Full Length Article

Combining Ability Analysis and Genetic Inheritance of Salt Tolerance Indicators in Maize (*Zea mays*) Following Diallel Mating Design

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Abstract

Saline soils are the source of severe abiotic stress, which hinders crop productivity. To compete the challenges of food security for rapidly growing population of the world, it is necessary to utilize marginal lands for cultivation by developing saline adapted varieties. Total six elite maize lines were used as parents following diallel mating design. Resultantly 30 F_1s were generated. Data were recorded for different adaptability indicators under saline environments in maize. Differences among mean squares for general combining ability (GCA), specific combining ability (SCA) and reciprocal effects for all the indicators were highly significant. Root length, shoot length, Na^+ and K^+ ion contents were governed by non-additive type of gene action whereas; leaf area was controlled by additive gene action. Under different saline environments, better adaptability level regarding GCA, SCA and their reciprocal effects were indicated in maize genotypes L7-2, OH-41 and WFTMS. The cross Q67 × L7-2 exhibited comparatively highest level of adaptability regarding SCA effects under saline environments. For reciprocal effects maize genotypes L7-2, Q67, OH-41 and WFTMS could be used in different crossing combinations for the development of maize hybrids adapted to different saline environments. © 2015 Friends Science Publishers

Keywords: Maize; Adaptability; Gene action; Saline environment; Griffing's approach

Introduction

Maize is an important cereal all around the world. Each and every part of maize plant is used either in food or in non-food products. It ranked third on the basis of production and consumption among cereals after wheat and rice. Its seed comprises of high nutritive value i.e., 72% starch, 17% ash, 10% protein, 8.5% fiber, 4.8% oil and 3% sugar (Ahsan *et al.*, 2007). In Pakistan the leading producers in maize are Punjab and Khyber Pakhtunkhwan (KPK) provinces.

Soil salinity is one of the most critical abiotic stresses widely distributed in the world. Globally about 20% irrigated land is salt affected (Prochazkova *et al.,* 2013). Almost 12 billion US$ are the estimated losses in world's irrigated land due to salinity (Zahoor *et al.,* 2011). Total area of Pakistan is 80 million hectares out of which salt affected soils are 6.30 million hectares and it is increasing at the rate of about 40,000 ha annually (Nawaz, 2007). Different crops are differentially affected by salinity stress (Saleem *et al.,* 2011; Rauf *et al.*, 2012; Aslam *et al.*, 2013a). For a plant breeder existence of genetic variability among genotypes at different evaluating standards is a key source for plant improvement (Bello *et al.,* 2012). Maize has significant variation among different characters (Aslam *et al.*, 2013b; Naveed *et al.,* 2014) which could be used for further selection or improvement. Seedling emergence along with different morphological traits is the most viable selection standard for adaptability to saline environments (Radic *et al.*, 2007).

Concept of hybrid development in maize was initiated in 1933 and now prevailed worldwide. Potential of inbred lines in different combinations of hybridization is determined by general combining ability (GCA) and specific combining ability (SCA). Different inbred lines have different GCA due to presence of additive, additive × additive and higher order gene interactions whereas, differences in SCA of crosses is credited to non-additive genetic variance (Falconer, 1981). Diallel mating design is most appropriate for the assessment of potential of inbred lines, because they are crossed in all possible combinations (Yan and Kang, 2003). This technique provides the information about inheritance pattern of gene action in early filial generations to breeders for development of hybrid (Hayman, 1954; Jinks, 1954). Griffing's numerical diallel approach (Griffing, 1956) was used for combining ability analysis of maize inbred lines. This approach is based on first order statistics and gives very sound, robust and precise results. The majority of yield related traits are controlled by additive. Dominance and additive gene actions are effectively used for the improvement of hybrids (Kumar *et*

al., 2012). The purpose of this study was to assess the level of adaptability of different maize accessions, inheritance pattern of different traits related to adaptability under different saline environments and selection of parents based on their combining ability to be used in different breeding programs for the development of well adapted hybrids for saline environment.

