

## Genetic Analysis for Drought Tolerance of Cotton (*Gossypium Hirsutum* L.) for Yield Related Components

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### Abstract

Germplasm of Cotton plant was analysed to examine its ability for tolerance of water stress in future varieties. Four tolerant (VH-142, CIM-482, NIAB-78 and BH-121) and for four susceptible (CIM-446, FH-900, FH-901 and FH-1000) lines were recognized from 50 accessions on the basis of their root length at seedling stage. Full diallel crosses were made between selected eight genotypes were genetically examined related to yield traits following Hayman and Jinks(1954). Both additive and non-additive variances were observed in the inheritance for all traits under normal and water stress condition. Major fraction for genetic variance was additive which further was supported by high value of narrow sense heritability for characters. The graph of Variance vs covariance represents that gene action is of additive type with partial dominance and there is no epistasis interaction for the inheritance of these traits. The results of present study suggested that improvement can be brought for drought tolerance in cotton genotypes through crosses between tolerant genotypes with the help of conventional breeding approach in segregating generations.

**Keywords:** Additive Variance, non-additive variances, Cotton, Diallel seed cotton, root length, water stress

**Tob Regul Sci.** <sup>TM</sup> 2023;9(1): 4840-4859

**DOI:** [doi.org/10.18001/TRS.9.1.337](https://doi.org/10.18001/TRS.9.1.337)

### Introduction

The fibre of cotton has worldwide significance and it is very vital agricultural product of Pakistan, as an item for export it provides a large quantity of foreign exchange. It is also a source of raw material for textile industry in our country. The crop of cotton is of great importance of the economy of Pakistan. During the summer, cotton crop is widely grown in irrigated parts of southern Punjab, and the province of Sindh. The Production of cotton crop is effected in large areas of province Punjab and Sindh due to inadequate water or limited rainfall during the growth and development of cotton. Deficiency in ground water and high costs of energy are major problems in cotton cultivation in Pakistan. Therefore in present era the cotton breeders have started to develop cotton germplasm for various aspects particularly drought tolerance to bring modifications in the genetics of best cultivars to use as a parents for new populations, and to utilize new genetic material to use in breeding programmes. However, this research work is at the initial stage (Basal *et al.*, 2005, Iqbal *et al.*, 2005). The occurrence of additive type of gene action will give assurance to go forward in the improvement of tolerance to water deficient condition.

The limited availability of water to cotton plants causes slow development, decrease in bolls size and shedding of cotton squares. In addition, the stress of moisture causes many changes in plant phenotypes during development such as stunted plant growth and reduction in leaf area (Turner *et al.*, 1986; Ball *et al.*, 1994; Gerik *et al.*, 1996), shoot growth reduction, decrease in plant height and yield (McMichael and Quisenberry, 1991). Flowering process of cotton plant is very critical to water stress than vegetative growth and stage of ripening (Kar *et al.*, 2005).

The current research was conducted to investigate the capacity for breeding of *Gossypium hirsutum* L. under water stress condition, Fifty lines/accessions of cotton were tested for limited water supply in green house at stage of seedling. The genotypes were selected on basis of their root length parameter as recommended by Basal *et al.*, 2005, to develop the material to conduct the current research work.

### Materials and Methods

The current research was performed in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. The material for experiment was developed from 50 cotton lines taken from genetic material collected from the department and evaluated through screening. Eight accessions, Tolerant (VH-142, CIM-482, NIAB-78 and BH-121) and Susceptible: (CIM-446, FH-900, FH-901 and FH-1000) were finalized on the base of parameter root length.

The finally selected genotypes were grown in the glasshouse in the pots of mud filled with nutrient rich soil. Two seeds were sown in each pot. One seedling were allowed to grow after germination. The cultural practices such as fertilization, irrigation and hoeing were properly

continued during all the stages of plant developmental stages. During flowering the plants were crossed in a way to make a full set of all diallel crosses including self crosses. For the purpose crossing emasculation of the suitable buds were carried out in afternoon and covered stigma and the style of selected flowers with the help of soda straw tube and labeled to identify the parentage. The Pollens of the open flowers from male parents were used for the purpose to pollinate the emasculated buds in the morning, and the buds were covered again with the help soda straw tube to prevent contamination. The record of crosses was kept. At the stage of maturity, the selfed and crossed bolls were chosen and seed of cotton were ginned to obtain seed.

The response of genotypes under normal and water stress condition were evaluated in field conditions. All the sixty four entries were sown in the fields in randomized complete block design with three replications. The seeds of entries were planted in 75 cm apart rows each with plants has space of 30 cm in the rows. For each entry there was a single row and 10 plants were present in each row. Normal irrigation was given to the plants for studying under control condition while for water stress condition 50 % less water was given. Data of 5 plants for each entry of each treatment were collected for genetic analysis of the following characters:

#### **Number of bolls**

Seed cotton was harvested in three pickings. The total number of bolls in the all three picks was collected and all the bolls per plant were recorded. The average of bolls from each entry was calculated in each replication of the all three treatments.

#### **Boll weight**

Weight of the boll of a plant was obtained by dividing yield of seed cotton per plant by the respective total bolls of that plant. Average weight of boll of plant was calculated over the replication.

#### **Seed cotton yield**

Three picks of the seed cotton were done at regular gaps of three weeks. The Seed cotton per plant was separately picked and placed in bags of kraft paper. The total product for each plant after three picks was cleaned and then weighed with the help of electrical balance, and average per plant was noted for each replication.

#### **Ginning out turn**

The samples of clean and dry seed cotton were weighed for each plant and then ginned with the help a single roller electric gin. Ginning out turn was calculated by using following formula:

$$\text{GOT(\%)} = \text{Lint weight} / \text{Seed cotton yield} \times 100$$

**Statistical analysis of data**

The data were statistically analyzed for its variance as recommended by Steel *et al.* (1997) which showed that significant differences were present among the genotypes for all the traits. Genetic analysis was done by using diallel analysis following the approach of Hayman (1954a, b), Jinks (1954) and exemplified by Mather and Jinks (1982).

