

**PJN**

ISSN 1680-5194

PAKISTAN JOURNAL OF  
**NUTRITION**

**ANSI***net*

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## Generation Means Analysis in Cotton (*Gossypium hirsutum* L.) for Drought Tolerance

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**Abstract:** Four genotypes of *Gossypium hirsutum* L.; two drought tolerant (NIAB-78, CIM-482) and two susceptible (CIM-446 and FH-1000) were selected to make cross combinations. The parents, F<sub>1</sub>, F<sub>2</sub> and backcross generations of two crosses were studied under drought and normal conditions in the field to find gene action involved in the inheritance of the traits; number of bolls per plant, boll weight, seed cotton yield and ginning out turn. There were significant differences among six generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of two crosses for all the plant traits both under normal and drought conditions. Generation means analysis revealed additive, dominance and epistatic genetic effects operating in the phenotypic manifestation of the plant characters under both the conditions.

**Key words:** Cotton, drought tolerance, gene action, heritability, Pakistan

### INTRODUCTION

Cotton plays an important role in Pakistan's economy. Besides catering local textile industry and contributing significantly in labour employment sector it earns a lot of foreign exchange through exports of its lint and textile products. Pakistan ranks fifth in production in the list of cotton growing countries in the world (Economic Survey of Pakistan, 2010-11). Total area of Pakistan is 79.61 mha and out of which 4.40 mha is drought affected (Economic Survey of Pakistan, 2000). Like in many regions of the world, drought is one of the serious abiotic factors which adversely affect general agriculture including cotton crop in Pakistan. Negative effects of drought on cotton plant and production have been reported by many researchers like Le Houerou (1996) and Saranga *et al.* (2001). Similarly, decrease in number of bolls and lint yield has been reported by Krieg and Sung (1986); Guinn and Mauney (1984); Kimball and Mauney (1993); Gerik *et al.* (1996) and Saranga *et al.* (1998). The availability of irrigation water in Pakistan is going down day by day and there is a need to develop cotton varieties which are able to resist drought and perform better under low water availability. For any effective and efficient cotton breeding programme genetic information of basic nature including the type of gene action involved in the inheritance pattern of plant traits of interest is necessary which helps a breeder in selecting the parents and/or crosses for further studies for improvement in the character. An attempt was made to generate such information in the present study.

### MATERIALS AND METHODS

The present studies were conducted in the Department of Plant Breeding and Genetics, University of Agriculture,

Faisalabad. The materials used in the studies consisted of two drought tolerant (NIAB-78 and CIM-482) and two susceptible (CIM-446 and FH 1000) cotton cultivars along with their F<sub>1</sub>s (NIAB-78 x CIM-446) and (CIM-482 x FH-1000), F<sub>2</sub>s and back crosses. The material was planted in the field under drought as well as normal conditions during May, 2009 using randomized complete block design with three replications. There was a single row, each for parents and F<sub>1</sub> generations, three for each back cross generation and five each for F<sub>2</sub> generations in a replication. Each row accommodated 15 plants with 30 cm plant to plant distance. The row to row distance was kept at 75 cm. Ten plants from the middle of all the rows were tagged for recording the data. During the crop season, water stress was imposed by supplying 50% less irrigations in the drought treatment. All other cultural operations were performed according to the standard practices. At the time of maturity (during month of November) data were recorded for number of bolls per plant, boll weight, seed cotton yield and Ginning Out-Turn (GOT).

The data were subjected to analysis of variance (Steel *et al.*, 1997) to determine significance of genetic differences among generations used in the experiment both under normal as well as drought conditions. Generation means analysis was performed following Mather and Jinks (1982). Means and variances of the two parents, BC<sub>1</sub>, BC<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub> generations used in the analysis were calculated from individual plant basis pooled over replications. A weighted least square analysis was performed on the generation means commencing with the simplest model using parameter *m* only. Further models of increasing complexity (*md*, *mdh*, etc.) were fitted if the chi-squared value was

significant. The best fit model was chosen as the one which had significant estimates of all parameters along with non-significant chi-squared value. For each trait the higher value parent was taken as P<sub>1</sub> in the model fitting.

