

# NUTRITION OF



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# Genetic Analysis of Water Stress Tolerance and Various Morpho-Physiological Traits in *Zea mays* L. Using Graphical Approach

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Abstract: Fifty inbred lines of  $Zea\ mays\ L$ . were screened against water stress in glass house experiment. Six inbred lines selected on the basis of various tolerance levels at seedling stage were hybridized in a diallel mating system. The F1 hybrids along with the parents were evaluated in field under normal and water stress regimes to determine the nature and magnitude of genetic variances and heritability estimates. Highly significant ( $p \le 0.01$ ) differences were noted among the genotypes for all the traits studied under both regimes. The scaling test disclosed full adequacy for traits like plant height, ear leaf area, grain yield, Cell Membrane Thermostability (CMT) and net Photosynthetic rate ( $P_0$ ) under normal condition. Similarly characters like ear leaf area, 100-grain weight, cell membrane thermostability and net photosynthetic rate under water stress condition showed additive genetic effect with partial dominance which suggested that these traits might be useful during selection for developing synthetics. The model was partially adequate for anthesis-silking interval and 100-grain weight under normal condition and plant height, anthesis-silking interval and grain yield under moisture deficit condition. Moderate to high heritability estimates for grain yield and yield related parameters revealed maximum ability to transfer the genes to the next generation.

Key words: ASI, CMT, Pn, additive components, graphical analysis, heretibility, maize, diallel

### INTRODUCTION

Maize (Zea mays L.), the only cultivated species of the genus Zea is one of the oldest domesticated food crops in the world. Maize, belongs to a group of C4 crops, is essential to present and future worldwide food security (Brown, 1999; Pingali, 2001). It is world's widely grown leading cereal crop and ranks third in Pakistan after wheat and rice. In Pakistan, currently it is planted on an area of 949.83 thousand hectares with annual production of 3476.98 thousand tones and average yield of 3661 kg/hectare (Anonymous, 2009-2010). Maize can adapt to wide range of environmental conditions due to the presence of genotypic and phenotypic diversification. Therefore, it is, grown over a variety of environments ranging from tropical to temperate regions of the world. Paterniani (1990) pinpointed that maize cultivation problems in the tropics are numerous and more challenging than in temperate areas.

Water stress affects maize plant by causing poor crop stand, low plant density, stunted growth, wilting, top firing, tassel blast, silk delay, poor seed set and barrenness which eventually result in reduced grain yield. Drought is single most important abiotic stress limiting crop production worldwide. Water deficient or lack of adequate soil moisture affects the plant ability to grow and complete a normal life cycle (Moussa and Abdel-Aziz, 2008). Drought severely impairs plant growth and development, limits production and the performance

of crop plants, more than any other environmental factor (Shao *et al.*, 2009). Continuous moisture deficiency results stunted stem growth and reduced root expansion (Banziger *et al.*, 2000). Pakistan is already one of the water-stressed countries in the world, a situation which is going to aggravate due to high population growth. About 150 million (ha) of total world area is grown under water scarce conditions and among cereals maize is considered most vulnerable to drought stress except rice (Banziger and Araus, 2007). Drought stress losses to yield are expected to raise due to fluctuation in temperature and rainfall distribution in main production areas (Campos *et al.*, 2004).

Information on the genetic architecture of traits related to drought tolerance and their mode of inheritance is first pre-requisite to launch an efficient and target oriented breeding programme. Breeding for high yield under drought condition is more difficult than breeding for the same under favorable condition. Higher plants exhibit a range of biological, physiological, morphological adaptation in their response to water stress. However, success in breeding for stress tolerance is limited (Hollington and Steele, 2007). To evolve superior genotypes possessing drought tolerance understanding of genetic mechanism based on various morphophysiological traits is a pre-requisite either through conventional breeding or genetic engineering (Mitra, 2001; Chen et al., 2004). Therefore recognition and

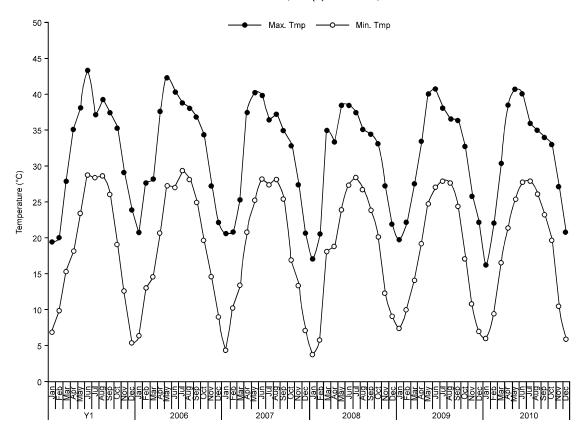


Fig. 1: Average maximum and minimum temperature of five years (2005-2010)

understanding of plant traits having strong positive correlation with drought tolerance and higher yield under drought is necessary (Richards, 2004; Rauf and Sadaqat, 2008). Many plant traits contribute to enhanced tolerance to stressful growing conditions. Drought tolerance has complex and polygenic tolerance mechanisms associated with epistatic effects and large genotypes by environments effects. The present study was planned with a view to improve maize genetically for grain yield under water stress condition.

