

RESEARCH ARTICLE

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Studies of genetic variability and correlation among morphological traits of maize (*Zea mays* L.) at seedling stage.QURBAN ALI¹, MUHAMMAD AHSAN¹, HAFIZ SAAD BIN MUSTAFA^{2*} AND EJAZ-UL-HASAN²¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.²Oilseeds Research Institute, AARI, Faisalabad, Pakistan.**Abstract:**

The present investigations aimed to evaluate the genetic diversity and character association in twenty maize accessions at seedling stage. The experiment was laid out in completely randomized design and correlation analysis both at genotypic and phenotypic levels were practiced. Heritability estimates were used to determine the selection criteria under drought stress conditions. The higher magnitude of heritability and genetic advance were recorded for fresh shoot weight, fresh and dry biomass of seedlings. The significant genotypic and phenotypic correlations were found between root and shoot length, fresh and dry biomass of the seedlings. However, fresh shoot weight had positive association with fresh biomass of seedlings and dry root weight with dry biomass of seedlings. It was suggested that traits like fresh and dry biomass of seedling, root and shoot length may be used as selection criteria to obtain high yielding maize genotypes under normal and drought stress conditions.

Key words: genotype, drought, heritability, genetic advance, inbred lines.

1. Introduction

Maize is one of the most important cereal crop in the world after wheat and rice. It is grown in Pakistan as a major cash crop under the area of 1083 thousand hectares with production of 3990 thousand tones [3]. Maize is dual purpose crop it is used as a food for human and feed for livestock. It is also used as a raw material in medicine, food and textile industries. Maize has high nutritive value as it contains 72 % starch, 10 % protein, 4.80 % oil, 8.50 % fiber, 3.0 % sugar, and 1.70 % ash [4].

The intelligent exploitation of maize inbred lines for genetic analyses requires a detailed knowledge of genetic and historical relationships between these lines and an understanding of the partitioning of genetic diversity among them. For example, developmental mutants of maize can exhibit strikingly different phenotypes when assayed in the genetic backgrounds of different maize inbred lines [8]. Knowledge of the relationships among lines would help to identify a set of inbred lines that have maximal diversity for the analysis of the effects of genetic background. Single-nucleotide polymorphism discovery in maize can be optimized by selecting a set of lines that capture the maximum number of alleles or haplotypes [13]. The present study was conducted to evaluate various maize genotypes for seedling traits.

2. Materials and methods

The present study was conducted in the glass-house of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during crop season of 2011. The genetic material was comprised of twenty accessions given in Table-1. The germplasm was collected from the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan and National Agricultural Research Centre, Islamabad, Pakistan.

These genotypes were sown in polythene bags (18 × 9 cm) filled with sandy loam soil (pH 7.8 and EC 1.7 dS m⁻¹) in the iron trays with three replications following completely randomized design. Field capacity of the soil was determined before sowing. Two seeds per polythene bag were sown and thinned up one healthy seedling after emergence. All the recommended agronomic and cultural practices were carried out. The moisture level was maintained by volume on alternate days by using a moisture meter (ΔT-NH2, Cambridge, England). The average temperature throughout the experimental period was 42 °C. At five leaf stage, five plants were selected randomly from each genotype and data were recorded for fresh root length, fresh shoot length, fresh root weight, fresh shoot weight, fresh biomass of

seedling, dry root weight, dry shoot weight and dry biomass of seedlings.

Table1: The detail of experimental material

Genotype	Status	Source
B-316	Inbred line	PBG, UAF
F-96	Inbred line	PBG, UAF
F-113	Inbred line	PBG, UAF
F-111	Inbred line	PBG, UAF
F-114	Inbred line	PBG, UAF
EV-340	Inbred line	PBG, UAF
EV-347	Inbred line	PBG, UAF
EV-335	Inbred line	PBG, UAF
B-322	Inbred line	PBG, UAF
F-146	Inbred line	PBG, UAF
EV-323	Inbred line	PBG, UAF
F-140	Inbred line	PBG, UAF
F-143	Inbred line	PBG, UAF
F-130	Inbred line	PBG, UAF
F-117	Inbred line	PBG, UAF
B-327	Inbred line	PBG, UAF
Sh-139	Inbred line	PBG, UAF
EV-1097Q	Variety	NARC
Pop/209	Variety	NARC
Raka-poshi	Variety	NARC

2.1. Statistical Analysis

The data were subjected to analysis of variance [12]. The genotypic and phenotypic correlations were calculated by Kwon and Torrie technique [7]. The genetic advance was calculated by using Falconer formula [5].

