# Estimation of Additive, Dominance and Epistatic Components of Genetic Variation in Fibre Quality Characters of Up-land Cotton Grown in Salinized Conditions

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# ABSTRACT

The role of additive, dominance and epistatic components of genetic variance in the inheritance of staple length, fibre strength, and fibre fineness in (*Gossypium hirsutum* L.) grown in 10 and 20 dSm<sup>-1</sup> NaCl salinities was assessed using triple test cross analysis. Results of the genetic analysis revealed that although both additive and non-additive genes affected the characters, genes acting cumulatively were predominant. It was further revealed that additive x dominance and dominance x dominance epistatic component was important in the inheritance of the characters studied. Since there was strong evidence of the presence of significant epistasis in the inheritance of the characters, therefore no precise conclusion could be drawn about the relative importance of the three components of genetic variation. However, for the improvement of these fibre traits showing predominantly additive gene effects, early generation selection may be effective.

Key Words: Triple test cross; (Gossypium hirsutum L.); NaCl; Salinity; Epistasis; Additive; Dominance

# **INTRODUCTION**

Yield potential of all agricultural crops is limited by environmental stresses all over the world (Wittwer, 1980). Amongst the stresses, the adverse effects of soil salinity on crop production are more drastic. Although the problem of salinity has become alarming throughout the world, the spread of this menace is of greater magnitude in arid and semi-arid areas (Shannon, 1985; Ashraf, 1994; Lin *et al.*, 1997). Soils of Pakistan provide the best illustration of the development of salinity. According to an estimate, about 5.7 x 10<sup>6</sup> ha of arable land had been affected by salinity in Pakistan due to continuous use of low quality irrigation water for agricultural purpose (Mujtaba *et al.*, 2003). It had been reported that due to the decrease in agricultural production in Pakistan, losses occur to the tune of about 20 billion rupees per annum (Qayyum & Malik, 1988).

Cotton (*Gossypium hirsutum* L.) is the most important cash crop of Pakistan and is grown in canal-irrigated soils affected by varying concentrations of salts. This situation warrants the development of cultivars of cotton suitable for the adverse soil conditions adopting "biological approach" (Shannon, 1984; Foy, 1997; Hollington, 1998). The success of developing salt tolerant cultivars, through exploitation of genetic resources, depends upon availability of variability in the germplasm for salinity tolerance provided that it is genetically based. Thus in order to speed up the research work, collection of information on the genetic components of variation is essential.

Various biometrical methods were used in the past for estimating the mode of gene action controlling different agronomic and quality characters. In most of the genetic designs used, it is assumed that non-allelic interactions are absent, whereas the fact is often contrary to this assumption. However, most methods yield a much larger standard error for the dominance component and the additive and dominance components are differently affected by linkage disequilibrium. The triple test cross (TTC) method described by Kearsev and Jinks (1968), which is basically an extension of the Comstock and Robinson (1952) design III, specifically evaluates the role of non-allelic interaction in the inheritance of plant characters and in its absence provides equally precise estimates of additive and dominance components of variation. In the present investigations on salinity tolerance in (Gossypium hirsutum L.), TTC technique was used to detect epistasis, in addition to the presence of additive and non-additive components of variation, in fibre characters tested under salinity conditions.

# MATERIALS AND METHODS

For the present genetic investigations, the plant material was developed following the procedure of triple test cross given by Kearsey and Jinks (1968). For this purpose, two locally developed varieties; CIM-1100 and MNH-93 of (*Gossypium hirsutum* L.), differing in NaCl tolerance (Malik & Makhdum, 1987; Qadir & Shams, 1997; Noor *et al.*, 2001) were used to study the genetic basis of

variation in fibre traits in the plant material tested under salinity conditions. The two cultivars CIM-1100 (P<sub>1</sub>) and MNH-93 (P<sub>2</sub>) were hybridized to develop F<sub>1</sub> seed. From F<sub>2</sub> generation, 25 plants were selected randomly and crossed as male parents to P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> plants (used as female testers) to develop L<sub>1i</sub> (P<sub>1</sub> x F<sub>2</sub> (i)), L<sub>2i</sub> (P<sub>2</sub> x F<sub>2</sub> (i)) and L<sub>3i</sub> (F<sub>1</sub> x F<sub>2</sub> (i)) families, where 'i' denotes plant number 1 - 25, selected as male from F<sub>2</sub>. Each male, therefore had three progenies and a total of 75 families were developed for genetic investigations.