**Table 1. Mean squares of various cotton plant traits in a 8x8 diallel cross under normal water regime**

Source	DF	Number of bolls	Boll weight	Seed cotton yield	Ginning-out-turn
Replications	2	6.630	0.449	13.94	7.454
Genotypes	63	5.794**	4.510**	48.76**	9.727**
Error	126	3.577	0.0339	18.09	2.630

\*\* = Highly significant

**Table 2. Mean squares of various cotton plant traits in a 8x8 diallel cross under water stress regime**

Source	DF	Number of bolls	Boll weight	Seed cotton yield	Ginning-out-turn
Replications	2	0.661	0.0217	4.94	9.870
Genotypes	63	7.311**	3.987**	47.98**	13.283**
Error	126	3.487	0.0392	17.07	3.570

\*\* = Highly significant

**Results**

The Joint regression analysis and analysis of variance of  $W_r + V_r$  (difference between the arrays) and  $W_r - V_r$  (differences within the arrays) were applied to check the adequacy of the additive-dominance model regarding yield related parameters of cotton plant under both normal and water stress environmental regimes. The values of the scaling tests are given in Table3.

Table3. Scaling tests for adequacy of additive-dominance model for data regarding different plant traits under normal and water stress regimes.

Traits (Normal)	D	H <sub>1</sub>	H <sub>2</sub>	F	(h <sup>2</sup> )	E	(H <sub>1</sub> / D) <sup>0.5</sup>	( $\sqrt{4D}$ H <sub>1</sub> + F / $\sqrt{4D}$ H <sub>1</sub> - F)	(H <sub>2</sub> / 4H <sub>1</sub> )	h <sup>2</sup> (n.s)
NOB	2.98 ± 0.07*	2.78 ± 0.14*	1.94 ± 0.12*	1.38 ± 0.14*	0.55 ± 0.08*	1.27 ± 0.02*	0.96	1.63	0.17	0.49
BW	0.09 ± 0.01**	0.03 ± 0.003*	0.01 ± 0.002*	0.03 ± 0.02 <sup>NS</sup>	0.006 ± 0.004 <sup>NS</sup>	0.01 ± 0.005*	0.57	0.53	0.08	0.49
SCY	15.98 ± 0.59*	12.53 ± 1.36*	8.75 ± 1.18*	9.32 ± 1.40*	2.57 ± 0.80*	6.31 ± 0.20*	0.88	1.98	0.18	0.69
GOT	5.12 ± 0.20*	1.21 ± 0.46*	0.55 ± 0.20*	1.26 ± 0.78 <sup>NS</sup>	1.19 ± 0.27*	0.94 ± 0.06*	0.48	0.59	0.11	0.78
Water stress										
NOB	1.75 ± 0.12*	1.52 ± 0.74*	0.91 ± 0.26*	1.87 ± 0.31*	-0.20 ± 0.17 <sup>NS</sup>	1.20 ± 0.28*	0.93	3.69	0.14	0.54
BW	0.07 ± 0.03**	0.03 ± 0.001*	0.02 ± 0.001*	-0.04 ± 0.03 <sup>NS</sup>	-0.005 ± 0.003 <sup>NS</sup>	0.01 ± 0.001*	0.65	0.38	0.16	0.57
SCY	14.67 ± 0.44*	11.79 ± 0.99*	8.03 ± 0.867*	6.49 ± 1.02*	2.25 ± 0.58*	5.91 ± 0.15*	0.9	1.65	0.17	0.7

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GOT	7.1 6± 0.1 9*	1.32± 0.44*	0.71±0. 29*	- 0.88±0.4 6 <sup>NS</sup>	0.74±0.2 6*	1.28±0.0 64*	0.4 3	0.75	0.1 3	0.7 7
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Traits (Normal)	Joint regression analysis	Mean squares		Remarks
		W <sub>r</sub> + V <sub>r</sub>	W <sub>r</sub> – V <sub>r</sub>	
Number of bolls	1.055±0.090	8.726 <sup>NS</sup>	0.285 <sup>NS</sup>	Partially adequate
Boll weight	0.871±0.140	0.0005 <sup>NS</sup>	0.0001 <sup>NS</sup>	Partially adequate
Seed cotton yield	1.106±0.1216	116.871 <sup>NS</sup>	13.767 <sup>NS</sup>	Partially adequate
Ginning out turn	0.966±0.009	14.073 <sup>NS</sup>	2.086 <sup>NS</sup>	Partially adequate
<b>Water Stress</b>				
Number of bolls	0.893±0.134	5.562 <sup>NS</sup>	0.418 <sup>NS</sup>	Partially adequate
Boll weight	0.920±0.07	0.0001 <sup>NS</sup>	0.0001 <sup>NS</sup>	Partially adequate
Seed cotton yield	1.106±0.1216	78.587 <sup>NS</sup>	33.725 <sup>NS</sup>	Partially adequate
Ginning out turn	0.998±0.064	37.484 <sup>NS</sup>	2.213 <sup>NS</sup>	Partially adequate

Table4 :Components of genetic variation under normal and water stress regimes

D= Additive variance, H<sub>1</sub>= Component of variation due to dominant effects of genes

H<sub>2</sub> = Component of variation due to dominant effects of genes correlated with gene distribution

F = Relative frequency of dominant and recessive alleles in the parents

h<sup>2</sup> = Overall dominance effects of heterozygous loci

E = Environmental variance

(H<sub>1</sub> /D)<sup>0.5</sup> = Mean degree of dominance

$\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F}$  = Proportion of dominant and recessive genes in the parents

H<sub>2</sub> / 4H<sub>1</sub> = Proportion of genes with positive and negative effects in the parents

h<sup>2</sup><sub>NS</sub> = Heritability, Narrow sense

The analyses revealed that the model was partially adequate for the data regarding all the traits. The regression coefficient 'b' for all the parameters deviated from zero but not from unity which indicated the absence of non-allelic interaction, independent genes distribution for the characters among the parents and independence of gene actions. As suggested by Mather and Jinks, 1982 the unit slope of the regression lines for all the characters revealed that all the assumptions of the additive dominance model were met.

**Number of bolls:**

Study of Table 4 indicated the involvement of additive and non-additive effects of genes in the inheritance of number of bolls per plant under both the water regimes as D and H ( $H_1, H_2$ ) components were statistically significant.