### RESULTS AND DISCUSSION

Significant differences were observed among generations of two crosses for all the traits under normal as well as drought conditions. Generation means, population effects and LSD values to compare the generation means are shown in the Table 1 and 2.

**Number of bolls per plant:** For number of bolls per plant, two parameters [md] in cross-1 and four parameters [mdjl] model in cross-2 appeared to be adequate under normal conditions (Table 3). Under drought, 5 parameters [mdhij] model in cross-1 and 3 parameter [mdh] model in cross-2 showed best fitness of the observed to the expected generation means for the trait (Table 4). Under normal conditions significant additive component in cross-1 revealed that additive variance is pronounced for this trait and there existed a scope for its genetic improvement through selection. However, in cross-2 epistatic effects of the type j and l are unfixable, therefore, heterosis breeding may be rewarding for this trait. As far as, the situation under droughtfull conditions is concerned, both additive and non-additive gene actions indicated their involvement in the inheritance pattern of this trait in both the crosses. In cross-2 higher magnitude of d than h without any complication due to epistatic effects revealed the scope of its fixation through

selection. Pathak and Singh (1970); Kalsy and Garg (1988) and Esmail (2007) also studied the inheritance of number of bolls per plant in cotton and reported additive, dominance and epistatic effects for this trait. Similarly Singh *et al.* (1971) studied genetics of number of bolls per plant in cotton and found additive and dominance genetic variances along with the interactions for this trait. Silva and Alves (1983) studied the gene action in cotton (*G. hirsutum*) and reported additive and dominance affects for number of bolls per plant.

**Boll weight:** Under normal conditions 4 parameter [mdhi] model showed its adequacy to the data set for boll weight in both the crosses (Table 3). Whereas under droughtful conditions, 4 parameter [mdhi] in cross-1 and 5 parameter [mdhij] model in cross-2 appeared adequate (Table 4). Both the crosses behaved almost consistent over the stress regimes with positive values of all the parameters involved in the inheritance of boll weight. Dominance component is there but almost of equal magnitude in cross-1 under normal and in cross 2 under drought. Overall, both the crosses seemed convincing to be considered as far as improvement in boll weight, an important component of yield of seed cotton, is concerned. Different types of gene actions involved in the inheritance of boll weight in cotton have been reported in the literature by the researchers like, Pathak and Singh (1970) reported additive and epistatic effects for this trait, Singh *et al.* (1971); Kaseem *et al.* (1984); Kalsy and Garg (1988) observed additive and dominance genetic variance

Table 1: Generation means of the traits in cross-1 (NIAB-78 x CIM-446) and Cross-2 (CIM-482 x FH-1000) under normal conditions

Traits	Cross (C)	Generations						Pop. Effects	LSD (0.05)
		P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	BC <sub>1</sub>	BC <sub>2</sub>		
No of bolls	C1	35.03a	30.40c	32.13bc	31.14c	34.14ab	30.85c	**	2.26
	C2	32.06a	22.70c	31.36a	27.63b	31.52a	24.15c	**	2.56
Boll weight (gm)	C1	4.21a	3.42c	4.08ab	3.183	4.04ab	3.60c	**	0.22
	C2	4.05a	3.39c	3.91ab	3.42c	3.81b	3.33c	**	0.21
Seed cotton yield (gm)	C1	119.66a	110.53c	117.60b	117.38b	118.13ab	112.09c	**	1.90
	C2	118.67a	90.37e	113.77b	106.57c	118.34a	95.43d	**	3.41
GOT (%)	C1	36.99a	35.68bc	37.50a	36.04b	37.44a	35.22c	**	0.76
	C2	38.83ab	37.59c	39.05a	37.10c	38.26b	37.07c	**	0.64

\*p<0.05; \*\*p<0.01; ns = non-significant

Table 2: Generation means of the traits in Cross-1 (NIAB-78 x CIM-446) and Cross-2 (CIM-482 x FH-1000) under drought conditions

