

Correlation analysis of maize genotypes under saline stress and its impact on morphological characteristics

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Abstract: Screening of salt tolerant genotypes of agricultural crops is a necessary aspect for future food security. In this study, fifteen genotypes of maize were used to analyze their performance under saline condition. An experiment was performed as factorial under Completely Randomized Design (CRD) with three replications. Estimation of genetic variations of yield and yield related contributing traits under saline environment was done. Seeds of fifteen genotypes were grown on saline soil (0ds/m, 5ds/m and 10ds/m) under field condition. At seedling stage all of the genotypes were used for correlation analysis between shoot fresh weight, shoot dry weight, root fresh weight, and root dry weight. Root fresh weight and shoot length was positive and highly significant at genotypic level under various saline conditions. On the base of significant results, seven selected genotypes were used for measurement of morphological characteristics like plant height (PH), Number of leaves per plant (LPP), number of cob per plant (CPP), cob length (CL), cob diameter (CD), number of grains per row (GPR), number of grain rows per cob (GRPC), 100-grain weight (GW) and seed yield per plant (SYPP). Genotypic and phenotypic correlation indicated that plant height was highly significant with cob length, cob diameter, and grain yield per plant. Path coefficient regression analysis also indicated that same factors were positive having direct effect on grain yield. Results indicated that salinity causes adverse effect on maize plant and with the increase of salinity stress on maize genotypes there was significant decrease in root shoot length and root shoot weight. While correlation and path coefficient studies concluded that number of grains per cob and 100-grain weight could be used as important characters to improve maize grain yield.

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1. Introduction

Maize (*Zea mays* L.) is an important cereal crop throughout the world. It is also known as corn especially in USA. It belongs to the grass family Poacea (Gopalan et al., 2007). The largest producer of maize is United States and ranks first in the world with the production of 4096190 thousand million tons while Mexico produced 765545 thousand million tons (FAO, 2012). In Pakistan, maize crop covers an area of about 1085 thousand hectares with an average yield of 4268 kg/ha (Economic Survey of Pakistan, 2012-13). Worldwide, it has been estimated that approximately 21% of the total grain produced is consumed as food.

Along its importance, several maize-growing countries are facing many problems such as insect, pest, salinity and drought which are produce hindrance in high yield. Salinity is the most important abiotic stress that limits plant growth, development and productivity of a wide range of crops (Flowers, 2004; Jaleel et al., 2007; Khan and Ashraf, 2008). In Pakistan, approximately 6.8 million hectares land is

salt affected. More than 100 million hectares of agricultural land remains uncultivated due to salinity stress. Saline soil are producing more adverse effect elements (P, Zn, Mn, Na⁺ Cl⁻) as compared to essential elements (K and Fe) which are not necessary for plant growth and better yield (Flowers and Flowers, 2005; Turan et al., 2009). Plant's response to high salinity is complex and causes changes in their morphology, physiology and metabolism (Parida and Das, 2005).

Saline injury produce major effect on reduction of plant growth (Azooz et al., 2004; Jaleel et al., 2008), which results in several physiological responses like modification of ion balance, water status, mineral nutrition, photosynthetic efficiency, carbon distribution and utilization (Sultana et al., 2002; Taylor et al., 2004; Yildirim et al., 2006). In case of salinity tolerance, growth stage of the crop plants becomes an important factor. During germination and seedling stage plants are more sensitive to high salinity because it affects seed germination, survival percentage, and morphological

characteristics (Bilgin et al., 2008). It also decreases the photosynthesis and respiration rate of plants (Jouyban, 2012).

