

GENOTYPIC VARIATIONS IN SALINITY TOLERANCE AMONG BT COTTON

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Abstract

Salinity stress is one of the most serious environmental problem that negatively affects the growth of plants, especially in arid and semi-arid regions. Scientists have been struggling to address this problem through land reclamation methods and by adding various organic manures into the soil. However, the most cost effective method is to develop salt tolerant varieties. Keeping this in view, fifty cotton genotypes were collected from different areas and were subjected to evaluation. Plants were irrigated with nutrient solution with an electrical conductivity of 10dSm⁻¹ and 15dSm⁻¹ from 10th day seedlings stage to 40th day. Plants were harvested when they were 40 days old and the data was compared at absolute value and relative values from the seedlings. Analysis of variance indicated that there were significant differences among genotypes at control and both salinity levels. Results showed that salinity adversely affected the root length, shoot length, fresh root weight, fresh shoot weight, dry shoot weight, dry root weight in comparison to chlorophyll contents. Magnitude of Sodium under NaCl stress increased many folds and reduction in potassium was also witnessed in the leaves. Broad sense heritability was high whereas phenotypic variance is equal or less than genotypic variances. The genotypes that perform better for the trait that had high broad sense heritability were selected as salt tolerant genotypes such as KEHKSHAN, S-3, NIAB-824 and MNH-988 whereas C-26, FH-114 and FH-173 were conceived as salt sensitive genotypes. The results indicate that selection for cotton will be problematic due to masking effects of environment, and imply rigorous and careful selection of salt tolerant genotypes.

Key words: Salinity, Salt tolerance, Upland cotton, Genetic variation, Seedlings traits, *Gossypium hirsutum* L.

Introduction

Salinity is the rise of salt level in the soil that obstructs the healthy growth of the plant. Around the world, the accumulation of salts in the soil is negatively affecting the yield of different crops. Due to salinity and sodicity, every year, almost 800 million hectare or 7% of the entire earth goes out of cultivation results in less area for crop production (FAO, 2008). Main reasons for the rise of salt level in the soil is due to high evapotranspiration rate and poor quality of irrigation water. Arid and semi-arid regions are mainly affected by salinity in the country. Soil is considered saline if its electrical conductivity is 4dSm⁻¹ or higher value. The primary criteria for selection of salinity tolerance is the ability of the plant to take up a good stand after germination and emergence of seedlings (Rozema & Schat, 2013). The plants that successfully pass the germination and seedlings stages in high salt areas will be vigorous and tolerant to salt stress because at germination and seedling stages, growth will be much crucial due to accumulation of salts at surface soil due to high evaporation and climbing water by capillary action (Taghizadeh *et al.*, 2018).

Cotton is a major fiber crop in Pakistan. It can grow up to 7.7 dS/m, for which it is regarded as moderately salt tolerant (Kamran *et al.*, 2016) moreover, it is proven that with the increase of salt stress, it shows decline in the germination and emergence percentage (Sevik & Cetin, 2015). With the onset of salinity, plants show reduced rate of germination in cotton seeds (Yue *et al.*, 2007). At seedling stage water efficiency, evaporation rate and

photosynthesis are reduced while respiration rate increases (Parihar *et al.*, 2015). Phenotypically, the height of plant, stem thickness, shoot and root weight and expansion of leaves size halts that gravely affects the yield of cotton (Cheng *et al.*, 2018).

Variability in the germplasm is the prerequisite for the success of every breeding program. Number of morphological and physiological markers have been utilized to assess the variations under salinity stress. Morphological traits include root and shoot weight, longer tap root length, reduced chlorophyll contents and transpiration rate can be exploited for the development of salt tolerant cultivars (Ta'ibi *et al.*, 2016). Among various physiological markers enhanced K⁺/Na⁺ ratio and low Na⁺ uptake are important for salinity tolerance (Liu *et al.*, 2017). Further, genetic variability and heritability plays an important role in breeding strategy for specific traits and to estimate the amount of genetic advance to be expected from the selection. Therefore, it is necessary that screening for salt tolerance should be carried out for the available germplasm so that genetic resource for increasing salt tolerance can be found.

In the present study, 50 cotton genotypes were examined for the variations in cotton plants under salinity stress at seedling stage. The results from this research may help breeders for the selection of potential germplasm for the salinity tolerance breeding mechanisms under salt affected areas.

