents and presence of dominant alleles were confirmed for these trait by the value of  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ . The values of average degree of dominance  $(H_1/D)^{1/2}$  for all traits except seedling shoot length were less than one which suggested partial-dominance for these traits, while value of  $(H_1/D)^{1/2}$  for seedling shoot length was larger than unity which suggested the presence of over dominance in this set of diallel cross. The value of ratio  $1/2F / [D (H_1-H_2)]^{1/2}$  for all seedling parameters was less than unity. This implied that dominance level is not constant in all loci and it varied in some loci. It was observed that different number of genes controls the seedling parameters. The maximum dominance ( $h^2/H_2$ ) value of seedling shoot/ root by length suggested the involvement of nine groups of genes having dominance at seedling stage. Correlation between parental means (Yr) and the parental order of dominance (Wr + Vr) provided a meaningful estimate of the direction of dominance. The significant and negative value of (r) for seedling root length, seedling shoot weight and seedling root weight

suggested that the dominant genes were responsible for the increase of these traits and most dominant genes acted in one direction and majority of recessive genes in opposite direction. The positive significant correlation between Wr + Vr and parental value indicated that recessive alleles are associated with the increase of seedling shoot length, seedling shoot/root by length and seedling shoot/root by weight. Estimates of narrow sense and broad sense heritability estimates were high but the amount of narrow sense heritability was low as compared to broad sense heritability (Table 4). The Fr and  $H_{1r}$  values indicated that SLH279 carried maximum number of dominant alleles and BH 160 possessed maximum number of recessive alleles for seedling shoot length. The data (Table 5) showed that  $H_{1r}$  that is, non additive effect of array into different parents confirm the findings of Fr value. The Fr and  $H_{1r}$  values indicated that MNH 552 had maximum number of dominant genes and VH142 had maximum number of recessive alleles for seedling root length and shoot/ root by length. It also revealed that variation due to dominance effect of genes controlled for gene distribution was mainly due to MNH 552 for seedling root length and shoot/root by length. The distribution of varietales values revealed that MNH-700 had the greatest number of dominant genes followed by FH-1000 for seedling shoot weight. The  $H_{1r}$  value confirmed the presence of recessive alleles in BH160 for seedling root weight and Fr for shoot/ root by weight revealed that MNH-552 carried the most dominant genes.

## DISCUSSION

There is a wide degree of variation within species in response to seedling growth and inheritance in the cotton plant. The robustness of cotton crop at seedling stage can be an indicator of healthy crop at maturity. Systemic work to examine genetic variability within crops is still in its infancy (Srivastava and Java, 1984). Different scientists studied the plant growth at early stage of plant

**Table 4.** Estimates of genetic components of variances and their standard error.

Genetic component	Shoot length	Root length	Shoot/Root length	Shoot weight	Root weight	Shoot/root weight
D	0.330* ± 0.025	2.698* ± 0.110	0.121* ± 0.005	6061.999* ± 355.905	684.986* ± 57.129	0.810* ± 0.051
H <sub>1</sub>	0.438* ± 0.062	2.455* ± 0.280	0.098* ± 0.012	4566.176* ± 903.497	611.507* ± 145.028	0.524* ± 0.130
H <sub>2</sub>	0.403* ± 0.056	2.288* ± 0.250	0.080* ± 0.011	3933.180* ± 807.117	543.716* ± 129.557	0.370* ± 0.117
h <sup>2</sup>	2.122* ± 0.037	4.999* ± 0.168	- 0.736* ± 0.007	176.629* ± 543.243	66.344 <sup>NS</sup> ± 87.201	- 0.529 <sup>NS</sup> ± 0.078
F	- 0.62 <sup>NS</sup> ± 0.060	- 0.184 <sup>NS</sup> ± 0.269	0.050* ± 0.012	1642.755* ± 869.476	- 29.841 <sup>NS</sup> ± 139.567	0.536 <sup>NS</sup> ± 0.126
E	0.012 <sup>NS</sup> ± 0.009	0.024 <sup>NS</sup> ± 0.042	0.001 <sup>NS</sup> ± 0.002	93867 <sup>NS</sup> ± 134.519	10.781 <sup>NS</sup> ± 21.593	0.011 <sup>NS</sup> ± 0.019
Derived components						
(H <sub>1</sub> /D) <sup>1/2</sup>	1.152	0.954	0.901	0.868	0.945	0.804
H <sub>2</sub> /4H <sub>1</sub>	0.230	0.233	0.204	0.215	0.222	0.177
H <sub>1</sub> - H <sub>2</sub>	0.03518	0.166079	0.018	632.9959	67.7905	0.153637
(4DH <sub>1</sub> ) <sup>1/2</sup> + F	0.849	0.931	1.601	1.37	0.955	2.396
(4DH <sub>1</sub> ) <sup>1/2</sup> - F						
1/2F/[D(H <sub>1</sub> - )] <sup>1/2</sup>	- 0.288	- 0.138	0.538	0.419	- 0.069	0.759
h <sup>2</sup> /H <sub>2</sub>	5.2	2.18	9.1	0.045	0.122	1.43
r.= correlation b/w Wr +Vr and parental value	- 0.99265	- 0.97751	0.914	- 0.99741	- 0.98192	0.497159
h <sup>2</sup> NS = (heritability narrow sense)	0.654	0.719	0.674	0.718	0.727	0.674
h <sup>2</sup> b = heritability broad sense)	0.962	0.988	0.978	0.997	0.980	0.964