Materials and Methods

Present study was conducted in the research area of the department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan. This program comprised of hybridization under field conditions and evaluation in screen house experiment. Total six elite maize lines (A556, OH-41, WFTMS, Q67, 82Pi and L7-2) with diverse origin, collected from National Agricultural Research Centre (NARC), Islamabad, Maize and Millet Research Institute (MMRI), Sahiwal, University of Agriculture Faisalabad and Ayub Agriculture Research Institute, Faisalabad (Table 1). Parental lines were sown in the field by keeping plant to plant and row to row distances 30 cm and 75 cm, respectively. All the recommended agronomical practices were applied to raise a good crop. At maturity the parents were crossed (direct and indirect) by following diallel mating design. Resultantly 30 F_1s were generated. Healthy seed of parents (6) and crosses (30) were sown in iron trays to raise seedlings. Seedlings of age 15 days were transplanted to hydroponic culture. Hoagland nutrient solution (Hoagland and Arnon, 1950) was used to supply the nutrients to seedlings and was refreshed after 15 days. Treatments were applied after three days of transplantation after ensuring stability of seedlings in aquaculture. Three salinity levels viz., control (natural salinity of water) (T_0), 60 mM NaCl (T_1) and 100 mM NaCl (T_2) were developed with NaCl in hydroponic culture in two installments. Seedlings were harvested 30 days after treatment application. Root length (cm), shoot length (cm), leaf area (cm^2), Na^+ ions (mmol/L), K^+ ions (mmol/L) and plant biomass (g) were the traits used to evaluate the performance of inbred lines. Leaf area was measured with the help of portable leaf area meter (Model LI-3000C, LI-COR Biosciences Lincoln, Nebraska USA). Na^+ and K^+ contents were determined by procedure devised by Gorham *et al.* (1984). Flame photometer (Model 410, Sherwood Scientific Ltd., UK) was used for measurement of sodium and potassium ions. The morphological parameters like shoot length, root length, leaf area and plant biomass were also recorded right after harvesting.

Statistical Analysis

The data collected were analyzed statistically by using analysis of variance (Steel *et al.,* 1997) to find the differences among various F_1 hybrids and their parental lines. Analysis of general and specific combining abilities and components of variances were calculated following the procedure given by Griffing (1956) method 1, model 1.

Results

Analysis of Variance

Various attributes in the present study regarding general combining ability and specific combining ability were analyzed using statistical techniques. Significance of differences among inbred lines for general and specific combining ability was estimated by using analysis of variance. Subjected inbred lines were significantly different for GCA, SCA and reciprocal effects under T_0, T_1 and T_2 treatments for root length, shoot length, leaf area, Na^+ ions, K^+ ions and plant biomass (Table 2).

Combining Ability Analysis

Parent L7-2 had higher GCA value at T_0 and T_1 for root length, while Q67 had higher GCA effects at T_2 for root length (Table 4). WFTMS × L7-2 cross showed higher SCA value for root length under T_0 and T_1 while OH-41 × Q67 cross exhibited higher SCA value for root length under T_2 (Table 4). Crosses 82Pi × Q67, 82Pi × A556 and L7-2 × Q67 had higher values of reciprocal effects for root length at T_0, T_1 and T_2 respectively (Table 4). For shoot length, parent L7-2 showed higher GCA value at T_0 and T_1 whereas parent OH-41 had higher GCA value at T_2. Cross Q67 × L7-2 at T_0, cross A556 × 82Pi at T_1, and cross WFTMS × Q67 at T_2 had higher SCA effects for shoot length (Table 5). Maximum reciprocal effects for shoot length were exhibited by crosses L7-2 × OH-41 at T_0, L7-2 × Q67 at T_1 and L7-2 × WFTMS at T_2 (Table 5).

Parental combination of WF86TMS showed higher GCA value for leaf area under T_0 and T_2 while Q67 had higher GCA value under T_1. Cross combination of A556 × 82Pi had higher SCA value for leaf area under T_0 and T_1 whereas, cross A556 × OH-41 had higher SCA value at T_2. Cross combinations WFTMS × OH-41 at T_0, 82Pi × A556 at T_1, L7-2 × Q67 at T_2 had highest values for reciprocal effects for leaf area (Table 6).

Lesser intensity of Na^+ ions is preferred as selection criteria as it reflects high level of tolerance to saline conditions, so, minimum values of GCA, negative heterosis in case of SCA and reciprocal effects were desirable for this trait under salinity stress. Parent A556 was with lowest GCA effects for Na^+ at T_0 and T_2 while Q67 parent showed least GCA (Table 7).

