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Discrimination of Salt Tolerant and Susceptible Cotton Genotypes at Seedling Stage using Selection Index

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ABSTRACT

This research work was planned to screen a part of cotton germplasm to find out their salt tolerance potential at seedling stage measuring root length, shoot length, root fresh weight, root dry weight, root dry weight and shoot dry weight. A control and two levels of NaCl (10 & 20 dS m^{-1}) and 50 cotton genotypes in completely randomized design were used. Data indicated that there was significant reduction in all seedling traits. It was also observed that 24 genotypes could not show even emergence at 20 dS m^{-1} salinity level. Moderate to high genetic variability was observed in all traits at all levels of salinity except at relative salinity of 10 dS m^{-1}. High heritability and high genetic advance was also found for most of the traits. Some genotypes were ranked top on the basis of root length, while others performed well on the basis of shoot dry weight. Thus, to get rid of this complication, selection index was performed by giving an equal weight to all the seedling traits studied. As a result, top 6 genotypes (NIAB-999, CIM-707, NIAB-78, MNH-93, CIM-446 & CIM-443) performing well at 20 dS m^{-1} were declared salt tolerant. © 2011 Friends Science Publishers

Key Words: Upland cotton; Salt stress; Component of variance; Heritability; Genetic advance; Selection index

INTRODUCTION

Drought and salinity are two mains causes of crop yield losses throughout the globe. Salinity will result in up to 30% land deterioration in coming 25 years and 50% up to 2050 (Wang *et al.*, 2003). It has been estimated that more than 800 million hectare (Mha) of world lands are affected by both saline and sodic conditions, which covers almost 6% of the total world area. In Iran, Egypt, Argentina and Pakistan, 23.8, 8.7, 33.1 and 10.0 Mha, respectively are badly affected by salinity, comprising of 14.6, 8.7, 13.9 and 12.9% of country land (FAO, 2008). Presence of toxic ions in the plant system cause many negative impacts on plant growth and development due to 3 main phenomenon: (1). Low water potential of root environment resulting in water shortage in the plants, (2). Toxicity due to Na+ and Cl- ions, and (3). Imbalance in the plant nutrition due to decreased nutrient uptake and transport to the above ground portion of the plants (Munns & Tester, 2008).

Pakistan is basically an agricultural dominant country as here agriculture is the vital to country's economy, accounting a share of 23% in GDP and employing 44% of the labor force. At present, Pakistan is facing a severe problem in national food security because of loss of precious arable land caused by drought, water logging and salinity. It is estimated that every day, approximately 500 acres of farm land is taken out of agriculture due to expansion of roads, factories, urbanization. According to Qureshi and Barrett-Lennard (1998), approximately 6.3×10^6 of irrigated land has been severely affected due to salinity, resulting in low agricultural productivity. These salt affected areas result in a loss of Rs 20 billion every year (Qayyum & Malik, 1988).

As a cash crop, cotton accounts for 8.6% of value added commodity in agriculture sector and 1.6% to overall GDP of the country (Anonymous, 2010). Having promising share in fiber and oil production, cotton is rightly called "Silver Fibre" crop of Pakistan. It has been revealed that Pakistan is the 4th largest producer (10.5 m metric tons) and 3rd largest consumer (11.4 m metric tons) of seed cotton (ASA, 2010). In 2009, the cotton crop was sown in the country on an area of 3.1 Mha with production of 12.7 million bales, comprising per unit yield of 695 Kg/ha (Anonymous, 2010). Still average national yield is very far lower than obtained in other countries. Although, the cotton crop had been declared fairly salt tolerant crop at vegetative stage (Maas & Hoffman, 1977; Maas, 1986), its low germination along with abnormal growth at seedling stage appealed the cotton breeders to enrich a salt tolerance characteristics in it, resulting in more seed-cotton yield than the existing cultivars (Ali *et al.*, 2005).