D, Additive; H<sub>1</sub>, variation due to dominant effect of gene; H<sub>2</sub>, variation due to dominant effect of gene correlated with gene distribution; h<sup>2</sup>, net dominance over all loci in heterozygous phase; F, relative frequency of recessive alleles; E, environmental variance.

development (Noor et al., 2001; Bhatti et al., 2006; Azhar et al., 2007; Sharifi, 2008). For the evaluation of crop plant at seedling stage, use of biometrical techniques can be helpful to understand the genetic mechanism of these traits. Among these techniques, diallel matting system is an imperative technique which provided information on the inheritance of quantitative traits (Sharifi, 2008). Diallel analysis is also helpful in identification of parents with additive and non additive genetic effects for a specific trait with a benefit in selection of best parents to be included in breeding program (Murtaza et al., 2005). In the present study, the results revealed the presence of both additive and non-additive genetic variation in the in-heritance of traits under study and retes-

ted value of 'c' for seedling shoot length suggested that selection for this trait could be useful. Azhar et al. (2007) also found that root length is controlled by both additive and non additive effects and selection can play vital role for the improvement of this trait. The estimates of genetic components D, H<sub>1</sub> and H<sub>2</sub> confirmed the presence of both additive and non-additive genetic effects for all these traits. Preponderance of additive genetic was observed for seedling root length, shoot root ratio by length, root weight, shoot weight and shoot root ratio by weight. Lee et al. (1986) reported that the weight of 12 days old rice seedling was under the control of both additive and non-additive gene effects but additive effect were more important. On the other hand for

seedling shoot length, non-additive genetic effects were found to be more important as compared to additive effects.

Li and Rutger (1980) and Akram et al. (2007) also found both additive and non additive effects in F<sub>1</sub> and F<sub>2</sub> generations, and additive effects were consistent over both generations. This little contradiction in the finding was may be due to different crop and environmental conditions. The negative F component and value of (4DH<sub>1</sub>)<sup>1/2</sup> + F / (4DH<sub>1</sub>)<sup>1/2</sup> - F less than unity revealed more recessive alleles in the parents for seedling root length, shoot length, root weight where as more dominant allele appeared in seedling shoot root ratio by length, shoot weight and shoot root ratio by weight. Partial-dominance gene action was found

