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Genetic behavior of yield contributing and ionic concentration traits under salt stress conditions in cotton (*Gossypium hirsutum* L.)

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Abstract
The objective of study was exploitation of genetic interaction, and variability shown by yield contributing and ionic concentration traits for development of salt tolerance genotypes. Thus, genetic variation was created by hybridizing six tolerant and three susceptible genotypes. Thus, 27 genotypes were tested at salinity level of NaCl@ 20dSm^{-1} long with control (normal soil). Moderate to high variability by PCV and GCV values indicated the possibility to get salt tolerant genotypes. High broad-sense heritability and increased variability suggested that yield contributing traits were strictly under genetic control. High heritability with moderate to high genetic advance for yield contributing traits suggested selection may result in considerable improvement under salinity stress. Additive gene action was exhibited by plant height, number of bolls plant^{-1}, Na^+, K^+ and K^+/Na^+ ratio. While, mixed trend of additive and non-additive gene action was observed for boll weight and seed-cotton yield plant^{-1}. Total variance indicated that salt tolerance in NIAB-999, CIM-707, NIAB-78, MNH-93, CIM-446, CIM-443 was due to high uptake of K^+ and thus maintaining a highest K^+/Na^+ ratio in their leaves. This highest uptake of K^+ and balancing ratio of K^+/Na^+ ratio may lead to increased seed-cotton yield plant^{-1}. The derived information could be helpful to design breeding scheme against salt stress.

Keywords: cotton, salinity, gene action, heritability, salt stress

Introduction
Salt affected soils are distributed in 120 countries covering 953 M ha and reduced productivity to 7-8% at the global scale (Yadav 2003) [40]. The salinity of soils not only causes severe reduction in yield but also diminishes nutritional quality of agricultural crops (Machado and Serralheiro 2017; Yokoi *et al*. 2002) [24]. Although cotton has been considered as fairly tolerant crop when exposed to salinity stress (Anonymous 2018; Maas 1986; Maas and Hoffman 1977) [6, 23, 22]. yet its yield is drastically reduced due to low germination % and abnormal plant growth and development (Khan 1987) [18]. Various earlier researchers have studied the effect of salt stress on the germination, growth and yield of cotton crop (Julkowska *et al.* 2015; Liang *et al.* 2018; Sakina *et al*. 2016; Shrivastava *et al.* 2015) [16, 32, 37]. A wide range of variability for salinity tolerance has been observed in many crop plants (Gill and Kumar 1999; Lu *et al.* 2014; Noor *et al*. 2001; Sakina *et al*. 2016; Saqib *et al*. 2002; Zeng *et al.* 2015) [13, 32, 21, 27, 34, 42]. At present, sufficient amount of information existed in the literature mentioning the availability of significant differences among different genotypes (Ali *et al*. 2002; Khan *et al*. 2003, Nazeer *et al*. 2014) [3, 19, 24]. In the same context, information is also available to know the physiological aspects of salinity tolerance (Ashraf 2004) [10]. However, very less research work was conducted to find the genetic basis of salinity tolerance (Ali *et al*. 2007; Azhar *et al*. 2007) [5, 11]. For developing salt tolerance cultivars, apart from existence of variability, information about the genetic basis of salt tolerance may play a promising role. Various biometrical techniques can be applied for finding-out the genetic architecture of salt tolerance through combining ability analysis and gene action estimates. Among various mating designs, line×tester analysis (Kempthorne 1957) [17]. was employed here as large number of parents and crosses can be evaluated with ease along with the advantage that the analysis is also based free from any assumptions. This analysis also provides very reliable information about the genetic architecture of inheritance pattern from its combining ability estimates in addition of studying the inheritance of yield contributing traits, and ionic concentration traits of cotton genotypes exposed to normal (control level) and salinity stress environment.
For bringing effective progress in getting salt tolerance, the knowledge of variability, heritability, genetic advance, proportional contribution to total variance, combining ability variances and gene action are very necessary and this information collectively constitute the genetic basis of pattern of inheritance, which may assist the cotton breeders to find salt tolerant parental genotypes and F_1 hybrid genotypes.

Materials and Methods
Description of experiment site
The research work was carried out in the department of Plant Breeding & Genetics, University of Agriculture, Faisalabad, Pakistan. The experimental site is situated at latitude 31°25′N, longitude 73°09′E and altitude 184.4 m

from sea level.

