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Genetics of Agronomic and Fiber Traits in Upland Cotton under Drought Stress

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ABSTRACT

Genetics of agronomic (plant height, boll number, boll weight, seed weight, seed cotton yield & lint percentage) and fiber (staple length, fiber strength & fiber fineness) traits was investigated using generation means analysis of parental, F_1, F_2 and backcross generations involving drought sensitive (FH-87, MNH-329) and tolerant (CIM-446, MNH-513) cotton genotypes under drought and normal conditions. The genotype, FH 87 was highest in number of bolls per plant and seed cotton yield under normal environment. Significant differences were observed among generations for the traits studied in both crosses under both conditions. The traits studied were controlled by additive and dominance type of gene action along with interactions under both conditions. It may be suggested that selection for drought tolerant plants should be delayed until later segregating generations in a breeding program. Difference of gene action within the crosses under well watered and drought stress conditions suggest that selection for drought tolerant plants should be carried out under simulated drought conditions. © 2010 Friends Science Publishers

Key Words: Genetics; Gene action; Generation means analysis; Yield and yield components; Drought; Cotton

INTRODUCTION

Drought stress affects plant growth, hence reduces yield of a plant (Ritchie, 1980; Malik & Wright, 1998; Ahmed *et al*., 2000; Basal *et al.,* 2005). Drought is a serious problem that limits cotton production in many regions of the world including Pakistan. High temperature and scarcity of water significantly reduce cotton production in the country. The crop is affected by drought even in irrigated areas due to high temperature and scarcity of irrigation water. Heatherly *et al.* (1977) has stated that the growth and yield of many species are repressed severely even by moderate water stress.

Cotton is classified as a drought sensitive crop as it is not an efficient water consumer. Nevertheless, it has mechanisms that make it well adapted to semi-arid regions, such as its deep penetrating and extensive root systems, leaves and fruits that can be shed when plants are stressed and a flexible fruiting period (Ray *et al*., 1974). Drought resistance is a complex trait with multigenic components, which interact in a holistic manner in plant systems (Mussell & Staples, 1979; Cushman & Bohnert, 2000; Ahmad *et al*., 2009). Drought resistance is genetically controlled and is associated with various morphological and physiological features of crop plants (Singh, 2004).

Fiber yield in cotton is a complex trait due to multigenic and substantial genotype-environment interactions (Song & Zhang, 2009). Breeding for yield under stress conditions is even more complex due to difficulties to define and apply a precise set of environmental conditions relevant to the range of naturally occurring stress scenarios (Levi *et al*., 2009). The comparative performance of genotypes under drought stress conditions is a common study point in identification of drought tolerance and selection of genotypes for use in dry environments. However, high yield could arise as a result of drought escape or high yield potential in the absence of drought (Cattivelli *et al*., 2009) rather than, or as well as, the possession of adaptations specifically favoring performance under drought (Fischer & Maurer, 1978; Malik & Wright, 1998). Plant breeders have suggested the use of component traits as selection criterion for yield improvement (Misra *et al.,* 1994; Munir *et al.,* 2007), therefore, selection of a certain morphological trait, which contributes towards high yield under drought rather than selecting for only yield, would increase the efficiency of breeding programs for drought resistance (Malik & Wright, 1998).

For a successful breeding programme, the availability of genetic variability and knowledge of gene action to improve drought tolerance are essential, otherwise choice of

breeding methods used may not result in appreciable improvement (Munir *et al.,* 2007). The present studies were thus undertaken to get comprehensive information about the nature of gene action involved in the inheritance of yield and yield components under drought and normal conditions. The data were statistically analyzed to determine gene action using six different populations, viz., P_1, P_2, F_1, F_2, BC_1 and BC_2 of a cross. This method provides estimates of various components (i.e., additive, dominance, epistasis etc.) of genetic variance from the generation means. This information would help breeders to develop cotton cultivars with improved drought resistance.