The families were grown in earthen pots of 30 cm diameter lined with polythene sheet filled with 8.5 Kg soil, having ECe 0.16 dSm<sup>-1</sup>, pH value 7.65 and saturation percentage 38.95. There were four pots each having two plants for each of the 75 families assessed in three NaCl treatments i.e. control, 10 and 20 dSm<sup>-1</sup>. The pots were arranged in three replications according to complete block randomized design. When seedlings emerged, all the pots were watered once with 1/2 strength Hoagland nutrient solution (Hoagland & Arnon, 1950). Salt treatment was started four weeks after sowing and maintained up to maturity. The plants to be evaluated as control were given only nutrient solution. At maturity, total seed cotton was obtained and ginned. Lint was tested for staple length, fibre strength and fibre fineness. The results of each character of each family tested in 10 and 20 dSm<sup>-1</sup> were compared with that in control called relative salt tolerance or indices of salt tolerance based upon the three characters (Maas, 1986).

The means of indices of salt tolerance of 75 families measured in 10 and 20 dSm<sup>-1</sup> NaCl salinity were subjected to analysis of variance technique. The test of epistasis ( $L_{1i} + L_{2i} - 2L_{3i} = 0$ ) was carried out according to Perkins and Jinks (1970). The sum of squares due to epistasis was partitioned in to 'i' (additive x additive) type of interaction for 1 degree of freedom and 'j' (additive x dominance) and 'l' (dominance x dominance) type of interactions for the remaining 24 degree of freedom. The variances of the sums ( $L_{1i} + L_{2i}$ ) and differences ( $L_{1i} - L_{2i}$ ) were used to estimate additive (D) and dominance (H) components, respectively (Singh & Chaudhary, 1985). The estimates of degree of dominance were worked out as the square root of the ratio of H and D components ( H/D) following Wigan (1944).

### RESULTS

Results of analyses of variance revealed that 75 families differed significantly ( $P \le 0.01$ ) from each other for the three fibre traits studied in 10 and 20 dSm<sup>-1</sup> NaCl stress (Table I). The effect of the two NaCl salinities on the characters was also highly significant ( $P \le 0.01$ ). The mean squares due to interaction of families x salinities appeared to be significant ( $P \le 0.05$ ) for staple length and highly significant ( $P \le 0.01$ ) for fibre strength indicating that the two levels of NaCl salinity had affected the characters in 75 families differently, however the mean squares for fibre fineness were reduced to non-significant ( $P \ge 0.05$ ).

Table I. Mean squares from analyses of variance of indices of salt tolerance based upon three fibre traits measured on 75 families in 10 and 20 dSm<sup>-1</sup> NaCl salinities

Sources of variation	d.f	Staple length	Fibre strength	Fibre fineness
Families	74	9.47**	147.60**	47.71**
Salinities	1	815.70**	2193.96**	1559.31**
Families x Salinities	74	2.91*	11.79**	3.51 <sup>NS</sup>
Error	300	2.10	5.32	7.43

\*, \*\*, denote significant (P $\leq$ 0.05) and Highly significant (P $\leq$ 0.01) differences respectively, whilst NS denotes non-significant (P $\geq$ 0.05) differences

Non-significant mean squares due to deviations of families ( $L_{1i} + L_{2i} - 2L_{3i}$ ) from zero for staple length and fibre fineness showed the absence of epistasis in 10 dSm<sup>-1</sup> salinity, whilst it was present in case of 20 dSm<sup>-1</sup>. However, epistasis was revealed to be involved for fibre strength in both the salinity levels (Table II). It was evident that 'i' type epistasis (additive x additive interaction) was non-significant in low and high NaCl stresses, whereas 'j' (additive x dominance) and 'l' (dominance x dominance) type epistasis appeared to be highly significant (P 0.01) in the inheritance of fibre strength (Table II). For staple length and fibre fineness, j + l type epistasis was significant (P 0.01) in 20 dSm<sup>-1</sup> stress.