Pakistani saline soils contain a mixture of different salts (Sandhu & Qureshi, 1986). Various earlier researchers have suggested the development of salt tolerant cultivars

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either through conventional techniques of plant breeding or through non-conventional techniques of molecular biology (Shannon, 1985; Flowers & Yeo, 1995; Khan *et al.*, 2001). For the evolution of salt tolerant cotton varieties, the presence of genetic variability is a pre-requisite. Earlier findings of various researchers suggested the presence of sufficient variation in various crop species e.g., in cotton (Ashraf & Ahmad, 2000; Noor *et al.*, 2001; Bhatti & Azhar, 2002), in maize (Khan & McNeilly, 2005), in tomato (Shaaban *et al.*, 2004) and in sorghum (Azhar & McNeilly, 2001). Thus, improving seed cotton yield against salt stress is a very essential practice of cotton researchers and a regular screening of available germplasm is need of the time because of (1) fast spreading saline areas with increasing salinity toxicity and (2) deterioration in genetic makeup of already salt tolerant genotypes due to natural mutation and segregation.

For starting breeding program against salt stress, information about the parental material to be used for hybridization is mandatory. Thus, the research work was planned to screen a part (available at the department) of cotton germplasm to find out their salt tolerance potential.

MATERIALS AND METHODS

The screening experiment was conducted in the glass house of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during January-February, 2009. The standard procedure was followed for developing a salinity concentration of 10, 20 and 30 dS m^{-1} by mixing calculated amount of table salt (NaCl) in normal field soil, while normal field soil (ECe=2.3 dS m^{-1}) without any mixing of table salt was considered as control level treatment. Hence experiment comprises of 4 treatments. (1). Polythene bags were filled with a soil of required ECe followed by irrigation. Seven undelinted seeds from each of 50 genotypes were sown to get a minimum of 5 plants per bag. The experiment was laid out in 2 factors (accessions & salinity concentration) completely randomized design in triplicated fashion in such a way that each polythene bag represented one experimental unit and thus, total 150 polythene bags were used in each treatment. No sign of insect-pest damage was noticed, while small weeds were removed with hands. No emergence was observed for any genotypes even in any replication at highest level of salinity 30 dS m^{-1}, so it was skipped from the statistical analysis. Light irrigation was applied to the seedling grown in polythene bags as the soil surface appeared dry and seedlings were raised till 40 days of sowing. The data of seedling traits like root and shoot length, root and shoot fresh and dry weight were recorded after 40 days of sowing.

Five seedlings from each polythene bag were uprooted and washed with tap water. Clean and blotted dry seedlings were dissected at the point of cotyledonary node to separate shoot and root. Length of shoots and roots of five seedlings was measured and fresh weight taken immediately. Shoots and roots were separately packed in a labeled kraft paper bag, placed in an oven at 70°C for 48 h and dry weights of roots and shoots taken.

Both absolute and relative means of each trait were used for the statistical analysis. Analysis of variance (ANOVA) was performed and means comparisons were made by Least Significant Difference (LSD) test at 5% probability value (Gomez & Gomez, 1984). The whole analysis was performed in Statistix® 8.1 statistical software. One-way analysis of variance separately for control and salinity level (10 & 20 dS m^{-1}) was performed to get valuable information about the differences among the genotypes. Coefficient of phenotypic (PCV) and genotypic variance (GCV) and genetic advance as percentage of mean were classified as suggested by Singh and Narayanan (2000). Broad-sense heritability was calculated with the formula of Lush (1940). Selection index (Smith, 1936) based on the equal weight of all seedling traits was calculated and the genetic similarities within the tolerant and susceptible genotypes selected on the basis of selection index score, were determined by cluster analysis.

RESULTS AND DISCUSSION

Mean squares for absolute and relative salt tolerance revealed highly significant differences ($P>0.01$) among genotypes, salinity levels and significant accession×concentration interactions for root and shoot length, fresh and dry weights Highly significantly reduction in germination of cotton varieties was noted at 10 dS m^{-1} under salinity stress in saline germination medium. Twenty four out of 50 genotypes showed no emergence at 20 dS m^{-1}. Decreased emergence in salt susceptible genotypes was caused by low accumulation of K^+, Ca^{2+} and NO_3^- in the cells due to damaging effect of Na^+ and Cl^- (Singh *et al.*, 2000; Ali *et al.*, 2005 & 2007). Mean data of 50 genotypes indicated significant reductions in all seedling traits of plants with increased salinity stress (data not shown). High concentration of ions in the rooting medium caused a reduction in root length at both salinity levels. Root permeability for water uptake decreases at increased salinity and Ca^{2+} displacements from the plasmalemma takes place causing a reduction in root length (Khan *et al.*, 2001; Saqib *et al.*, 2002). The reduction in shoot length may be due to toxic effects of Na^+ and Cl^- on the metabolic pathways, which in turn produce some sticky material on the cell walls, causing a decrease in cell elasticity and cell expansion. As a result, new cells created quickly and shoot remained dwarf (Ashraf, 2002).