2.2. Statistical Analysis Formulae:

Phenotypic and genotypic coefficients of variation were calculated according to the formula given below:

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

GCV = Genotypic coefficient of variation (%)

PCV = Phenotypic coefficient of variation (%)

\bar{X} = Grand mean of the trait

$\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = genotypic variance

Broad sense heritability for each recorded trait was calculated as a ratio of the genotypic variances to phenotypic variances. Phenotypic (r_p) and genotypic (r_g) correlation coefficient was calculated as outlined by Kwon and Torrie [7].

$$r_p = \frac{M_{ij}}{\sqrt{(M_{ii})(M_{jj})}}$$

Where,

r_p = the estimate of phenotypic correlation coefficient

M_{ij} = the mean product of genotypes for the i^{th} and j^{th} traits

M_{ii} and M_{jj} = Variety mean squares for i^{th} and j^{th} traits, respectively.

$$r_g = \frac{Cov_{gij}}{\sqrt{(Var_{gi})(Var_{gj})}}$$

Where,

r_g = Genotypic correlation coefficient

Cov_{gij} = Genotypic covariance of i^{th} and j^{th} traits

Var_{gi} = Genotypic variance of i^{th} traits

Var_{gj} = Genotypic variance of j^{th} traits

Standard error of genotypic correlation coefficients (SE of r_g) was calculated according to Reeve [9]. The Genotypic correlation coefficient was considered significant if their absolute value exceeded twice their standard error.

$$S.E. \text{ of } r_g = \frac{1 - r_g^2}{\sqrt{2}} \sqrt{\frac{\sqrt{h_i^2} \sqrt{h_j^2}}{h_i^2 \cdot h_j^2}}$$

Where,

r_g^2 = The genotypic correlation coefficient between the traits i and j .

h_i^2 = The heritability of i^{th} trait.

h_j^2 = The heritability of j^{th} trait.

The estimates of heritability and genotypic correlation coefficient were considered significant if their absolute value exceeded twice of their standard error. Phenotypic correlation coefficients were tested using t-test according to Steel and Torrie [12] as given below.

$$t = \frac{r}{\sqrt{(1 - r^2) / n - 2}}$$

Where,

r = the phenotypic correlation coefficient, $n-2$
= correlation error degree of freedom

Genetic advance (GA) was calculated by the following formula [5].

$$GA = \sigma_p \times h^2 \times i$$

Where, σ_p = the phenotypic standard deviation,
 h^2 = Estimate of broad sense heritability,

i = constant value (1.755) that reflects the selection intensity (10%)

3. Results and discussion:

It is clear from Table 2 that higher genotypic and phenotypic variances were recorded for fresh biomass

of seedling (80.793, 81.471) followed by fresh shoot weight (43.450, 44.241) respectively. The higher genotypic and phenotypic coefficient of variation was recorded for dry root weight (42.419, 43.911) followed by dry shoot weight (47.271, 40.442) respectively. The higher environmental variance and coefficient of variance were recorded for fresh root weight (8.140, 7.176) respectively. Similar results were found by [10, 11 & 2]. The highest estimates of heritability and genetic advance were recorded for fresh and dry shoot weight, fresh and dry biomass of seedlings. Selection of higher yielding maize genotypes may be helpful on the basis of higher genetic advance and heritability.

