SCREENING OF MAIZE (ZEA MAYS L.) INBRED LINES UNDER WATER DEFICIT CONDITIONS

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Abstract: *Development of the selection criteria and selection of crop plant genotypes is a crucial and important task of plant breeders. The present study was designed to screen out the drought or water deficit tolerant maize genotypes. Fifty genotypes were taken from maize germplasm restored by the Department of Plant Breeding and Genetics University of Agriculture, Faisalabad, Pakistan. One set of genotypes were grown under 100% field capacity while other set at 50% field capacity in wire house conditions. The significant contrasts were observed in genotypes of various attributes under ordinary and stress timeframe. The traits root length and root shoot ratio by mass showed the high heritability and genetic advance and genotypic correlation with each other under water deficit condition provided the basis for the selection. The principle component analysis showed that the genotypes A545, AES204, WM13RA were chosen on the premise of better performance for most of the traits under study. These lines may be used in further breeding program as candidate parents for the development of drought tolerant hybrids.*

Introduction

The rise in atmospheric CO_2 could lead to global warming and changes in precipitation patterns. Increasing temperature and altered soil moisture due to climate change are expected to decrease food crop yield over the next 50 years. The productivity and plant growth of many crops plants are mainly affected by the drought in most of the tropical and sub tropic regions of the world. Maize is an important C_4 cereal crop plant grown in many countries of the world. It has been grown on an area of 183 million hectare and production of about 1021 Mt throughout the world (FAO, 2013). In Pakistan, maize is ranked third after wheat and rice among the cereals (Anonymous, 2013). Due to its multipurpose utilization, its demand will become double around 2050. The maize grain yield has been influenced by many environmental factors, among all of them the drought has been considered to be the most significant (Yin *et al*. 2016). In fact, both drought occurrence and severity are projected to be increased by 2050 (Zhao and Luo 2007)**.** Drought is known to affect morphology, photosynthesis, dry matter (DM) and grain yield (Hao *et al*. 2016, Gheysari *et al*. 2017). It has been widely recognized that maize during the growing season is prone to drought (Çakir 2004, Saseendran *et al*. 2014). It has been reported that the drought stress induced stomata closure and caused damaging in photosynthetic system (Lawlor and Uprety 1993, Flexas *et al*. 2012). Sunlight deficit (solar radiation) usually resulted in photoinhibition (light-induced decrease in photochemical activity) (Terashima *et al*. 1994, Sharwood *et al*. 2014). Genetic variability is basic tool for the plant breeder to develop the tolerant genotypes which can cope with agro-climatic changing in near future. The well structured knowledge of plant genetics o for the climate change is necessary to understand the ground realities of the conditions (Thirunani *et al*., 2000). The present study was designed to develop selection criteria of such traits with high genotypic correlation, genetic advance, and heritability to produce maize genotypes, effective in water usage even under water deficit conditions.

Material method

Site description

The experiment was conducted during the maize-growing season of 2015 at wire house of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan (31.4504° N, 73.1350° E). The climate of the region is continental monsoon with four distinct seasons. It is at its peak in July and August during monsoon season. The annual high temperature was recorded as 31.3°C while 743mm the mean annual precipitation. About 60% of precipitation received between July

and August. The soil is the typical soil consists of young stratified silt loam or very fine sand loam which makes the subsoil weak in structure.

Collection of the germplasm

Fifty exotic and elite inbred lines were collected from the germplasm of the Department of Plant Breeding and Genetics. Two sets of genotypes were grown in the wire house according the factorial randomized complete block design. One set of inbred lines were seeded under normal condition (100% field capacity). The second set was sown in wire house under water deficit condition (50% FC) in the polythene bag. All other agronomic suggested procedures were implemented. The data was recorded after 21 days of the sowing. The following plant characters were studied; root length (RL: cm), shoot length (SL: cm), fresh root weight (FRW: g) fresh shoot weight (FSW: g), dry root weight (DRW: g), dry shoot weight (DSW: g) and root shoot length ratio (RSL ratio)