# **MATERIALS AND METHODS**

Description of experimental materials: The present study was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material comprises six maize inbred lines: F-188, F-133, F-199, F-191, F-127, B-54 which were selected after screening against water stress. These were planted in the field for attempting all possible crosses in a complete diallel fashion during spring 2008. The female parents were hand emasculated and pollinated to produce sufficient seed of all crosses. The 15 F<sub>1</sub>S crosses, their reciprocals along with the six parents were planted in the field during autumn 2008 under normal and

moisture stress conditions. The layout of the experiment was a triplicate Randomized Complete Block Design comprising of two rows of 15.3 m length with 75 cm row to row and 23 cm plant to plant distance. For soil analysis four soil samples were collected from each replication which resulted in maximum average water holding capacity (38%) of soil dry weight and the permanent wilting point of 14%. Two seeds per hill were dibbled and later thinned to one seedling per hill. Non experimental rows were also planted to minimize the border effects. Insecticide was sprayed to control shoofly and borer attack. Each experimental unit was treated similar for all the agronomic and cultural practices from sowing to harvesting. Normal irrigations were applied to normal set of experiment whereas, 50% of the normal irrigation was applied to water stress experiment (Khan et al., 2004). Data regarding mean minimum and maximum temperature, relative humidity and monthly rainfall were taken all through the growing season. Pattern of rainfall, temperature and humidity depicted in Fig. 1 and 2.

Morph-physiological traits related to grain yield: At maturity, 10 equally competitive random plants were selected from each treatment and data for the following morpho-physiological traits were recorded.

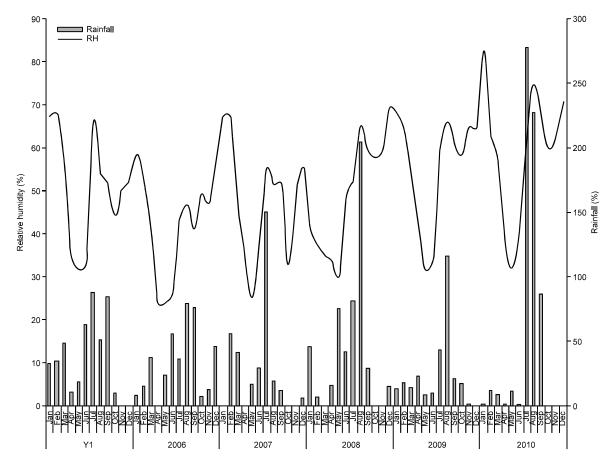


Fig. 2: Rainfall and relative humidity of five years (2005-2010)

Cell memberane thermostability: Cell Membrane Thermostability (CMT) under water stress conditions was determined according to Sullivan (1972). The percentage injury to leaf tissue due to water stress was calculated using first and second electrical conductivity measurements following the formula:

Percent injury =  $[1- (1-T1/T2)/(I-C1/C2)] \times I00$ 

T1 = First conductivity measurement of plant sample treated at 45°C before autoclave,

T2 = Second conductivity measurement of plant sample treated at 45°C after autoclave,

C1 = First conductivity measurement at room temperature (22°C) before autoclave,

C2 = Second conductivity measurement at room temperature (22°C) after autoclave.

Gas exchange parameter: Net photosynthetic rate  $(P_n)$  measurements were made on the second intact leaf from top of each plant using a CI-340 Hand-held Photosynthesis System (a portable battery operated system with a clamp on leaf chamber connected to infrared gas analyzer). Measurements were performed

at noon between 11.00-1400 P.M. Data were recorded at PAR $\geq$ 1250  $\mu$ mol m $^2$  s $^{-1}$  on clear cloudless days. Measurements were recorded when the crop is at flowering stage. Average of three plants was subjected to statistical analysis.

Plant height (cm): At physiological maturity, plant height was measured in cm as the distance from ground level to the apex of the tassel (Guzman and Lamkey, 2000) with the help of a measuring rod on 10 randomly selected plants. The average was used for the analysis of data.

Ear leaf area (cm²): Leaf area was measured as the product of the ear leaf length from the base to the tip and the maximum breadth in the center. Leaves of ten randomly selected plants from each replication were collected and leaf area was measured by using the formula suggested by Mckee (1964).

Leaf area = leaf length (cm) x leaf width (cm) x 0.73

Anthesis-silking interval (ASI): The Anthesis-Silking Interval (ASI) was calculated by using the following formula:

ASI = Days to 50% silking-Days to 50% anthesis

**100-grain weight (gm):** Three one-hundred grains samples were collected from the bulk produce, each obtained from the selected plants and weighed in grams using an electronic balance and average was used for data analysis.

**Grain yield per plant (gm):** Grain yield per plant was obtained by weighing the grains from the selected plants and average was worked out.

Statistical/biometrical analysis: The data pertaining to various physiological and agronomic parameters were statistically analyzed to determine significant differences among the genotypes under normal and water stress regimes according to Steel *et al.* (1997). The simple Additive-Dominance (AD) model proposed by Hayman (1954a) and Jinks (1954) and exemplified by Mather and Jinks (1982) for diallel analysis, was employed for further investigations.