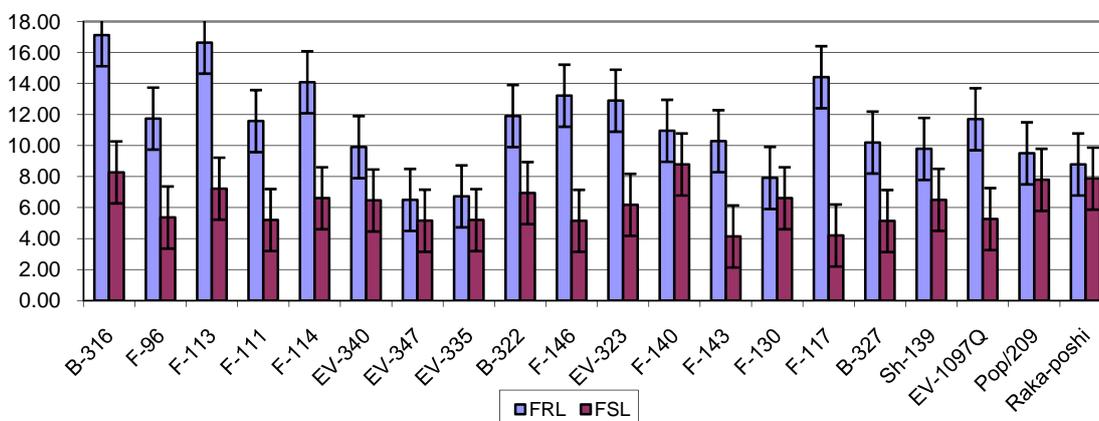


Figure1: Fresh Root length (FRL) and Fresh shoot length (FSL) of maize seedling

It is shown in Figure-1 that higher root length was recorded for B-316, F-113, F-117 and F-114 while lower for EV-335 and EV-347 but higher shoot length was recorded for F-114, B-316 and Raka-poshi while lower shoot length was for F-117 and F-143. The higher root and shoot length of B-316, F-114 and F-117 indicated that these lines may be selected for developing drought tolerance genotypes [1&2].

It is persuaded from Figure-2 that higher fresh root weight was recorded for F-143, F-117, B-327 and Sh-139 while lower for F-96, F-130 and EV-335 but higher dry root weight was recorded for F-117, EV-340, B-322 and B-327 while lower for F-114 and Raka-poshi. The higher values of fresh and dry root weights indicated that the lines F-117 may be used to develop drought tolerant genotype [1&2].