Table 1. Maize inbred lines for the experiment

Inbred lines	Name	Inbred lines	Name
1	M-14	26	PB77
2	A50-2	27	52B-4
3	A495	28	53P4
4	A509	29	83P1
5	A545	30	20P2-1
6	A556	31	L7-2
7	AES204	32	70NO-2
8	Antigua-1	33	150P1
9	OH-28	34	HY7
10	OH 33-1	35	IC654
11	OH410	36	JY12
12	W64SD	37	ML1
13	W64TMS	38	ML3
14	WMBRA	39	ML4
15	WF-9	40	ML6
16	W187R	41	ML8
17	W10	42	ML9
18	WA3748	43	ML11
19	W82-3	44	ML12
20	B-34	45	ML14
21	B-34-2B	46	ML15
22	B-42	47	ML17
23	Q-66	48	ML18
24	Q-97	49	ML20
25	N48-94	50	ML21

Statistical and Biometrical analysis

The means were separated by the least significant difference (LSD) test at the probability level of 0.05%. The Estimate of broad sense heritability was recorded as the method outlined by Reeve and Robertson (1953) respectively. Genetic advance was calculated according to the method suggested by Johnson *et al*. (1955). Low water stress effects of several traits were observed in the graph under both normal and water deficit conditions using XLSTAT.

Principle component analysis was performed according to Gabriel, (1981) for both of the treatments separately using most variable principle factor in the form of biplot that was 2D scatter diagram showed the scattering pattern of genotypes and traits.

Results

Summary Statistics

The mean comparisons, minimum values, maximum values and standard deviation for normal and stress conditions were presented in the statistics summary (Table 2). Under normal condition the RL was ranged from 5cm to 13.5 cm with mean 10.1±1.425cm whereas under water deficit condition it was ranged from 7 cm to 16.5 cm with mean 10.85±2.16cm. The SL was ranged from 10.75 cm to 21 cm with mean 14.22±2.21cm under well water or normal condition while under low moisture stress condition it was ranged from 9.75 cm to 18.25 cm with mean value 13.86±1.46cm. Under normal condition the RW was ranged from the 2.49g to 11.98g with mean 5.05±1.70g whereas under stress condition it was ranged from 2.64g to 6.4g with mean 4.06 ±0.742g. The SW was ranged from 0.885g to 4.26g with mean 1.93±0.61g under well water condition while under low moisture stress it was ranged from 0.675g to 2.59g with mean value 1.49±0.379g. Under normal condition the DRW ranged from the 0.403g to 2.335g with mean 1.04± 0.40g whereas under stress condition it was ranged from 0.385g to 1.86g with mean 0.9g±0.35g. The DSW was found from 0.168g to 0.67g with mean 0.327±0.109g under well water while under low moisture stress it was ranged from 0.178g to 0.683g with mean value 0.298g ±0.094g. Under normal condition the RS ratio was ranged from the 1.366 to 10.59 with mean 3.018±1.528 whereas under stress condition it was ranged from 1.188 to 6.493 with mean 3.763±1.265.

Genetic components in seedling traits

Heritability helps to estimate the reliability of the phenotypic value in genetic research of the quantitative attributes of the plant (Ahmed *et al*., 2011; Falconer and Mackay, 1996). Under normal condition, heritability was found moderate and low for most of the attributes under consideration. The heritability was found for different traits under normal condition; RL (51.182%), SL (63.425%), RW (69.65%), SW (67.35%), DRW (49.789%), DSW (47.941%), RS ratio (57.701%). The genetic advance was found for RL (17.1%), SL (22.54%), RW (52.51%), SW (48.472%), DRW (46.02%), DSW (38.236%), RS ratio (67.78%), whereas under low moisture stress, heritability was found for RL (89.696%), SL (51.172%), RW (43.371%), SW (34.142%) DRW (34.142%), DSW (46.372%), RS length ratio (73.311%) while genetic advance was found for RL (37.810%), SL (12.83%) RW (19.268%), SW