### **RESULTS AND DISCUSSION**

ANOVA revealed highly significant genotypic variations for all characters among 36 genotypes under both

regimes. Mean squares for parental inbred lines and the crosses were significant at p≤0.05 for all the characters under normal and moisture deficit conditions except anthesis-silking interval which was non-significant under normal condition as shown in Table 1.

Adequacy test for various morpho-physiological traits both under normal and water stress conditions and validity of assumptions underlying the genetic model, were tested by joint regression analysis and analysis of variance of (Wr + Vr) and covariance (Wr - Vr). The results of the two tests under normal and water stress environment are given in Table 2.

The regression coefficient 'b' for all the parameters departed significantly from zero but did not deviate from one. This property of the regression line suggested the presence of intra-allelic gene interaction, independent distribution of genes among the parents for the trait. The unit slope of regression lines for all the traits indicated that the assumptions underlying the additive-dominance model were met (Mather and Jinks, 1982).

Mean squares of (Wr + Vr) and (Wr - Vr) revealed highly significant differences between the arrays (Wr + Vr) and non-significant variation within the arrays (Wr - Vr) for plant height, ear leaf area, grain yield per plant, cell membrane thermostability under normal irrigated

Table 1: Mean squares of various plant traits in a 6 x 6 diallel cross under normal and water stress conditions

	df	PH	ELA	ASI	CMT-S	NPR	100-GW	GYPP
Source (normal)								
Replicate	2	62.01	32.55	0.84	6.92	0.60	0.31	21.31
Genotypes	35	768.82**	8089.3**	0.97 <sup>NS</sup>	155.14**	81.07**	21.58**	1337.51**
Error	70	37.07	481.23	0.95	8.82	3.45	3.18	104.17
Mean		161.87	440.31	5.29	70.86	34.08	27.99	124.82
CV (%)		3.76	4.98	18.41	4.19	5.45	6.38	8.18
Source (water stress)								
Replicate	2	58.05	101.65	2.06	13.03	0.89	0.15	30.743
Genotypes	35	709.29**	19834**	22.17**	123.03**	185.62**	35.40**	1552.03**
Error	70	47.34	66.55	1.86	8.10	0.91	1.16	29.06
Mean		124.65	358.38	8.56	47.56	16.20	23.45	92.05
CV (%)		5.52	2.28	15.94	5.99	5.91	4.59	5.86

CV: Coefficient of Variation. PH = Plant Height, ELA = Ear Leaf Area, ASI = Anthesis Silking Interval; CMT-S = Cell Membrane Thermo-Stability, NPR = Net Photosynthetic Rate, 100-GW = 100-Grain Weight, GYPP = Grain Yield per Plant

Table 2: Scaling tests for adequacy of additive-dominance model for various plants traits under normal and water stress conditions

	Regression	slope	Mean squares	<b>S</b>		
Traits (normal)	<b>b</b> <sup>0</sup>	b <sup>1</sup>	 Wr + Vr	 Wr - Vr	Remarks	Joint regression (b)
Plant height	8.59**	0.383 <sup>NS</sup>	272294.6**	2811.68 <sup>NS</sup>	Fully adequate	b = 0.95±0.11
Ear leaf area	12.01**	0.505 <sup>NS</sup>	7713779*	93636.6 <sup>NS</sup>	Fully adequate	$b = 0.95 \pm 0.079$
ASI	4.84**	0.864 <sup>NS</sup>	0.65 <sup>NS</sup>	0.210 <sup>NS</sup>	Partially adequate	$b = 0.84 \pm 0.17$
CMT	3.24**	0.917 <sup>№</sup>	2519.827**	128.136 <sup>NS</sup>	Fully adequate	$b = 0.78 \pm 0.24$
Pn	4.613**	0.059 <sup>NS</sup>	1488.64**	53.30*	Fully adequate	$b = 0.98 \pm 0.21$
100-grain weight	9.184**	-0.169 <sup>NS</sup>	49.18 <sup>№</sup>	0.92 <sup>NS</sup>	Partially adequate	b = 1.02±0.11
Grain yield per plant	5.385**	1.475 <sup>NS</sup>	390119.4**	19089.9 <sup>№</sup>	Fully adequate	$b = 0.78 \pm 0.15$
Traits (water stress)						
Plant height	9.310**	-0.713 <sup>NS</sup>	33570.5 <sup>№</sup>	538.375 <sup>NS</sup>	Partially adequate	b = 1.082±0.116
Ear leaf area	15.89**	0.857 <sup>№</sup>	2059361**	89452.8 <sup>NS</sup>	Fully adequate	$b = 0.948 \pm 0.0596$
ASI	7.079**	1.294 <sup>NS</sup>	42.66NS	1.679 <sup>№</sup>	Partially adequate	$b = 0.845 \pm 0.119$
CMT	8.219**	1.737 <sup>NS</sup>	4781.31**	125.897 <sup>NS</sup>	Fully adequate	$b = 0.825 \pm 0.1004$
Pn	11.63**	1.32 <sup>NS</sup>	7884.38**	76.29 <sup>NS</sup>	Fully adequate	b = 0.897±0.0771
100-grain weight	10.87**	0.366 <sup>NS</sup>	533.038**	4.557 <sup>NS</sup>	Fully adequate	b = 0.967±0.0889
Grain yield per plant	3.244**	0.749 <sup>NS</sup>	54320.2 <sup>NS</sup>	5609.51 <sup>NS</sup>	Partially adequate	b = 0.8122±0.250