Materials and Methods

In the present study, fifty genotypes of upland cotton were selected from different research institutes

and were subjected to salt stress at two levels in the Department of Plant Breeding and Genetics in the University of Agriculture, Faisalabad (Table 1). Sand filled polystyrene cups (Height 5 inches, Diameter 3.5 inches) were used for the sowing of genotypes in three replications. Each genotype was sown in five cups and one treatment per replication was maintained according to the Factorial Complete Randomized design. For the 1st 10 days only Hoagland solution was provided to the plants then Hoagland solution of 10 d Sm⁻¹ and 15 d Sm⁻¹ concentration was applied (Hoagland and Arnon 1950) as it has been done by (Saeed *et al.*, 2011) to screen tomato germplasm for salinity tolerance. The salinity levels were maintained in the pots by continuous testing of electrical conductivity of the sand material in cups by pour through extraction method (Wright 1986). One seedling was sown in each cup. From 10 days of sowing to 40th day of harvesting saline solution was applied on alternate days. Chlorophyll meter (Model: SPAD 502 PLUS Japan) was used to measure the chlorophyll contents in the leaves when 1st true leaf had reached maturity. After harvesting, seedlings were uprooted and rinsed with deionized

water and swapped with the paper towel. Then seedlings were cut into two portions i.e. root and shoot, and measurement were taken for their length, fresh root and shoot weight. Then the roots and shoots were dried in an oven for 72 hours at 70 c° to take dry weight of the given samples. For Na⁺ and K⁺ analysis, the dried leaves were grinded down with mortar and pestle and then digested with concentrated Nitric acid and Sulfuric acid 1:2 ratio (molar ratio) on the hot plate. After digestion they were cooled at room temperature by adding distilled water and readings were taken by flame photometer (Model: 410 Flame Photometer).

Relative values are expressed as percent change which were calculated by dividing the value of parameter under salt stress by value of parameter under control conditions and multiplied by 100 (Nabi *et al.*, 2010). Analysis of variance was carried out by the method outlined by (Steel *et al.*, 1997) to see whether the genotypic differences are significant. Broad Sense Heritability was estimated by the formula outlined by (Falconer & Mackay, 1996) and Genetic Advance was calculated following the equation given by (Johnson *et al.*, 1955).

Table 1. Institutes and names of 50 genotypes of *Gossypium hirsutum L.* examined for salinity tolerance

Sr. No.	Genotypes	Institute name	Sr. No.	Genotypes	Institute name
1.	FH-458	CRI, Faisalabad	26.	KZ-189	Private Seed Company
2.	BS-80	Private Seed Company	27.	C-26	China
3.	Mubarak	CRI, Faisalabad	28.	SB-149	Private Seed Company
4.	Debal	CRI, Faisalabad	29.	IUB-222	IUB, Bhawalpur
5.	Kehkshan	CRI, Faisalabad	30.	MG-6	Private Seed Company
6.	Lalazar	CRI, Faisalabad	31.	IR-901	NIBGE, Fsd
7.	FH-312	CRI, Faisalabad	32.	VH-333	CRS, Vehari
8.	FH-444	CRI, Faisalabad	33.	NIAB-824	NIAB
9.	MNH-888	CRI, Multan	34.	AS-01	Private Seed Company
10.	FH-173	CRI, Faisalabad	35.	AGC-2	Private Seed Company
11.	FH-113	CRI, Faisalabad	36.	RH-647	CRI. R.Y.Khan
12.	FH-177	CRI, Faisalabad	37.	CRS-456	CRS, Multan
13.	FH-187	CRI, Faisalabad	38.	AA-802	Private Seed Company
14.	FH-171	CRI, Faisalabad	39.	NS-131	Neelum Seeds
15.	MNH-988	CRI, Multan	40.	FH-154	CRI, Faisalabad
16.	FH-170	CRI, Faisalabad	41.	VH 259	CRS, Vehari
17.	MNH-992	CRI, Multan	42.	CIM 595	CCRI, Multan
18.	FH-142	CRI, Faisalabad	43.	VH 295	CRS, Vehari
19.	FH-118	CRI, Faisalabad	44.	VH 329	CRS, Vehari
20.	FH-941	CRI, Faisalabad	45.	CIM 602	CCRI, Multan
21.	FH-4243	CRI, Faisalabad	46.	AA 703	Ali Akbar Seeds
22.	VH-325	CRS, Vehari	47.	CIM 622	CCRI, Multan
23.	FH-114	CRI, Faisalabad	48.	FH 169	CRI, Faisalabad
24.	CIM-612	CCRI, Multan	49.	S 3	Private Seed Company
25.	CRS-2007	CRS, Multan	50.	IR 3701	NIBGE, Fsd

Table 2. Mean squares from relative values of analysis of variance for various seedling traits of 50 upland cotton accessions grown at two NaCl concentration levels (combine analysis at all levels).