Since screening is considered as an essential part of the breeding programs, several screening and selection schemes have been proposed for salt tolerance improvement in many crops. Also, selection for improved salt tolerance based on seedling stage has been used in various crop species, for example in rice (Khan et al., 2003; Shannon et al., 1998), maize (Khan et al., 2003), wheat (Qureshi et al., 2003) and tomato (Soloviev et al., 2003). Screening of germplasm is required to identify salt tolerant accessions and developing high yielding varieties. In different crops including maize, screening is useful for understanding the responses of plants at different growth stages under various saline environments (Khan et al., 2003). According to (Flowers and Yeo, 1995) one of the important method to develop salt tolerant genotype in shorter time is to use the variation already present in the existing crops. Because of the importance of maize crop the main objective of all maize breeders is to develop new inbred lines and hybrids with high grain yield with additional quality of tolerance to salt stress environment.

Before planning of any breeding program, information about the correlations among the traits an important for success. From breeder's point of view, screening of germplasm totally depends upon correlation analysis of morphological traits of crop plants which are producing direct effect on grain yield. Grain yield is a complex quantitative character that depends on a number of factors. Therefore, analysis of correlation coefficients the most widely used one among numerous other methods (Yagdi and Sozen, 2009). Sometimes improvement made in one character is at the expense of other character due to association among them (Salahuddin et al., 2010).

For complete analysis of plant response to saline soil, path coefficient regression analysis and phenotypic genotypic correlation are necessary to be performed. Path coefficient analysis permits the separation of direct and indirect effect through the other related characters. Path coefficient analysis produces exact picture of a set of independent variables on the dependent variable and gives a more realistic relationship of the characters and helps in identifying the effective components. This technique was first used for plant selection by (Dewey and Lu, 1959) while it was originally developed by (Wright, 1921).

With the use of selection and breeding techniques, improvement in salt tolerance in different plant species would be possible. Therefore, the purpose of the present study was to generate information on the genetic variability for salinity

tolerance at early seedling and late morphological stage in maize genotypes.

2. Material and Methods

Experiment design

The research work was conducted in the green house of the Department of Plant Breeding and genetics, University of Agriculture, Faisalabad, Pakistan. These studies were carried out in solution culture and in greenhouse to find out the performance of maize genotypes in saline environment. The details of experimentation are given as under. Total 17 maize genotypes (Pearl, Sadaf, Hybrid-1898, Yousafwala, MMRI yellow, Agati-2002, Sahiwal-2002, Pak-1, Pak-2, Agati-85, Golden, EV-1089, Sultan, Sunahri, Agati-2000, 12-population, EV-6089) were collected from Maize and Millet Research Institute (MMRI), Yousafwala, Sahiwal, Pakistan. The germplasm was sown in iron trays filled with distilled water washed sand.

Solution culture studies

The maize genotypes were sown in iron trays filled with an equal amount of fresh sand. The experiment was conducted following completely randomized design (CRD) with three replication and three treatments (0ds/m, 5ds/m and 10 ds/m). At two-leaf stage, seedlings of uniform size were transplanted in foam-plugged holes of polystyrene sheets floating over half strength Hoagland's nutrient solution that was prepared according to (Hoagland and Arnon, 1950). Salinity was developed in respective treatments by adding NaCl in three/four applications, starting two days after transplanting. Proper aeration of the culture solution was provided for 8 hours daily by an aeration pump. The pH of the solution was monitored daily and adjusted at 6.0 ± 0.5 , when needed. The substrate solutions were changed fortnightly.

Estimation of Seedling parameters

After three weeks few plants of all genotypes were harvested manually and following seedling traits were recorded regarding Root length (cm), Shoot length (cm), Fresh Root weight (g) and Fresh Shoot weight (g). The seedlings from each maize genotype and replication were carefully washed free of sand. The plants were uprooted and root and shoot length were measured with the help of measuring tape in centimeters. Similarly, shoots and roots were weighed separately in grams using electronic balance. After a critical examination of genotypes for seedling parameters, seven genotypes were selected for field experiment on the basis of data collected for better performance under saline condition.