Table 3: Estimation of the components of genetic variations under normal and water stress conditions

									(/4DH1 + F		
Traits	raits Condition D	D	H1	H2	F	(h²)	Е	(H <sub>1</sub> /D) <sup>0.5</sup>	(H <sub>1</sub> /D) <sup>0.5</sup> //4DH <sub>1</sub> - F)	(H2/4H1)	h² (n.s)
PL,HT	Normal	509.60±26.60	150.86±67.63	141.02*±60.41	14.44±65.08	163.30±40.66	13.73±10.07	0.5441	1.05	0.234	0.84
	W.stress	516.51±10.28	98.62±26.10	94.73*±23.32	57.25±25.12	-6.21±15.70	17.32±3.89	0.4370	1.291	.2401	0.79
ELA	Normal	5170.83±106.27	920.77±269.77	620.62±240.99	-2.69.25±259.61	335.41±162.20	$170.45\pm40.165$	0.423	0.883	0.168	0.83
	W.stress	13251.65±133.72	1579.57±339.46	1281.07±303.25	-1177.63±326.67	804.63±204.10	24.55±50.54	0.345	0.772	0.203	0.85
ASI		0.05±0.041	-0.650±0.106	-0.449±0.09	-0.369±0.102	-0.132±0.06	0.343±0.01	0.42	-0.352	0.173	0.31
	W.stress	14.73±0.404	1.481±1.02	1.183±0.916	-0.469±0.987	-0.08±0.617	$0.680\pm0.152$	0.317	0.904	0.199	0.68
CMT		91.90±6.19	35.84±15.72	23.55±14.04	2.179±15.12	-0.268±9.450	3.188±2.340	0.62	1.03	0.16	0.85
	W.stress	86.88±4.39	30.38±11.15	22.70±9.96	13.21±10.73	-0.165±6.70	1.576±1.66	0.59	1.2	0.18	08.0
-H	Normal		25.05±8.800	19.28±7.86	9.67±8.47	1.02±5.29	1.22±1.31	0.67	1.30	0.19	08.0
	W.stress		50.11±9.500	35.98±8.56	-4.35±9.22	23.10±5.76	0.333±1.42	0.68	0.94	0.17	98.0
100-GW	Normal		1.499±0.942	1.70±0.84	-1.641±0.91	-0.616±0.56	1.130±0.140	0.34	0.68	0.28	0.72
	W.stress		26.95±9.37	26.25±8.36	5.75±9.01	37.23±5.63	1.02±1.39	0.61	1.29	0.19	0.79
ĕ	Normal	885.56±57.58	217.22±146.19	161.20±80.18	42.84±140.69	-19.26±87.90	37.04±21.76	0.49	1.10	0.18	0.85
	W.stress	1127.13±31.58	161.20±80.18	156.69±71.63	30.72±77.17	-1.50±48.21	10.58±11.93	0.38	1.07	0.24	92.0

Dominance effect (over all loci in heterozygous phase) (h²), Environnemental variance (E), Mean degree of dominance (H₁/D)û², Proportion of genes with positive and negative effects GY: Grain in the parents (H⅓Hh), Proportion of dominant and recessive genes in the parents (√4DH₁ - F), Heritability (Narrow sense).
PL.HT: Plant Height; ELA: Ear Leaf Area; ASI: Anthesis-silking Interval; CMT: Cell Membrane Thermostability; pn: net phohtosynthetic rate, 100-GW: 100 Grain Weight, Yield

Additive variance (D), Dominance variance (H1), Proportion of positive and negative genes in the parent (H2), Relative frequency of dominant and recessive alleles in the parents (F),

conditions and for the characters like ear leaf area, 100 grain weight, cell membrane thermostability, net photosynthetic rate under water stress condition indicated the presence of dominance. Thus, the results of both the tests suggested that the simple genetic model was fully adequate for these characters. While, non-significant differences at (p>0.05) between the arrays (Wr + Vr) for traits like anthesis silking interval, 100-grain weight under normal condition and the traits like plant height, anthesis silking interval, grain yield per plant under water stress condition showed the absence of dominant effects and presence of epistasis. Nonsignificant differences within the arrays (Wr-Vr) for all the traits except net photosynthetic rate under normal condition. Thus, based upon the results of two tests simple genetic model was partially adequate for analyzing the data set for plant traits like anthesis-silking interval and 100- grain weight under normal conditions and the traits like plant height, anthesis-silking interval, grain yield per plant under moisture deficit condition.