The decreasing trend of shoot fresh weight in this study appears to be due to increased uptake of excessive salts, which are assigned to reduction in stored or newly produced photosynthates and less uptake of water (Yeo & Flowers, 1984; Qadir & Shams, 1997; Saqib *et al.*, 2002). Reduction in root fresh weight was attributed to decreased

Table I: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for root length under salt stress

Source of Variations	Absolute root length (mm)			Relative root length (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	147.31	108.42	38.59	73.04	23.87
Minimum	122.01	79.53	0.00	65.12	0.00
Maximum	190.48	154.79	98.99	81.19	51.87
Variance	307.89	375.52	1471.47	18.35	542.46
CV %	11.91	17.87	99.39	5.86	97.58
Environmental variance	61.61	72.31	36.60	3.75	4.82
Genotypic variance	287.36	351.42	1459.27	17.10	540.86
Phenotypic variance	348.96	423.72	1495.87	20.85	545.68
Environmental coefficient of variance %	5.33	7.84	15.68	2.65	9.20
Genotypic coefficient of variance %	11.51	17.29	98.98	5.66	97.44
Phenotypic coefficient of variance	12.68	18.99	100.22	6.25	97.87
Heritability % (broad-sense)	82.35	82.93	97.55	82.02	99.12
Genetic advance (i=10%=1.76)	27.07	30.05	66.41	6.59	40.75
Genetic advance as % of mean	18.38	27.71	172.06	9.02	170.73

Table II: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for shoot length under salt stress

Source of Variations	Absolute shoot length (mm)			Relative shoot length (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	210.23	163.13	56.65	77.01	24.35
Minimum	162.90	114.05	0.00	69.94	0.00
Maximum	260.93	220.69	133.94	84.49	51.29
Standard Deviation	26.49	28.96	55.55	4.13	23.69
CV (%)	12.60	17.75	98.06	5.37	97.29
Environmental variance	58.35	202.66	31.92	18.43	1.49
Genotypic variance	682.44	770.92	3075.57	10.93	560.50
Phenotypic variance	740.79	973.58	3107.48	29.36	561.99
Environmental coefficient of variance (%)	3.63	8.73	9.97	5.58	5.01
Genotypic coefficient of variance (%)	12.43	17.02	97.89	4.29	97.24
Phenotypic coefficient of variance	12.95	19.13	98.40	7.04	97.37
Broad-sense heritability (%)	92.12	79.18	98.97	37.22	99.74
Genetic advance (i=10%=1.76)	44.13	43.48	97.10	3.55	41.61
Genetic advance as % of mean	20.99	26.66	171.40	4.61	170.92

Table III: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for root fresh weight under salt stress

Source of Variations	Absolute root fresh weight (mg)			Relative root fresh weight (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	1939.79	1643.19	643.90	81.27	30.13
Count	50.00	50.00	50.00	50.00	50.00
Minimum	1658.52	1299.07	0.00	75.32	0.00
Maximum	2157.96	1948.98	1404.47	86.85	62.61
Standard Deviation	138.06	173.07	629.72	2.86	29.35
CV %	7.12	10.53	97.80	3.52	97.44
Environmental variance	6655.54	30449.93	7251.59	18.51	3.33
Genotypic variance	16841.70	19804.78	394133.73	2.03	860.59
Phenotypic variance	23497.24	50254.71	401385.33	20.55	863.92
Environmental coefficient of variance %	4.21	10.62	13.23	5.29	6.06
Genotypic coefficient of variance %	6.69	8.56	97.50	1.75	97.38
Phenotypic coefficient of variance	7.90	13.64	98.39	5.58	97.57
Heritability % (broad-sense)	71.68	39.41	98.19	9.90	99.61
Genetic advance (i=10%=1.76)	193.37	155.49	1094.90	0.79	51.53
Genetic advance as % of mean	9.97	9.46	170.04	0.97	171.06

osmotic potential at root surface causing low water uptake (Terry & Waldron, 1984), toxicity of salts and unavailability of essential nutrients (Levitt, 1980; Brugnoli & Lauter, 1991). The decreased root dry weight was also due to toxicity of salts and decreased availability and transportation of photosynthetic materials to the roots in growing medium. Shoot dry weight had also shown significant variation among all the genotypes and it showed reducing trend with increasing salinity. Other causes of decreased shoot dry weight were the shortage of essential nutrients (Ashraf, 2002).