Field Experiment

The selected genotypes from previous experiment were subjected to field experiment under saline and control soil for the measurement of

morphological characteristics, their correlation and direct and indirect effect. For these purpose seven genotypes such as Sultan, Sadaf, Sunahri, 12-population, EV-6089, Golden, EV-1089 was planted in the area of University of Agriculture, Faisalabad which was affected with high salt concentration was laid out following randomized complete block design (RCBD). Plant to plant and row to row distance were kept 15cm and 25cm respectively while line length was kept 4 meters. At maturity, plants were harvested manually and different yield parameters were recorded. Study was carried out to find the association of yield and yield related contributing traits in maize genotypes under saline conditions.

Measurement of Quantitative Characters

The measurement of quantitative parameters is important for the performance of a crop in field at saline and control conditions. A variety of agronomic characteristics were measured, including the plant height (cm), number of leaves per plant, number of cobs per plant, cob length (cm), cob diameter (cm), number of grain per cob row, number of grain rows per cob, 100 seed weight (gram) and seed yield per plant (gram). All of the morphological characteristics of selected corn genotypes were collected both at saline and control conditions. System International (SI) unit was used for measurement of these characters.

Statistical Analysis

The statistical analysis of the data on individual characters was carried out using mean values of randomly selected plants. The collected data was used for estimating simple analysis of variance by following (Steel et al., 1980). Tukey HSD test was used for mean comparison of genotypes and treatments for salinity experiment. LSD test was used for mean comparison of maize genotypes for field experiment. The values of correlations among various characters were determined by following (Kwon and Torrie, 1964). Genotypic, phenotypic variance and genotypic, phenotypic coefficient of variation was measured according to (Singh and Chaudhary, 1985). Path analysis was performed in accordance with (Dewey and Lu, 1959).

Results

Corn genotypes under saline environment

Seeds of seventeen genotypes of maize were sown under saline condition in green house. Data was collected for root length, shoot length, fresh root weight and fresh shoot weight for 17 maize accessions at three different salinity treatments. Visual pictures of length of shoot and root are shown in figure 1. Data was subjected to analysis of variance under two factor factorial arrangements. Following maize genotypes were used for analysis of response against salinity

stress such as Pearl, Sadaf, Hybrid-1898, Yousafwala, MMRI yellow, Agati-2002, Sahiwal-2002, Pak-1, Pak-2, Agati-85, Golden, EV-1089, Sultan, Sunahri, Agati-2000, 12-population, EV-6089.

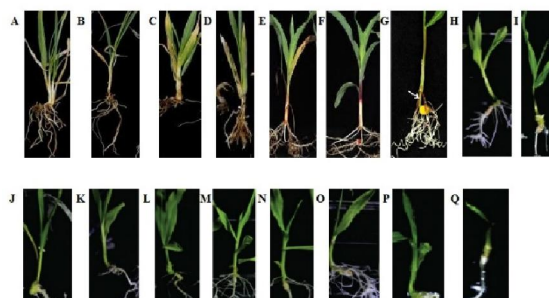


Figure 1: Pictorial explanation of seedling of maize genotypes; A) Sadaf; B) pearl; C) hybrid-1898; D) EV-6089; E) Golden; F) EV-1089; G) Sultan; H) MMRI yellow; I) Agati2002; J) Sahiwal-2002; K) Pak-1; L) Pak-2; M) Sunahri; N) Agati-85; O) 12-population; P) Yousafwala; Q) Agati-2000.

Statistical analysis of root and shoot parameters

Root length and root fresh weight

Data of seventeen genotypes of maize regarding root fresh weight and root length were used for statistical analysis such as analysis of variance (ANOVA), coefficient of variability and genotypic comparison. On the base of analysis of variance results, all of the genotypes of maize depicted highly significant differences among maize genotypes for root length and root fresh weight on three salinity treatments (0ds/m, 5ds/m and 10ds/m). Analysis of variance (ANOVA) did not produce exact picture of significant resistance of all genotypes to different soil saline condition. Other statistical analysis were applied for reconfirmation of maize genotypes resistance against saline condition such as phenotypic and genotypic correlation.