Source of variation	d.f	Chlorophyll contents	Root length	Shoot length	Fresh root weight	Fresh shoot weight	Dry root weight	Dry shoot weight	Sodium (Na)	Potassium (K)	K/Na ratio
Accessions	49	37.13**	246.8**	45.31**	431.4**	273.7**	168.3**	192**	13394**	81.2**	19.37**
Conc.	1	5053.27**	14983.6**	5849.37**	24813.4**	12152.5**	38153.2**	53993.3**	864392**	10000.8**	4536.05**
Accessions × Concentration	49	13.14**	48.7**	12.41**	142.8**	38.7**	74.2**	106.2**	1011**	13.2**	2.85**
Error	198	1184.57	6159.2	4.88	6.1	8.2	118.2	36.6	448	1.8	1.06

F. Tab 5% 1.75* F.tab1% 2.15

Table 3. Components of variance, broad sense heritability and genetic advance to salinity stress in the cotton seedlings.

Components	Potassium (ppm)					Chlorophyll contents			
	Absolute values			Relative values		Absolute values			Relative values
	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹	Control	10dSm ⁻¹	15dSm ⁻¹	15dSm ⁻¹
Genotypic variance	155.87	215.51	191.56	13.18	17.10	17.59	16.68	14.25	11.39
Phenotypic variance	159.39	218.85	194.12	15.23	18.59	18.15	16.98	14.72	17.29
Heritability Broad sense	97.79	98.48	98.68	86.55	92.02	96.93	98.22	96.83	65.86
Genetic advance i=1.76	21.61	25.49	24.06	5.91	6.94	7.23	7.08	6.50	4.79
Genetic advance %	12.95	18.59	20.41	7.20	9.85	19.80	20.91	21.06	5.67

Results

The analysis of variance showed that there were significant difference between control and two levels of salinity. Moreover, significant interaction of genotypes with salinity levels indicated differential response under salt stress (Table 2).

Analysis of variance showed that the chlorophyll contents in the leaves were not significantly different at lower level of salt stress which explains that minor salt stress does not affect leaves chlorophyll contents, however salt stress at 15 d Sm⁻¹ resulted in significant change in chlorophyll contents. FH 173 and VH 259 were the most affected genotypes under the salt stress while S-3 and MNH-888 were least affected under salt stress. High broad sense heritability and low genetic advance indicated that characters are genetically controlled (Table 3).

Relative values pointed out that the highest root length under 10 dSm⁻¹ was for SB-149 while under 15 d Sm⁻¹ S-3 and AA-802 performed best (Table 4). However the most susceptible genotypes for salt stress were CM-595 and FH-173. Genotypes differed significantly from each other under both levels of stress. High heritability and low genetic advance was observed, moreover the phenotypic variance and genotypic variances were almost equal in absolute values whereas, high phenotypic variance than genotypic in relative values was indicated in the results. For shoot length NS-131 and AS-01 performed better under 10 d Sm⁻¹ while MNH-888 and FH-154 had the highest length under 15 d Sm⁻¹. There was moderate heritability for relative values and low genetic advance, moreover the high phenotypic variance than genotypic variance showed that environment has influence on the characters studied (Table 5) (Salam *et al.*, 2011).

The fresh root weight of NIAB-824 and FH-458 performed best under 10 d Sm⁻¹ while KEHKSHAN and NIAB-824 produced best results under 15 d Sm⁻¹ (Table 6). High heritability and low genetic advance was observed and slightly high phenotypic variance than genotypic variance was witnessed (Table 7). The maximum root dry weight was found for CIM-612 under 10dSm⁻¹ and 15dSm⁻¹ salt stress conditions. However, SB-149 performed the poorest for root dry weight under salt stress conditions. Genotypic variance was lower than the phenotypic variance for root dry weight.

Among the fifty genotypes subjected to salt stress for fresh shoot weight at two levels FH-113 and CM-595 performed well under 10 d Sm⁻¹ salt stress while KEHKSHAN, FH-187 and VH-329 did best under 15 d Sm⁻¹ salt stress. Analysis of variance pointed out that there exist a significant difference between both levels of salt stress. Expected broad sense heritability was high for all treatments in absolute and relative values and moderate genetic advance was observed. For shoot dry weight, AA-703 and CM-622 performed best under 10 d Sm⁻¹ salt stress while MNH-888 and MUBARAK were found high salt stress tolerant under 15 d Sm⁻¹ (Table 8) Analysis of variance indicated that there was significant difference between two levels of stress level when genotypes were subjected to salt stress. There was moderate level of broad sense heritability while genetic advance was low (Table 10).