Components of variance, heritability and genetic

Table IV: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for shoot fresh weight under salt stress

Source of Variations	Absolute shoot fresh weight (g)			Relative shoot fresh weight (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	2273.730	1494.107	595.732	65.203	24.292
Count	50.00	50.00	50.00	50.00	50.00
Minimum	1948.43	1121.57	0.00	57.52	0.00
Maximum	2881.97	2193.70	1505.71	76.05	52.32
Standard Deviation	242.47	266.38	591.81	4.50	23.68
CV %	10.66	17.83	99.34	6.91	97.47
Environmental variance	9932.189	13188.180	225.299	5.553	3.191
Genotypic variance	55483.116	66561.858	350160.670	18.432	559.579
Phenotypic variance	65415.305	79750.038	350385.970	23.984	562.769
Environmental coefficient of variance %	4.383	7.686	2.520	3.614	7.353
Genotypic coefficient of variance %	10.360	17.268	99.331	6.584	97.380
Phenotypic coefficient of variance	11.249	18.901	99.362	7.511	97.657
Heritability % (broad-sense)	84.817	83.463	99.936	76.849	99.433
Genetic advance (i=10%=1.76)	381.798	414.832	1041.134	6.624	41.515
Genetic advance as % of mean	16.792	27.765	174.766	10.159	170.902

Table V: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for root dry weight under salt stress

Source of Variations	Absolute root dry weight (mg)			Relative root dry weight (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	253.68	176.43	78.93	68.97	27.89
Minimum	207.14	121.84	0.00	58.94	0.00
Maximum	367.53	291.64	215.13	79.52	58.56
Standard Deviation	41.05	41.57	79.55	5.08	27.17
CV %	16.18	23.57	100.78	7.37	97.42
Environmental variance	204.62	26.70	35.89	18.65	1.05
Genotypic variance	1616.63	1719.58	6316.23	19.61	737.83
Phenotypic variance	1821.25	1746.28	6352.12	38.25	738.88
Environmental coefficient of variance %	5.64	2.93	7.59	6.26	3.68
Genotypic coefficient of variance %	15.85	23.50	100.69	6.42	97.40
Phenotypic coefficient of variance	16.82	23.69	100.97	8.97	97.46
Heritability % (broad-sense)	88.76	98.47	99.44	51.25	99.86
Genetic advance (i=10%=1.76)	66.67	72.42	139.48	5.58	47.77
Genetic advance as % of mean	26.28	41.05	176.70	8.09	171.29

Table VI: Components of variance, heritability and genetic advance estimates of 50 cotton genotypes for shoot dry weight (g) under salt stress

Source of Variations	Absolute shoot dry weight (mg)			Relative shoot dry weight (%)	
	Control	10 dS m^{-1}	20 dS m^{-1}	10 dS m^{-1}	20 dS m^{-1}
Grand mean of trait	377.25	291.55	98.92	76.89	24.61
Count	50.00	50.00	50.00	50.00	50.00
Minimum	336.82	243.44	0.00	72.17	0.00
Maximum	476.35	402.23	249.77	84.32	52.54
Standard Deviation	35.78	40.30	97.99	3.10	23.96
CV %	9.48	13.82	99.06	4.04	97.36
Environmental variance	741.51	910.35	18.68	7.70	2.22
Genotypic variance	1032.78	1320.61	9595.80	7.07	573.31
Phenotypic variance	1774.30	2230.95	9614.48	14.77	575.53
Environmental coefficient of variance %	7.22	10.35	4.37	3.61	6.05
Genotypic coefficient of variance %	8.52	12.46	99.02	3.46	97.30
Phenotypic coefficient of variance	11.17	16.20	99.12	5.00	97.49
Heritability % (broad-sense)	58.21	59.19	99.81	47.89	99.61
Genetic advance (i=10%=1.76)	43.15	49.21	172.24	3.24	42.06
Genetic advance as % of mean	11.44	16.88	174.11	4.21	170.92

advance estimates have been presented in the Tables I−VI. The lowest value of genotypic and phenotypic coefficient of variance at 10 dS m^{-1} revealed the existence of very low variability for most of the traits. However, the highest genotypic and phenotypic variance along with lowest environmental variance was evident at 20 dS m^{-1}. This showed that variance at 20 dS m^{-1} is genetically determined and selection at all level of salinity stress for seedling traits may be possible. Similarly, high heritability along with high genetic advance at 20 dS m^{-1} suggested that selection is