The mean squares due to sums and differences of  $L_{1i}$ and  $L_{2i}$  families were highly significant (P  $\leq 0.01$ ) in both moderate and high salinity levels, whilst the level of significance was reduced to significant ( $P \le 0.05$ ), due to differences for staple length in 10 dSm<sup>-1</sup> and thus provided a clue of the presence of genes that acted cumulatively and non-cumulatively (Table III). The magnitudes of additive components (D) were higher than those of dominance components (H) for the fibre traits assessed in low and high salinities, which indicated that genes showing additive properties were much important than those showing nonadditive effects. The degree of dominance ( $\sqrt{H/D}$ ) was significantly lesser than 1 for staple length in 10 dSm<sup>-1</sup>, fibre strength in 20 dSm<sup>-1</sup> and fibre fineness in both the NaCl levels, indicating the presence of partial dominance of genes controlling inheritance of the characters. The magnitude of degree of dominance for staple length in 20 dSm<sup>-1</sup> and fibre strength in 10 dSm<sup>-1</sup> was nearly equal to 1 revealing the involvement of complete dominance of genes for these two characters (Table III).

# DISCUSSION

Selection of plants combining good plant characters is the main goal of plant breeding and in recent years much of the improvements have been possible due to genetic advances made through intercrossing existing varieties (Fehr, 1987). For the development of plant material of (*Gossypium hirsutum* L.) having acceptable fibre

Items	d.f.	Staple length		Fi	bre strength	Fibre fineness	
		10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>	10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>	10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>
Total epistasis	25	23.89 <sup>NS</sup>	63.23**	192.74**	446.89**	112.94 <sup>NS</sup>	209.46**
i type epistasis	1	4.54 <sup>NS</sup>	638.02 <sup>NS</sup>	33.24 <sup>NS</sup>	158.04 <sup>NS</sup>	150.29 <sup>NS</sup>	454.36 <sup>NS</sup>
j+l type epistasis	24	24.71*	39.28**	199.39**	479.76**	11.38*	199.26**
Total epistasis x replicates	50	26.24	28.71	80.99	61.65	102.52	61.26
i type epistasis x replicates	2	355.17	392.40	1055.18	786.45	1287.77	784.37
j+l type epistasis x replicates	48	12.53	13.56	40.4	31.45	53.13	31.13

Table II. Test of epistasis using  $(L_{1i} + L_{2i} - 2 L_{3i})$  comparisons based upon relative values of three plant characters measured in two NaCl salinities

\*, \*\*, denote significant ( $P \le 0.05$ ) and Highly significant ( $P \le 0.01$ ) differences respectively, whilst NS denotes non-significant ( $P \ge 0.05$ ) differences

Table III. Mean squares due to sums  $(L_{1i} + L_{2ii})$  and differences  $(L_{1i} - L_{2i})$ , estimates of additive (D) and dominance (H) components, and degree of dominance ( $\sqrt{H/D}$ ) based upon relative values of three plant characters measured in two NaCl salinities

Items	d.f.	Staple length		Fi	bre strength	Fibre fineness		
		10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>	10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>	10 dSm <sup>-1</sup>	20 dSm <sup>-1</sup>	
Sums	24	7.65**	15.06**	186.00**	305.34**	56.06**	96.44**	
Sums x replicates	50	2.82	3.36	7.69	9.96	18.84	13.77	
Differences	24	7.54*	13.15**	154.56**	123.73**	33.60**	56.67**	
Differences x replicates	50	4.24	3.53	9.99	9.55	13.91	11.28	
D		6.44	15.60	237.75	393.84	49.62	110.22	
Н		4.41	12.83	192.75	152.24	26.26	60.52	
√H / D		0.83	0.91	0.90	0.62	0.71	0.74	

\*, \*\*, denote significant (P≤0.05) and Highly significant (P≤0.01) differences respectively

characteristics i.e. staple length, fibre strength and fibre fineness suitable for saline conditions, the desired plant material must be developed under salt stress conditions. For effective selection of plants, variability in fibre characters must be genetically based. In present investigations, the genetic material was subjected to constant NaCl stress of 10 and 20 dSm<sup>-1</sup> from fourth week of sowing till the final picking of plants. In previous studies, salinity response in corn (Kaddah & Ghowail, 1964), bean (Meiri & Poljakoff-Mayber, 1970), and sorghum (Azhar & McNeilly, 1989) had been assessed using the same procedure and therefore the present method provided better evaluation of cotton breeding material for enhanced salinity tolerance. Previous work revealed that indices of tolerance in different crops had been frequently used by research workers to investigate genetic mechanism of stress tolerance, for example, aluminium tolerance in sorghum (Boye-Goni & Marcarian, 1985) salinity tolerance in sorghum (Azhar & McNeilly, 1988). Recently, Khan and McNeilly (2005) and Ali et al. (2005) have used indices of salt tolerance for investigating genetic mechanism controlling salinity tolerance in (Zea mays L.) and (Triticum aestivum L.), respectively.