Potassium accumulation inside the plant is a key parameter to know about the ability of plant to cope the salt stress. Among 50 genotypes KEHKSHAN and FH-118 were found salt tolerant under 10 d Sm⁻¹ salt stress while MNH-988 and FH-312 performed well under 15 d Sm⁻¹ salt stress conditions. Expected broad sense heritability was found high which confirms that the characters are genetically controlled while low genetic advance was noted for the given trait. Whereas, higher the sodium concentration in the leaves the lower will be the ability of genotypes to cope up salt stress. In our study, FH-114 and C-26 pooled highest amount of Na⁺ under 10 d Sm⁻¹ level of stress whereas MNH-888 performed better under 15 d Sm⁻¹ while LALAZAR, DEBAL and S-3 accumulated the lowest amount of Na⁺ in their leaves under high salt stress and were regarded as a candidate for the salt tolerant genotypes (Table 8). Phenotypic variance was found higher than the genotypic variance which represents that the impact of environment on genotypes is eminent. The expected broad sense heritability was found higher at both stress levels while genetic advance was low (Table 9).

Among 50 genotypes, LALAZAR and FH-113 indicated the maximum K/Na ratio under 10dSm⁻¹ salt stress while FH-113 and NIAB-824 were promising lines under 15dSm⁻¹ salt stress (Table 11). All genotypes under studied were significantly different from each other. Expected broad sense heritability was found moderate while genetic advance was found lower for this trait. Phenotypic variance was less than genotypic variance (Table 9).

Table 4. Percent change in the chlorophyll contents, root length and shoot length of 50 genotypes grown in two levels of salt stress.

	Chlorophyll contents		Root length		Shoot length	
	10dSm ⁻¹	15dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹
FH-458	95.12	89.10	78.95	66.03	90.72	82.81
BS-80	95.78	87.94	86.10	71.04	90.86	80.83
MUBARAK	93.63	89.98	86.42	73.37	88.20	83.67
DEBAL	93.76	88.13	76.45	61.96	86.89	77.33
KEHKSHAN	93.62	86.51	86.50	76.43	89.86	79.37
LALAZAR	95.01	84.50	80.54	65.77	87.35	80.61
FH-312	94.93	87.76	85.52	72.60	93.03	86.56
FH-444	94.40	88.45	82.50	71.56	89.29	78.77
MNH-888	95.26	92.19	84.94	76.30	92.28	88.26
FH-173	92.56	75.77	74.80	67.89	89.13	80.97
FH-113	92.66	86.25	69.97	48.51	88.63	79.16
FH-177	87.97	76.95	81.47	69.89	89.39	75.97
FH-187	90.88	85.91	78.95	66.80	90.41	79.14
FH-171	92.16	86.13	77.33	55.00	89.60	79.62
MNH-988	92.93	79.44	83.30	75.37	91.33	82.02
FH-170	90.84	77.96	78.76	55.18	90.66	83.90
MNH-992	93.86	85.21	82.01	72.53	90.56	84.60
FH-142	94.23	84.00	87.60	74.81	89.62	82.39
SB-149	90.33	81.93	82.10	75.76	86.38	78.21
FH-941	91.01	82.24	74.93	58.22	87.57	81.92
FH-4243	94.08	85.66	84.69	69.06	91.37	80.20
VH-325	93.42	83.00	74.92	63.84	92.32	86.67
FH-114	93.77	87.16	81.06	54.63	83.80	72.49
CIM-612	91.89	85.14	84.85	79.50	90.53	84.88
CRS-2007	93.74	82.71	82.71	68.42	90.73	78.83
KZ-189	92.05	86.14	75.00	50.00	92.53	76.56
C-26	93.33	83.43	81.91	63.82	91.36	79.91
FH-118	92.74	84.31	94.57	62.50	87.63	74.23
IUB-222	92.70	85.87	75.67	61.67	91.92	85.66
MG-6	91.67	85.64	81.62	67.65	87.80	82.54
IR-901	92.46	88.04	81.31	66.89	92.94	84.07
VH-333	89.85	85.77	88.46	78.67	90.08	83.97
NIAB-824	92.04	84.94	84.76	76.38	93.68	84.04
AS-01	93.20	82.06	83.28	68.69	94.44	87.86
AGC-2	91.47	85.45	88.83	73.40	90.52	74.06
RH-647	90.86	84.76	87.30	68.57	91.92	83.64
CRS-456	93.62	85.20	87.54	72.90	92.72	83.51
AA-802	91.59	81.27	89.06	81.42	92.18	85.89
NS-131	94.60	86.03	84.97	71.90	94.32	85.20
FH-154	92.04	80.81	76.95	63.67	93.83	89.09
VH 259	92.56	75.77	74.80	67.89	89.13	80.97
CM 595	92.66	86.25	69.97	48.51	88.63	79.16
VH 295	87.97	76.95	81.47	69.89	89.39	75.97
VH 329	90.88	85.91	78.95	66.80	90.41	79.14
CM 602	92.16	86.13	77.33	55.00	89.60	79.62
AA 703	91.01	82.24	74.93	58.22	87.57	81.92
CM 622	94.08	85.66	84.69	69.06	91.37	80.20
FH 169	93.42	83.00	74.92	63.84	92.32	86.67
S 3	97.99	91.41	93.23	81.20	91.92	83.64
IR 3701	93.53	85.12	70.28	65.00	92.72	83.51