Traits	Cross (C)	Generations						Pop. Effects	LSD (0.05)
		P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	BC <sub>1</sub>	BC <sub>2</sub>		
No of bolls	C1	26.30a	22.06c	21.86c	24.04b	25.67a	22.31c	**	1.25
	C2	23.03a	16.56e	21.86b	20.72c	21.94b	18.68d	**	0.92
Boll weight (gm)	C1	3.68a	3.05bc	3.32b	2.93c	3.35b	2.99c	**	0.30
	C2	3.26a	2.54e	2.93c	2.75d	3.11b	2.48e	**	0.13
Seed cotton yield (gm)	C1	101.77a	93.23b	102.30a	95.85b	101.03a	95.06b	**	4.24
	C2	86.60b	66.53d	84.86b	82.50c	94.744a	68.45d	**	2.31
GOT (%)	C1	36.05a	35.18c	36.20a	35.45bc	35.75ab	35.25bc	**	0.55
	C2	37.27b	36.09e	37.88a	36.83cd	37.02bc	36.46de	**	0.44

\*p<0.05; \*\*p<0.01; ns = non-significant

Table 3: Best model fit estimates for generation means parameters ( $\pm$  standard error) by weighted least squares analysis of the traits in cross-1 (Niab-78 x CIM-446) and cross-2 (CIM-482 x FH-1000) under normal conditions

Traits	Genetic effects							$\chi^2$	(df)	Prob.
	Cross (C)	[m]	[d]	[h]	[l]	[j]	[i]			
Number of bolls	C1	32.22 $\pm$ 0.20	2.54 $\pm$ 0.32					9.420	4	1.0000
	C2	27.03 $\pm$ 0.26	4.67 $\pm$ 0.34			2.65 $\pm$ 0.76	4.09 $\pm$ 0.59	2.584	2	0.2747
Boll weight (gm)	C1	3.60 $\pm$ 0.09	0.40 $\pm$ 0.03	0.45 $\pm$ 0.12	0.19 $\pm$ 0.09			5.350	2	0.0689
	C2	2.90 $\pm$ 0.11	0.36 $\pm$ 0.03	0.98 $\pm$ 0.15	0.81 $\pm$ 0.12			4.102	2	0.1286
SCY (gm)	C1	124.40 $\pm$ 2.78	4.94 $\pm$ 0.41	-21.28 $\pm$ 6.77	-9.31 $\pm$ 2.73		14.48 $\pm$ 4.23	2.408	1	0.1207
	C2	99.14 $\pm$ 1.58	14.15 $\pm$ 0.74	14.05 $\pm$ 2.38	5.07 $\pm$ 1.76	8.68 $\pm$ 1.25		2.097	1	0.1476
GOT (%)	C1	34.51 $\pm$ 0.27	0.65 $\pm$ 0.10	2.93 $\pm$ 0.40	1.79 $\pm$ 0.30	1.56 $\pm$ 0.21		1.450	1	0.2285
	C2	35.07 $\pm$ 0.26	0.62 $\pm$ 0.11	3.87 $\pm$ 0.37	3.08 $\pm$ 0.28	0.58 $\pm$ 0.20		3.309	1	0.0689

Prob. = Probability

Table 4: Best model fit estimates for generation means parameters ( $\pm$  standard error) by weighted least squares analysis of the traits in cross-1 (Niab-78 x CIM-446) and cross-2 (CIM-482 x FH-1000) under drought conditions