MATERIALS AND METHODS

The present study comprising of two drought susceptible (FH-87, MNH-329) and two drought tolerant cotton varieties (CIM-446, MNH-513) along with their F_1 (FH-87 × CIM-446, MNH-329 × MNH-513), F_2 and backcross generations was conducted under drought and normal conditions in the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. The experimental material was sown in the field on 05-06-2007 in a randomized complete block design with three replications under both conditions. There were two rows for each of the parents and F_1 generations, three rows for each back-cross and six rows for each F_2 generation in each replication. Length of each row was 3 m and there were 10 plants in each row. Row to row and plant to plant distance was 75 and 30 cm, respectively. Ten plants from each of the parents and F_1 generations, 20 plants from each backcross and 50 plants from each F_2 population were selected at random from each replication for recording the data. All the cultural operations were same under both conditions except irrigations. Three irrigations (73, 84 & 108 days after sowing) were applied to normal trial and only one irrigation (84 days after sowing) was applied to trial under drought conditions in addition to 29.9, 149.7, 19.5 and 12.2 mm rainfall during the month of June, July, August and September, respectively. During the month of November-December data were recorded for plant height, boll number/plant, boll weight, seed weight, seed cotton yield, staple length, fiber strength and fiber fineness.

The data were subjected to analysis of variance following the method as in Steel *et al.* (1997) and a generation means analysis was performed following the method described by Mather and Jinks (1982) using the computer program, Xmean-fit to find out gene action for the traits. Means and variances of each population (parents, backcrosses, F_1 & F_2) used in the analysis were calculated from individual plants pooled over replications. A weighted least square analysis was performed on the generation means commencing with the simplest model using parameter *m* only and tested for goodness of fit. If the chi-squared value of one parameter model [*m*] was significant then further models of increasing complexity [*md, mdh,* etc.]

Table 1: Generation means for plant height (PH, cm), boll number (BN), boll weight (BW, g), 100 seed weight (SW, g), seed cotton yield (SCY, g), lint percentage (LP, %), fiber length (FL, mm), fiber strength (FS, g/tex) and fiber fineness (FF. Mic) in two crosses FH 87 × CIM-446 (1), MNH-329 × MNH-513 (2) of cotton under normal (N) and drought (D) conditions in the field

Traits	Cross No	Generations						Pop. Effects	LSD (0.05)
		P_1	P_2	F_1	F_2	BC_1	BC_2		
PH	N1	109.89	108.50	110.28	93.77	107.40	107.40	**	6.10
	D1	101.28	98.47	101.39	81.66	96.67	96.00	**	7.88
	N2	109.81	108.33	109.88	96.86	107.75	107.00	**	5.12
	D2	101.00	98.50	101.05	85.09	95.78	95.83	**	7.20
BN	N1	11.33	7.42	10.22	7.31	9.47	13.47	**	2.19
	D1	7.06	7.00	10.00	6.56	6.44	10.00	**	1.31
	N2	12.19	8.27	11.63	9.60	11.00	9.22	**	1.29
	D2	11.00	7.61	10.05	7.41	8.33	8.08	**	2.21
BW	N1	2.53	2.42	2.72	2.64	2.64	2.29	**	0.14
	D1	2.14	2.31	2.58	2.27	2.22	2.66	**	0.26
	N2	2.48	2.26	2.29	2.36	2.20	2.21	*	0.17
	D2	2.22	2.08	2.44	2.07	2.11	2.06	*	0.12
SW	N1	7.18	7.08	8.02	7.47	7.63	7.52	**	0.13
	D1	7.03	6.96	7.86	7.36	7.10	7.12	*	0.14
	N2	7.29	7.06	7.08	7.17	7.35	7.22	**	0.09
	D2	7.13	6.94	6.99	7.04	6.70	6.59	**	0.13
SCY	N1	28.58	17.85	27.81	18.95	24.48	31.38	**	8.21
	D1	15.07	15.95	25.75	14.79	14.54	26.03	**	6.25
	N2	30.14	18.66	26.57	22.53	24.51	20.74	**	8.41
	D2	24.30	15.79	24.53	15.30	17.75	16.83	**	7.32
LP	N1	38.70	39.58	39.22	39.69	37.98	38.08	**	0.21
	D1	39.55	40.64	40.23	38.18	39.58	38.67	*	0.18
	N2	39.06	39.33	39.24	40.90	37.79	38.96	**	0.28
	D2	39.71	40.55	40.28	39.84	39.47	39.81	**	0.31
FL	N1	28.33	27.22	27.84	27.58	27.71	27.41	**	0.19
	D1	27.57	27.66	27.96	26.18	28.23	27.71	**	0.16
	N2	27.54	27.59	27.11	27.61	26.89	27.56	**	0.09
	D2	27.06	27.02	26.99	26.55	26.72	27.36	**	0.10
FS	N1	26.29	28.13	27.00	25.55	27.33	27.08	*	0.28
	D1	26.52	28.34	26.98	23.57	28.23	26.73	**	0.36
	N2	26.54	27.16	26.83	25.92	27.45	28.17	**	0.25
	D2	26.02	27.01	26.88	24.04	28.19	28.38	**	0.36
FF	N1	3.87	4.54	4.32	4.46	4.23	4.15	*	0.13
	D1	3.83	4.67	4.04	4.38	4.36	3.79	**	0.24
	N2	4.72	4.80	4.87	4.55	3.69	4.37	**	0.34
	D2	4.90	4.87	5.01	4.56	3.80	4.28	**	0.27