The estimates of  $(H_1/D)^{0.5}$  also revealed partial dominance. Greater values of  $H_1$  than  $H_2$  under both the conditions indicated an unequal allele frequency at all loci. The gene frequencies in the parents was unequal as it is evident from the ratio  $H_2/4H_1$ , which is 0.17 and 0.14 under normal and drought conditions respectively. The positive and significant value of  $F$ , under both the conditions indicated higher frequencies of dominant alleles. This suggestion was further supported by the value of  $\sqrt{4DH_1+F}/\sqrt{4DH_1-F}$  (1.63 and 3.69) under both the conditions which are greater than 1. Significant value of  $h^2$  was observed under normal conditions which showed unidirectional dominance towards higher number of bolls under normal condition. Under water stress the dominance seemed bidirectional where the relative frequency of positive and negative dominant genes were almost equal. Effect of environment was also observed on the expression of this trait. Heritability ( $N_s$ ) of this trait was moderate under both the water regimes.

$$b = 0.893 \pm 0.134$$

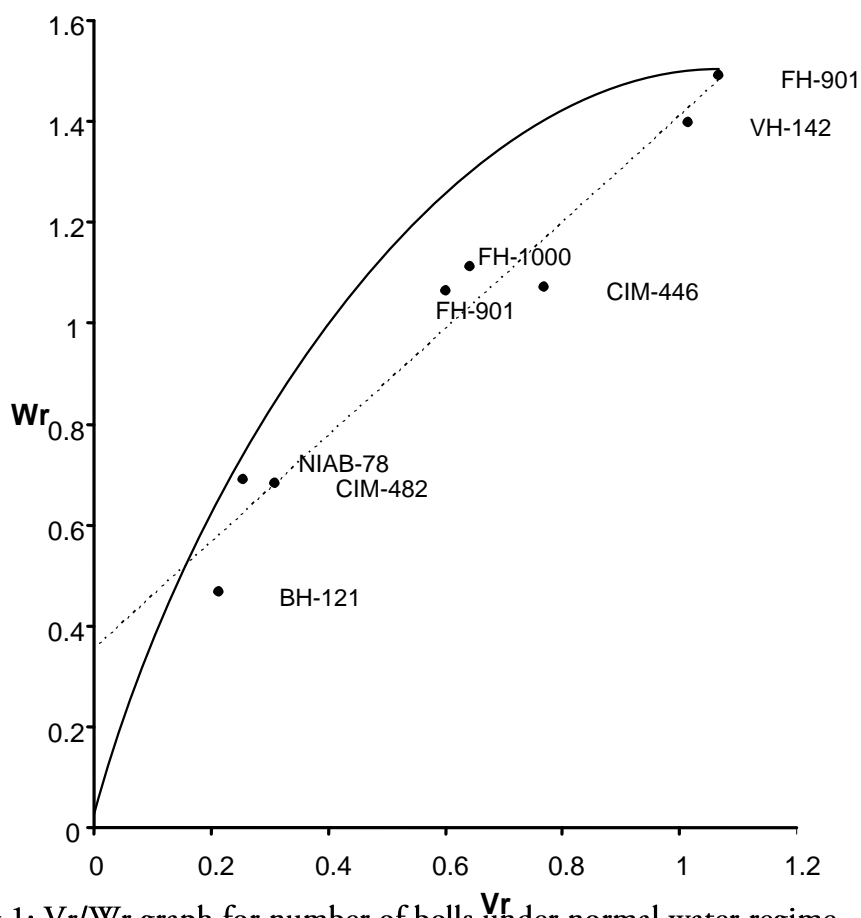


Fig 1:  $V_r/W_r$  graph for number of bolls under normal water regime

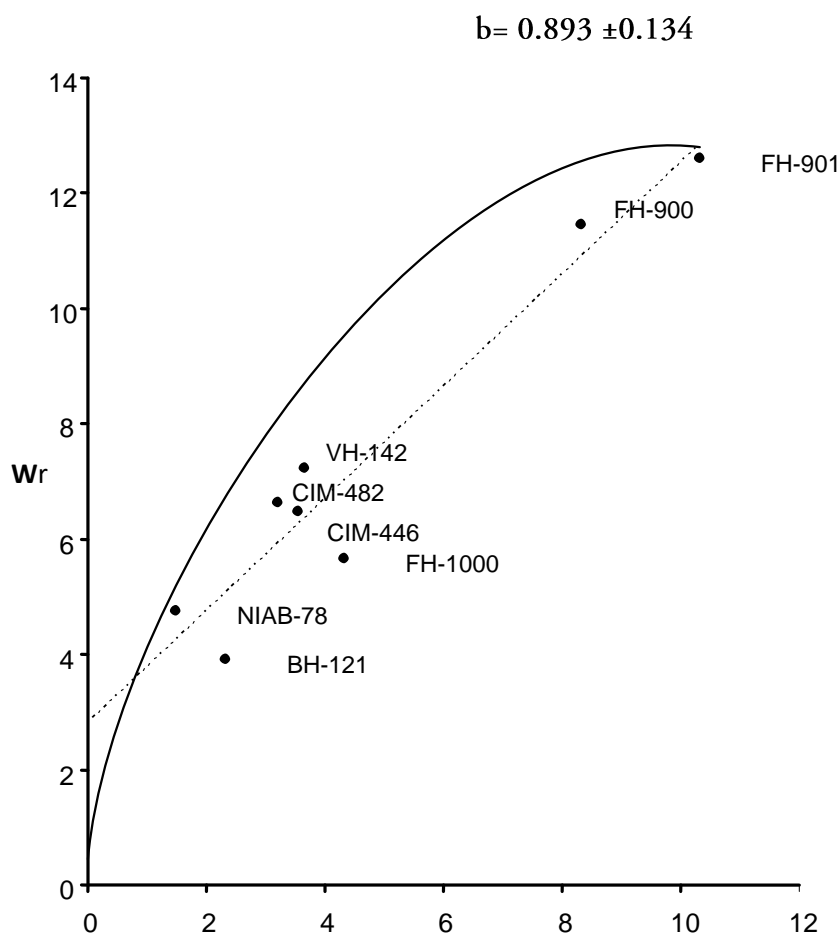


Fig 2: Vr/Wr graph for number of bolls under water stress regime

The Vr/Wr graph in Fig.1 and 2 revealed that additive type of gene action with partial dominance involved in the inheritance of number of bolls as the regression lines intercepted Wr axes on positive side of the origin. As far as the varietal positions on the regression lines were concerned, BH-121 secured maximum dominant and FH-901 the recessive genes under both the conditions because of their closest and farthest positions from the origins respectively. All other varieties had variable number of dominant and recessive genes depending upon their positions. The parent BH-121 proved to be best general combiner under both the water regimes as it got maximum array means (17.04 and 14.98 under normal and stressed conditions respectively). Specifically it made good combinations with CIM-482 both under normal and stressed conditions by securing maximum values within the arrays. (Tables 5 and 6)