On the base of results obtained from phenotypic and genotypic correlation, Genotype Ev-1089 had highest, while genotype Sadaf had lowest mean value for root length over all of three salinity treatments. Root length of maize accessions was highest under 0ds/m and shortest under 10ds/m. This showed that with the increase of salinity stress on maize genotypes there was a significant decrease in root length. Analysis of variance also showed that interaction of maize accessions with salinity treatments was highly significant for root fresh weight. Genotype Pak-2 had the maximum root fresh weight but genotype Sadaf had minimum mean value for root fresh weight. Maximum root fresh weight of maize accessions was observed at 0ds/m to 5ds/m but root fresh weight of

maize genotypes at 10ds/m was non-significantly different from each other. (Table 1 and 2).

Results of treatment mean comparison showed that root fresh weight of maize accessions was decreased with the increase of salinity stress.

Table 1: Analysis of variance and coefficient analysis of root fresh weight of maize genotypes at different saline condition

Source of variable	DF	SS	MS
Replications	2	1.690	0.8452
Accessions	14	51.017	3.6441**
Treatment	2	22.114	11.0571**
Genotype*treatment	28	23.436	0.8370**
Error	90	29.932	0.3401
Total	134	128.190	

Ns=non-significant, *=significant, **=highly significant

Variances and coefficients of variability of maize genotypes for root fresh weight under three salinity treatments

Coefficient of variability (CV %)	3.36%
Genotypic Variance	0.76
Phenotypic Variance	0.76
Genotypic Coefficient of Variability	70.46
Phenotypic Coefficient of Variability	70.58

Table 2: Analysis of variance and coefficient analysis of root length of maize genotypes at different saline condition

Source of variable	DF	SS	MS
Replications	2	15.01	7.506
Accessions	14	352.07	25.148**
Treatment	2	591.49	295.747**
Genotype*treatment	28	135.43	4.837
Error	90	273.42	3.107
Total	134	1367.43	

Ns=non-significant, *=significant, **=highly significant

Variances and coefficients of variability of maize genotypes for root length under three salinity treatments

Coefficient of variability (CV %)	1.58%
Genotypic Variance	10.88
Phenotypic Variance	10.92
Genotypic Coefficient of Variability	93.85
Phenotypic Coefficient of Variability	94.02

Statistical analysis of shoot fresh weight and shoot length

The analysis of variance indicated that there were highly significant differences among maize accessions for shoot length. Effects of three salinity treatments (0ds/m, 5ds/m and 10ds/m) were also highly significantly different for 15 maize accessions. Interaction of accessions with treatments was observed to be non-significant for shoot length of maize. Genotype Pak-2 had highest mean value for shoot length over all of three salinity treatments while

genotype Pak-1 had the lowest mean value for shoot length over all of three salinity treatments (Table 3). Analysis of variance also showed that interaction of maize accessions with salinity treatments was non-significant for shoot fresh weight. Genotype Sadaf has the maximum shoot fresh weight but genotype Sunahri has minimum mean value for shoot fresh weight. Maximum shoot fresh weight of maize genotypes was observed at 0ds/m but shoot fresh weight of maize genotypes at 10ds/m was minimum (Table 4). Results of treatment mean comparison showed that shoot fresh weight of maize genotypes was decreased with the increase of salinity stress. Shoot length of maize accessions was higher under 0ds/m while shortest under 10ds/m. This showed that with the increase of salinity stress on maize accessions there was significant decrease in shoot length.

Table 3: Statistical analysis of shoot fresh weight of maize genotypes

Source	DF	SS	MS
Replication	2	1.1217	0.5608
Accessions	14	4.7573	0.3398**
Treatment	2	13.6985	6.8492**
Genotype*treatment	28	1.0956	0.0391
Error	88	8.8583	0.1006
Total	134	29.5315	

Ns=non-significant, *=significant, **=highly significant

Variances and coefficients of variability of maize genotypes for shoot fresh weight under three salinity treatments

Coefficient of variability (CV %)	3.87%
Genotypic Variance	1.29
Phenotypic Variance	1.29
Genotypic Coefficient of Variability	158.78
Phenotypic Coefficient of Variability	158.80