**Table 5.** Relative frequencies of dominant to recessive alleles in parents Fr and H<sub>1r</sub> values.

Parents	Shoot length	Root length	S/R ratio length	Shoot weight	Root weight	S/R ratio weight
<b>Fr</b>						
MNH700	0.5380	-1.099	0.0813	1228.40	137.2922	0.838
VH142	- 0.09263	- 5.552	- 0.220	- 1361.02	- 1336.11	- 0.119
SLH279	0.8487	1.486	0.1400	- 1253.38	469.0922	0.535
FH1000	- 0.565	3.335	0.1783	1419.24	536.5588	1.290
BH160	- 0.9414	- 4.408	- 0.091	- 1882.76	- 1628.91	- 0.817
MNH552	0.1603	5.1335	0.213	1193.08	1643.026	1.4862
<b>H<sub>1r</sub></b>						
MNH700	1.0383	1.54	0.129	1520.74	778.6399	0.826
VH142	0.408	- 2.913	- 0.173	1562.39	- 694.76	- 0.131
SLH279	1.349	4.124	0.187	- 9610.4	110.44	0.523
FH1000	- 0.0644	5.973	0.225	4342.66	1177.907	1.278
BH160	- 0.441	- 1.769	- 0.0434	1040.66	-987.56	- 0.828
MNH552	0.340	7.772	0.261	1485.42	2284.37	1.474

Fr = Covariance of additive and non additive effect in r<sup>th</sup> array; H<sub>1r</sub> = variations due to dominant effect of genes in r<sup>th</sup> array.

in root length, shoot root ratio by length, root weight, shoot weight and shoot root ratio by weight whereas over dominance was found in shoot length. Asymmetry of positive and negative homozygotes among the six parents at non-additive loci was observed for all traits under study. The ratio  $1/2F / [D (H_1-H_2)]^{1/2}$  was less than unity for all traits hence it implied that dominance level was not constant in all loci and it varied in some loci. Dominant genes were responsible for the increase of seedling root length, shoot length, root weight shoot weight however recessive genes were accountable for the increase of shoot root ratio by length and by weight. Seedling root length, shoot length and root weight can be improved through heterosis breeding. Among seedling parameters roots are most sensitive part of plant and heterosis may lead to robust of rooting system. The modification of rooting system can lead to cotton plant to be more tolerant to against drought (Basal et al., 2003).

The estimation of heritability has a great value in prediction of the genotypic and phenotypic effects during the selection of plant material (Johnson et al., 1955; Teran et al., 1990). Both estimates of heritability are effected by environmental factors, therefore selection of breeding material based on heritability should be with great care. The low amount of narrow sense heritability than broad sense heritability reduced the efficiency of selection based on all seedling traits in early segregation generation because heritability is ratio of variance due to hereditary differences and genotypic variance to total phenotypic variance (Cruz et al., 2006). Azhar et al. (2007) also found the very low amount of narrow sense heritability for seedling root length and diminish the scope of selection in early generations. The high amount of broad sense heritability for root length and root weight seems to be genetically controlled. These findings are in agreement with the studies of Hanif et al. (2008). Relative

frequencies (Fr and H<sub>1r</sub>) showed that MNH 552 and FH 1000 can prove a good parental lines for the achievement of heterosis in F<sub>1</sub> generation as both have maximum dominant genes for root length and seedling root weight.

It may be suggested that the study of genetic bases at seedling stage can be a good indicator for the selection of robust parental line to be used in future breeding programme for development of hybrid and elite genotypes and it is concluded from the study of gene action and heritability estimates that pedigree-breeding method could be helpful for the improvement of all these seedling traits in cotton.

## REFERENCES

- Akram M, Ajmal S, Munir M (2007). Inheritance of traits related to seedling vigor and grain yield in rice (*Oryza sativa* L.). Pak. J. Bot. 39: 37-45.
- Andrew RH (1982). Factors influencing early seedling vigour of Shrunken-2 maize. Crop Sci. 22: 263-266.
- Azhar FM, Khan AA, Saleem N (2007). Genetic mechanism controlling the salt tolerance in *Gossypium hirsutum* L. seedling. Pak. J. Bot. 39 115-121
- Basal H, Bebeli C, Smith CW, Thaxton P (2003). Root growth parameters of converted race stock of upland cotton and two BC<sub>2</sub>F<sub>2</sub> populations. Crop Sci. 43: 1983-1988.
- Bhatti MA, Azhar FM, Alvi AW (2006). Estimation of additive dominance and epistatic components of cotton grown in salinized conditions. Int. J. Agric. Biol. 8: 624-627.
- Crosbie TM, Mock JJ, Smith OS (1980). Comparison of grains predicted by several selection methods for cold tolerance traits of two maize populations. Crop Sci. 20: 549-655.
- Cruz RP, Milach SCK, Luiz CF (2006). Inheritance of rice cold tolerance at germination stage. Genet. Mol. Biol. 29: 314-320.
- EI-Zik KM, Namken NL, Thaxton PM (1990). Effect of weather on cotton seedling survival and its association with lint yield and fiber quality. National cotton council America, pp. 88-93.
- Endrizzi JE (1962). The diploid-like cytological behavior of tetraploid cotton. Evolution, 16: 325-329.
- Hanif M, Noor E, Murtaza N, Qayyum A, Malik W (2008). Assessment of