Table-5. Mean 8×8 diallel table for number of bolls under normal water regime  
NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	14.67	16.67	17.00	16.50	14.83	15.50	14.17	15.83
CIM-482	16.67	17.33	17.83	17.50	16.00	16.17	16.00	15.33
BH-121	17.00	17.83	18.00	17.83	16.17	17.00	16.17	16.33
VH-142	16.50	17.50	17.83	17.67	15.33	16.33	15.33	16.00
FH-900	14.83	16.00	16.17	15.33	15.00	15.83	14.67	15.50
CIM-446	15.50	16.17	17.00	16.33	15.83	16.00	15.50	15.67
FH-1000	14.17	16.00	16.17	15.33	14.67	15.50	14.00	14.83
FH-901	15.83	15.33	16.33	16.00	15.50	15.67	14.83	15.33
Mean	15.65	16.60	17.04	16.56	15.42	16.00	15.08	15.60

Table-6. Mean 8×8 diallel table for number of bolls under water stress regime  
NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	12.67	14.50	14.67	14.67	12.67	13.50	11.17	13.00
CIM-482	14.50	15.33	15.83	16.00	13.83	13.00	14.00	13.83
BH-121	14.67	15.83	16.00	16.17	14.17	14.33	14.17	14.50
VH-142	14.67	16.00	16.17	15.67	13.33	14.00	12.83	12.83
FH-900	12.67	13.83	14.17	13.33	13.00	12.33	13.33	11.83
CIM-446	13.50	13.00	14.33	14.00	12.33	14.00	13.33	12.50
FH-1000	11.17	14.00	14.17	12.83	13.33	13.33	12.00	12.50
FH-901	13.00	13.83	14.50	12.83	11.83	12.50	12.50	13.33
Mean	13.35	14.54	14.98	14.44	13.06	13.38	12.92	13.04

#### Boll weight :

A perusal of the Table 4 revealed significant additive as well as dominance variances under normal and water stress conditions. Degree of dominance was also noted as partial as the values of  $(H_1/D)^{0.5}$  was less than one. The frequency of alleles was unequal at all the loci under both the regimes as indicated by difference in the values of  $H_1$  and  $H_2$  which was further evidenced by the values of  $H_2/4H_1$  being lesser than 0.25. The negative value of  $F$ , though non significant under both conditions indicated higher frequencies of recessive alleles. This suggestion was further supported by the value of  $\sqrt{4DH_1+F}/\sqrt{4DH_1-F}$  (0.53 and 0.38) under both the conditions which are lesser than 1. The non significant value of  $h^2$  was observed under both the conditions showing bidirectional dominance. Significance of  $E$  components indicated an effect of environment in the phenotypic expression of this character. Narrow sense heritability was

observed to be moderate with values for 0.49 under normal and 0.57 under water stress conditions.