Table 4: Statistical analysis of shoot length of maize genotypes at different doses of saline condition

Source	DF	SS	MS
Replications	2	28.85	14.427
Accessions	14	419.24	29.946**
Treatment	2	1484.81	742.403**
Genotype*treatment	28	428.52	15.304
Error	90	980.49	11.142
Total	134	3341.90	

Ns=non-significant, *=significant, **=highly significant

Variances and coefficients of variability of maize genotypes for shoot length under three salinity treatments

Coefficient of variability (CV %)	1.16%
Genotypic Variance	35.18
Phenotypic Variance	35.26
Genotypic Coefficient of Variability	120.03
Phenotypic Coefficient of Variability	120.17

Measurement of morphological characteristics

Out of fifteen genotypes of maize, seven genotypes (EV-6089, Sadaf, Sultan, Sunahri, 12-population, EV-1089 and Golden) indicated good results against different doses of salinity and salinity treatments produce. The seedlings of these seven genotypes of maize were used for further field analysis for their important morphological characteristics at natural saline soil of experimental

area. The analysis of variance designated that the performance of genotypes was highly significantly different for number of leaves under field saline conditions (Figure 2). Results of coefficient of variance also indicated significant differences for number of leaves, plant height, cob length, cob diameter, grain per row, grain rows per cob, number of cob per plant, 100 grain weight and seed yield that different maize accessions have at maturity as depicted by least significant differences (LSD) test.