(21.718%), DRW (43.84%), DSW (51.184%), RS ratio (58.43%)

Genotypic correlation

Association under normal conditions

It was found that the RL showed significant genotypic correlation with SL (0.133), DSW (0.259), RS ratio (0.217), SL had significant genotypic correlation with RW (0.46), SW (0.80) DRW (0.39) ,DSW (0.75) and RS ratio (0.36), RW exhibited significant genotypic association with SW (0.57), DRW (0.30) and DSW (0.588), SW showed the positive and significant genotypic association with DSW (0.77) and RS ratio (0.499) under ordinary situation. While in water stress, RL showed the significant genotypic association with SL (0.28), RW (0.29), DRW (0.44) RS ratio (0.11), SL had genotypic correlation with RW (0.30), SW (0.74), DSW (0.50) RS ratio (0.19), SW with RS length ratio (0.42).

Table 2. Summary statistics for various maize traits under normal and stress conditions

Variable		Min	Max	Mean	S.D
RL	**Normal**	5.000	13.500	10.106	1.425
	Stress	**7.000**	**16.500**	**10.850**	**2.162**
SL	**Normal**	10.750	21.000	14.223	2.218
	Stress	**9.750**	**18.250**	**13.869**	**1.468**
RW	**Normal**	2.495	11.980	5.050	1.702
	Stress	**2.645**	**6.460**	**4.062**	**0.742**
SW	**Normal**	0.885	4.265	1.936	0.619
	Stress	**0.675**	**2.595**	**1.497**	**0.379**
DRW	**Normal**	0.403	2.335	1.049	0.407
	Stress	**0.385**	**1.863**	**0.900**	**0.353**
DSW	**Normal**	0.168	0.673	0.327	0.109
	Stress	**0.178**	**0.683**	**0.298**	**0.094**
RS	**Normal**	1.366	10.591	3.018	1.528
	Stress	**1.188**	**6.493**	**3.763**	**1.265**

Table 3. Genotypic correlation of various traits of maize under normal and water stress condition

Traits		SL	RW	SW	DRW	DSW	RS
RL	Normal	0.1338*	0.06	0.1472	0.2597*	0.0760	0.2171*
	Stress	**0.2897***	**0.2991***	**0.1474**	**0.4497***	**0.2032**	**0.1088***
SL	Normal		0.4699*	0.8071*	0.3946*	0.7547*	0.3665*
	Stress		**0.3066***	**0.7493***	**0.0373**	**0.5027***	**0.1968***
RW	Normal			0.5764*	0.3028*	0.5888*	0.1035
	Stress			**0.3348**	**0.3357**	**0.308**	**0.1277**
SW	Normal				0.171	0.7748*	0.4990*
	Stress				**0.2438**	**0.2846**	**0.4211***
DRW	Normal					0.4653	0.2364
	Stress					**0.1277**	**0.4568**
DSW	Normal						0.3926
	Stress						**0.2092**

Table 4. Genetic components of various traits of maize under normal and water stress condition

SOV		RL	SL	RW	SW	DRW	DSW	RS
MS	Normal	4.063	9.843	5.795	0.766	0.332	0.024	4.67
	Stress	**9.352**	**4.307**	**1.1**	**0.287**	**0.25**	**0.018**	**3.198**
h^2_{bs}	Normal	51.182	63.425	69.65	67.35	49.789	47.941	57.701
	Stress	**89.696**	**51.172**	**43.371**	**34.142**	**34.142**	**46.372**	**73.311**
GA	Normal	17.1	22.54	52.51	48.472	46.02	38.236	67.78
	Stress	**37.81**	**12.83**	**19.268**	**21.718**	**43.84**	**51.184**	**58.43**

Association under moisture stress situation

Principle component analysis

Biplot were formed by PCA for the normal and moisture stress condition separately to assess the genetic variability in the germplasm of maize. The genotypes near the origin of the biplot showed average performance for the characters. Genotypes for away from the origin in the direction of the vector arrow were indicators of the high mean and genotype with opposite the vector showed the poor performance for subjected traits. The biplot showed that RL, SL, RW, SW, DRW, DSW were found positive discriminator under normal conditions. The graph also depicted that 66.09% genetic variability in the mean data, PC1 and PC2 contribute 45.42% and 20.67% respectively. RL showed the acute angle