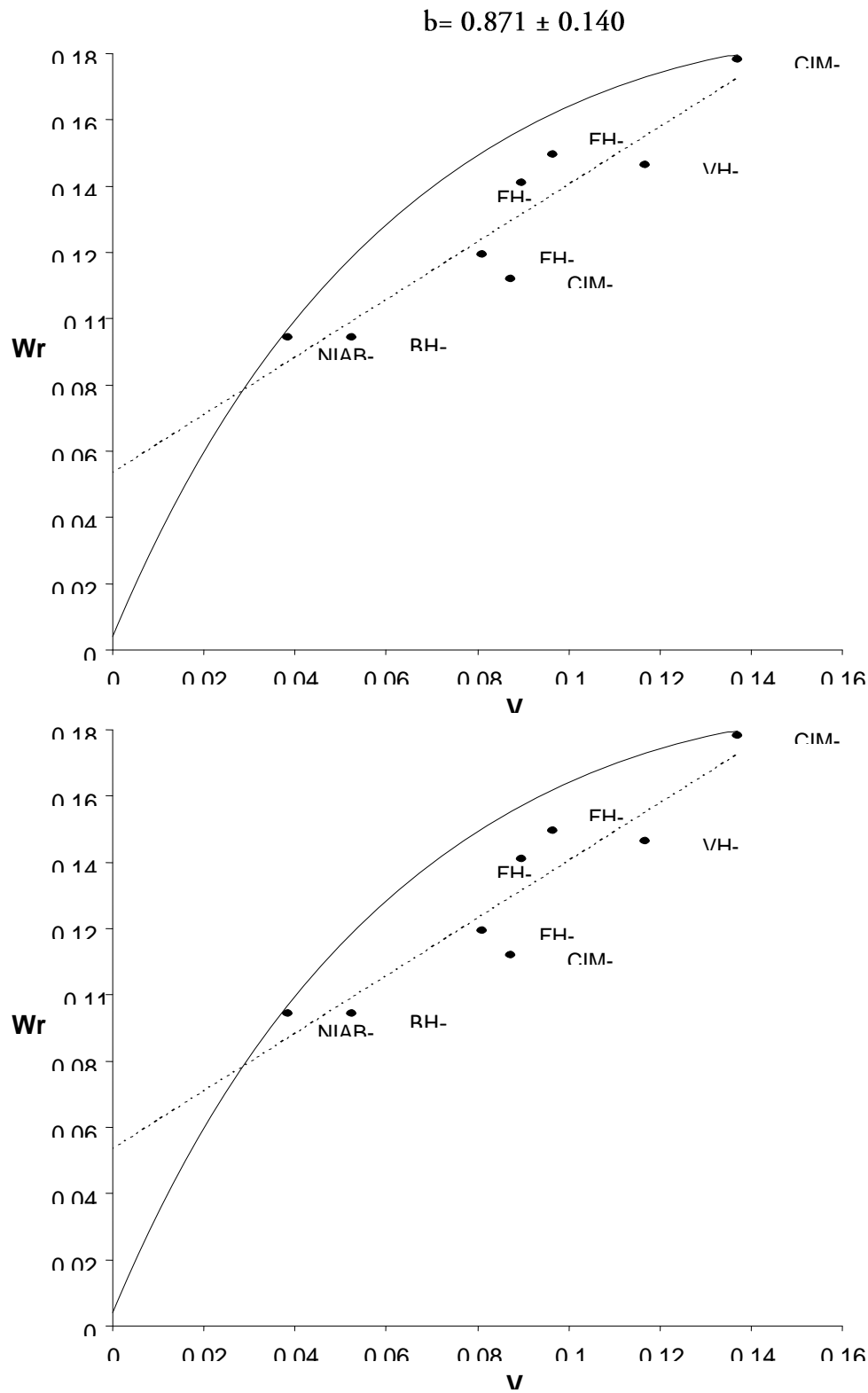


Fig 3: Vr/Wr graph for boll weight under normal water regime

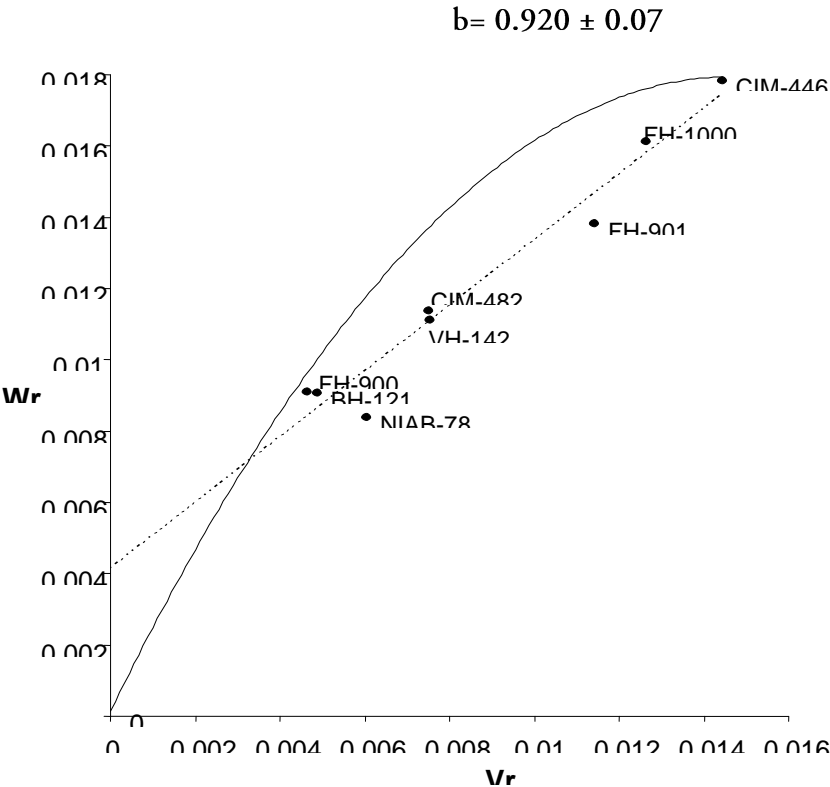


Fig 4: Vr/Wr graph for boll weight under water stress regime

Fig 3 and 4 for boll weight under normal and water stress regimes indicated additive type of gene action with partial dominance as the regression lines with unit slopes intercepted the Wr axes below the origins. The positions of array points on the regression lines in both the figs. remained same as far as the possession of maximum number of dominant as well as recessive genes. The variety NIAB-78 got dominant and CIM-446 the recessives because of their closest and farthest locations from the origin.

Table-7 Mean 8×8 diallel table for boll weight under normal water regime  
NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	2.80	2.71	2.74	2.68	2.55	2.69	2.57	2.69
CIM-482	2.71	2.61	2.64	2.59	2.62	2.60	2.47	2.57
BH-121	2.74	2.64	2.41	2.60	2.46	2.51	2.44	2.36
VH-142	2.68	2.59	2.60	2.59	2.55	2.57	2.46	2.49
FH-900	2.55	2.62	2.46	2.55	2.45	2.49	2.47	2.37
CIM-446	2.69	2.60	2.51	2.57	2.49	2.58	2.51	2.48
FH-1000	2.57	2.47	2.44	2.46	2.47	2.51	2.50	2.44
FH-901	2.69	2.57	2.36	2.49	2.37	2.48	2.44	2.38
Mean	2.68	2.60	2.52	2.57	2.50	2.55	2.48	2.47

Table-8 Mean 8×8 diallel table for boll weight under water stress regime

NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	2.63	2.55	2.53	2.50	2.38	2.59	2.44	2.51
CIM-482	2.55	2.43	2.33	2.41	2.38	2.44	2.25	2.35
BH-121	2.53	2.33	2.20	2.35	2.26	2.26	2.23	2.19
VH-142	2.50	2.41	2.35	2.40	2.36	2.36	2.29	2.21
FH-900	2.38	2.38	2.26	2.36	2.22	2.28	2.24	2.24
CIM-446	2.59	2.44	2.26	2.36	2.28	2.37	2.25	2.23
FH-1000	2.44	2.25	2.23	2.29	2.24	2.25	2.24	2.25
FH-901	2.51	2.35	2.19	2.21	2.24	2.23	2.25	2.20
Mean	2.52	2.39	2.29	2.36	2.30	2.35	2.27	2.27

Table-7 and Table-8 show the mean values of the parents as well as their  $F_1$  progenies under both the water regimes. The best GCA was shown by NIAB-78 securing the highest array means. However it showed good SCA with BH-121 under normal and with CIM-446 under water stress condition by securing highest values (2.74 and 2.59) respectively.