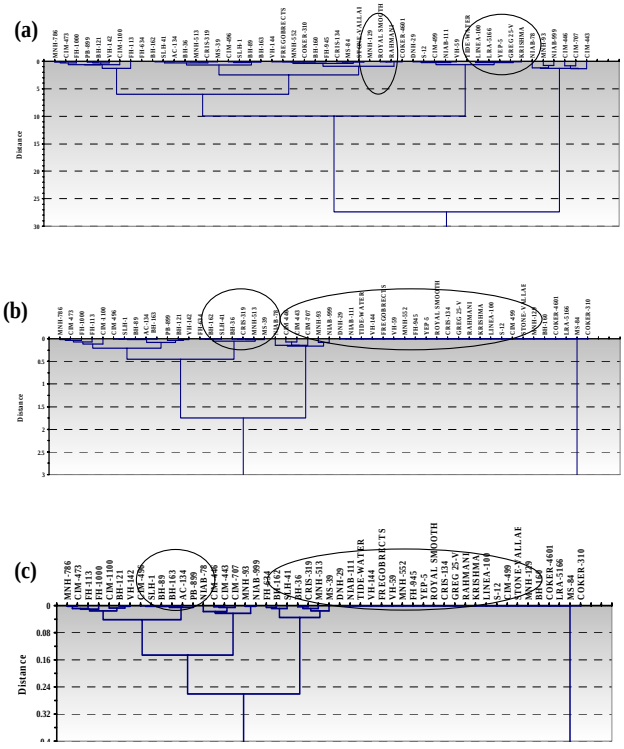
Table VII: Ranking of 50-Cotton accession on the basis of selection index at 20 dS m^{-1}

Absolute Control		Absolute salinity (20 dS m^{-1})		Relative salinity (20 dS m^{-1})	
Accessions	**Index**	**Accessions**	**Index**	**Accessions**	**Index**
NIAB-78	1.000	NIAB-78	1.000	NIAB-999	1.000
CIM-707	0.945	CIM-707	0.967	CIM-707	0.970
NIAB-999	0.935	NIAB-999	0.959	NIAB-78	0.965
CIM-446	0.910	CIM-446	0.950	CIM-443	0.951
MNH-93	0.908	CIM-443	0.948	MNH-93	0.950
CIM-443	0.900	MNH-93	0.948	CIM-446	0.913
FH-113	0.707	CIM-473	0.846	MNH-786	0.778
CIM-473	0.682	FH-113	0.844	CIM-473	0.767
FH-1000	0.680	MNH-786	0.842	FH-1000	0.765
MNH-786	0.677	FH-1000	0.839	FH-113	0.763
CIM-1100	0.623	CIM-1100	0.809	BH-121	0.709
VH-142	0.614	BH-121	0.801	CIM-1100	0.700
BH-121	0.609	VH-142	0.801	VH-142	0.694
PB-899	0.574	PB-899	0.778	BH-89	0.662
BH-89	0.532	BH-89	0.757	SLH-1	0.633
CIM-496	0.520	CIM-496	0.753	CIM-496	0.624
BH-163	0.505	BH-163	0.748	PB-899	0.618
SLH-1	0.505	SLH-1	0.747	AC-134	0.617
AC-134	0.471	AC-134	0.734	BH-162	0.601
FH-634	0.449	BH-162	0.706	BH-163	0.569
BH-162	0.446	FH-634	0.704	SLH-41	0.567
SLH-41	0.444	SLH-41	0.700	FH-634	0.557
MNH-513	0.406	MNH-513	0.666	CRIS-319	0.512
BH-36	0.401	BH-36	0.665	BH-36	0.503
CRIS-319	0.400	CRIS-319	0.664	MNH-513	0.502
MS-39	0.390	MS-39	0.662	MS-39	0.497
VH-144	0.359	FH-945	0.000	FH-945	0.000
FH-945	0.346	GREG 25-V	0.000	GREG 25-V	0.000
MNH-552	0.339	RAHMANI	0.000	RAHMANI	0.000
COKER-310	0.326	YEP-5	0.000	YEP-5	0.000
FREGOBRECTS	0.324	FREGOBRECTS	0.000	FREGOBRECTS	0.000
BH-160	0.320	KRISHMA	0.000	KRISHMA	0.000
MS-84	0.294	TIDE-WATER	0.000	TIDE-WATER	0.000
CRIS-134	0.286	LINEA-100	0.000	LINEA-100	0.000
STONEVALLAE	0.255	MNH-552	0.000	MNH-552	0.000
MNH-129	0.251	DNH-29	0.000	DNH-29	0.000
COKER-4601	0.226	VH-59	0.000	VH-59	0.000
RAHMANI	0.197	ROYAL SMOOTH	0.000	ROYAL SMOOTH	0.000
ROYAL SMOOTH	0.190	CRIS-134	0.000	CRIS-134	0.000
KRISHMA	0.156	COKER-310	0.000	COKER-310	0.000
GREG 25-V	0.143	STONEVALLAE	0.000	STONEVALLAE	0.000
YEP-5	0.136	MNH-129	0.000	MNH-129	0.000
LRA-5166	0.103	BH-160	0.000	BH-160	0.000
LINEA-100	0.099	VH-144	0.000	VH-144	0.000
TIDE-WATER	0.084	COKER-4601	0.000	COKER-4601	0.000
DNH-29	0.062	LRA-5166	0.000	LRA-5166	0.000
VH-59	0.044	MS-84	0.000	MS-84	0.000
S-12	0.035	S-12	0.000	S-12	0.000
NIAB-111	0.029	CIM-499	0.000	CIM-499	0.000
CIM-499	0.026	NIAB-111	0.000	NIAB-111	0.000