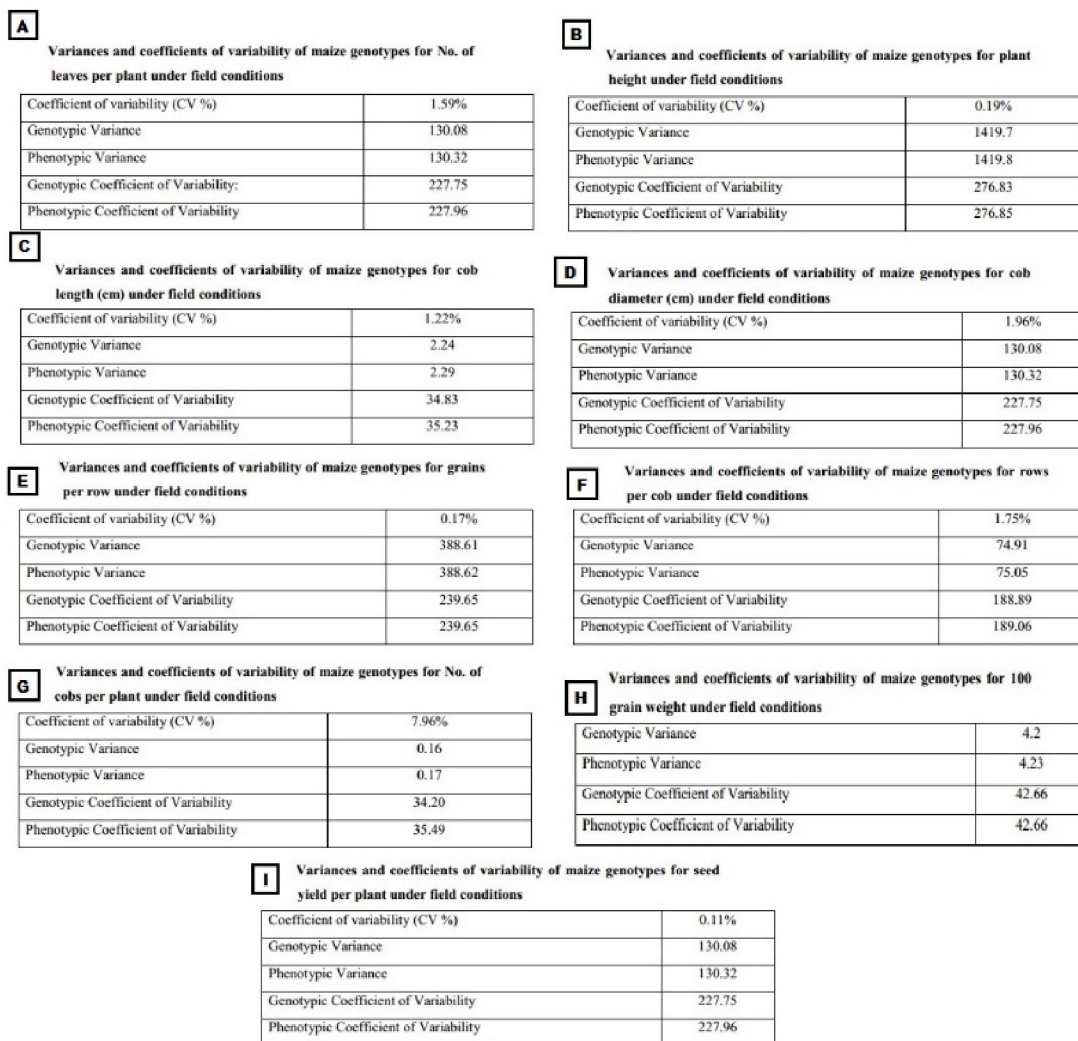


Figure 2: Coefficient of variability of all morphological characteristics of maize plants under saline field condition; A) number leaves per plant, B) Plant Height, C) cob length, D) cob diameter, E) number of grain per row, F) grain rows per cob, G) Number of cob per plant, H) 100 grain weight, I) seed yield per plant.

The comparison of accession means presented that the highest number of leaves per plant was produced by genotype Sadaf (13.0) while minimum number of leaves was recorded in EV-6089 (10.8). The magnitude of coefficient of variability of plant height was presented as (0.19%), cob length (1.22%),

cob diameter (1.96%), grain per row (0.17%), grain row per cob (1.75%), number of cob per plant (7.69%), 100 grain weight (4.2%) and seed yield per plant (0.11%). Results of coefficient of variability showed that the maximum plant height was produced by EV-6089 (228.38cm) followed by Sultan

(218.4cm) (Figure 2B). The minimum plant height was observed in Sadaf (140.44cm). Maximum cob length was produced by EV-6089 (20.19cm) followed by Sadaf (19.25 cm) (Figure 2C) whereas minimum cob length was observed in Golden (15.5 cm). Results indicated that maximum cob diameter was produced by Sunahri (36.5cm) and Sultan (34.9cm) while minimum in Golden (12.37cm) (Figure 2D).

The comparison of accession means showed that the maximum number of grains per row was produced by Golden (84.3) while minimum was observed in Sunahri (34.07) (Figure 2E). Mean comparison of accessions showed that the maximum number of grain rows per cob was produced by Sadaf (37.963) while minimum in Golden (13.667) (Figure 2F). Mean comparison of maize genotypes was showed that the maximum number of cobs per plant was produced by Sunahri (1.99) while minimum value was observed in EV-1089 (1.00) (Figure 2G). Genotypes EV-1089, I2-population and Golden were similar statistically. Differences in the 100 grain weight showed that the size of grains of different genotypes was different under filed saline conditions (Figure 2H). Genotypic variance was 4.24 while the phenotypic variance was also 4.24. Mean comparison of genotypes showed that the maximum seed yield per plant was produced by Sunahri followed by Sultan with the mean values of 245.81g while minimum seed yield per plant was observed in Golden with the mean value of 79.08 (Figure 2-I).