Table 5. Components of variance, broad sense heritability and genetic advance to salinity stress in the cotton seedlings.

Component	Root length (cm)					Shoot length (cm)				
	Absolute values			Relative values		Absolute Values			Relative Values	
	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹
Genotypic variance	8.83	6.76	6.63	20.02	57.58	5.29	4.83	4.92	2.97	12.99
Phenotypic variance	9.14	6.94	6.79	54.99	85.25	5.41	4.88	4.98	8.67	17.13
Heritability broad sense	96.59	97.40	97.61	36.41	67.55	97.74	98.84	98.80	34.26	75.81
Genetic advance $i=1.76$	5.11	4.49	4.45	4.72	10.91	3.98	3.82	3.86	1.77	5.49
Genetic advance %	47.72	51.43	61.11	5.80	16.19	23.68	25.14	28.06	1.95	6.73

Table 6. Percent change in the Fresh root weight, Fresh shoot weight and Root dry weight of 50 genotypes grown in two levels of salt stress.

	Fresh root weight		Fresh Shoot Weight		Root dry weight	
	10dSm ⁻¹	15dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹
FH-458	92.47	36.56	87.26	74.13	66.67	48.15
BS-80	83.54	45.57	75.10	63.98	79.31	51.72
MUBARAK	74.76	63.81	78.23	74.18	77.27	54.55
DEBAL	68.33	59.62	71.30	56.48	76.09	52.17
KEHKSHAN	86.05	80.00	80.98	83.82	64.52	48.39
LALAZAR	80.49	70.73	69.25	58.92	78.26	58.70
FH-312	82.35	69.68	87.50	75.83	79.10	52.24
FH-444	79.04	65.27	83.30	55.31	75.00	54.55
MNH-888	84.97	70.52	75.81	66.87	71.25	52.50
FH-173	84.70	70.49	91.34	75.99	75.00	55.00
FH-113	72.44	49.36	94.61	79.51	75.00	50.00
FH-177	57.63	38.98	83.45	71.43	74.29	51.43
FH-187	81.25	61.88	90.26	82.47	69.23	43.59
FH-171	65.08	44.44	74.63	48.01	75.00	48.21
MNH-988	79.93	74.72	76.52	69.51	72.97	56.76
FH-170	87.65	61.73	92.79	72.89	61.11	42.59
MNH-992	87.88	73.64	81.20	74.00	70.42	46.48
FH-142	90.16	72.13	90.37	74.07	78.00	60.00
FH-118	83.33	75.51	86.50	73.57	73.08	49.23
FH-941	70.62	56.50	86.23	67.96	67.24	53.45
FH-4243	89.52	70.16	91.04	82.08	70.27	59.46
VH-325	80.39	68.63	90.16	77.32	80.49	58.54
FH-114	76.84	60.00	91.29	79.68	74.07	35.33
CIM-612	72.39	61.97	87.14	76.07	82.00	64.21
CRS-2007	72.86	59.52	86.92	75.93	67.24	51.72
KZ-189	85.62	43.14	87.76	82.29	67.33	45.24
C-26	86.05	51.16	88.54	79.86	70.00	50.00
SB-149	75.68	48.65	84.64	70.26	63.33	33.33
IUB-222	75.12	56.22	87.83	68.70	77.29	56.25
MG-6	77.78	46.03	91.90	78.54	69.23	34.62
IR-901	75.17	64.83	83.15	69.57	70.83	45.83
VH-333	88.54	66.24	90.63	82.10	75.00	54.17
NIAB-824	91.10	78.42	87.35	76.94	68.49	50.68
AS-01	85.89	67.48	85.00	72.25	75.00	54.55
AGC-2	80.68	65.91	87.99	77.60	80.77	57.69
RH-647	82.08	53.76	86.11	75.76	71.82	61.36
CRS-456	78.99	63.77	89.08	77.87	76.74	62.79
AA-802	75.38	67.42	80.66	67.77	73.68	52.63
NS-131	80.00	67.72	83.07	74.60	73.33	53.33
FH-154	81.44	59.28	81.34	66.18	80.49	56.10
VH 259	82.45	68.62	91.34	75.99	75.00	55.00
CM 595	72.44	49.36	94.61	79.51	75.00	50.00
VH 295	57.63	38.98	83.45	71.43	74.29	51.43
VH 329	79.27	60.37	90.26	82.47	69.23	43.59
CM 602	65.08	44.44	74.63	48.01	75.00	48.21
AA 703	70.62	56.50	86.23	67.96	67.24	53.45
CM 622	89.52	70.16	91.04	82.08	70.27	59.46
FH 169	80.39	68.63	90.16	77.32	80.49	58.54
S 3	67.62	44.76	83.15	69.57	75.00	56.25
IR 3701	71.24	67.97	90.63	82.10	68.75	56.25