(<90) with most of the traits, had association with other seedling traits. The genotypes AES204, WM13RA were found high performance for most of the traits and ML 17 fall most distantly in the region of the RS ratio while W10,ML11, ML12, ICS65 showed poor performance under study under well water condition (Fig 1). The biplot showed that RL, SL, RW, SW, DRW, DSW were found positive discriminator under low moisture conditions. The graph also depicted 59.29% genetic variability in the mean data, PC1 and PC2 contribute 33.31% and 25.99% respectively. RL showed the acute angle (<90) with most of the traits, had association with other seedling traits. The genotypes A545, AES204, WM13RA were found high performance for most of the traits while Q-66, ML 1, ML4 showed poor

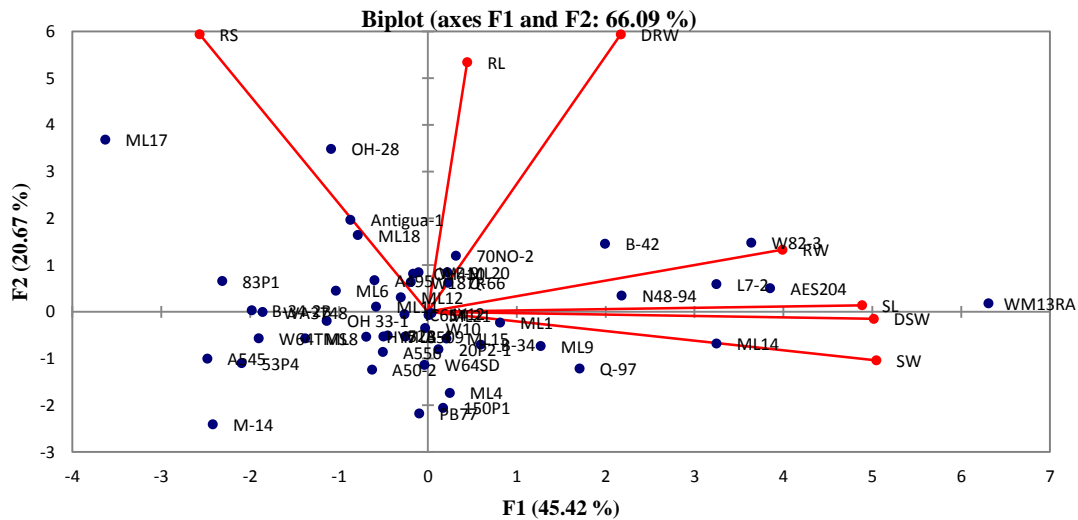performance under study low water stress condition   (Fig 2).

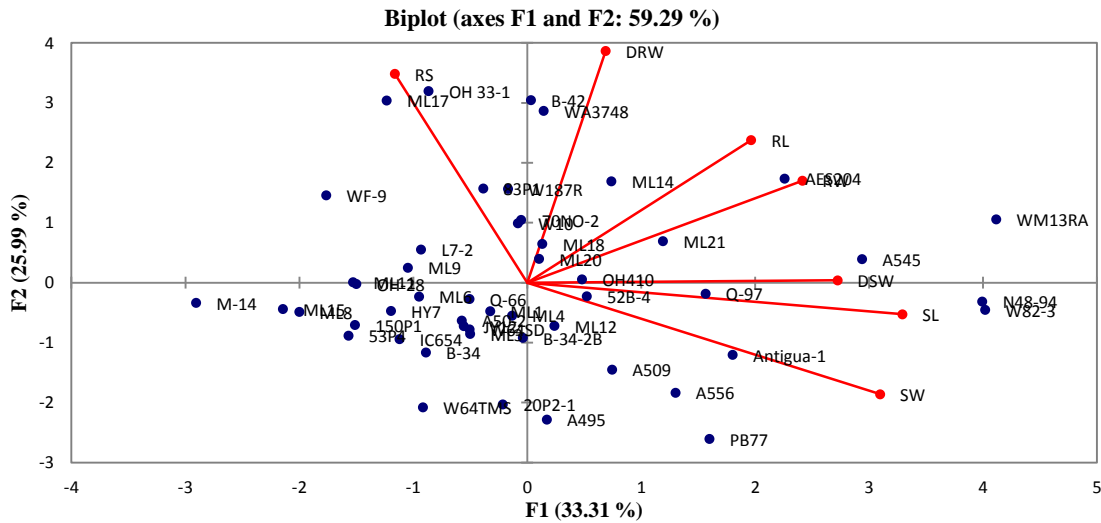**Fig. 1. Biplot of maize genotype under normal conditions**