Plant Material

The plant material used in this study includes six salt tolerant varieties viz., NIAB-999, CIM-707, NIAB-78, MNH-93, CIM-446, CIM-443, and three salt susceptible genotypes viz., CIM-499, NIAB-111, S-12. The varietal response against salt tolerant and susceptibility was based on our previous results given in Abbas *et al*. (2011) [1]. while treated these varieties at NaCl @ 20 dSm^{-1} and NaCl @ 10 dSm^{1}, respectively. The seed source of the varieties along with their distinguishes features is given in Table 1.

Table 1 Seed sources of different cotton varieties used in the experiment

Variety	Year of release	Source
Female parents: salt tolerant varieties		
NIAB-999	2003	Nuclear Institute for Agriculture and Biology, Faisalabad
CIM-707	2004	Central Cotton Research Institute, Multan
NIAB-78	2006	Nuclear Institute for Agriculture and Biology, Faisalabad
MNH-93	1980	Cotton Research Station, Multan
CIM-446	1998	Central Cotton Research Institute, Multan
CIM-443	1998	Central Cotton Research Institute, Multan
Male parents: salt susceptible genotypes		
CIM-499	2003	Central Cotton Research Institute, Multan
NIAB-111	2004	Nuclear Institute for Agriculture and Biology, Faisalabad
S-12	1988	Cotton Research Station, Multan

Maintenance of genetic purity and Development of F_1 hybrids

For each genotype, nine pots were allocated and 6 seeds were dibbled to raise a minimum of three plants per pot. At the time of flowering, hybridization/crossing among six tolerant genotypes and three susceptible genotypes were attempted keeping tolerant genotypes as lines (females) and susceptible genotypes as male parent, following the procedure given by Kempthorne (1957) [17]. To keep the genetic purity of parents, selfing was also conducted. Thus, the outcome of the experiment was selfed seeds of 9 parents and crossed seed of 18 F_1 hybrids (Table 2). Selfed and crossed bolls (fully opened) of each combination were picked for getting seed cotton and ginning was accomplished to get F_1 seed. Utmost care was done to prevent mixing of seeds of different genotypes during ginning process.

Table 2 List of F1 recombinations comprises 6 females and 3 male parents

Sr. No	Recombinations
1	NIAB-999 × CIM-499
2	NIAB-999 × NIAB-111
3	NIAB-999 × S-12
4	CIM-707 × CIM-499
5	CIM-707 × NIAB-111
6	CIM-707 × S-12
7	NIAB-78 × CIM-499
8	NIAB-78 × NIAB-111
9	NIAB-78 × S-12
10	MNH-93 × CIM-499
11	MNH-93 × NIAB-111
12	MNH-93 × S-12
13	CIM-446 × CIM-499
14	CIM-446 × NIAB-111
15	CIM-446 × S-12
16	CIM-443 × CIM-499
17	CIM-443 × NIAB-111
18	CIM-443 × S-12

Experiment Layout

Selfed seeds of nine parents (6-tolerant & 3-susceptible) and their F_1 crossed seeds comprises of 18 combinations were sown during the year June 2013 in earthen pots (12 × 10”). These pots were laid out according to randomized complete block (RCB) design in 2 factors (genotypes and salinity) arrangement in 2 replications.

Direct mixing of NaCl salts in the field soils as a medium of growth was not applied as it may hinder the germination of salt susceptible genotypes as were observed in screening experiment. As susceptible parental genotypes (testers) were also necessary for making various comparisons, so NaCl solutions were applied to get a desirable salinity level of NaCl@ 20dSm^{-1}. After a desirable emergence achieved, first dose of calculated amount of brine solution (NaCl @ 10dSm^{-1}) was applied to two-week-old seedlings whereas final increment to raise the salinity concentration of NaCl @ 20 dSm^{-1} was applied after four weeks of sowing. All kinds of recommended crop husbandry practices from seed sowing to seed cotton picking were provided.