Estimation of genetic components of variation and graphical analysis under normal and water stress conditions: Genetic components of variation were estimated according to Hayman (1954b) and are presented in Table 3. For plant height, significant value of D and H under normal and moisture stress conditions revealed the importance of additive and dominant genetic effects. The value of H<sub>1</sub> and H<sub>2</sub> are less than D indicating that genes showing additive effects for plant height were more important than dominant genes.

The importance of dominant variation was also indicated by significant H components (H1 and H2) under both conditions. Equal value of H1 and H2 under normal water regime displayed similar distribution of dominant genes. While, unequal value of H<sub>1</sub> and H<sub>2</sub> under water stress environment displayed different distribution of dominant genes. Non significant estimates of F indicated that positive or dominant genes were not frequent under normal planting conditions. Whereas, positive and significant value of F under water stress conditions indicated that positive genes were more frequent. The significance of values of h2 indicated the important effect of heterozygous loci for plant height under normal water conditions. But non-significant value of h2 showed the unimportant effect of heterozygous loci under moisture deficit condition. The effects due to E were nonsignificant under normal but significant under water stress condition suggesting the unimportant role of environment for the expression of plant height under normal condition but played a significant role in the development of the character under water stress condition.

Mean degree of dominance  $(H_1/D)^{0.5}$  under normal (0.5441) and water stress (0.4370) conditions was less than one indicating partial dominance. Heritability in

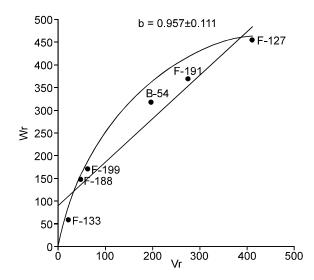


Fig. 3: Wr/Vr graph for plant height under normal water regime

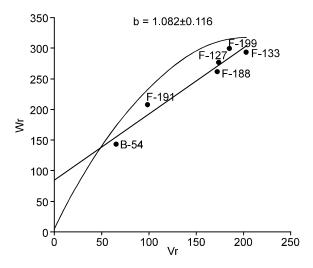


Fig. 4: Wr/Vr graph for plant height under water stress regime

narrow sense was 0.84% and 0.79% under normal and water stress conditions. Graphical presentation of the data displayed additive gene action for the inheritance of plant height. The position of varietal points along the regression line (Fig. 3) showed that F-133 followed by F-188 and F-199 carried the maximum dominant genes while F-127 being farthest, possessed maximum recessive genes under normal water regime. Figure 4 showed that B-54 had more dominant genes for plant height whereas; F-133 and F-188 had maximum recessive genes for plant height under water stress condition. The findings are in compatible with the work of Kuriata et al. (2003); Mendes et al. (2003); Kumar and Gupta, (2004); Muraya et al. (2006); Tabassum et al. (2007) and Hussain et al. (2009) who supported additive gene action for this trait.

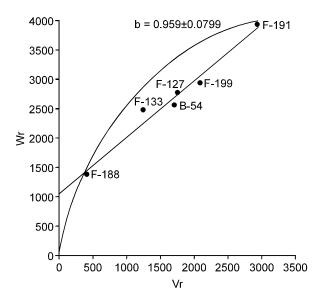


Fig. 5: Wr/Vr graph for ear leaf area under normal water regime

The relative value of H<sub>1</sub> and H<sub>2</sub> indicated different distribution of dominant and recessive genes. Genetic components D and H were significant under normal and moisture stress condition indicating the presence of additive and dominant genes (Table 3). The value of H<sub>1</sub> and H2 were less than D which indicated that additive genetic effects for ear leaf area were more important than dominant genetic effects. The value of H<sub>2</sub>/4H<sub>1</sub> ratio was <0.25, indicating unequal distribution of genes for ear leaf area among the parents. The F value was negative and non-significant showing the presence of recessive genes which was supported by high value of v4DH<sub>1</sub> + F/v4DH<sub>1</sub> - F. The significant value of h<sup>2</sup> was noted under both environmental conditions showing important effect of heterozygous loci for this trait. The degree of dominance was <one revealing the presence of partial dominance in F1 hybrid which was also shown by the slope on the regression line (Fig. 3). Environmental variation (E) was found significant under normal and non-significant under water stress conditions. Narrow sense heritability was 0.83% and 0.85% under normal and moisture deficit condition. The results are in line with Khotyleva and Lemesh (1994); Shabbir and Saleem (2002); Tabassum (2004); Akbar (2008) and Hussain et al. (2009) who reported additive and dominant type of gene action for ear leaf area. The graphical representation (Fig. 5) indicated that the parental inbred line F-188 had maximum dominant genes while F-191 had maximum recessive genes under normal environment. Under water stress environment, F-188 followed by F-127 possessed maximum dominant genes, whereas F-191 and B-54 carried maximum recessive genes for the inheritance of ear leaf area (Fig. 6).