Traits	Genetic effects							$\chi^2$	(df)	Prob.
	Cross (C)	[m]	[d]	[h]	[l]	[j]	[i]			
Number of bolls	C1	26.41 $\pm$ 0.560	2.120 $\pm$ 0.24	-4.33 $\pm$ 0.820	-2.11 $\pm$ 0.62	1.21 $\pm$ 0.45		3.490	1	0.0618
	C2	19.69 $\pm$ 0.200	3.230 $\pm$ 0.20	1.94 $\pm$ 0.370				2.475	3	0.4798
Boll weight (gm)	C1	2.58 $\pm$ 0.080	0.310 $\pm$ 0.02	0.74 $\pm$ 0.107	0.78 $\pm$ 0.088			1.175	2	0.5557
	C2	2.53 $\pm$ 0.071	0.360 $\pm$ 0.028	0.39 $\pm$ 0.092	0.36 $\pm$ 0.070	0.28 $\pm$ 0.05		1.174	1	0.2786
SCY (gm)	C1	89.56 $\pm$ 1.290	4.640 $\pm$ 0.41	12.80 $\pm$ 1.760	7.95 $\pm$ 1.400			3.048	2	0.2178
	C2	76.56 $\pm$ 0.310	10.030 $\pm$ 0.31	13.03 $\pm$ 1.550		16.34 $\pm$ 0.77	-4.73 $\pm$ 1.580	2.154	1	0.1422
GOT (%)	C1	35.41 $\pm$ 0.080	0.458 $\pm$ 0.10				0.64 $\pm$ 0.219	5.096	3	0.1649
	C2	36.58 $\pm$ 0.072	0.550 $\pm$ 0.081				1.17 $\pm$ 0.195	3.640	3	0.3031

Prob. = Probability

along with the epistatic effects and Tyagi (1988) and Esmail (2007) observed additive and dominance variance.

**Seed cotton yield:** Under normal conditions, 5 parameters model i.e., m, d, h, l and i in cross-1 and m, d, h, l and j in cross-2 were indicated to be adequate for seed cotton yield (Table 3). Whereas, under drought, 4 parameters [mdhi] in cross-1 and 5 parameter [mdhjl] model in cross-2 provided the best fit for this trait (Table 4). Opposite signs of h and l indicated the presence of duplicated type of gene interaction in cross-1 under normal conditions. Under drought (in cross-1) both additive and dominance effects were present the genes showing non-additive influence appeared to be more important than the additive genes. The additive x additive [li] interaction, however, indicated that fixation of additive alleles is possible in the later segregating generations as suggested by Singh and Narayanan (2000). In cross-2, again additive x non-additive gene actions with epistatic effects were operative for the expression of yield of seed cotton. Pathak and Singh (1970); Kaseem *et al.* (1984); Kalsy and Garg (1988) and Esmail (2007) studied the inheritance of seed cotton yield per plant in cotton and reported additive, dominance and epistatic gene effects for this trait. Similarly Randhawa *et al.* (1986) reported the presence of additive and epistatic effects in the inheritance of this trait.

**Ginning Out-Turn (GOT):** Under normal irrigation regime five parameters [mdhij] model gave the best fitness in both the crosses. Similarly, three parameters (mdl) model provided good fit for ginning out turn percentage. Under droughtful regime both the crosses again showed the same genetic picture. Three parameters (mdl) model was fit in both the crosses. Both additive and non-additive genes alongwith their epistatic effects were evident to be involved in the inheritance of this trait under normal and drought conditions in both the crosses. Greater values of h than those of d indicated the presence of heterosis. Positive signs showed the effect of favourable or increasing alleles for GOT but the presence of non-additive genetic and epistatic effects do not favour the effectiveness of selection. However, heterosis breeding may be exploited. Additive, dominance and interactions were reported to be responsible for the inheritance of lint percentage by Singh and Yadavendra (2002); Mert *et al.* (2003) while analyzing generation means in cotton.

Generation variance analysis has widely been used by plant breeders for partitioning the total variance into genetic and environmental components. The partitioning of phenotypic variance into its genotypic and environmental components is not sufficient to study the genetic properties of a breeding material, so genotypic variance is further partitioned into additive (D),

Table 5: Components of variance, D (additive), E (environmental), standard errors ( $\pm$ SE) and narrow sense heritability estimates of the traits in cross-1 (Niab-78 x CIM-446) and cross-2 (CIM-482 x FH-1000) under normal conditions