effective at this level in improving these seedling traits, because of presence of additive type of gene action. Selection at other levels may be misleading due to presence of non-additive type of gene action as low heritability and genetic advance values were obtained. For making any improvement in salt tolerance at seedling stage or even at higher stage, the presence of heritable variation is a key to success. Without any genotypic variability, selection practice can not be performed. Similarly, high heritability and high genetic advance were also found for all traits except root fresh weight (Tables I−VI). Intra-specific and intra-varietals variability has been previously reported in cotton (Bhatti & Azhar, 2002; Azhar *et al.*, 2007; Hanif *et al.*, 2008).

For the selection of salt tolerant genotypes, selection index was prepared at 20 dS m^{-1} by utilizing the both absolute and relative means because of presence of huge variability at this level (Table VII). Data indicated that NIAB-78 occupied the top rank at absolute salinity of 20 dS m^{-1} while NIAB-999 showed overall best performance at relative salinity of 20 dS m^{-1}. Similarly, 24 varieties that could not emerge were at the bottom of relection index. Thus, top 6 varieties on the basis of selection index at 20 dS m^{-1} were selected due to their best performance at increased

Fig. 1: Cluster analysis of 50 cotton accessions for seedling traits at (a) control, (b) absolute values and (c) relative values of 20 dS m^{-1} NaCl



salinity stress. There was also observed significantly positive correlation among all seedling traits (data not presented here). Different genotypes occupied variable rank for all traits at all salts levels. For example, MNH-93 showed longest root length followed by NIAB-78 but CIM-446 produced highest shoot dry weight followed by CIM-707. Thus, making selection on this material is very difficult and many complications may results. Earlier researchers used one or two traits as a criteria for selection of tolerant or susceptible genotypes to avoid confusion and complication e.g., root and shoot length (Bhatti & Azhar, 2002), root and shoot fresh and dry weight (Azhar *et al.*, 2007; Hanif *et al.*, 2008). However, in the present study, selection criteria were based on 6 seedling traits studied and those genotypes were selected, which performed well on the basis of all seedling traits.

For finding the similarity among 6 genotypes, dendrogram was prepared using the mean performance at all seedling traits through 'win-stat' software. The cluster analysis indicated that the above 6 genotypes selected were in one group, while the 24 genotypes were in other group (Fig. 1).