were tried and tested for goodness of fit. The best model was chosen as the one which had significant estimates of all parameters along with non-significant chi-squared value. The higher value parent was always taken as P_1 in the model fitting for each trait.

A weighted least squares analysis of variance based on the method as described by Mather and Jinks (1982) was also employed on the data of the experiment containing six generations (Parents, F_1, F_2, BC_1 & BC_2). Model fitting was started using the E parameter only. When the chi-squared value was significant D, H and F parameters were successively included until a satisfactory fit was obtained. The best fit model was chosen as the one with all significant parameters and non-significant chi-squared value.

RESULTS AND DISCUSSION

Significant differences were observed among the generations for the traits, plant height, number of bolls per

Table II: Estimates of the best fit model for generation means parameters (±, standard error) by weighted least squares analysis in respect of Plant Height (PH, cm), boll number (BN), boll weight (BW, g), 100 seed weight (SW, g), seed cotton yield (SCY, g), lint percentage (LP, %), fiber length (FL, mm), fiber strength (FS, g/tex) and fiber fineness (FF. Mic), in two crosses FH-87 × CIM-446 (1), MNH-329 × MNH-513 (2) of cotton under normal (N) and drought (D) conditions in the field

Traits	Cross No	Genetic Effects						X^2(df)
		[m]	[d]	[h]	[i]	[j]	[l]	
PH	N1	06.21±6.93	0.67±0.23	78.77±14.81	54.52±6.93	-	-45.17±8.04	0.34(1)
	D1	95.91±7.19	1.40±0.26	70.10±17.02	59.50±7.18	-	-43.09±10.09	0.09(1)
	N2	06.61±8.56	0.74±0.20	76.57±18.52	42.08±8.56	-	-33.69±10.17	0.00(1)
	D2	96.21±7.80	1.23±0.24	72.05±17.46	44.01±7.79	-	-26.75±9.90	0.44(1)
BN	N1	9.87±0.84	-	6.42±0.85	3.46±0.84	6.71±1.99	-	1.75(2)
	D1	7.84±1.93	0.44±0.09	20.21±1.94	9.97±1.93	23.26±4.67	-	3.09(1)
	N2	10.32±0.98	1.96±0.07	4.18±1.00	2.79±0.98	-	-	0.10(2)
	D2	8.75±0.78	1.67±0.11	5.40±0.78	4.64±0.79	-	-	2.68(2)
BW	N1	2.54±0.02	0.06±0.02	-	0.53±0.17	-	0.25±0.03	5.93(2)
	D1	2.36±0.02	0.04±0.02	-	0.54±0.17	-	0.22±0.03	5.89(2)
	N2	2.30±0.01	0.17±0.02	-	0.49±0.07	-	-	7.34(4)
	D2	2.16±0.07	0.07±0.02	0.78±0.07	-	-	-	3.26(2)
SW	N1	7.48±0.01	0.05±0.01	0.89±0.01	-	-	-	2.55(3)
	D1	7.24±0.01	0.03±0.01	-	-	-	0.80±0.01	3.31(3)
	N2	7.20±0.01	0.11±0.01	-	-	-	-0.10±0.01	1.33(3)
	D2	6.90±0.52	0.10±0.01	-4.77±1.32	-1.62±0.52	-	3.11±0.81	0.01(1)
SCY	N1	24.84±2.38	0.39±0.10	8.26±2.39	8.64±2.38	-10.46±4.60	-	3.41(1)