Collection of data

At the time of harvesting, data regarding yield contributing traits viz., plant height (cm), number of bolls $plant^{-1}$, boll weight (g) and seed-cotton yield per plant (g). Ionic concentration traits like Na^+ mM/L, K^+ mM/L and K^+/Na^+

concentration traits were recorded. The absolute data values at control and NaCl @ 20dSm^{-1} and relative means at NaCl @ 20dSm^{-1} for each trait were used for statistical analysis. The relative means were calculated by following formula:

$$\text{Relative (\%) means} = \frac{\text{Absolute mean value in NaCl @ 20 dsm}^{-1}}{\text{Absolute mean value in Control treatment}} \times 100$$

Statistical analysis

After getting absolute and relative mean values, the data were analyzed for Analysis of Variance (ANOVA) technique with 2 factors RCB Design as described by Steel *et al*. (1997) [39]. To have a deep look into the variation, the statistical analysis was also performed at each salt level separately. For the estimation of gene action of parents (lines and testers) and F_1 combinations, source of variation (SOV) for genotypes from Analysis of variance (ANOVA) table was further partitioned into its components parts (Kempthorne 1957) [17]. Data showing significant differences at each salinity level were subjected to further estimation of components of variations, heritability and genetic advances (Singh and Narayanan 2000) [35].

The detailed procedure of all kinds of statistical data analysis has been given below:

Components of variances were calculated by the following formulas:

Genotypic variance (σ_g) = V_g = ($MS_g - MS_e$) / r.
Environmental variance (σ_e) = V_e = ($MS_g - MS_e$) / r.
Phenotypic variance (σ_p) = V_p = $V_g + V_e$.

The coefficients of variation on environmental, genotypic and phenotypic basis were determined as described by Burton (1952) and revealed by Singh and Narayanan (2000) [35].

Genotypic coefficient of variance (GCV) = (σ_g /trait mean) × 100.
Environmental coefficient of variance (ECV) = (σ_e /trait mean) × 100.
Phenotypic coefficient of variance (PCV) = (σ_p / trait mean) × 100.

The PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon (1973) and are given below:

Low	:	less than 10%
Moderate	:	10-20%
High	:	more than 20%.

Broad-sense heritability was calculated by the formula given by Lush (1940) [20].

$$H^2 \text{ (b.s.) \%} = (V_g / V_p) \times 100.$$

Categorization of broad-sense heritability was made according to Johnson *et al*. (1955) [15]. and has been given below.

Low	:	less than 30%
Moderate	:	30-50%
High	:	more than 50%.

Genetic advance and genetic advance as percentage of mean was calculated by the following formula given by Johnson *et al*. (1955) [15].

$$\text{Genetic advance (G.A.)} = K \times \{V_g / (V_p)^{1/2}\},$$

Genetic advance (G.A.) % = (Genetic Advance / Trait Mean) × 100,

Where,

$(V_p)^{1/2}$ = phenotypic standard deviation
K = selection differential and its value at selection intensity of 10% (i = 10%) is 1.76 (Falconer and Mackay 1996).

The classification of genetic advance as percentage of mean was made as suggested by
Johnson *et al*. (1955) [15]. and is given below:

Low	:	less than 10%
Moderate	:	10-20%
High	:	more than 20%.

Results

1. Combine analysis of variance

Mean square values from combine analysis of variance with respect to all the accession and salinity levels for all the traits have been presented in the Table 1 and it was found that all the accessions/genotypes showed significant (P<0.05) differences for all the traits studied. There were also highly significant (P<0.01) differences between salinity levels among yield contributing traits. It was also revealed that all the varieties showed significant differences for accession×concentration interaction with respect to all the yield contributing traits, reflecting that all the genotypes showed different responses to salinity at control level and NaCl@ 20 dSm^{-1}.

With respect to ionic traits (Na^+, K^+ and K^+/Na^+ ratio), there were found highly significant (P<0.01) differences among all the accessions and salinity stress (Table 3). The interaction between accession×concentrations was found highly for Na^+ and K^+/Na^+ ratio but non-significant for K^+ in their leaves which clearly revealed that all the varieties (whether susceptible or tolerant) showed consistent behavior with respect to K^+ concentration in their leaves in control and increased salinity stress.