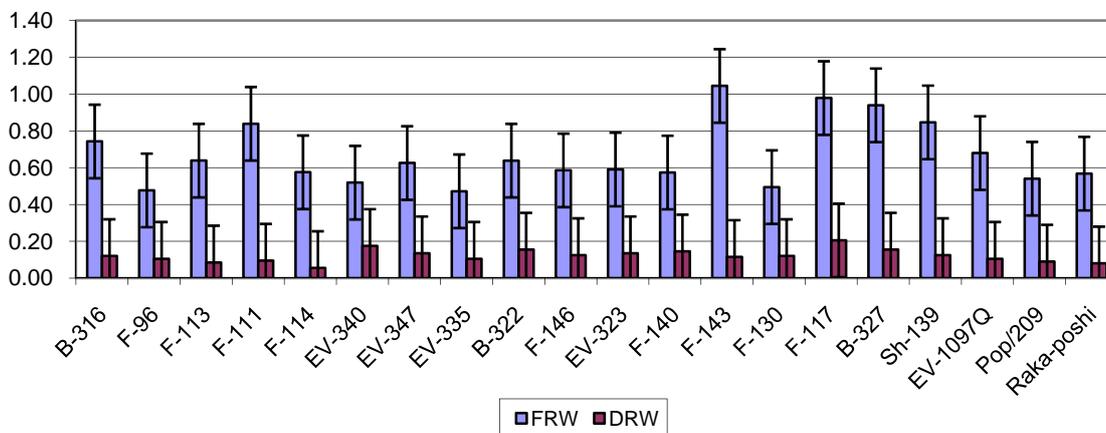


Figure 2: Fresh root weight (FRW) and Dry root weight (DRW) of maize seedlings

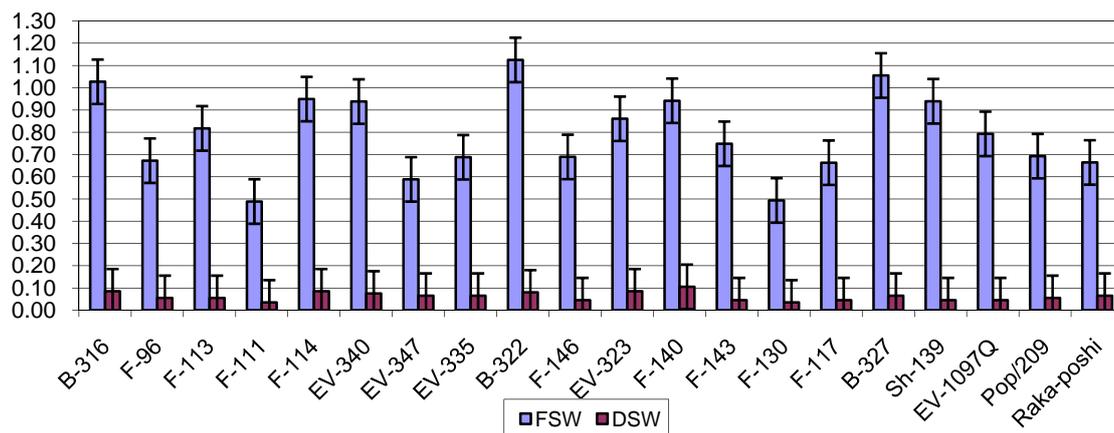


Figure 3: Fresh shoot weight (FSW) and Dry shoot weight (DSW) of maize seedlings

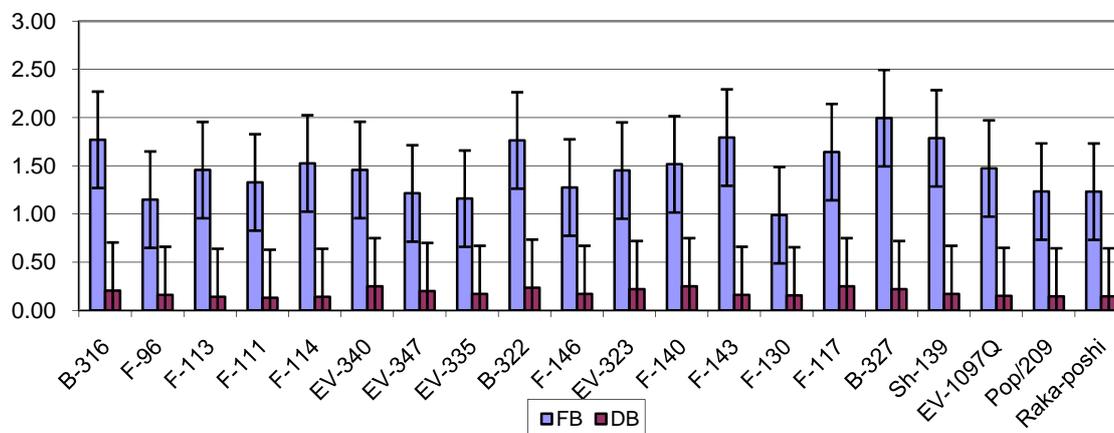


Figure 4: Fresh biomass of (FB) and Dry biomass of (DB) of maize seedlings

It is clear from Figure- 3 that higher fresh shoot weight was recorded for B-322, B-327 and B-316 while lower for F-111 and F-130 but dry shoot weight was for F-140, EV-323, B-316 and F-114 while lower for F-111 and F-130. The higher values of fresh and dry shoot weights indicated that lines B-316 may be used to develop drought tolerant genotype [1&2].

It is clear from Figure-4 that higher fresh biomass of seedlings were recorded for B-327, Sh-139, B-316 and F-143 while lower for F-96 and F-130 but higher dry biomass of seedlings were recorded for F-140, B-327 and F-117 while lower for F-111, F-113 and F-114. The higher values of fresh and dry biomass of seedlings indicated that line B-327 may be used for developing drought tolerance genotypes [1&2].