Although, screening of salt tolerant genotypes was made at seedling stage in polythene bags but the positive correlation between seedlings traits and yield contributing traits in the earlier research findings (Salam *et al.*, 1999; Bhatti & Azhar, 2002) suggested that selection was effective. The genotypes selected at seedling traits were also salt tolerant in earlier experiments. NIAB-78 has been declared as a salt tolerant in many earlier findings (Khan *et al.*, 1995; Ashraf & Ahmad, 2000). The salt tolerant lines CIM-707 and NIAB-999 (in this experiment) also proved its consistency in earlier salinity stress experiments at 25 and 36.1 dS m^{-1} under naturally salt affected fields (Ali *et al.*, 2005). In other study, the genotype MNH-93 remained runner up for salt tolerance followed by NIAB-78 under salinity stress imposed until flower initiation (Qadir & Shams, 1997). Similarly, the genotype CIM-446 also exhibited salt tolerance in earlier experiments (Saqib *et al.*, 2002).

CONCLUSION

On the basis of selection index and cluster analysis, top 6 genotypes (NIAB-999, CIM-707, NIAB-78, CIM-443, MNH-93 & CIM-446) showed best performance at absolute and relative salinity of 20 dS m^{-1} were declared as salt tolerant and used as a female parent (line) in line×tester mating design (being submitted through other manuscript). However, the bottom three genotypes (S-12, CIM-499 & NIAB-111), which exhibited very poor performance were selected as salt susceptible and used as male parent (tester) for hybridization with above selected salt tolerant lines.

REFERENCES

Aceves, N.E., L.H. Stolzy and G.R. Mehyus, 1975. Effect of soil osmotic potential produced with two salt species on plant water potential, growth and grain yield of wheat. *Plant Soil*, 42: 619–627

Ali, Z., A.S. Khan, I.A. Khan and F.M. Azhar, 2005. Heritability (h^2 b) estimates for NaCl tolerance in wheat (*Triticum aestivum* L.). *J. Agri. Soc. Sci.*, 1: 126–128

Ali, Z., A. Salam, F.M. Azhar and I.A. Khan, 2007. Genotypic variation in salinity tolerance among spring and winter wheat (*Triticum aestivum* L.) accessions. *South African J. Bot.*, 73: 70–75

Anonymous, 2010. *Economic Survey of Pakistan. 2009-2010*. Govt. of Pakistan, Finance Division, Economic Advisory Wing, Islamabad, Pakistan

ASA, 2010. *Cotton Market Monthly Economic Letter May 12, 2010*. Available online at http://www.cottoninc.com/MarketInformation/MonthlyEconomicLetter/#5American cotton association, newsletter, Accessed 6 June, 2010

Ashraf, M. and S. Ahmad, 2000. Influence of sodium chloride on ion accumulation, yield components and fibre characteristics in salt-tolerant and salt-sensitive lines of cotton (*Gossypium hirsutum* L). *Field Crop. Res.*, 66: 115–127

Ashraf, M., 2002. Salt tolerance of cotton: Some new advances. *Crit. Rev. Plant Sci.*, 21: 1–30

Azhar, F.M., A.A. Khan and N. Saleem, 2007. Genetic mechanisms controlling salt tolerance In *Gossypium hirsutum* L. Seedlings. *Pakistan J. Bot.*, 39: 115–121

Azhar, F.M. and T. McNeilly, 2001. Compartmentation of Na^+ and Cl^- ions in different parts of *Sorghum bicolor* (L.) moench during plant development. *Pakistan J. Bot.*, 33: 101–107

Bhatti, M.A. and F.M. Azhar, 2002. Salt tolerance of nine *Gossypium hirsutum* L. varieties to NaCl salinity at early stage of plant development. *Int. J. Agric. Biol.*, 4: 544–546

FAO, 2008. *FAO Land and Plant Nutrition Management Service.* Available online at: http://www.fao.org/ag/agl/agll/spush/. Accessed 25 April 2008

Flowers, T.J. and A.R. Yeo, 1995. Breeding for salinity resistance in crop plants; where next. *Australian J. Plant Physiol.*, 22: 875–884

Gomez, K.A. and A.A. Gomez, 1984. *Statistical Procedures for Agricultural Research,* 2nd edition, pp: 467–469. John Wiley and Sons, New York, Chichester, Brisbane and Singapore

Hanif, M., E. Noor, N. Murtaza, A. Qayyum and W. Malik, 2008. Assessment of variability for salt tolerance at seedling stage in *Gossypium hirsutum* L. *J. Food Agric. Environ.*, 6: 134–138

Kent, L.A. and A. Lauchli, 1985. Germination and seedling growth of cotton: salinity calcium interactions. *Plant Cell Environ.,* 8: 115–159