Table 3: Mean squares from analysis of variance for yield contributing traits of 27 upland cotton accessions grown at control level and NaCl @ 20 dSm-1 (combine analysis at all levels)

SOV	d.f.	Plant height (cm)	Number of bolls plant^{-1}	Boll weight (g)	Yield plant^{-1}(g)	Na^+	K^+	K^+ / Na^+ ratio
Replications	1	39.194 $^{n.s}$	0.182 n.s	0.093 **	23.561 **	0.086 $^{n.s}$	64.175 **	0.496 **
Accessions (Acc.)	26	596.664 **	6.571 **	0.082 **	68.326 **	1.73 **	8.293 **	0.191 **
Concentrations (Conc.)†	1	53616.51 **	332.629 **	23.634 **	10143.57 **	327.447 **	37.277 **	34.584 **
Acc. × Conc.	26	59.282 **	0.666 **	0.033 **	5.946 *	2.289 **	1.195 $^{n.s}$	0.195 **
Error	54	10.111	0.25	0.005	3.035	0.29	0.768	0.025

n.s.= non-significant, *=significant at P<0.05, **= highly significant at P<0.01. †= Control level (salinity @ 2.3 dSm^{-1}) and NaCl @ 20 dSm^{-1}.

2. Variability, heritability and genetic advance.

Yield contributing traits

Lower values of environmental variance were obtained for all the yield contributing traits at control level as well as under salinity stress, indicating the minor influence of environment on the expression of above traits (Table 4, 5, 6). Narrow gap between phenotypic variance and genotypic variance also confirmed low environmental influences on the expression of these traits. Highest values of genotypic variances were observed for plant height under control level while it was less under saline conditions. Low values of coefficient of variance, a reliable and relative statistical measure for studying of variability, were observed for all the yield contributing traits at all levels of salinity, which indicated that these traits are being controlled by genetic factors with minimum influences of environment. Under control level, genotypic and phenotypic coefficient of variance was lower (<10) for number of bolls per plant and individual boll weight while moderate (10~20) coefficient of variance on genotypic and genotypic basis was observed for plant height and seed-cotton yield per plant. As the plants were exposed to salt stress, genotypic and phenotypic coefficient of variance showed increasing trend. The phenotypic and genotypic coefficient of variance values were moderate for plant height, number of bolls per plant while high for yield per plant at absolute level of salinity of NaCl@ 20 dSm^{-1} while all traits showed higher values of phenotypic and genotypic coefficient of variance for yield contributing traits on the basis of relative level of salinity of NaCl@ 20 dSm^{-1}. Although, broad-sense heritability was in 'high group' (h^2>50) for most of the yield contributing traits at all levels of salinity, yet its value increased under salinity stress. In contrast, narrow-sense heritability was moderate under control level while lower under salt stress environment for plant height. Narrow-sense heritability for number of bolls per plant, individual boll weight and seed-cotton yield per plant occupied 'low category' at all salinity levels but there were observed decreasing trend of broad-sense heritability for most of the traits under salinity stress. It has been depicted (Table 4,5,6) that genetic advance had exhibited a mixed trend of increase or decrease for all yield contributing traits under salinity stress levels. However, a genetic advance as % of mean (a relative estimate) indicated low value for individual boll weight under control level, moderate value under absolute salinity of NaCl@ 20 dSm^{-1} and high value under high salinity stress of NaCl@ 20 dSm^{-1}. The genetic advance increased from 'moderate category' (10~20) under control level to 'high category' (>20)under absolute and relative salinity of NaCl@ 20 dSm^{-1}.

Table 4: Proportional contribution to total variance of lines and tester; Components of variance, heritability and genetic advance along with combining abilities variance and gene action of absolute values at control level for yield contributing and ionic concentration traits in 9 parents and 18 F_1 crosses of upland cotton

Description	Plant height (cm)	Number of bolls plant^{-1}	Boll weight (g)	Yield plant^{-1} (g)	Na^+	K^+	K^+ / Na^+ ratio
Absolute control level (salinity @ 2.3 dSm^{-1})							
s^2e	14.65	0.40	0.01	5.09	0.07	0.76	0.02
s^2g	203.34	1.04	0.03	16.45	0.11	1.07	0.05
s^2p	217.98	1.44	0.03	21.54	0.17	1.83	0.06
ECV	3.08	4.85	2.57	5.71	3.60	3.13	3.17
GCV	11.48	7.80	5.20	10.26	4.57	3.70	5.50
PCV	11.89	9.19	5.80	11.74	5.82	4.85	6.35
h^2 (b.s) %	93.28	72.14	80.37	76.35	61.75	58.39	75.16
H^2 (n.s) % (F=1)	54.23	23.58	2.97	15.21	17.34	59.68	12.52
GA (10% i)	24.24	1.52	0.25	6.24	0.45	1.39	0.33
GA% of X (10% i)	19.52	11.67	8.21	15.78	6.32	4.98	8.39
s^2gca	59.11	0.17	0.00	1.64	0.01	0.55	0.00
s^2sca	17.52	-0.07	0.01	2.97	0.03	-0.18	0.01
s^2gca / s^2sca	3.37	-2.45	0.04	0.55	0.50	-3.09	0.45
s^2sca / s^2gca	0.30	-0.41	28.39	1.81	1.98	-0.32	2.25
s^2A (F=1)	118.21	0.34	0.00	3.28	0.03	1.09	0.01
s^2D (F=1)	17.52	-0.07	0.01	2.97	0.03	-0.18	0.01
s^2D / s^2A (F=1)	0.15	-0.20	14.19	0.91	0.99	-0.16	1.12
s^2A / s^2D (F=1)	6.75	-4.86	0.00	1.10	1.01	-6.06	0.89