Desire for K^+ ions is opposite to Na^+ ions. Among parents, 82Pi at T_0, A556 at T_1, OH-41 at T_2 showed higher values of GCA effects. Among direct crosses, A556 × 82Pi at T_0, A556 × OH-41 at T_1, WFTMS × 82Pi at T_2 had higher SCA values for K^+ ions. Among indirect or reciprocal effects, 82Pi × WFTMS at To, L7-2 × 82Pi at T_1, and 82Pi × A556 at T_2 had higher values for reciprocal effects

Table 1: List of parents and crosses

Parents					
A556	0H-41	WFTMS	Q67	82Pi	L7-2
Crosses					
A 556 × OH-41	OH-41 × A 556	WFTMS×A556	Q67 × A 556	82Pi × A 556	L7-2 × A 556
A556× WFTMS	OH-41×WFTMS	WFTMS×0H-41	Q 67 × 0H-41	82Pi × OH-41	L7-2 × OH-41
A 556 × Q 67	OH-41 × Q 67	WFTMS×Q 67	Q67×WFTMS	82Pi×WFTMS	L7-2×WFTMS
A 556 × 82Pi	OH-41 × 82Pi	WFTMS×82Pi	Q 67 × 82Pi	82Pi × Q 67	L7-2 × Q 67
A 556 × L7-2	WFTMS × L7-2	WFTMS×L7-2	Q 67 × L7-2	82Pi × L7-2	L7-2 × 82Pi

Table 2: Mean squares for different seedling traits under different salinity levels.

SOV	Treatment	DF	RL	SL	LA	Na^+	K^+	PB
GCA	To	5	57.612*	33.446*	9.726*	67.913*	93.076*	28.24*
	T1	5	65.326*	93.220*	39.755*	84.567*	76.36*	50.934*
	T2	5	95.463*	56.483*	15.82*	14.402*	9.19*	64.289*
SCA	To	15	8.294*	3.827*	22.251*	4.056*	7.547*	3.782*
	T1	15	6.687*	2.157*	10.967*	6.249*	3.634*	7.351*
	T2	15	11.763*	36.73*	18.998*	2.55*	3.449*	4.159*
RECI	To	15	24.851*	28.293*	13.55*	31.882*	9.128*	56.60*
	T1	15	35.037*	24.603*	17.738*	5.597*	10.52*	47.905*
	T2	15	31.128*	32.694*	18.798*	10.509*	6.135*	45.408*
Error	To	70	2.319	0.764	23.601	1.757	5.672	1.411
	T1	70	1.010	0.513	21.164	6.223	8.406	0.485
	T2	70	0.723	0.203	5.152	21.792	8.031	0.387

Where, RL = root length, SL = shoot length, LA = leaf area, Na^+ = sodium ions, K^+ = potassium ions and PB = plant biomass

Table 3: Estimates of relative proportion of variance components for general combining ability (GCA), specific combining ability (SCA) and reciprocal effects for quantitative traits in maize under salt conditions.

	Treatment	δ^2GCA	δ^2SCA	δ^2Recpl	δ^2A	δ^2D	Dominance of Effects	Breeding Program
RT	To	9.57	9.82	27.64	19.14	9.82	Dominance > Additive	Heterosis Breeding
	T1	4.95	3.34	17.19	9.9	3.34	Dominance > Additive	Heterosis Breeding
	T2	5.08	4.5	10.93	10.16	4.53	Dominance > Additive	Heterosis Breeding
SL	To	1.89	1.25	10.43	3.78	1.25	Dominance > Additive	Heterosis Breeding
	T1	3.89	0.34	6.052	7.79	0.34	Dominance > Additive	Heterosis Breeding
	T2	0.34	4.22	3.223	0.71	4.22	Additive > Dominance	Simple Selection/Population Improvement by recurrent selection
LA	To	-23.3	291.3	148.3	-46.6	291.3	Additive > Dominance	Simple Selection/Population Improvement by recurrent selection
	T1	51.34	122.5	177.1	102.7	122.48	Additive > Dominance	Simple Selection/Population Improvement by recurrent selection
	T2	-1.12	53.83	45.84	-2.23	53.83	Additive > Dominance	Simple Selection/Population Improvement by recurrent selection
Na^+	To	9.36	3.117	27.13	18.73	3.12	Dominance > Additive	Heterosis Breeding
	T1	40.7	18.97	14.3	81.42	18.97	Dominance > Additive	Heterosis Breeding
	T2	21.64	19.4	103.5	43.28	19.4	Dominance > Additive	Heterosis Breeding
K^+	To	40.53	21.56	23.05	81.05	21.56	Dominance > Additive	Heterosis Breeding
	T1	51	12.86	39.93	102.1	12.85	Dominance > Additive	Heterosis Breeding
	T2	3	11.37	20.61	7.8	11.37	Additive > Dominance	Simple Selection/Population Improvement by recurrent selection
PB	To	2.87	2.26	38.97	5.74	2.26	Dominance > Additive	Heterosis Breeding
	T1	1.77	1.79	11.38	3.54	1.79	Dominance > Additive	Heterosis Breeding
	T2	1.94	0.71	8.59	3.88	0.71	Dominance > Additive	Heterosis Breeding