Traits	Cross (C)	Components of variance					
		[D]	[E]	$[\chi^2]$	(df)	$h^2 (F_2)$	$h^2 (F_{\infty})$
Number of bolls	C1	15.620 $\pm$ 02.150	2.707 $\pm$ 0.390	5.50	4	0.66	0.85
	C2	49.517 $\pm$ 06.297	7.224 $\pm$ 1.057	1.26	4	0.64	0.84
Boll weight (gm)	C1	0.450 $\pm$ 00.060	0.090 $\pm$ 0.013	6.59	4	0.60	0.83
	C2	0.647 $\pm$ 00.085	0.102 $\pm$ 0.015	6.04	4	0.66	0.84
SCY (gm)	C1	67.060 $\pm$ 09.720	12.880 $\pm$ 1.870	1.80	4	0.65	0.82
	C2	46.669 $\pm$ 16.165	33.301 $\pm$ 4.559	0.41	4	0.37	0.56
GOT (%)	C1	2.760 $\pm$ 00.480	0.740 $\pm$ 0.100	0.93	4	0.537	0.74
	C2	1.949 $\pm$ 00.432	0.757 $\pm$ 0.107	1.07	4	0.50	0.69

Table 6: Components of variance, D (additive), E (environmental), standard errors ( $\pm$ SE) and Narrow sense heritability estimates of the traits in cross-1 (Niab-78 x CIM-446) and cross-2 (CIM-482 x FH-1000) under drought conditions

Traits	Cross (C)	Components of variance					
		[D]	[E]	$[\chi^2]$	(df)	$h^2 (F_2)$	$h^2 (F_{\infty})$
Number of bolls	C1	9.855 $\pm$ 02.149	3.739 $\pm$ 0.528	0.82	4	0.43	0.66
	C2	37.461 $\pm$ 03.860	3.037 $\pm$ 0.449	0.29	4	0.76	0.91
Bolls weight (gm)	C1	0.453 $\pm$ 00.048	0.039 $\pm$ 0.006	0.54	4	0.78	0.91
	C2	0.306 $\pm$ 00.038	0.043 $\pm$ 0.006	4.21	4	0.72	0.87
SCY (gm)	C1	84.745 $\pm$ 11.119	13.254 $\pm$ 1.936	0.57	4	0.69	0.85
	C2	65.131 $\pm$ 06.926	5.877 $\pm$ 0.868	2.10	4	0.79	0.91
GOT (%)	C1	0.274 $\pm$ 00.0555	0.093 $\pm$ 0.013	1.16	4	0.42	0.63
	C2	4.269 $\pm$ 00.552	0.647 $\pm$ 0.095	7.69	4	0.58	0.81

dominance (H) and interaction (F). Genetic and environmental variance can be measured from an experiment which includes some non segregating (e.g. pure lines, inbred lines, F<sub>1</sub> etc.) and segregating populations (e.g. back crosses, F<sub>2</sub> etc.). In the present studies a model incorporating DE (additive and environmental) components gave the best fit for all the traits in both the crosses, both under normal and drought conditions (Table 4 and 5). Additive and dominance genetic variance of various traits in cotton has been reported by Tyagi (1988); Mukhtar *et al.* (2000); Bertini *et al.* (2001).

Both generation means and generation variance analyses indicated presence of additive and dominance variance for various traits, but epistatic effects were not detected in the generation variance analysis. This discrepancy might have arisen due to the differences in the estimation precision of the two analyses. However Malik *et al.* (1999) reported that generation means analysis is relatively more reliable compared to generation variance analysis.

The narrow sense heritability estimates were higher for yield and yield related traits (Table 4 and 5). These high heritability estimates were due to additive gene effects which suggested that these traits can be improved by selection during successive generations. The narrow sense heritability estimates of infinity generation (F<sub>∞</sub>) were consistently higher than F<sub>2</sub> generation. Moderate to high narrow sense heritability for various plant traits including seed cotton yield, number of bolls and boll weight was reported by Ahmed *et al.* (2006); Kumari and

Chamundeswari (2005); Ulloa (2006). However, low estimates of narrow sense heritability for different plant traits in cotton have been observed by Murtaza (2005) and Esmail (2007).

#### ACKNOWLEDGEMENT

This study was a part of Ph. D thesis (Genetic studies of drought tolerance in cotton (*Gossypium hirsutum* L.) and all necessary funds were provided by the higher education commission of Pakistan to PIN No:074-1143-Av4-124.

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