Table 5: Proportional contribution to total variance of lines and tester; Components of variance, heritability and genetic advance along with combining abilities variance and gene action of absolute values at NaCl @ 20 dSm^{-1} for yield contributing and ionic concentration traits in 9 parents and 18 F_1 crosses in upland cotton

Description	Plant height (cm)	Number of bolls plant^{-1}	Boll weight (g)	sYield plant^{-1} (g)	Na^+	K^+	K^+ / Na^+ ratio
Absolute salinity of NaCl @ 20 dSm^{-1}							
s^2e	5.96	0.108	0.004	0.96	0.44	0.73	0.029
s^2g	114.33	2.327	0.028	17.66	1.65	2.93	0.124
s^2p	120.3	2.435	0.032	18.62	2.09	3.66	0.154
ECV	3.07	3.446	2.889	4.87	6.21	2.94	6.137
GCV	13.43	15.993	8.009	20.86	12.09	5.88	12.671
PCV	13.77	16.36	8.514	21.42	13.59	6.57	14.079
h^2 (b.s) %	95.04	95.562	88.485	94.84	79.11	79.98	80.998
H^2 (n.s) % (F=1)	31.9	6.13	4.384	4.66	4.48	44.66	18.463
GA (10% i)	18.35	2.625	0.277	7.2	2.012	2.692	0.559

GA% of X (10% i)	23.04	27.52	13.259	35.76	18.92	9.248	20.07
s^2gca	19.19	0.07	0.001	0.43	0.05	0.82	0.014
s^2 sca	2.98	-0.02	0.003	0.14	-0.1	-0.05	-0.006
s^2 gca / s^2 sca	6.43	-3.6	0.223	3.03	-0.45	-16.31	-2.487
s^2 sca / s^2 gca	0.16	-0.28	4.476	0.33	-2.24	-0.06	-0.402
s^2 A (F=1)	38.38	0.15	0.001	0.87	0.09	1.63	0.028
s^2 D (F=1)	2.98	-0.02	0.003	0.14	-0.1	-0.05	-0.006
s^2 D / s^2A (F=1)	0.08	-0.14	2.238	0.16	-1.12	-0.03	-0.201
s^2A / s^2 D (F=1)	12.88	-7.5	0.33	6.21	-0.9	-32.6	-4.67

Table 6: Proportional contribution to total variance of lines and tester; Components of variance, heritability and genetic advance along with combining abilities variance and gene action of relative values at NaCl @ 20 dSm^{-1} for yield contributing and ionic concentration traits in 9 parents and 18 F_1 crosses in upland cotton

Description	Plant height (cm)	Number of bolls plant^{-1}	Boll weight (g)	Yield plant^{-1} (g)	Na^+	K^+	K^+ / Na^+ ratio
Relative salinity of NaCl @ 20 dSm^{-1}							
s^2 e	2.31	6.27	3.87	3.19	37.2	4.11	0.001
s^2 g	36.06	154.03	90.9	58.51	556.83	12.87	0.009
s^2 p	38.37	160.3	94.77	61.7	594.03	16.99	0.01
ECV	4.13	9.02	5.85	6.31	4.08	1.95	4.463
GCV	64.47	221.66	137.33	115.7	15.78	3.44	13.464
PCV	68.6	230.68	143.18	122.01	16.3	3.95	14.184
h^2 (b.s) %	93.98	96.09	95.92	94.83	93.74	75.8	90.1
H^2 (n.s) % (F=1)	12.28	2.92	6.62	3.34	4.98	7.36	10.045
GA (10% i)	11.99	25.06	19.24	15.34	40.21	5.498	0.16
GA% of X (10% i)	21.44	36.06	29.06	30.34	26.895	5.275	22.493
s^2gca	2.23	2.26	3.04	1.03	14.8	0.63	0.001
s^2 sca	0.14	0.32	-0.15	4.84	2.19	-0.94	0
s^2 gca / s^2 sca	15.6	7	-19.63	0.21	6.77	-0.66	2.345
s^2 sca / s^2 gca	0.06	0.14	-0.05	4.7	0.15	-1.51	0.426
s^2 A (F=1)	4.46	4.53	6.07	2.06	29.61	1.25	0.001
s^2 D (F=1)	0.14	0.32	-0.15	4.84	2.19	-0.94	0
s^2 D / s^2A (F=1)	0.03	0.07	-0.03	2.35	0.07	-0.75	0.213
s^2A / s^2 D (F=1)	31.86	14.16	-40.47	0.43	13.52	-1.33	4.69