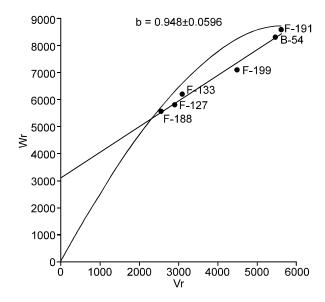


Fig. 6: Wr/Vr graph for ear leaf area under water stress regime

For anthesis-silking interval, the value of D was positive and non-significant under normal water regime indicating the absence of additive effects. While positive and significant value of D showing presence of additive genetic effects under water stress environment. The values of H<sub>1</sub> and H<sub>2</sub> were < D denoting that genes showing dominance effect were less important than additive genes. While values of H<sub>1</sub> and H<sub>2</sub> are under both planting environment displayed the distribution of dominant genes among the parental inbred lines. Negative and non-significant F value showed lower frequency of dominant alleles under both environmental conditions. The value of H<sub>2</sub>/4H<sub>1</sub> ratio was <0.25. The value of h^2 was negative observed under both environmental conditions. Environmental variation (E) was found significant under normal and water stress conditions indicating predominance role of environment. The mean degree of dominance was < one signifying partial dominance in F1 hybrid which was denotedby the regression slope. The estimate of narrow sense heritability was 31% and 68% under normal and moisture deficit environments, respectively. Afarinesh et al. (2005) reported that dominance variance was responsible for controlling anthesis to silking interval. These results are in accord with the work of Farooq (2008); Bello and Olaoye, (2009) and Khodarahmpour (2011) who found additive dominance model for anthesis-silking interval. Graphical representation in (Fig. 7) showed inbred line F-127 and B-54 had more dominant genes whereas, F-188 had maximum recessive genes for anthesis silking interval under normal condition. Under stress environment (Fig. 8) inbred line F-133 possessed maximum dominant genes whereas, maximum recessive genes were carried by F-127 being away from the origin.

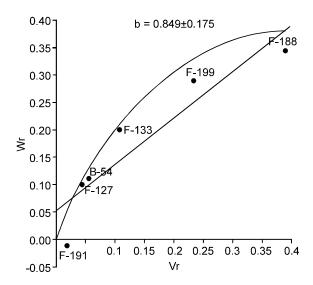


Fig. 7: Wr/Vr graph for ASI under normal water regime

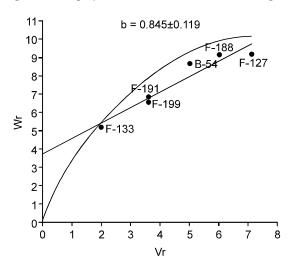


Fig. 8: Wr/Vr graph for ASI under water stress regime

Estimates of genetic components of variations for cell membrane thermostability under both environmental conditions were found positive and significant. The value of H<sub>1</sub> and H<sub>2</sub> was <D under normal and water deficit condition indicated that genes showing dominance effect for cell membrane thermostability were less important than additive genes. The values of H<sub>1</sub> and H<sub>2</sub> are not equal indicated gene distribution for relative cell injury seem to be unequal, which was further supported by the ratio of H<sub>2</sub>/4H<sub>1</sub> having value <0.25 under normal water and stress environment. Non-significant and Positive value of F signified the positive genes were less frequent under normal and water stress conditions. The value of h^2 was negative. Environmental variation (E) was positive and non significant under both conditions depicting that environmental variation were less important for this trait. The degree of dominance was

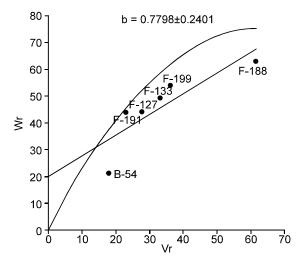


Fig. 9: Wr/Vr graph for CMT under normal water regime

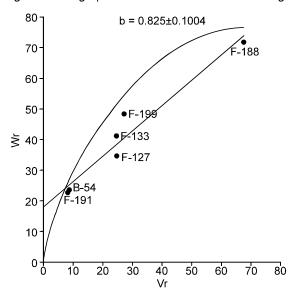


Fig. 10: Wr/Vr graph for CMT under water stress regime

less than one suggesting the presence of partial dominance in F<sub>1</sub> hybrid. The estimate of narrow sense heritability was 85% and 80% under normal and water stress condition, respectively. The results are in accord with Farooq (2010) who reported additive genetic effects for this trait. Hussain *et al.* (2009) however, reported over-dominance type of gene action for inheritance of this trait. Distribution of array points in the graphs revealed that B-54 carried maximum number of dominant genes and F-188 carried maximum recessive genes for the inheritance of cell membrane thermostability under normal regime (Fig. 9).