3.1. Correlation:

It is clear from Table 3 that high and positive genotypic correlation of fresh root length was found with fresh shoot length, dry root and shoot weight. The high and significant phenotypic correlation was

found for fresh shoot length, fresh biomass of seedling and dry root weight while negative and significant phenotypic correlation was found for dry shoot weight. Similar results were described by [2]. A positive and significant genotypic correlation was found between fresh shoot length and fresh root weight, fresh shoot weight and dry root weight but negative and significant genotypic correlation was found for dry biomass of seedlings. A positive phenotypic correlation was found between fresh shoot length and fresh shoot weight. Similar results were found by [6, 14 &15]. Fresh root weight was positive and significantly correlated with fresh and dry biomass of seedling and dry shoot weight both at genotypic and phenotypic levels while positively with fresh shoot length at the genotypic level but negatively at the phenotypic level. Fresh shoot weight was positive and significantly correlated with fresh root and shoot length and fresh biomass of seedling at

genotypic and phenotypic levels. Fresh biomass of seedling was highly and significantly correlated with fresh and dry root weight, shoot weight and dry biomass of seedling both at genotypic and phenotypic levels. The strong genotypic correlation of fresh and dry biomass indicated that selection on the basis of fresh and dry weight may be useful to improve the yield of maize genotypes. Similar results were reported by [11, 2]. Dry root and shoot weight were

significantly correlated with each other and with fresh and dry biomass of seedling at genotypic and phenotypic levels. Dry biomass of seedling was highly and significantly correlated with fresh root weight dry root and shoot weight at genotypic and phenotypic levels. The significant genotypic correlations indicated that selection can be made on the basis of these traits [11, 10&2].

Table 2: Estimates of various genetic components for maize genotypes

Traits	GCV%	PCV%	GV	PV	ECV%	EV	GA	h ² _{BS} %
FRL	31.861	29.431	3.451	4.391	0.940	1.319	2.890	78.60
FSL	39.349	38.478	7.910	8.456	0.546	2.322	4.774	93.50
FRW	3.413	4.933	11.231	19.371	8.14	7.176	4.472	57.90
FSW	29.239	28.321	43.450	44.241	0.791	0.898	11.464	98.20
FB	37.424	38.988	80.793	81.471	0.678	1.769	15.709	99.20
DRW	42.419	43.911	6.518	7.213	0.695	2.176	4.259	90.40
DSW	47.271	40.442	26.729	28.471	1.742	3.769	8.791	93.90
DB	21.899	20.781	38.437	39.271	0.834	5.631	10.764	97.90

GV = Genotypic variance, PV = Phenotypic variance, EV = Environmental Variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, ECV = Environmental coefficient of variance, GA = Genetic advance, h²_{bs} = Broad sense heritability.

Table 3: Genotypic and phenotypic correlation for various morphological traits of maize seedlings

Traits	R	FSL	FRW	FSW	FB	DRW	DSW	DB
FRL	G	0.7512**	0.0311	0.4579*	-0.0641	0.6398**	0.6647**	-0.0112
	P	0.6213**	0.1213	0.0943*	0.2139**	0.6121**	-0.3411**	0.0449
FSL	G		0.4311*	0.4421**	-0.0129	0.3528**	0.0292	-0.2176*
	P		-0.2179**	0.3701*	-0.2101	0.1732	0.4471**	0.2911*
FRW	G			-0.0211	0.4319**	-0.1762	0.2123*	0.2921*
	P			0.1101	0.4421**	-0.2711*	0.2679**	0.3129**
FSW	G				0.6671**	0.0217	0.0044	0.0121
	P				0.6319**	-0.0023	0.0203	0.0373
FB	G					0.3172*	0.4144**	0.9127**
	P					0.3319**	0.4324**	0.9087**
DRW	G						0.4811**	0.8921**
	P						0.4789**	0.8131**
DSW	G							0.1443*
	P							0.2376*

** = Highly significant, * = Significant, DRW = Dry root weight, DSW = Dry shoot weight, FRL = Fresh root length, FSL = Fresh shoot length, FB = Fresh biomass of seedling, DB = Dry biomass of seedling, FSW = Fresh shoot weight, FRW = Fresh root weight

4. Conclusion

It was concluded from the present study that the strong genotypic and phenotypic correlation was found between root and shoot length, fresh and dry biomass of seedling, fresh shoot weight and fresh biomass of seedling and dry root weight with dry

biomass of seedlings. It was suggested that fresh and dry biomass of seedling, root and shoot length may be helpful to select higher yielding maize genotypes for normal and drought stress conditions.

5. References

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