#### Seed cotton yield :

The significant values of  $D$  and  $H_1$  in table confirmed the additive and dominance effects of genes for seed cotton yield. The values of  $H_2$  were also significant for this trait under both the water regimes. The positive and significant values of  $F$  for the trait indicated the presence of excess of dominant alleles in the genetic material. The positive and significant  $h^2$  confirmed the direction of dominance was towards the higher seed cotton yield. Significant  $E$  indicated the effect of environment on the expression of this trait. The amount of dominance effects can be seen from the value of  $(H_1/D)^{0.5}$  which was less than one indicating partial dominance. The Value of  $H_2/4H_1$  was less than 0.25 thus indicated unequal frequency of alleles. Estimates of  $\sqrt{4DH_1+F}/\sqrt{4DH_1-F}$  under both the environments were more than one indicated that the parents contain more dominant genes. Heritability ( $N_s$ ) estimates were moderately higher (0.69 and 0.70) under both the water regimes.

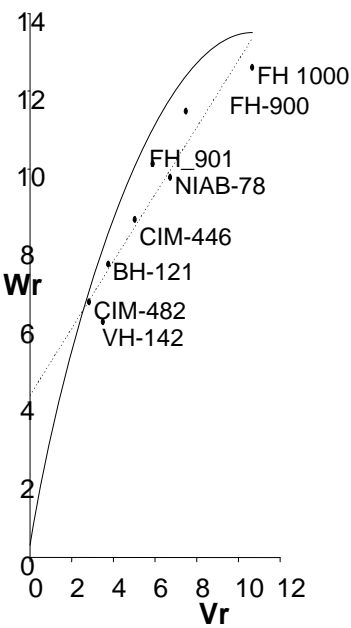


Fig 5: Vr/Wr graph for seed cotton yield under normal water regime  
 $b = 1.106 \pm 0.1216$

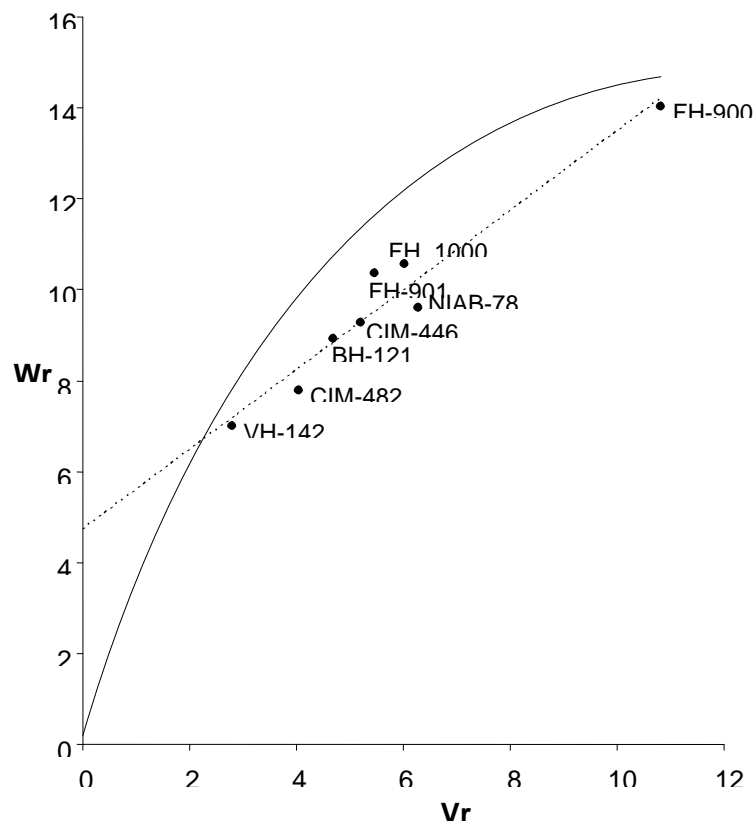


Fig 6: Vr/Wr graph for seed cotton yield under water stress regime

The position and slope of regression in  $V_r/W_r$  graphs ( Fig 5 and Fig 6) revealed additive type of gene action with partial dominance and no epistatic effects in the expression of this trait under both the environments. The location of array points on the regression lines indicated that VH-142 possessed maximum dominant genes under both the regimes being the closest to the origin whereas FH-1000 under normal and FH-900 under water stress conditions had maximum recessive genes for yield of seed cotton because of their farthest positions from the origin.

**Table-9 Mean 8×8 diallel table for seed cotton yield under normal water regime**

NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	39.33	43.50	41.17	44.00	37.33	40.33	37.33	37.17
CIM-482	43.50	45.33	44.67	45.50	43.17	43.17	40.00	41.17
BH-121	41.17	44.67	43.67	43.50	40.67	42.17	41.17	39.83
VH-142	44.00	45.50	43.50	46.00	39.67	43.33	38.83	37.17
FH-900	37.33	43.17	40.67	39.67	36.33	37.33	35.67	36.50
CIM-446	40.33	43.17	42.17	43.33	37.33	41.33	38.17	37.83
FH-1000	37.33	40.00	41.17	38.83	35.67	38.17	35.00	35.50
FH-901	37.17	41.17	39.83	37.17	36.50	37.83	35.50	36.67

Mean 40.02 43.31 42.10 42.25 38.33 40.46 37.71 37.73

**Table-10 Mean 8×8 diallel table for seed cotton yield under water stress regime**

NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	31.33	34.33	33.00	36.33	29.83	32.00	30.33	29.00
CIM-482	34.33	37.33	36.00	38.83	35.17	34.50	32.00	33.50
BH-121	33.00	36.00	35.67	36.17	31.67	34.17	33.17	33.00
VH-142	36.33	38.83	36.17	39.67	31.67	35.83	31.67	31.33
FH-900	29.83	35.17	31.67	31.67	28.33	29.33	27.33	28.67
CIM-446	32.00	34.50	34.17	35.83	29.33	33.33	30.17	30.50
FH-1000	30.33	32.00	33.17	31.67	27.33	30.17	27.00	28.17
FH-901	29.00	33.50	33.00	31.33	28.67	30.50	28.17	29.33

Mean 29.98 30.44 32.02 35.21 34.10 35.19 30.25 32.48

The estimates given in Table-9 and Table-10 depicted that the parent CIM-482 secured the highest array means thus showing the best GCA effects. Similarly, within the respective arrays it showed best SCA with VH-142 under both conditions.