	D1	18.69±1.93	0.44±0.09	10.21±1.94	9.97±1.93	13.26±4.67	-	3.09(1)
	N2	23.86±0.11	5.74±0.11	-9.72±4.14	-	-	11.89±4.14	0.37(2)
	D2	19.08±1.73	4.25±0.08	19.04±1.75	14.55±1.73	-	-	2.58(2)
LP	N1	38.88±1.38	0.42±0.12	-7.77±3.56	-6.63±1.37	-	11.21±2.24	0.43(1)
	D1	39.48±0.65	0.56±0.12	4.16±0.72	4.02±0.67	-	-	0.24(2)
	N2	39.21±1.49	-	-22.83±4.03	-9.85±1.49	-	13.01±2.58	5.04(2)
	D2	39.94±0.08	0.40±0.11	-	-	-	-	3.56(4)
FL	N1	27.68±0.05	0.53±0.12	-	-	-	-	4.96(4)
	D1	27.55±0.89	-	14.65±2.43	6.92±0.89	-	-7.40±1.57	2.27(2)
	N2	27.38±0.09	-	-0.49±0.10	-	-	-	6.74(4)
	D2	26.95±0.03	-	-	-	1.30±0.73	-	8.14(4)
FS	N1	26.90±1.02	0.84±0.12	13.01±2.50	6.47±1.01	-	-6.75±1.52	3.77(1)
	D1	26.73±1.02	0.28±0.11	15.33±2.50	6.61±1.01	-	-8.29±1.56	0.01(1)
	N2	27.01±1.10	-0.34±0.11	18.31±2.85	7.34±1.09	-	-10.99±1.79	0.88(1)
	D2	26.75±1.28	-0.49±0.04	20.22±3.04	6.82±1.28	-	-13.04±1.80	0.62(1)
FF	N1	4.26 ± 1.02	0.28±0.11	15.33 ± 2.50	6.61 ± 1.01	-	-8.29 ± 1.56	0.01(1)
	D1	4.18 ± 0.35	-	-7.67 ± 0.94	-2.09 ± 0.35	0.97 ± 0.27	5.71 ± 0.60	0.12(1)
	N2	4.50 ± 0.35	-	-7.13 ± 0.96	-2.07 ± 0.35	-1.35 ± 0.29	5.18 ± 0.63	0.59(1)
	D2	4.57 ± 0.35	-	-7.67 ± 0.94	-2.09 ± 0.35	-0.97 ± 0.27	5.71 ± 0.60	0.12(1)

plant, boll weight, seed weight, seed cotton yield, lint percentage, fiber length, fiber strength and fiber fineness. Generation means, population effects and LSD values to compare the generation means are shown in the Table I. The results of generation means analysis are given in Table II and the results of generation variance analysis, as well as heritability estimates (ns & F∞) are given in Table III.

In quantitative traits, gene action is described as additive, dominance and epistatic effects (additive x additive [i], additive x dominance [j] & dominance x dominance [l]). Additive effect is normally the average effect of genes from both parents; dominance is the interaction of allelic genes and epistasis is the interaction of non-allelic genes affecting a particular trait. Gene action has been estimated using diallel crosses following the methods described by Hayman (1954) and Jinks (1954) or by using generation means and variance of different populations (parents, F_1, segregating & backcross populations) by the method as by Mather and

Jinks (1982). Gene action has been studied through generation means and variance analyses by various workers in cotton (Pathak, 1975; Dhillon & Singh, 1980; Singh & Sandhu, 1985; Kalsy & Garg, 1988) and in other crops (Malik *et al.,* 1999; Munir *et al.,* 2007).