Ionic concentration traits

Components of variance, heritability and genetic advance for ionic concentration traits have been presented in the Table 4 for control level, Table 5 for absolute salinity level of NaCl @ 20 dSm^{-1} and in Table 6 for relative level of salinity of NaCl@ 20 dSm^{-1}. The genotypic and phenotypic coefficients of variance were relatively higher than environmental coefficient of variance at control level as well as at absolute salinity level of NaCl @ 20 dSm^{-1}.

The genotypic and phenotypic coefficient of variance occupied a 'lower category' for Na^+, K^+ and K^+/Na^+ ratio at absolute and relative salinity stress level of NaCl @ 20 dSm^{-1}. In contrast, no change in phenotypic and genotypic coefficient of variance was noted at control level and salinity stress levels (Table 4, 5, 6). Broad-sense heritability increased for all ionic concentration traits when exposed to salinity stress while narrow-sense heritability gradually decreased. Broad-sense heritability occupied a 'high category' for Na^+, K^+/Na^+ ratio at control level along with 'medium category' for K^+ concentration in their leaves. But at absolute and relative level of salinity of NaCl@ 20 dSm^{-1}, broad-sense heritability increased and occupied a 'high category' than at control level (Table 4, 6).

Narrow-sense heritability for K^+ concentration decreased gradually from 59.68% in control level to 44.66% in absolute salinity level of NaCl @ 20 dSm^{-1} and 7.36% in relative salinity stress of NaCl@ 20 dSm^{-1}. Lower values of genetic advance and genetic advance as % of mean for all ionic concentration traits were observed at control level. Genetic advance as % of means for K^+/Na^+ ratio increased from 8.391% (low category) to 20.07% in absolute salinity level of NaCl @ 20 dSm^{-1} and 22.493% in relative salinity level of NaCl @ 20 dSm^{-1}

3. Combining ability variance and gene action.

Yield contributing traits.

The general combining ability variance were higher than specific combining ability variances for plant height and number of bolls per plant at control level and salinity level of salinity of NaCl@ 20 dSm^{-1} (Table 4,5,6). The individual boll weight had expressed relatively higher values of GCA variances than SCA variances at relative level of salinity of NaCl @ 20 dSm^{-1} than at control level and absolute salinity level of NaCl @ 20 dSm^{-1}. For seed-cotton yield per plant, SCA showed highest values (4.84) at relative level of salinity of NaCl @ 20 dSm^{-1} than at other levels. Among yield contributing traits, the ratio of GCA/SCA variance was more than 1 for plant height and number of bolls per plant at control level while less than 1 for individual boll weight and seed-cotton yield per plant. In plants exposed to salinity stress, higher values of GCA/SCA ratio were observed for all yield contributing traits at absolute salinity level of NaCl @ 20 dSm^{-1}. The GCA/SCA ratio increased at relative level of salinity of NaCl@ 20 dSm^{-1} for plant height, number of bolls per plant and individual boll weight (Table 5). Additive components of variance showed rapid decline for plant height under salt stress conditions from its value of 118.21 at control level, to its value of 38.38 at absolute salinity level of NaCl @ 20 dSm^{-1} and 4.46 at relative salinity level of NaCl @ 20 dSm^{-1}. For number of bolls per plant, individual boll weight and seed-cotton yield per plant, additive variance were highest at relative salinity level of