#### Ginning out turn:

The estimates given in Table 4, for ginning out turn, indicated that  $D$ ,  $H_1$  and  $H_2$  are significant which revealed the involvement of additive and non additive effects in the inheritance of this trait both under both the water regimes. Higher estimates of  $H_1$  than  $H_2$  indicated unequal allele frequency at all the loci. Unequal gene frequencies in the parents was further indicated by the ratio  $H_2/4H_1$ , which are 0.11 and 0.13 (less than 0.25) under both the conditions. Non significant value of  $F$  revealed that parents carried same number of dominant and recessive genes but negative sign indicates higher frequencies of recessive allele. It was further supported by the estimates of  $\sqrt{4DH_1+F}/\sqrt{4DH_1-F}$  (0.59 and 0.75) under both the conditions which are lesser than 1. Positive and significant estimates of  $h^2$  were observed under both the conditions. In the presence of dominance it means that the number of dominant genes which increase the ginning out turn are more frequent. Significance of  $E$  indicated the effect of environment on the expression of trait. The observed estimates of  $(H_1/D)^{0.5}$  were 0.48 and 0.43 i.e, lesser than 1.0 indicating the partial dominance. The estimates of heritability ( $N_s$ ) were moderately higher.

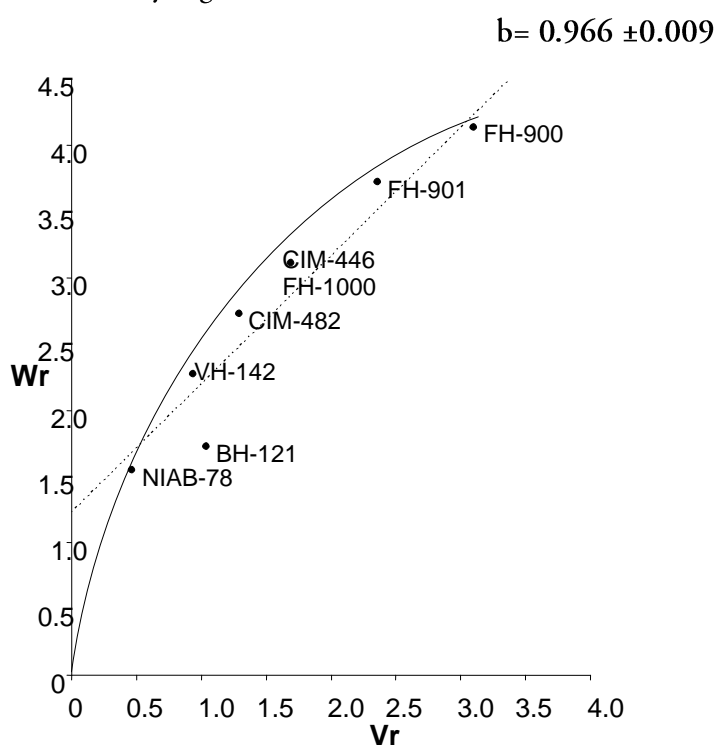


Fig 7: Vr/Wr graph for ginning out turn under normal water regime

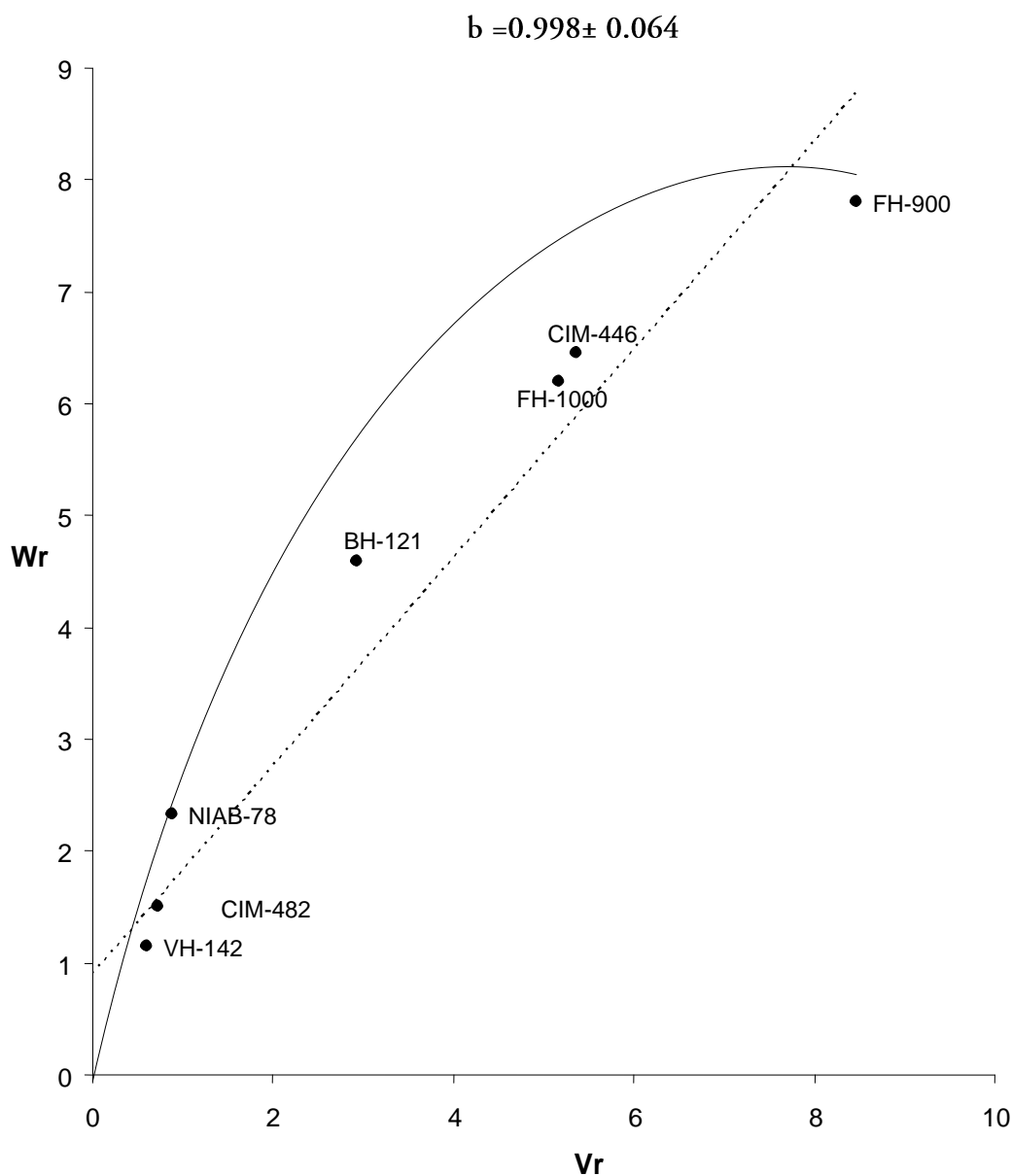


Fig 8:  $V_r/W_r$  graph for ginning out turn under water stress regime

The gene action involved in the inheritance of ginning out turn percentage under both the environments was of additive type along with partial dominance as the regression lines passed through the  $W_r$  axes above the origins (Fig 7 and Fig 8). There was no involvement of any non-allelic interaction as the line was with a unit slope. From the position of array points the variety NIAB-78 possessed most of the dominant genes under normal whereas, VH-142 under water stress conditions being closest to the origins. However most of the recessive genes were possessed by FH-900 under both the regimes because of their farthest positions from the origins. Highest GCA effects were shown by VH-142 under both the conditions because of its highest array



means .Within the arrays it showed good SCA effects in the crosses with CIM-482 under normal and with BH-121 under water stress regime.(Table 11 and 12)

**Table-11 Mean 8×8 diallel table for ginning out turn under normal water regime**

NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	41.73	41.68	42.13	42.77	39.65	40.60	40.94	38.88
CIM-482	41.68	41.63	41.77	43.75	40.17	40.43	40.97	37.00
BH-121	42.13	41.77	42.50	43.00	40.83	40.39	41.22	38.10
VH-142	42.77	43.75	43.00	44.10	41.02	40.41	41.57	39.00
F H-900	39.65	40.17	40.83	41.02	39.33	39.37	40.06	37.97
CIM-446	40.60	40.43	40.39	40.41	39.37	39.40	40.00	38.70
FH-1000	40.94	40.97	41.22	41.57	40.06	40.00	40.40	37.93
FH-901	38.88	37.00	38.10	39.00	37.97	38.70	37.93	36.00
Mean	41.05	40.93	41.24	41.95	39.80	39.91	40.38	37.95

**Table-12 Mean 8×8 diallel table for ginning out turn under water stress regime**

NIAB-78 CIM-482 BH-121 VH-142 FH-900 CIM-446 FH-1000 FH-901

NIAB-78	38.60	37.92	39.23	39.29	35.38	36.45	37.87	35.40
CIM-482	37.92	37.60	37.82	38.85	35.17	35.98	35.48	34.48
BH-121	39.23	37.82	39.93	40.25	35.05	35.15	36.72	34.70