Table 7. Components of variance, broad sense heritability and genetic advance to salinity stress in the cotton seedlings.

Components	Fresh root weight (mg)					Shoot fresh weight (mg)				
	Absolute values			Relative values		Absolute values			Relative values	
	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹
Genotypic variance	0.05	0.03	0.03	64.69	122.63	0.07	0.04	0.04	33.75	65.10
Phenotypic variance	0.05	0.03	0.03	70.33	129.19	0.07	0.04	0.04	42.02	72.69
Heritability broad sense	99.60	99.81	99.73	91.98	94.92	98.64	98.65	97.63	80.30	89.56
Genetic advance $i=1.76$	0.38	0.32	0.31	13.50	18.88	0.46	0.37	0.35	9.11	13.36
Genetic advance %	64.57	69.54	84.65	17.12	31.13	34.64	32.64	36.65	10.65	18.36

Table 8. Percent change in the Shoot dry weight, Potassium and Sodium of 50 genotypes grown in two levels of salt stress.

	Shoot dry weight		Potassium		Sodium	
	10dSm ⁻¹	15dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹	10 dSm ⁻¹	15 dSm ⁻¹
FH-458	73.68	52.63	77.48	67.57	331.67	435.00
BS-80	77.78	57.14	84.49	72.45	350.88	468.42
MUBARAK	71.97	61.36	88.79	76.69	339.53	460.47
DEBAL	71.61	58.62	85.17	73.52	310.17	389.83
KEHKSHAN	82.26	52.42	90.16	77.05	373.17	509.76
LALAZAR	74.29	43.81	80.54	68.32	295.24	380.95
FH-312	76.64	48.91	87.81	77.42	345.00	475.00
FH-444	63.64	54.55	81.16	68.53	339.29	417.86
MNH-888	74.44	63.16	87.37	75.80	428.57	580.00
FH-173	73.87	53.76	82.88	73.15	335.29	452.94
FH-113	78.95	51.32	83.75	76.25	312.50	403.57
FH-177	76.00	47.00	82.35	66.08	361.11	433.33
FH-187	65.69	50.00	78.76	64.93	384.31	470.59
FH-171	75.73	50.49	80.73	66.86	370.83	510.42
MNH-988	72.99	51.82	84.93	77.48	360.00	426.21
FH-170	68.11	55.79	82.03	65.23	324.53	454.72
MNH-992	74.44	60.90	85.18	77.68	402.63	523.68
FH-142	81.62	47.12	79.59	67.76	352.94	421.57
FH-118	76.52	56.06	90.40	80.07	414.17	542.23
FH-941	66.67	42.86	77.17	65.86	350.94	435.85
FH-4243	66.32	44.21	84.72	67.66	360.78	472.55
VH-325	69.31	42.57	80.38	71.35	347.06	447.06
FH-114	63.64	39.39	77.80	65.30	445.00	570.00
CIM-612	65.04	41.46	84.01	75.84	350.00	422.35
CRS-2007	75.00	46.00	80.12	68.56	348.36	491.80
KZ-189	77.67	37.86	75.15	64.68	333.96	450.94
C-26	72.22	30.00	80.69	70.57	442.62	586.07
SB-149	68.42	36.84	81.50	73.30	338.33	445.00
IUB-222	70.48	41.90	77.83	69.30	393.18	570.45
MG-6	65.34	45.21	79.19	68.68	337.70	444.26
IR-901	73.27	50.50	78.21	69.86	309.09	463.64
VH-333	76.31	59.77	81.25	66.46	329.03	425.81
NIAB-824	78.94	51.47	82.83	71.86	290.12	403.70
AS-01	73.27	48.51	78.95	69.68	356.36	467.27
AGC-2	68.18	28.79	85.52	70.38	370.91	480.00
RH-647	77.08	53.13	79.09	71.60	377.08	460.42
CRS-456	75.00	52.78	86.67	68.63	373.08	446.15
AA-802	74.30	45.45	89.52	75.67	334.77	515.38
NS-131	79.44	53.27	80.65	68.43	367.92	441.51
FH-154	75.76	49.49	76.53	69.27	382.00	456.00
VH 259	63.87	53.76	82.88	73.15	335.29	452.94
CM 595	78.95	51.32	83.75	76.25	312.50	403.57
VH 295	76.00	47.00	82.35	66.08	361.11	433.33
VH 329	65.69	50.00	78.76	64.93	384.31	470.59
CM 602	75.73	50.49	80.73	66.86	370.83	510.42
AA 703	86.67	42.86	77.17	65.86	387.50	481.25
CM 622	86.32	44.21	84.72	67.66	353.85	463.46
FH 169	69.31	42.57	80.38	71.35	321.82	414.55
S 3	73.27	50.50	78.21	69.86	291.94	387.10
IR 3701	93.10	59.77	81.25	66.46	366.04	450.94