Khan, A.A. and T. McNeilly, 2005. Triple test cross analysis for salinity tolerance based upon seedling root length in maize (*Zea mays* L.). *Breed. Sci.*, 55: 321–325

Khan, A.A., T. McNeilly and F.M. Azhar, 2001. Stress tolerance in crop plants. *Int. J. Agric. Biol.,* 3: 250–255

Khan, A.N., R.H. Qureshi, N. Ahmad and A. Rashid, 1995. Response of cotton cultivars to salinity in various growth development stages. *Sarhad J. Agric.*, 11: 729–731

Levitt, J., 1980. *Response of Plants to Environmental Stresses*, Vol. 2, 2nd edition. water, radiation, salt and other stresses. Academic Press, New York

Lush, J.L., 1940. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *American Soc. Anim. Prod. Proc.*, 33: 293–301

Maas, E.V. and G.J. Hoffman, 1977. Crop salt tolerance-current assessment. *J. Irrig. Drain. Div. Civ. Eng.*, 103: 115–134

Maas, E.V., 1986. Salt tolerance of plants. *Appl. Agric. Res.*, 1: 12–26

Munns, R. and M. Tester, 2008. Mechanisms of Salinity Tolerance. *Annu. Rev. Plant Biol.*, 59: 651–681

Noor, E., F.M. Azhar and A.A. Khan, 2001. Diffeerences in responses of *Gossypium hirsutum* L. varieties to NaCl salinity at seedling stage. *Int. J. Agric. Biol.*, 3: 345–347

Qadir, M. and M. Shams, 1997. Some agronomic and physiological aspects of salt tolerance in cotton (Gossypium hirsutum L.). *J. Agron. Crop Sci.*, 179: 101–106

Qayyum, M.A. and D. Malik, 1988. Farm production losses in salt affected soils. *In: Managing Soil Resources Proc. 1st. Nat. Cong on Soil Sci., Oct: 6-8, 1985*, pp: 356–364. Lahore, Pakistan

Qureshi, R.H. and E.G. Barrett-Lennard, 1998. *Saline Agriculture for Irrigated Land in Pakistan*, p: 142. A Handbook. ACIAR Monograph No. 50, Canberra, Australia

Salam, A., P.A. Hollington, J. Gorham, R.G. Wyn Jones and C. Gliddon, 1999. Physiological genetics of salt tolerance in (*Triticum aestivum* L): Performance of wheat varieties, inbred lines and reciprocal F1 hybrids under saline conditions. *J. Agron. Crop Sci.*, 183: 145–156

Sandhu, G.R. and R.H. Qureshi, 1986. Salt affected soils of Pakistan and their utilization. *Proc. Rev. Res.*, 5: 106

Saqib, M., J. Akhtar, S. Pervaiz, R.H. Qureshi and M. Aslam, 2002. Comparative growth performance of five cotton (*Gossypium hirsutum* L.) genotypes against different levels of salinity. *Pakistan J. Agric. Sci.*, 39: 69–75

Shaaban, M.M., M.M. El-Fouly and El-Zanaty, 2004. Halophytes and Foliar Fertilization as a useful technique for growing processing tomatoes in the Saline Affected soils. *Pakistan J. Biol. Sci.,* 7: 503–507

Shannon, M.C., 1985. Principles and strategies in breeding for high salt tolerance. *Plant Soil*, 89: 227–241

Singh, A.K., V. Prakash and E.R.D. Sastry, 2000. *Effect of Salinity Stress on Seed Germination Seeding Growth of Wheat*, pp: 96–98. Agricultural Science-Digest, India

Singh, P. and S.S. Narayanan, 2000. *Biometrical Techniques in Plant Breeding*, 2nd edition. Kalyani Publication Ludhiana, India

Smith, H.F., 1936. A discriminant function of plant selection. *Ann. Eugenics*, 7: 240–250

Terry, N. and L.J. Waldron, 1984. Salinity, photosynthesis, and leaf growth. *California Agric.*, 38: 38–39

Wang, W., B. Vinocur and A. Altman, 2003. Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. *Planta*, 218: 1–14

Yeo, A.R. and T.J. Flowers, 1984 Mechanisms of salinity resistance in rice and their role as physiological criteria in plant breeding. *In*: Staples, R.C. and G.H. Toenniessen (eds.), *Salinity Tolerance in Plants*, pp: 151–170. Strategies for Crop Improvement, John Wiley and Sons, New York

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