The preliminary statistical analyses of indices of salt tolerance data revealed the existence of significant amount of genotypic variation in all the three characters measured in NaCl stress conditions (Table I). Triple test cross analysis of salt tolerance data led to the detection of epistasis in staple length and fibre fineness at 20 dSm<sup>-1</sup> and in both the salinity levels in case of fibre strength. It was revealed that additive x additive epistasis was absent in all the characters in both the salinities (Table II). In contrast, the significant 'j + l' type epistasis suggested the importance of additive x

dominance and dominance x dominance gene interactions in the genetic control of variation in staple length, fibre strength and fibre fineness measured in 10 and 20 dSm<sup>-1</sup> NaCl salinities (Table II). It had been reported that variation in root length of Sorghum bicolor (Azhar & McNeilly, 1988) and maize (Khan & McNeilly, 2005) seed cotton yield, boll weight and number of bolls in up-land cotton (Kumar & Raveendran, 2001) all crops grown in salinized conditions, were affected by the involvement of epistatic genetic component. Clearly, the results of present studies appeared to be in great agreement to the previous reports and suggest that additive x dominance and dominance x dominance epistasis were more important than additive x additive component, with in the limits of the present investigation, of salinity tolerance in Gossypium hirsutum L. The greater contribution of (j + l) type epistasis, in addition to pronounced effects of additive x additive gene effects, had been reported in barley grown in saline and alkaline soils (Tripathi & Singh, 1983). Absence of significant 'i' type epistasis for staple length, fibre strength and fibre fineness in both the salinities, however indicates that overall epistasis is a relatively minor component of epistasis for these characters (Singh & Singh, 1976).

In the absence of epistasis, analysis of variance for sums and differences provides direct tests of the significance of additive (D) and dominance (H) components. Both items, the sums and differences, were significant for all the characters in 10 and 20 dSm<sup>-1</sup> salinities, revealing the importance of both additive and non-additive properties of genes (Table III). In case of staple length in 20 dSm<sup>-1</sup> and fibre strength in 10 dSm<sup>-1</sup> the relative ratios ( $\sqrt{H/D}$ ) were almost equal to 1, suggesting that both additive and non-

additive genes affected these characters (Table III). For staple length in 10 dSm<sup>-1</sup>, fibre strength in 20 dSm<sup>-1</sup> and fibre fineness in both the salinities, genes acting cumulatively were predominant as ( $\sqrt{H/D}$ ) was lesser than 1. But since there was strong evidence of the presence of significant epistasis in the inheritance of all the characters, the estimates of D and H were biased by epistasis to an unknown extent. Therefore, no precise conclusion could be drawn about the relative importance of the three components of genetic variation. However, for the improvement of these fibre traits showing predominantly additive gene effects, early generation selection may be effective.

Estimates of h<sup>2</sup><sub>ns</sub> of the characters following triple test cross analysis, are usually un-common to make, but significant amount of additive gene effects suggest that these estimates might be high (Mather & Jinks, 1982). It would thus seem likely from the results that significant advance in NaCl tolerance in (Gossypium hirsutum L.) may be achieved through selection and breeding. Shannon (1985) suggested that the correlation between tolerance at low and high salinity conditions, if influenced by the same genes, should be positive. From the inheritance pattern of fibre quality characteristics of (Gossypium hirsutum L.) does indeed appear to be marked similarities between the genetic architecture of tolerance at 10 and 20 dSm<sup>-1</sup> salinity levels. It may thus well be that genes operating at low and high salinity conditions are the same. However, further work is needed to verify this suggestion. Nonetheless this is important, since breeding material exposed to salinity stress using high selection pressures would identify tolerant genotypes, resulting in a rapid and effective improvement in salinity tolerance at increased salinity in up-land cotton.

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