Where RL = root length, SL = shoot length, LA = leaf area, Na^+ = sodium ions, K^+ = potassium ions and PB = plant biomass

(Table 8).

L7-2 proved as good general combiner at T_0, T_1 and T2 for plant biomass. Cross combination Q67 × L7-2 was good specific combiner at T_0, T_1 and T_2 for plant biomass. Cross Q67 × OH-41 had higher value for reciprocal effects at T_0. For plant biomass at T_1 and T_2, indirect cross WFTMS × OH-41 had higher value for reciprocal effects (Table 9).

Estimate of Variance Components of Additive and Dominance Gene Action

Variance components for GCA, SCA and reciprocal effects were estimated to obtain an estimate of relative importance of additive and non-additive type of gene actions. Variances due to GCA effects for root length, shoot length, leaf area, Na^+ ions and K^+ ions were greater than variances due to SCA effects under three salinity treatments (Table 3).

The variance components for root length at T_0 (9.5694), T_1 (4.9520) and T_2 (5.079) were due to GCA. Similarly variances due to SCA were as for T_0 (9.8146), T_1 (3.337) and T_2 (4.530) and due to reciprocal effects were as for T_0 (27.6376), T_1 (17.1930) and T_2 (10.9262). The variance due to A (Dominance effect) for treatment T_0, T_1 and T_2 were 19.139, 9.90 and 10.1599, respectively and due to D

Table 4: Estimate of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for root length (cm) under salinity

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	-4.04*	1.06*	0.51	-3.52*	1.84*	2.39*
	T_1	-2.49*	1.56*	0.21	-0.48	-0.18	-2.04*
	T_2	-0.23	0.98	0.67	-0.65	-3.21*	-1.16*
OH-41	T_0	3.83*	-3.56*	2.04*	1.84*	-7.13*	0.43
	T_1	4.50*	0.39	-1.01*	0.63	0.60	-1.93*
	T_2	0.50	-0.68	-0.74	3.23*	0.70	-2.07*
WFTMS	T_0	-3.50*	10.50*	0.66	-1.88*	-1.68*	2.70*
	T_1	-0.67	7.00*	-2.44*	-1.04*	1.44*	4.57*
	T_2	1.17*	1.33*	-2.01*	-3.40*	1.06*	0.79
Q67	T_0	-0.17	5.00*	1.83*	0.35	2.12*	1.51*
	T_1	2.00*	-1.00*	0.50	1.93*	-0.59	1.38*
	T_2	0.67	-2.50*	-2.50*	4.52*	-2.29*	2.26*
82Pi	T_0	-1.00*	9.50*	-3.83*	10.67*	1.82*	-1.13*
	T_1	7.33*	1.67*	-1.67*	1.67*	-0.71	-1.65*
	T_2	0.00	0.83	2.50*	3.33*	-1.95*	1.23*
L7-2	T_0	-5.50*	-1.00*	-3.50*	-1.33*	-1.17*	4.76*
	T_1	6.17*	-0.17	-5.50*	-3.33*	-7.00*	3.31*
	T_2	5.33*	4.00*	-2.50*	4.50*	-8.00*	0.33

*Desired or higher GCA, SCA and Reciprocal values are highlighted as bold

Table 5: Estimates of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for shoot length (cm) under salinity