Genotypic and phenotypic correlation analysis

Phenotypic and Genotypic Correlation Coefficient Statistical analysis was done for the confirmation of response of maize genotypes at different doses of salinity at greenhouse and field condition. Morphological characteristics data of fifteen genotypes of maize at greenhouse condition were used for genotypic phenotypic correlation analysis. From initial experiment, seven selected genotypes of maize were used for the analysis of phenotypic and genotypic correlation analysis under field saline condition. On the base of statistical analysis, root length with shoot fresh weight, shoot fresh weight with shoot length of all maize genotypes were produced highly significant correlation at both genotypic and phenotypic level under greenhouse experiment. On the base of results, root length produce significant correlation with root fresh weight and shoot length at genotypic level but positive non-significant results at phenotypic level (Table 14). From field experiment of selected seven types, genotypic phenotypic correlation results indicated that plant height produce highly significant correlation between cob length, cob diameter, seed yield and cob length with cob diameter, cob per plant, grain row per cob and seed yield. It was persuaded from Table

15 that significant genotypic correlation was also found for cob diameter with cob per plant, seed yield per plant but negative and significant correlation was also found between some agronomic characteristics.

Table 5: Genotypic and phenotypic correlation analysis of fifteen genotypes for four characteristics (root length, root fresh weight, shoot length and shoot fresh weight) of maize.

Genotypic and Phenotypic Correlation Coefficients					
Traits	Type of correlation	RL	RFW	SFW	SL
RL	Genotypic	1.000*	0.33*	0.74**	0.22*
	Phenotypic		0.043	0.55**	0.11
RFW	Genotypic			0.03	0.57**
	Phenotypic			0.83**	0.33*
SFW	Genotypic				0.87**
	Phenotypic				0.74**

Table 6: Genotypic and phenotypic correlation analysis of selected seven genotypes for morphological characteristics of maize at field condition.

Genotypic and Phenotypic Correlation Coefficients									
Variables	PH	LFP	CL	CD	GPR	GRPC	100-GW	CPP	SYP
PH	Genotypic								
	Phenotypic		-0.24* -0.23	0.59** 0.59**	0.96** 0.96**	0.011 0.010	-0.17 -0.17	0.046 0.046	0.306* 0.295*
LFP	Genotypic								
	Phenotypic			-0.14 -0.12	-0.086 -0.082	0.35** 0.34*	0.47** 0.45*	-0.29* -0.28	0.22* 0.23
CL	Genotypic								
	Phenotypic				0.66** 0.65**	-0.14 -0.13	-0.55** 0.54**	-0.28* -0.27	0.71** 0.69**
CD	Genotypic								
	Phenotypic				-0.156 -0.16	-0.014 -0.01	0.055 0.054	0.48** 0.47**	0.60** 0.603**
GPR	Genotypic								
	Phenotypic					0.05 0.052	-0.31* -0.313	-0.25* -0.23	0.149 0.150
GRPC	Genotypic								
	Phenotypic						-0.27* -0.27*	0.801** 0.778**	-0.04 -0.043
100-GW	Genotypic								
	Phenotypic							0.124 0.12	0.313* 0.313*
CPP	Genotypic								
	Phenotypic								0.24* 0.23

4. Discussions

In biological system, most of the characters are linked with each other and such correlation may be the product of some pleiotropic effects of a gene, chromosomal segmental affiliation or due to environmental influences. Correlation analysis figures out the intensity of relationship between the two traits. To estimate the genetic inter-relationship of two characters under study, phenotypic (rp) and genotypic (gp) correlation coefficients were computed and measured for all possible combinations of characters of maize accessions under various saline environments.

The association among root fresh weight and shoot length was positive and highly significant at genotypic level while positive and significant at phenotypic level. Results revealed that correlation between root fresh weight and shoot fresh weight was positive and highly significant at phenotypic level while positive and non-significant at genotypic level under various saline environments (Table 1 and 2). Results of the correlation studies presented in explained the correlation among shoot fresh weight and shoot length was positive and highly significant at both genotypic and phenotypic levels (Table 5, Figure 2).

To estimate the genetic inter-relationship of the two characters under study, phenotypic (rp) and genotypic (gp) correlation coefficients were computed and measured for all possible combinations of characters of maize genotypes. It was revealed that (Table 6) correlation of plant height with cob length, cob diameter, and grain yield per plant was positive and highly significant at genotypic and phenotypic levels. A significant and positive correlation was observed between plant height and number of cobs per plant while positive correlation was found among number of grains per row and 100-grain weight both at phenotypic and genotypic levels. It was also found that correlation of plant height with number of grain rows per cob was negative and non-significant at both genotypic and phenotypic levels. The association of plant height with number of leaves per plant was negative and significant at genotypic level while negative and non-significant at phenotypic level.