In the present study, generation means analysis revealed that all the traits were complex in inheritance showing interactions under well-watered, as well as under drought condition. Therefore, delayed selection might be fruitful to breed cotton for the traits under both the environments. (Dhillon & Singh, 1980; Singh *et al.,* 1983; Randhawa *et al.,* 1986; Lin & Zhao, 1988; Singh & Yadavendra, 2002; Murtaza *et al.,* 2004; Rahman *et al.,* 2005; Ahmad *et al*., 2009). The absence of interactions in some studies (Gad *et al.,* 1974; Ma *et al.,* 1983; Nadarajan & Rangasamy, 1990; Pavasia *et al.,* 1999; Bertini *et al.,* 2001; Mert *et al.,* 2003) may be due to the difference in the genetic background of the populations used in the

Table III: Variance components D (additive), H (dominance), F (additive x dominance) and E (environmental) following weighted analysis of components of variance and heritability (ns, narrow sense and F generation) for plant height (PH, cm), boll number (BN), boll weight (BW, g), 100 seed weight (SW, g) and seed cotton yield (SCY, g), lint percentage (LP, %), fiber length (FL, mm), fiber strength (FS, g/tex) and fiber fineness (FF. Mic), in two crosses FH-87 × CIM-446 (1), MNH-329 × MNH-513 (2) of cotton under normal (N) and drought (D) conditions in the field

Traits	Cross No	Variance Components			x^2 (df)	Heritability	
		D	H	E		Ns	F∞
PH	N1	1076.80±154.55	-1042.06±155.61	21.43±4.34	1.51(3)	0.81	0.98
	D1	814.57±131.42	-714.07±142.41	20.29±3.98	2.70(3)	0.83	0.97
	N2	1611.32±230.17	-1565.25±231.87	31.56±5.86	0.50(3)	0.79	0.98
	D2	1201.55±176.98	-1137.70±181.00	31.77±5.92	5.09(3)	0.84	0.97
BN	N1	29.92±3.71	-	8.22±1.86	2.03(4)	0.65	0.78
	D1	40.42±5.06		10.10±2.02	5.36(4)	0.66	0.80
	N2	62.99±11.45	-82.06±22.59	12.21±2.32	1.05(3)	0.72	0.83
	D2	35.11±4.53	-	10.37±1.96	8.76(4)	0.63	0.77
BW	N1	0.53±0.07	-	0.10±0.02	7.26(4)	0.73	0.84
	D1	0.57±0.11	-0.44±0.14	0.10±0.01	4.36(3)	0.74	0.85
	N2	0.14±0.05	-	0.07±.0.01	0.08(4)	0.58	0.73
	D2	0.22±0.03	-	0.05±0.01	5.50(4)	0.69	0.81
SW	N1	1.55±0.33	-0.97±0.42	0.20±0.04	4.94(3)	0.79	0.88
	D1	1.16±0.14	-	0.20±0.04	5.05(4)	0.74	0.85
	N2	0.78±0.37	-1.98±0.74	0.15±0.04	4.19(3)	0.72	0.83
	D2	1.62±0.20	-	0.30±0.05	5.29(4)	0.73	0.84
SCY	N1	228.68±27.87	-	20.14±4.31	3.49(4)	0.64	0.91
	D1	334.69±74.91	-203.34.±99.93	20.23±4.39	1.44(3)	0.78	0.94
	N2	351.80±44.41	-	20.28±3.62	7.30(4)	0.72	0.94
	D2	169.06±21.38	-	20.28±3.62	4.41(4)	0.68	0.89
LP	N1	16.19±3.78	-10.60±5..05	4.46±0.87	3.14(3)	0.64	0.78
	D1	20.99±2.79	-	4.57±0.88	8.10(4)	0.70	0.82
	N2	8.65±1.23	-	2.43±0.45	4.45(4)	0.64	0.78
	D2	17.36±2.32	-	4.42±0.84	0.35(4)	0.66	0.80
FL	N1	4.71±0.60	-	1.07±0.30	3.94(4)	0.69	0.81
	D1	2.77±0.42	-	0.53±0.09	4.17(4)	0.72	0.83
	N2	1.31±0.29	-	0.32±0.06	4.09(4)	0.67	0.80
	D2	9.56±1.92	-6.96±2.44	2.50±0.50	0.35(5)	0.66	0.79
FS	N1	6.15±0.89	-	1.41±0.27	7.15(4)	0.69	0.81
	D1	19.97±3.34	-17.62±3.73	4.23±0.91	7.69(3)	0.70	0.82
	N2	0.22±0.20	-	0.39±0.07	9.00(4)	0.22	0.36
	D2	26.30±4.11	-23.72±4.38	5.60±0.93	0.90(3)	0.70	0.82
FF	N1	2.33±0.34	-	0.61±0.08	7.15(4)	0.66	0.79
	D1	0.41±0.07	-	0.10±0.03	8.15(4)	0.67	0.80
	N2	0.29±0.07	-	0.08±0.02	1.78(4)	0.64	0.76
	D2	0.91±0.21	-0.79±0.30	0.20±0.03	3.22(3)	0.69	0.81