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	-1.79*	1.74*	0.44	-0.54	-0.95	-1.98*
	T_1	0.99	0.23	-0.07	-0.91	1.56*	-0.38
	T_2	-0.14	-2.22*	0.81	0.96	0.50	-1.95*
OH-41	T_0	-4.50*	0.26	0.55	-0.43	-2.01*	-0.04
	T_1	-0.50	1.16*	0.26	-0.07	-1.60*	-0.05
	T_2	-1.49*	1.14*	-1.22*	0.18	0.32	2.94*
WFTMS	T_0	-1.00*	2.50*	-0.60	-1.06*	1.35*	-0.18
	T_1	-1.50*	2.00*	-1.87*	0.45	-0.41	-0.52
	T_2	-0.75	-2.50*	-1.15*	2.96*	-2.59*	-1.52*
Q67	T_0	-0.50	2.33*	-0.17	-0.79	0.88	1.85*
	T_1	0.00	0.00	-0.83	-1.20*	0.26	0.32
	T_2	-0.50	-2.00*	-0.50	-1.05*	-0.04	-1.43*
82Pi	T_0	0.33	-3.00*	-4.50*	1.83*	0.45	0.27
	T_1	-0.33	-1.00*	1.17*	0.17	-2.01*	0.62
	T_2	-2.10*	-0.20	2.00*	-1.65*	1.01*	-0.93
L7-2	T_0	3.00*	7.00*	4.00*	3.17*	3.50*	2.48*
	T_1	3.00*	-2.17*	5.00*	5.50*	4.00*	2.94*
	T_2	-4.16*	0.00	2.08*	-1.55*	1.00*	0.19

*Desired or higher GCA, SCA and Reciprocal values are highlighted as bold

(additive effect) were 9.814, 3.336 and 4.530, respectively. The variance components for shoot length for T_0, T_1 and T_2 due to GCA were 1.8927, 3.893 and 0.3444, due to SCA were 1.254, 0.3444 and 4.216 and due to reciprocal effects were 10.4325, 6.0528 and 3.223 respectively. The genetic component of variance due to A for T_0, T_1 and T_2 were 3.7854, 7.7872 and 0.7081 and due to D were 1.254, 0.3444 and 4.216, respectively (Table 3).

Due to GCA for leaf area the variance components were -23.294 (T_0), 51.339 (T_1) and -1.117 (T_2) and variance components due to SCA were 291.324 (T_0), 122.487 (T_1) and 53.831 (T_2) whereas due to reciprocal effects the values for variance components were for treatment T_0 (148.245), T_1 (177.123) and T_2 (45.841). The genetic component of variance due to A for T_0, T_1 and T_2 were -46.588, 102.679

and -2.235 and due to D were 291.32, 122.48 and 53.83, respectively. The degree of dominance showed that leaf area was controlled by additive type of gene action (Table 3).

The variance components due to GCA for Na^+ ions were as for treatments T_0 (9.3645), T_1 (40.7067) and T_2 (21.640) and for K^+ ions were for treatments T_0 (40.526), T_1 (51.007) and T_2 (3.009). Similarly in case of Na^+ ions variance components due to SCA were for treatments T_0 (3.117), T_1 (18.966) and T_2 (19.406) and for K^+ ions were for treatments T_0 (21.561), T_1 (12.856) and T_2 (11.367). For Na^+ ions reciprocal effects were for treatments T_0 (27.130), T_1 (14.3030) and T_2 (103.511) and the genetic component of variance due to A were for treatment T_0 (18.7290), T_1 (81.4135) and T_2 (43.281) and due to D were 3.117 (T_0), 18.966 (T_1) and 19.406 (T_2). The genetic component of

Table 6: Estimates of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for leaf area under salinity

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	-7.69*	12.53*	9.11*	-7.39*	19.69*	7.86*
	T_1	-14.31*	0.14	-8.00*	7.19*	18.39*	-4.56*
	T_2	-0.27	8.85*	1.29*	4.10*	5.96*	-2.32*
OH-41	T_0	15.50*	-0.53	6.94*	8.44*	0.53	-9.31*
	T_1	0.67	5.72*	-2.03*	6.67*	5.53*	-0.08
	T_2	6.50*	1.48*	-2.95*	1.35*	1.71*	5.43*
WFTMS	T_0	5.50*	32.50*	3.89*	0.53	1.11*	14.28*
	T_1	7.33*	24.67*	2.19*	1.19*	10.56*	14.44*
	T_2	7.50*	-10.00*	4.04*	5.29*	-8.34*	0.88
Q67	T_0	-21.00*	9.00*	3.50*	2.89*	5.61*	18.78*
	T_1	-10.50*	14.00*	12.00*	9.83*	-11.08*	8.47*
	T_2	0.50	-5.50*	12.00*	0.23	0.96	4.18*
82Pi	T_0	-1.50*	10.50*	5.50*	15.00*	-1.69*	-9.14*
	T_1	32.17*	10.00*	-1.50*	13.50*	-0.03	-3.33*
	T_2	-2.00*	3.50*	6.00*	9.50*	-3.13*	0.56
L7-2	T_0	-2.50*	4.508	-9.50*	5.00*	5.50*	3.13*
	T_1	2.17*	10.00*	-1.00*	16.67*	0.00	-3.42*
	T_2	-2.50*	-10.00*	-10.00	-1.50*	1.50*	-2.35*

*Desired or higher GCA, SCA and Reciprocal values are highlighted as bold

Table 7: Estimates of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for Na^+ ions under salinity.