Table 9. Components of variance, broad sense heritability and genetic advance to salinity stress in the cotton seedlings.

	Sodium (ppm)					Potassium to sodium ratio				
	Absolute values			Relative values		Absolute values			Relative values	
	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹
Genotypic variance	7.11	32.13	47.78	1658.95	2841.30	7.19	0.22	0.11	4.37	2.34
Phenotypic variance	7.66	33.96	50.08	2023.69	3380.25	7.47	0.22	0.11	5.84	2.97
Heritability broad sense	92.74	94.60	95.41	81.98	84.06	96.29	98.39	98.81	74.81	78.63
Genetic advance $i=1.76$	4.49	9.65	11.82	64.54	85.52	4.61	0.82	0.57	3.16	2.37
Genetic advance %	26.60	16.02	15.15	17.78	18.19	44.35	35.07	37.05	13.88	15.80

Table 10. Components of variance, broad sense heritability and genetic advance to salinity stress in the cotton seedlings.

Component	Shoot dry weight (mg)					Root dry weight (mg)			
	Absolute values			Relative values		Absolute values			Relative values
	Control	10dSm ⁻¹	15dSm ⁻¹	10dSm ⁻¹	15dSm ⁻¹	Control	10dSm ⁻¹	15dSm ⁻¹	15dSm ⁻¹
Genotypic variance	0.004	0.003	0.002	29.575	45.730	0.0025	0.0013	0.0008	45.7300
Phenotypic variance	0.005	0.003	0.002	73.390	74.177	0.0026	0.0014	0.0009	74.1774
Heritability Broad sense	93.745	91.955	90.707	40.298	61.649	98.6824	91.8416	86.4203	61.6495
Genetic advance $i=1.76$	0.113	0.091	0.077	6.041	9.292	0.0875	0.0601	0.0459	9.2919
Genetic advance %	33.864	35.932	46.472	7.955	18.920	54.1676	50.5947	54.4528	18.9196

Discussion

The genetic variability plays an important role in the selection of genotypes under salt stress. In the salt sensitive genotypes, chlorophyll contents were poorly degraded due to accumulation of salts inside the leaves (Parida and Das 2005; Tyagi *et al.*, 2014). However, salt tolerant genotypes S-3 and MNH-888 were not much affected. It can be due to high photosynthetic rate and high dry matter presence that ensures high chlorophyll contents and high crop yield (Alzahrani *et al.*, 2019; Ismail & Horie 2017). The root and shoot length are considered primary parameters for selection against salt stress. The cotton genotypes showed reduction of root and shoot length under high salt stress (Jiang *et al.*, 2016). S-3, AA-802, MNH-888 and FH-154 were found promising lines that had minimum impact of salt stress on the root and shoot length which indicates their capability to produce more dry matter and compartmentalization of salt into the cell at various places avoiding or escaping the salt stress (Shelke *et al.*, 2017). However, the susceptible genotypes could not perform well due to limited photosynthetic activities and diversion of available photosynthates towards reducing the toxic effects of salts (Hartmann *et al.*, 2015). Root and shoot related parameters have also been taken into account for the salt screening of tomato (Alsafari *et al.*, 2019; Elkhatib *et al.*, 2017), cotton (Parihar *et al.*, 2015), chickpea (Aslam *et al.*, 2018) and grasses (Van Tran *et al.*, 2018).