Rest of the parental lines held intermediate constitution having central position from the origin. Under water stress condition, F-191 and B-54 possessed maximum dominant genes, while F-188 had maximum recessive genes being away from the origin (Fig. 10). The

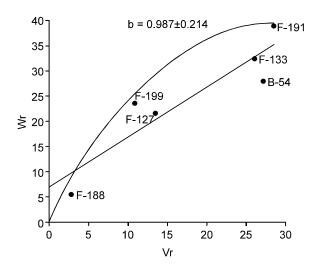


Fig. 11: Wr/Vr graph for Pn under normal water regime

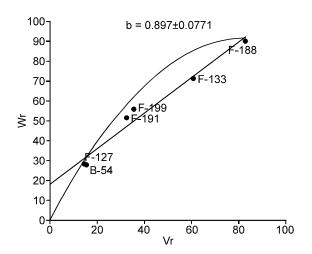


Fig. 12: Wr/Vr graph for Pn under water stress regime

remaining inbred lines were of intermediate gene constitution containing dominant and recessive genes. The positive F value revealed the importance of dominant genes for net photosynthetic rate under normal conditions. Whereas, negative value of F was noted under water deficit condition showing the unimportant role of dominant alleles. The positive value of h^2 was observed under both environmental conditions. The degree of dominance was <one, suggesting the presence of partial dominance in the F1 hybrids. The ratio of H<sub>2</sub>/4H<sub>1</sub> is greater than 0.25, indicating unequal distribution of the genes in the parents. The estimate of narrow sense heritability for net photosynthetic rate was 80% under normal and 86% under water stress conditions. The graph in the Figure 1 depicted that F-188 followed by F-127 contained maximum dominant genes and F-191 followed by F-133 carried maximum recessive genes as they are far from the origin for net photosynthetic rate under normal

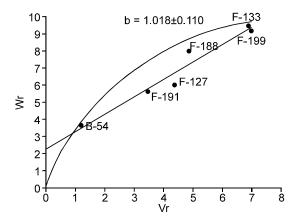


Fig. 13: Wr/Vr graph for 100-grain weight under normal condition

conditions. Similarly, Wr/Vr graph for net photosynthetic rate (Fig. 12) showed that B-54 and F-127 had maximum number of dominant genes for net photosynthetic rate, while F-188 and F-133 had maximum recessive genes for net photosynthetic rate under water stress conditions. Genetic components of variation were estimated for 100grain weight and significant value of D under both environments indicated additive genetic effects. Similarly significant value of H component (H1 and H2) under both normal as well as stress condition indicated importance of dominant variation. Unequal values of H1 and H2 under both environments revealed different distribution of dominant genes. Positive genes were found more frequent under water stress condition as revealed by the positive and significant value of F while under normal water condition. F value was negative and nonsignificant indicating positive genes were less frequent. Non-significant value of h2 denoted absence of heterozygous loci for 100-grain weight under normal and moisture deficit environment. Environmental variance (E) was significant indicating the role of environment effects for 100-grain weight under normal water conditions whereas it was non-significant expressing negligible effects of environment in the determination of this trait under water deficit condition. The narrow sense heritability estimates were more than 50% which indicated a greater proportion of additive genetic variation of the total variation was inherited. The degree of dominance was <one revealing partial dominance under both environments. Partial dominance was also evident in graphical presentation (Fig. 13).

Katna et al. (2005); Muraya et al. (2006); Srdic et al. (2007); Tabassum et al. (2007); Asefa et al. (2008); Farooq (2010); Khodarahmpour (2011) reported that 100-grain weight was under the control of additive type of gene action. The Wr/Vr graph (Fig. 12 and 13) revealed that under normal condition the parental line B-54 had frequent dominant genes being in close vicinity to the origin, while F-199 and F-133

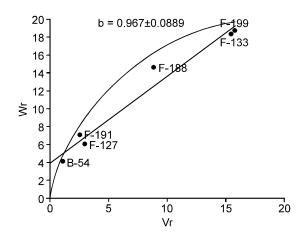


Fig. 14: Wr/Vr graph for 100-grain weight under water stress condition

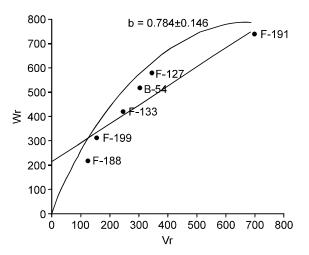


Fig. 15: Wr/Vr graph for grain yield per plant under normal condition

possessed more recessive genes being farthest from the origin. Under water stress condition, B-54 possessed maximum dominant genes, followed by F-127 and F-191, while the inbred lines F-199 and F-133 had maximum number of recessive genes conditioning 100-grain weight.

Genetic components for grain yield per plant revealed that D was significant. D was more than  $H_1$  and  $H_2$  indicating the presence of additive genetic effects in controlling grain yield under normal and water stress conditions. Unequal values of  $H_1$  and  $H_2$  under both environments revealed different distribution of dominant genes. The ratio of  $H_2/4H_1$  was <0.25, suggesting unequal distribution of genes among the parents. Environmental variation (E) was non-significant under both conditions expressing little role of environment in the determination of this trait. F value denoted the presence of dominant genes. The value of  $h^{\Lambda^2}$  was negative under both conditions. The degree of

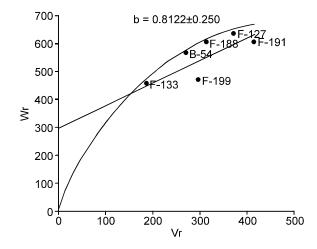


Fig. 16: Wr/Vr graph for grain yield per plant under water stress condition

dominance was < one suggesting the presence of partial dominance in F<sub>1</sub> hybrid also supported by the regression slope in the graph. The estimate of narrow sense heritability was 85% and 76% under normal and water deficit condition, respectively which is indicative of effective selection for this trait. The results are in line with Betran *et al.* (2003); Afarinesh *et al.* (2005); Ojo *et al.* (2007); Farooq (2008); Hussain *et al.* (2009); Farooq (2010) who reported additive gene action for grain yield. Distribution of array points in the graphs depicted that F-188 had maximum number of dominant genes for grain yield per plant under normal condition (Fig. 15).