experiments.

The gene action in the two crosses was different in some traits even under the same environment, which might be due to difference in genetic makeup of the parents involved. The results also showed difference of gene expression within the same cross under well watered and drought environment in some traits (seed weight, fiber length & fiber strength). There was similar gene expression under both the conditions in the other traits. So it may be suggested that cotton breeders interested in breeding cotton genotypes for drought stress environments should practice selection of breeding material under simulated drought stress. Different gene actions within the same cross under well-watered and drought stress shows that there is significant interaction of environment on seed development. Seed size directly relates to lint yield. fiber cells are produced on the epidermis of the seed. If seed size is smaller, more

seeds may be accommodated in a lock of the boll and hence higher lint yield per boll on the basis of surface area and volume relationship (Worley *et al.*, 1974 & 1976).

Generation variance analysis partitions variance further into additive (D), dominance (H), environmental (E) 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_1 etc.) and segregating populations (e.g., backcrosses, F_2 etc.). In the present studies a model incorporating additive, dominance and environmental components was generally found suitable to explain the variation in the crosses studied. Both generation means and generation variance analysis indicated presence of additive and dominance variance for various traits, however epistatic effects were not detected in the generation variance analysis. This discrepancy may be due to differences in the estimation precision of the two

analyses. Generation means analysis is relatively more reliable compared to generation variance analysis (Malik *et al.,* 1999).

The estimates of variance are also used to estimate the heritability, which indicates the amount of genetic variability relative to environmental affects and is considered a good index of transmission of characters from parents to their offspring. So the effectiveness of selection depends primarily on the magnitude of heritability. All the traits showed high narrow sense heritability estimates, except fiber strength in cross-2 under normal conditions, which had relatively low heritability. Infinity generation heritability was consistently higher than the narrow sense heritability for all the traits. High heritability estimates for the traits show that a large proportion of the genetic variance was composed of additive genetic component. Singh and Singh (1981), Gupta *et al*., 1987, Ulloa (2006) reported high heritability, while Murtaza (2005) and Esmail (2007) found low estimates of narrow sense heritability for various traits in cotton. The difference of the heritability estimates reported by workers may be due to the difference in the genetic makeup of the populations used in the experiments.

CONCLUSION

The traits, plant height, boll number/plant, boll weight, seed weight and seed cotton yield, staple length, fiber strength and fiber fineness are complex in inheritance, so it is suggested that selection for drought tolerant plants should be delayed until later segregating generations in a breeding programme. Difference of gene action within the crosses under well watered and drought stress condition suggests that selection for drought tolerant plants should be undertaken under simulated drought conditions.

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