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	-3.38*	0.85	1.10*	-3.09*	-1.56*	0.66
	T_1	0.88	-5.18*	3.62*	-4.91*	0.76	3.12*
	T_2	-6.07*	-1.18*	6.49*	-4.56*	-0.59	-4.68*
OH-41	T_0	1.00*	-0.18	0.41	-0.79	-2.09*	-0.04
	T_1	0.50	11.16*	9.18*	3.48*	2.82*	-4.33*
	T_2	-8.50*	0.12	-3.71*	5.91*	0.71	-4.87*
WFTMS	T_0	0.00	6.49*	-1.44*	-1.04*	3.32*	-1.95*
	T_1	2.67*	-2.50*	-2.15*	-1.05*	-3.55*	-5.85*
	T_2	-13.50*	17.50*	0.45	-0.93	-6.12*	5.79*
Q67	T_0	3.00*	-3.50*	-3.00*	2.76*	1.63*	2.52*
	T_1	4.00*	5.33*	-0.17	-6.62*	-0.24	4.12*
	T_2	-4.17*	1.50*	-11.00*	6.84*	9.99*	-2.09*
82Pi	T_0	6.50*	-7.83*	-8.67*	-3.17*	4.73*	0.55
	T_1	1.83*	3.17*	0.17	0.67	-6.12*	1.62*
	T_2	-4.50*	10.00*	3.50*	-19.0*	-5.46*	1.71*
L7-2	T_0	-1.17*	-4.00*	2.83*	-0.50	11.50*	-2.49*
	T_1	4.50*	0.00	9.17*	-7.0*	-6.00*	2.85*
	T_2	-2.00*	19.00*	-10.00*	7.50	0.00	4.12*

*Desired or higher GCA, SCA and Reciprocal values are highlighted as bold.

variance for K^+ ions due to A were for treatment T_0 (81.053), T_1 (102.018) and T_2 (7.801) and due to D were 21.561 (T_0), 12.856 (T_1) and 11.367 (T_2). The degree of dominance showed that Na^+ and K^+ ions were controlled by over dominance type of gene action (Table 3).

The variance components for plant biomass for treatment T_0, T_1 and T_2 due to general combining ability were 2.8681, 1.771 and -1.117 respectively. Similarly variance due to specific combining ability for treatment T_0, T_1 and T_2 were 2.264, 1.789 and 0.7094 and reciprocal effects for treatment T_0, T_1 and T_2 were 38.973, 11.384 and 8.57, respectively. The genetic component of variance; variance due to A (Dominance effect) for treatment T_0, T_1 and T_2 were 5.73, 3.54 and 3.88, respectively and due to D (additive effect) were 2.264, 1.789 and 0.7094, respectively (Table 3).

Discussion

Combining ability analysis provides the information about potential of certain accessions or parents. There is requirement of positive GCA and SCA for some traits whereas, negative GCA and SCA is required for others to decide about the selection of appropriate parents (Gopikannan and Ganesh, 2013). Genotypes Q67 and L7-2 showed good GCA for root length, L7-2 and OH-41 for shoot length, Q67 and WFTMS for leaf area, OH-41 and Q67 for Na^+ ions, A556 and OH-41 for K^+ ions under saline environments. GCA is fixable and is due to additive gene effects. GCA depicts the intrinsic genetic value of a parent for any trait (Simmonds, 1989). It is reported that parents having higher GCA values would be responsible for production of transgressive segregants in F_2 generation or

Table 8: Estimates of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for K+ ions under salinity