- variability for salt tolerance at seedling stage in *Gossypium hirsutum* L. J. Food Agric. Environ. 6: 134-138.
- Hayman BI (1954). The theory and analysis of diallel crosses. Genetics, 39: 789-809.
- Hoard RG, Crosbie TM (1985). S<sub>1</sub> line recurrent selection for cold tolerance in two Maize populations. Crop Sci. 25: 1041-1045
- Jinks JL (1954). The analysis of continuous variation in a diallel cross of *Nicotiana rustica*. Genetics, 39: 767-788
- Johnson N, Robinson HF, Comstock RE (1955). Genotypic and phenotypic correlations in sorghum and simplification in selection. Agron. J. 47: 477-482.
- Kassianenko VA (2003). Genetic analysis of the duration of vegetative period in cotton *Gossypium hirsutum* L. on soil with different nitrogen contents. Russian J. Gen. 39: 1400-1404.
- Kimber G (1961). Basis of the diploid-like meiotic behavior of polyploidy cotton. Nature (London). 19: 98-100.
- Lee CC, Li CC, Sung JM (1986). Physiological and genetic studies on seedling vigor in rice (*Oryza sativa* L.). II. Inheritance of alpha amylase activity and seedling vigor in rice. J. Agric. Ass. Chin. 135: 17-24.
- Li CC, Rutger JN (1980). Inheritance and cool temperature seedling vigor in rice and its relationship with other agronomic characters. Crop Sci. 20: 295-298.
- Li CC, Bhall JN, Borikar ST (1983). Combinability for seedling vigor in *Sorghum*. J. Maharashtra Agric. Univ. 8: 59-60.
- Mather K, Jinks JL (1982). Biometrical Genetics. 3<sup>rd</sup> Ed. Chapman and Hall. London.
- Mather K, Jinks JK (1977). Introduction to Biometrical Genetics. Chapman and Hall, London, (1<sup>st</sup> Ed).
- Mc Kenzie KS, Rutger JN, Peterson ML (1980). Relation of Seedling vigour to semi-dwarfism, early maturity and pubescence in closely related rice lines. Crop Sci. 20: 169-172.
- Murtaza N, Kitaoka M, Ali GM (2005). Genetic differences of cotton cultivars by polyacrylamide gel electrophoresis. J. Centr. Eur. Agric. 43: 61-166.
- Noor E, Azhar FM, Khan AA (2001). Differences in response of *Gossypium hirsutum* L. varieties to NaCl salinity level at seedling stage. Int. J. Agric. Biol. 3: 345-347.
- Sharifi P (2008). Inheritance of cold tolerance in rice at germination stage. Asian J. Plant Sci. 7: 485-489.
- Singh RK, Chaudhry BD (1985). Biometrical methods in Quantitative Genetic analysis. Kalyani Pub. Ludhiana, New Delhi, Revised Edition., pp. 102-118.
- Singh N (1992). Genotype and environment interaction for seed germination and seedling vigour in upland cotton. Seed Res. 20: 7-9.
- Srivastava JP, Java S (1984). Screening wheat and barley germplasm for salt tolerance. In: Salinity Tolerance, Plants Strategies for Crop Improvement, John Wiley New York. pp. 273-284.
- Steel RGD, Torrie JH, Dickey DA (1997). Principles and Procedures of Statistics, A Biometrical Approach. McGraw Hill Book Co., New York, USA.
- Teran HM, Maiti RK, Mercado RS, Moreno S (1990). Evaluacion Y Seleccion de Sorgo *Sorghum bicolor* L. Moench. Para resistencia a la sequia Y salinidad en etapa de plantula Ciencia Agropecuaria. 3: 18-25.