salinity of NaCl @ 20 dSm^{-1} (Table 6) while these values lower at control level and lowest at absolute salinity level of NaCl @ 20 dSm^{-1}. Maximum dominant variance was observed for plant height (17.52) at control level followed by dominance variance values of 4.84 for seed-cotton yield per plant at relative. Dominant variance had showed a mixed trend of increase or decrease for all traits at all salinity stress. The ratio of V_D/V_A was less than unity for plant height and number of bolls per plant at all levels of salinity stress indicating the presence of partial dominant gene action, whereas the ratio of V_A/V_D is more than unity (1) at all salinity levels. Higher values under salinity stress for plant height and number of bolls per plant indicated that the above partial dominance due to V_D/V_A ratio for plant height and number of bolls per plant is actually due to additive gene action. The presence of additive gene action has also been manifested from higher values of GCA/SCA ratio under control level and at salinity stress conditions.

Ionic concentration traits

Among the ionic concentration traits, Na^+ and K^+/Na^+ ratio showed relatively more values of SCA variance than GCA variance at control level (Table 4), whereas reverse was true for K^+ as here the ratio of GCA/SCA variance was more than unity for K^+. In the same context, the ratio of SCA/GCA was higher for Na^+ and K^+/Na^+ ratio and it was less than 1.

More than 1 value of GCA/SCA and SCA/GCA variance ratio is directly correlated with the additive and dominant type of gene action, respectively. Table 4 also indicated that additive gene action was higher for all the ionic concentration traits at control level. The ratio of V_D/V_A less than 1 for Na^+ and K^+ trait, which indicated the presence of partial dominant type of gene action for these ionic concentration traits. Over-dominant type of gene action was indicated for K^+/Na^+ due to V_D/V_A more than 1. The V_A/V_D ratio of Na^+ and K^+ was less than 1 and less than 1 for K/Na ratio, which reflected the presence of additive and non-additive type of gene action, respectively under control level. The ratio of GCA/SCA was more than 1 for K^+ and K^+/Na^+ ratio, indicating an association with additive gene action under absolute salinity level of NaCl @ 20 dSm^{-1} (Table 5). More than 1 ratio of V_D/V_A for Na^+ and less than 1 for K^+ and K^+/Na^+ ratio exhibited over-dominant and partial dominant gene action, respectively. This gene action is also verified by less than 1 value of V_A/V_D ratio for Na^+ and more than 1 for K^+ and K^+/Na^+ ratio reflecting non-additive and additive type of gene action, respectively. At relative level of salinity of NaCl@ 20 dSm^{-1}, less than 1 ratio of V_D/V_A for all the ionic concentration traits exhibited partial dominant gene action (Table 6). The presence of partial dominance gene action is verified from the V_A/V_D ratio of more than 1, which indicated that partial dominance is regulated by the genes having additive effects.

Discussion

For the development of salt tolerant lines or making any improvement in the existing salt tolerant cultivars, presence of sufficient variation within the crop species for salinity tolerant traits is pre-requisite for selection directly or followed by hybridization (Singh 2004, 2006) [36]. Degree of variability for salinity tolerance depends upon the type of germplasm screened, stage of crop exposed to salt stress as well as salt level applied (Akhtar and Azhar 2001; Poljakoff-Mayber and Lerner 1994) [2, 29]. At lower concentration of salinity stress, differences appeared among the varieties are not clear-cut as compare to high salinity stress (Ashraf 2002; Ali *et al*. 2005) [9, 4].

The values of environmental coefficient of variance for all yield contributing traits occupied a 'low category' which indicated that there was little influence of environment on the expression of these traits not only at control level but also at increased salinity level. The results relating to phenotypic and genotypic coefficient of variation reflected that there was moderate variability for plant height and seed-cotton yield per plant along with less variability for number of bolls per plant and individual boll weight at control level but under salt stress, increase in the variability has been noted. Moderate to high variability exhibited by PCV and GCV values suggested that selection at saline environment may be possible for getting desirable genotypes on the basis of yield contributing traits. High broad-sense heritability suggested that increased variability exhibited by these genotypes for yield contributing traits is purely based on genetic reasons and inheritance is through genetic control. Huge gap between broad-sense and narrow-sense heritability under salt stress environment reflected that number of bolls per plant, individual boll weight and seed-cotton yield per plant are controlled by genes producing non-fixable effects.