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	-2.67*	-1.50*	2.75*	-1.28*	6.89*	-6.86*
	T_1	7.75*	8.58*	-0.22	-1.42*	0.81	-3.39*
	T_2	1.94*	-0.86	-2.53*	-0.86	-4.25*	4.44*
OH-41	T_0	-0.67	-0.17	2.92*	-1.78*	-3.11*	5.14*
	T_1	0.00	-10.19*	-1.61*	-5.64*	-6.92*	2.39*
	T_2	-0.50	3.36*	0.56	-5.28*	-0.17	-1.47*
WFTMS	T_0	1.00*	2.67*	-8.42*	-0.03	-9.36*	5.22*
	T_1	1.17*	-4.17*	2.78*	1.56*	1.44*	-1.42*
	T_2	4.00*	-8.50*	-1.47*	1.56*	4.67*	-4.14*
Q67	T_0	5.67*	-3.33*	-0.83	-4.39*	6.28*	0.03
	T_1	1.67*	-9.17*	0.00	3.14*	2.25*	0.72
	T_2	-1.50*	2.50*	5.50*	-3.64*	-4.17*	2.53*
82Pi	T_0	-4.50*	8.00*	8.50*	9.17*	8.28*	-1.81*
	T_1	-2.00*	4.33*	-2.33*	1.17*	4.58*	-2.22*
	T_2	-6.00*	-1.50*	-2.50*	8.50*	0.25	2.14*
L7-2	T_0	4.50*	7.67*	0.50	-4.00*	-0.17	7.36*
	T_1	-4.50*	-6.33*	-14.50*	10.00*	12.50*	-8.06*
	T_2	0.00	-9.50*	2.00*	-5.50*	-1.00*	-0.44

*Desired or higher GCA, SCA and Reciprocal values are highlighted as bold

Table 9: Estimate of relative general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal (below diagonal) for plant biomass under salinity

	Treatment	A556	OH-41	WFTMS	Q67	82Pi	L7-2
A556	T_0	2.00*	0.76	-0.41	-1.98*	1.36*	-1.17
	T_1	1.35*	-0.91	0.78	-0.35	-0.80	0.83
	T_2	1.14*	-0.44	0.59	-0.21	-0.25	0.13
OH-41	T_0	10.45*	1.76*	-0.17	-1.04*	0.16	1.41*
	T_1	0.45	-0.67	0.12	-0.92	0.90	0.76
	T_2	0.93	-0.57	0.13	-0.58	0.11	0.61
WFTMS	T_0	0.75	10.18*	-1.57*	0.09	0.21	-0.16
	T_1	-0.90	7.92*	-0.32	-0.97	1.08*	-1.25*
	T_2	-0.85	7.52*	-0.16	-0.71	0.69	-0.88
Q67	T_0	-0.02	10.55*	2.65*	-0.57	0.57	4.05*
	T_1	-1.32*	2.67*	-2.37*	1.79*	0.18	3.45*
	T_2	-1.25*	2.54*	-2.25*	1.58*	-0.21	2.53*
82Pi	T_0	0.28	-11.42*	1.93*	3.35*	0.30	0.16
	T_1	1.05*	-6.23*	1.63*	3.58*	0.02	-1.54*
	T_2	1.42*	-4.92*	1.05*	2.57*	-0.07	-0.92
L7-2	T_0	-5.00*	5.68*	-4.02*	-1.48*	-6.50*	2.25*
	T_1	-5.00*	0.09	-1.32*	1.77*	-3.30*	2.17*
	T_2	-3.86*	0.25	-1.25*	0.35	-3.14*	2.01*

* Desired or higher GCA, SCA and Reciprocal values are highlighted as bold

lateral generations (Singh and Singh, 1985). It is recommended that parents with higher GCA values can be used for improvement of adaptability to saline environments by transgressive breeding.

Crosses WFTMS × L7-2 for root length and shoot length, A556 × 82Pi for leaf area, OH-41 × WFTMS for Na^+ ions, A556 × OH-41 for K^+ ions showed good SCA under subjected saline environments. Non-additive and non-allelic genetic effects were found to be responsible for SCA of any parent (Sprague and Tatum, 1942). SCA based hybrid selection excels the heterotic effects either due to presence of linkage or due to accumulation of beneficial genes from different parents (Sarasar *et al.*, 1986).

Probability of improvement through selections was evident because there were significant differences among parents in their adaptability levels to different saline environments. Previous studies reported the presence of genetic variability for different traits in maize under saline stressed environments (Betran *et al.*, 2003; Derera *et al.*, 2008). Significant differences among mean squares of GCA and SCA for different maize seedling traits showed that additive and non-additive gene effects are important for these parameters. Results showed that improvement of traits can be made through systematic or effective selection.