Fig. 2. Biplot of maize genotype under water deficit condition

Discussion

Many abiotic stresses, including low moisture enviro nment, severely affect maize production (Aslam *et al*, 2014). Maize plants are susceptible to low water tension during their life cycle with multiple morphophysiological and biochemical adversely specific growth and development levels (Anjum *et al*., 2017).

Genetic variability

A fundamental requirement for genetic advancement is the existence of genetic variability in any available germplasm at the alllic level.   The comprehensive knowledge on the nature and magnitude of genetic variability is available to direct breeders to map out genetic improvement for breeding programs. Summary statistics indicated that the root length parameter showed the high value of mean in water stress condition than the normal condition showed the change of the trend from the shoot to root the same

result was also reported by the Chohan, (2012); Ali *et al*., (2014) and Ahsan *et al*., (2008). The mean values of the SL, RW, SW, DRW, DSW, RS ratio decrease as compared to the normal conditions indicated the effect of drought on the plant growth (Farooq *et al*., 2009). The huge differences between maximum and minimum values and mean square showed the significant difference among the genotypes for most of the traits under study (Chohan, 2012, Ali *et al.*, 2014; Ahsan, *et al.,* 2008)

Development of selection criteria

High heritability and genetic advance may help a plant breeder to predict the rate of the gain through the selection (Wang *et al.,* 2011). The genetic reliability of the phenotypic values can be predicted from the heritability estimates, which may be used in the direction of the breeding improvement of the crops (Falconer and Mackay, 1996). The high heritability and genetic advance showed that trait can be fixed by simple selection (Najeeb *et al*., 2009).

Under moisture stress situation shoot length, root weight, shoot weight showed the high heritability and genetic advances. The traits like shoot length and root shoot length ratio with high heritability and genetic advance provide the basis of selection of tolerant lines for low moisture stress. Correlation assisted selection can be used to bring fast improvements in the maize germplasm (Ogunniyan and Olakojo, 2014). Root length showed the positive correlation with dry root weight indicated that the accumulation of the dry matter due to uptake of the root under the water stress condition and genotypic correlation of root length with the root shoot length ratio may be served as selection criteria to select tolerant line.

Selection of Genotype

Principle component analysis is one of the multivariate analyses used to assess the variability and performance of different crops under normal and water deficit conditions with help of PC biplots (Ashraf *et al*., 2015; Latif *et al*., 2015; Mustafa *et al*., 2015). Based on the results of PCA biplot best performing genotypes were selected from exotic and elite germplasm of maize under water deficit condition. The genotypes such as A545, AES204 and WM13RA were found high performance for most of the traits were found drought tolerant and while lines Q-66, ML 1 andML4 was found drought susceptible.

Conclusion

It was concluded that the variability was found among the genotypes for all the traits under study. The traits such as the root length and root shoot length ratio had high heritability and genetic advance may be served as selection criteria. The genotype such as A545, AES204 and WM13RA may be selected as tolerant genotypes, these lines may be used in the further breeding programs as a parents to develop water deficit tolerant genotypes and hybrids.

Conflict of interest

The authors declared absence of any conflict of interest.

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