Moderate to high genetic advance as % of mean value at control level indicated that considerable advancement by selection is possible. High heritability estimated along with moderate to high values under genetic advance for all yield contributing traits suggested that selection may be effective and may result in considerable improvement of seed-cotton yield under salinity stress conditions. Low values of genotypic and phenotypic coefficient of variance of fibre quality traits under control and salinity stress indicates that there existed less variability for these traits in the genotypes studied. Low to moderate broad-sense heritability for most of the fibre quality traits suggested the presence of low heritable variation and low values of narrow-sense heritability confirmed the presence of non-fixable inheritance exhibited by genes controlling fibre quality traits. Low to high heritability along with low genetic advance suggested that selection may not be effective in bringing any improvement in fibre quality traits. Low variability existed for all ionic concentration traits at control level while there has been observed a little increase in genotypic and phenotypic coefficient of variance under saline conditions. High broad-sense heritability followed by low narrow-sense heritability for ionic concentration traits reflected that these ionic traits are being controlled by non-additive genes having non-fixable expression. Moderated to high variability for these inorganic ions have previously reported by Ali *et al*. (2002) [3]. Although high heritability followed by high genetic advance values under salt stress were noted but selection on the basis of ionic concentration traits may still not effective due to low variability. Various earlier researchers had also reported high heritability under salt stress conditions (Hoffman and Parsons 1991) [14]. In contrast, some researchers found low heritability for few traits (Rumbaugh *et al.* 1984) [31]. and suggested that increase or decrease in heritability under stress conditions is because of diversified interaction of various genes under different environments and heritability values are specific to a particular population under particular environment.

Findings of earlier researchers revealed that interpretation of heritability values should be made with care. High heritability in the present research indicated that genetic improvement under salt stress is possible through selection.

Proportional contribution to total variance concluded that under stress conditions, variable share of lines and testers may be observed. Salt tolerant lines which has contributed very low share towards total variance at control level, showed increased contribution under stress for plant height, number of bolls per plant and seed-cotton yield while salt susceptible testers which contributed lower share for individual boll weight per plant at control salinity level, showed a highest contribution for individual boll weight. Thus, better performance of F_1 genotypes (also depicted from highest share of line×tester interaction for seed-cotton yield per plant) may be due to the maternal contribution for plant height and number of bolls per plant while paternal contribution for individual boll weight. Proportional contribution of ionic concentration traits indicated that under control and saline conditions, lines had performed maximum contribution for Na^+ while highest K^+ and K^+/Na^+ ratio was exhibited by testers (susceptible genotypes) at control and absolute salinity level of NaCl @ 20 dSm^{-1}. On the basis of index values of salt tolerance, lines had maximum share for all ionic traits. The results from proportional contribution of lines may lead to the conclusion that although lines have contributed highest share for Na^+ uptake and lowest share for K^+ and K^+/Na^+ ratio under control level but under salinity stress, lines have performed well for K^+ and K^+/Na^+ ratio. It may be concluded that salt tolerance in lines (tolerant parents) is due to high uptake of K^+ and thus maintaining a highest K^+/Na^+ ratio in their leaves. Earlier researchers also concluded that salt tolerant plants exhibited low Na^+ uptake and high K^+ (Munns, 1995) [25]. Plants uptake higher Na^+ in their leaves at the expense of K^+ and as photosynthesis slows down under salt stress, K^+ selectivity over Na^+ decreased leading to higher Na^+ and low K^+ in their leaves of salt sensitive species (Saqib *et al*. 2002) [34]. Thus, results of low K/Na ratio in the salt sensitive species are in accord with previous findings of Qadir and Shams (1997) [30]. and Pervaiz *et al*. (2002) [28]. This highest uptake of K^+ and balancing highest ratio of K^+/Na^+ ratio may lead to increased seed-cotton yield along with better growth and development under salt affected soils.

Additive gene action was exhibited by plant height and number of bolls per plant under salt stress environment while for individual boll weight and seed-cotton yield, mixed trend of additive and non-additive gene action was shown under salt stress. Similar results have been achieved in which researchers have found increased heritability and more additive components under salinity stress (Hoffman and Parsons 1991) [14]. Azhar *et al*. (2007) [11]. has also observed high additive gene action for seed-cotton yield under saline conditions. Similarly, with respect to Na^+, K^+ and K^+/Na^+ ratio, additive gene action was increased in saline conditions as compared to control level (Salam 1993) [33].

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