Root length, shoot length, Na^+ ions and K^+ ions were under the control of non-additive gene effects whereas leaf area was under the control of additive gene effects. Earlier it was reported that additive (Tabassum, 2004), dominance (Sharma and Bhalla, 1990) and over-dominance (Shabir and Saleem, 2002) gene effects for plant height (Khatoon *et al.,*

2010; Abbasi *et al.,* 2012). Leaf area was reported to be under the control of non-additive (Shabir and Saleem 2002) and additive (Sharma and Bhalla, 1990) gene effects according to different studie (Khatoon *et al.,* 2010; Zare *et al.,* 2011). Regarding root length results were in accordance with the findings of the Khatoon *et al.* (2010). Findings about Na^+ and K^+ ions results were in accordance with the findings of Ashrafuzzaman *et al.* (2000), Irshad *et al.* (2000), Gopal and Dube (2003), Karmoker *et al.* (2008), Tas and Basar (2009) and Carpici *et al.* (2009).

Prevalence of dominance effects triggers the breeder to proceed using heterosis breeding for improvement of traits whereas, in case of prevalence of additive effects argue to use simple selection and recurrent selection for improvement of traits in a population (Singh and Narayanam, 2011). Dominance effects were prevailing over additive effects for root length, shoot length, Na^+ ions, K^+ ions and plant biomass under different salinity treatments (Table 3). So, improvement in these traits can be brought through heterosis breeding under salinity stress. Additive effects were prevailing over dominance effects in leaf area at To, T1, T2, in shoot length and K^+ ions at T2 (Table 3). So, improvement in these traits can be brought about by simple selection or by population improvement through recurrent selection.

Physiological markers were used for screening of maize accessions under different saline environments. Salinity tolerance is very complex mechanism so, exploitation of physiological markers was preferred. Na^+ and K^+ ions were used as physiological markers in numerous previous studies (Shannon, 1997; Wahid *et al.,* 1999; Irshad *et al.,* 2000). In fact, measured trait should be in direct association with physiological trait and secondly test should be cost effective so that, large number of plant samples can be tested with low cost. Germination rate (Tajbakhsh *et al.,* 2006), growth rate (Greenway, 1962; Wahid *et al.,* 1999), leaf and root growth rate (Cramer and Quarrie, 2002), survival rate (Sayed, 1985; Hussain *et al.,* 2014), leaf injury (James *et al.,* 2002) and damage to photosynthetic apparatus (Krishnaraj *et al.,* 1993) were used for evaluation of different crops under salinity stress. K^+ ion flux induced by saline environment stress was found to be controlled mainly by additive gene effects in barley.

Genetic variation among different generations was mainly due to additive genetic effects whereas, non-allelic and dominant effects were minimum (Chen *et al.,* 2008). It was already reported that salinity tolerance at seedling stage is mainly under the control of recessive genes (Mano and Takeda, 1997) and in rice it was reported that over-dominance effects were discriminating for Na^+/K^+ (Gregorio and Senadhira, 1993). In genome of *Arabidopsis thaliana* only 5% genes were involved in cation transportation (Maser *et al.,* 2002) whereas, for K^+ transportation the involvement of 75 genes belonging to seven different gene families was reported (Shabala, 2003).

K^+ ions flux was found to be correlated with shoot biomass, grain yield, survival rate, plant height, and CO_2 assimilation (Chen *et al.,* 2007). Significant SCA and GCA were found for K^+ flux induced by saline environment in barley. Genotypes with higher GCA could be used as a source of salinity tolerance. CM72 and Numar were reported with higher GCA value under salinity stress and regarded as source of salinity tolerance (Chen *et al.,* 2008).

Conclusion

Combining ability of maize inbred lines was helpful to find out appropriate parents to be used in breeding program for saline conditions. Gene action (dominant or additive) showed that root length, shoot length, Na^+ ions, K^+ ions and plant biomass were under prevalence of dominance gene effects and heterosis breeding was recommended for improvement in these traits under saline conditions. Leaf area was under prevalence of additive gene effects and recurrent selection was recommended for improvement of this trait under saline conditions. L7-2 was good general combiner for comparatively more traits under different salinity treatments. Cross WFTMS × L7-2 showed good specific combining ability for most of the traits under different salinity levels. Cross WFTMS × OH-41 showed good reciprocal combination for relatively more traits comparative to other cross combinations under different salinity treatments.

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