VH-142	39.29	38.85	40.25	40.47	35.25	37.55	37.07	35.82
FH-900	35.38	35.17	35.05	35.25	33.97	34.20	34.38	34.02
CIM-446	36.45	35.98	35.15	37.55	34.20	34.80	34.55	34.28
FH-1000	37.87	35.48	36.72	37.07	34.38	34.55	34.23	33.40
FH-901	35.40	34.48	34.70	35.82	34.02	34.28	33.40	33.10
Mean	37.52	36.66	37.36	38.07	34.68	35.37	35.46	34.40

### Discussion:

The availability of variation in a plant character may be advantageous to a breeder, if it is genetically controlled. Diallel cross method used here provided such information on the pattern of inheritance of variation in the plant material assessed in the present research for the yield relating traits. The simple additive-dominance model was found partially adequate in all traits under both the water regimes (Table 3). Similar partial adequacy of additive dominance model to the data set was observed in different crops, for example in barley (Johnson and Aksel, 1964) ,

Sorghum (Azhar and McNeilly,1998) and cotton (Murtaza *et al.*2002; Khan *et al.*2003 ,Murtaza *et al.*2005).

Higher magnitudes of additive variance revealed that the effects of additive genes were more pronounced. This was further supported from Vr/Wr graphs for the traits where gene action was noted to be additive with partial dominance. Moderately higher estimates of narrow sense heritability for the traits are also the reflection of high magnitudes of additive variance. The additive variance without any epistatic effects and higher heritability seem to be encouraging for researchers for improving drought tolerance in cotton plant .Similar results were reported by Malik *et al.*(2013) in cotton, Akram *et al.* (2007) in rice and El-Rawy and Hassan (2014) in bread wheat.

The inheritance of seed cotton yield is a complex phenomenon because it is a product of interplay between many genetic and non- genetic components (Poehlman and Sleper, 1995).In the present studies seed cotton yield and its components i.e., number of bolls per plant and boll weight along with ginning out turn percentage (Lint perecentage) were found to be controlled both by additive and non- additive effects, however, the influence of additive effects was more prominent which was evident from the graphic representations of the characters where it was revealed that all of them were controlled by additive type of gene actions with partial dominance.

Heritability (Ns) was also observed to be moderately higher in case of yield and ginning out turn whereas it was moderate in number of bolls and boll weight .The situation offered a good enough scope for improvement of the characters through plant selection under drought conditions. Similar genetic information for seed cotton yield and its components has been reported by Punchal *et al.* (1994) Goudar *et al.* (1996),Tomar and Singh (1996), Saeed *et al.* (1996) Hussain *et al.*(1999)and Ahmad *et al.* (2000) while the observations of Ahmad *et al.*(1991) Khan *et al.* (1992),Hassan *et al.*(1993), Haq and khan (1993), Carvalho *et al* (1995), Iqbal *et al.*(2003) and Murtaza (2005) revealed that non additive effects were more important in their genetic control.

. All this information revealed a promising potential in the germplasm for possible improvement in water stress tolerance in cotton genotypes through conventional selection procedures in the segregating generations.

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