Concentration of sodium inside the plant in different parts is a reliable physiological parameter for salt stress (Wang *et al.*, 2017b). High sodium accumulation disrupts various metabolic processes in the plants. The ability of plant to uptake minimum sodium ions and retain them in the root zone so that they do not disturb plant metabolic pathways signifies the salt tolerance ability of the plants (Wang *et al.*, 2017a). In our experiment, LALAZAR, S-3 and DEBAL retained the lowest amount of Na⁺ ions inside the plants, whereas, MNH-888 and C-26 absorbed high amount of sodium ions inside their bodies and regarded as salt sensitive genotypes. High sodium concentration can be developed in the growing material due to lower efficiency of exclusion mechanisms or diffusion through damaged membranes (Wang *et al.*,

2017a). Overall, salinity stress reduced the growth of all traits in the experiment and this reduction of growth can be referred to ionic toxicity of sodium ions in the cell cytoplasm, water shortage in the plant due to the difference of osmotic pressure and ion imbalance or the combination of all above stated factors (Liu *et al.*, 2017).

Expected broad sense heritability was found moderate to high for the traits under both levels of salt stress that showed most of the characters were genetically controlled. Heritability estimates increased with the increase of salt stress might be a result of greater genetic variation due to expression of genes associated with salinity tolerance and a smaller environmental variation (Salam *et al.*, 2011). It can be further argued that hidden genetic variation, previously unselected, could be uncovered when stress is applied, thus possibly increasing heritability (Ali *et al.*, 2007). The genotypes that performed best for a given trait which had high broad sense heritability were regarded as salt tolerant genotypes whereas the genotypes that performed poor for the traits were regarded as salt sensitive genotypes. The substantially greater phenotypic variance pointed out a masking effect of the environment which may make genetic improvement through selection problematic. Genetic advance was low for most of the traits. It showed that the characters are controlled by dominant genes and selection for these traits will not be effective to have successful breeding program against salt stress (Nabi *et al.*, 2010). Besides cotton these kind of findings have been reported in tomato (Rivero *et al.* 2014), soybean (Shelke *et al.*, 2017) and wheat (Jan *et al.*, 2017).

Conclusion

The present study explored the genetic diversity of cotton germplasm for its ability to cope up salt stress. Increase in salt stress negatively effects the cotton yield and disturbs the metabolic activities inside the plant cells. The findings suggest that rigorous and careful selection is needed to be made for selection against salt tolerance. It also validates that these physiological parameters can be used for the screening and development of salt tolerant genotypes. These genotypes are precious resources to be used in breeding program aimed at increasing salt tolerance.

Table 11. Percent change in the Potassium-Sodium ratio of 50 genotypes grown in two levels of salt stress.

Genotypes	K/Na	
	10dSm ⁻¹	15dSm ⁻¹
FH-458	23.33	15.51
BS-80	24.05	15.44
MUBARAK	26.14	16.64
DEBAL	22.46	15.86
KEHKSHAN	23.99	15.01
LALAZAR	27.23	17.91
FH-312	20.56	13.39
FH-444	23.91	16.40
MNH-888	20.35	13.05
FH-173	24.67	16.12
FH-113	26.79	18.89
FH-177	22.76	15.22
FH-187	20.45	13.77
FH-171	21.72	13.07
MNH-988	16.97	13.21
FH-170	25.26	14.34
MNH-992	21.13	14.81
FH-142	22.50	16.04
FH-118	23.79	14.74
FH-941	21.94	15.08
FH-4243	23.44	14.29
VH-325	23.12	15.93
FH-114	22.51	14.49
CIM-612	18.63	13.00
CRS-2007	22.99	13.93
KZ-189	22.40	14.29
C-26	23.54	16.18
SB-149	19.04	16.43
IUB-222	19.78	12.13
MG-6	23.44	15.46
IR-901	25.31	15.06
VH-333	24.71	15.61
NIAB-824	26.23	18.26
AS-01	22.05	14.84
AGC-2	22.96	14.59
RH-647	20.95	15.52
CRS-456	23.21	15.37
AA-802	24.02	12.30
NS-131	21.91	15.49
FH-154	20.02	15.18
VH 259	24.67	16.12
CM 595	23.79	16.89
VH 295	22.76	15.22
VH 329	20.45	13.77
CM 602	21.72	13.07
AA 703	21.94	15.08
CM 622	23.44	14.29
FH 169	23.12	15.93
S 3	20.95	12.70
IR 3701	23.21	12.32

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