Correlation of number of leaves per plant with number of grains per row and number of grain rows per cob was positive and highly significant at genotypic level while positive and significant association at phenotypic level. Significant and positive correlation was observed between number of leaves per plant and number of cobs per plant at genotypic level and positive and non-significant at phenotypic level. Correlation of number of leaves per plant with cob length, cob diameter and seed yield per plant was negative and not significant at both genotypic and phenotypic levels. A negative and significant association of number of leaves per plant was developed with 100-grainweight at genotypic level while negative and not significant at phenotypic level. (Malik et al. 2005) recorded strong and positive correlation between number of leaves per plant and grain yield. It was also considered that plant height and number of leaves per plant was the most contributing attributes toward high grain yield and also selection for these trait can helpful for grain yield improvement in maize accessions.

Results presented in (Table 6) showed that correlation of cob length with cob diameter, seed yield

per plant, number of cob per plant and number of grain rows per cob was positive and highly significant at genotypic level and phenotypic level and with cob length and number of grain rows per cobs a non-significant and negative correlation was exhibited at genotypic and phenotypic levels. It was also found that association of cob length with 100-seed weight was significant but negative at genotypic level while negative and not significant at phenotypic level. (Kwaga 2014) also studied correlation among yield contributing traits and their results revealed that the grain yield had positively associated with cob length. The results of (Kwaga 2014) were similar to our findings.

(Ahmadi et al. 2014) also studied correlation coefficient and results revealed that number of grains per row was significantly and positively correlated with yield in maize accessions. (Khalili et al. 2013) reported that highest correlation was found among number of grains per row and grain yield. Results of (Wannows et al. 2010) and (Pavan et al. 2011) also indicated that number of kernel per row was also positively associated with grain yield at genotypic level. (Malik et al. 2005) also concluded that plant height and number of grains per row positively associated with seed yield at genotypic level. (Ahmed et al. 1992) concluded that positive and highly and significant genetic correlation was developed between number of grains per row and 100-seed weight.

Results of correlation analysis indicated that number of grain rows per cob with number of cobs per plant was positive and highly significant at genotypic and phenotypic levels. It was also found that correlation of number of grain rows per cob with 100-grain weight was negative and significant at genotypic and phenotypic levels but relationship with seed yield per plant was negative and non-significant at both the levels. (Munawar et al. 2013) revealed that significantly positive genotypic and phenotypic association was developed among number of grain rows per cob and grain yield. (Rafiq et al. 2010) concluded that number of grain rows per cob was significantly (positive or negative) correlated with grain yield. (Yousuf and Saleem 2001) reported that number of grains and number of grain rows per cob had significant genotypic correlation with grain yield per plant. Correlation of 100-grain weight and seed yield per plant was positive and significant at genotypic and phenotypic levels (Table 5).

Correlation of 100-grain weight with number of cob per plant was positive but non-significant at genotypic and phenotypic levels. (Aminu and Izge 2012) explained that the grain yield was positively and significantly associated with 100-kernel weight at both genotypic and phenotypic level even under water deficit conditions. Results of (Zarei et al. 2012)

showed that corn yield was associated in a positive way with plant height, number of grains per row and 100-grain weight. (Srećkov et al. 2010) concluded significant strong correlation was assessed among 100-seed weight and grain yield per plant. (Malik et al. 2005) reported that 100-grain weight had positive but no genetic association with grain yield but the results of (Rafiq et al. 2010) revealed that the grain yield was significantly (positive or negative) associated with 100-grain weight at genotypic level. From this study, it was concluded that correlation analysis of maize genotypes and soil condition have potential to improve farming techniques by selecting suitable genotypes which produce resistant against specific environment. This process is also play important role in upgrading of breeding program at field level.

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