Inbred F-191 had maximum recessive genes for grain yield under normal conditions. Wr/Vr graph (Fig. 16) showed that F-133 and F-188 had maximum number of dominant genes for grain yield, while F-127 and F-191 received maximum recessive genes for grain yield under water stress condition. F-191 maintained its gene expressions under both the environmental conditions.

Conclusion: From the foregoing study of genetic components of variation and the presence of additive genetic effects of plant height, ear leaf area, anthesis-silking interval, cell membrane thermostability, net photosynthetic rate, 100-grain weight and grain yield would be helpful to understand the genetic basis and physiological mechanism of water stress tolerance in maize and also their inheritance pattern coupled with moderate to high heritability in almost all traits is indicative of early generation trait selection.

## **REFERENCES**

Afarinesh, A., E. Farshadfar and R. Choukan, 2005. Genetic analysis of drought tolerance in maize (*Zea mays*.L) using diallel method. Seed Plant., 20: 457-473.

- Akbar, M., 2008. Genetic control of high temperature tolerance in *Zea mays* L. Ph.D thesis. Dept. Pl. Br. Genet., Univ. Agri. Faisalabad, Pakistan.
- Anonymous, 2009-10. Economic Survey of Pakistan. Economic Adviser's Wing, Finance Division, Government of Pakistan, Islamabad.
- Assessment of water stress tolerance in different maize accessions at germination and early growth stage. Pak. J. Bot., 38: 1571-1579.
- Banziger, M., G.O. Emeades, D. Beek and M. Bellon, 2000. Breeding for drought and nitrogen stress tolerance in maize: From Theory to practice. CIMMYT, Mexico, pp. 68.
- Banziger, M. and J.L. Araus, 2007. In Advances in molecular breeding toward drought and salt tolerant crops (M. A. Jenks. Ed.), Springerlink, Berlin, 587-601.
- Bello, O.B. and G. Olaoye, 2009. Combining ability for maize grain yield and other agronomic characters in typical southern guinea savanna ecology of Nigeria. Afr. J. Biotechnol., 8: 2518-2522.
- Betran, F.J., D. Beck, M. Banziger and G.O. Edmeades, 2003. Genetic analysis of inbred and hybrid grain yield under stress and non stress environments in tropical maize. Crop. Sci., 43: 807-817.
- Brown, R.H., 1999. Agronomic implications of C<sub>4</sub> photosynthesis. In: Sage RF, Monson RK. Eds. C<sub>4</sub> plant biology. San Deigo, CA: Academic Press, pp: 473-507.
- Campos, H., M. Cooper, J.E. Habben, G.O. Edmeades and J.R. Schussler, 2004. Improving drought tolerance in maize a view from industry. Field Crops Res., 90: 19-34.
- Chen, G., M. Sagi, S. Weining, T. Krugman, T. Fahima, A.B. Korol and E. Nevo, 2004. Wild barley eibi1 mutation identifies a gene essential for leaf water conservation. Planta, 219: 684-693.
- Farooq, A., 2008. Analysis of some physio-genetic parameters related to drought tolerance in maize. M.Sc thesis, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.
- Farooq, J., 2010. Genetic basis of heat tolerance in bread wheat (*Triticum aestivum* L.). Ph.D thesis, Department of Plant Breeding and Genetics, UAF, Faisalabad.
- Guzman, P.S. and K.R. Lamkey, 2000. Effective population size and genetic variability in the BS11 maize population. Crop Sci., 40: 338-346.
- Hayman, B.I., 1954a. The theory and analysis of diallel crosses. Genetics, 39: 789-809.
- Hayman, B.I., 1954b. The analysis of varience of diallel tables. Biometrics, 10: 235-244.

- Hollington, P.A. and K.A. Steele, 2007. Participatory breeding for drought and salt tolerant crops. In: M.A. Jenks, P.M. Hasegawa and S.M. Jain (Eds.). 226. Advances in molecular breeding toward drought and salt tolerant crops. Springer verlag, pp: 455-478.
- Hussain, I., M. Ahsan, M. Saleem and A. Ahmed, 2009. Gene action studies for agronomic traits in maize under normal and water stress conditions. Pak. J. Agri. Sci., 46: 108-112.
- Jinks, J.L., 1954. The analysis of continuous variation in a diallel crosses of *Nicotiana rustica* L. varieties. Genetics., 39: 767-788.
- Katna, G., H.B. Singh, J.K. Sharma and R.K. Mittal, 2005. Components of variation in maize (*Zea mays* L.) Ann. Biol., 21: 133-136.
- Khan, I.A., S. Habib, H.A. Sadaqat and M.H.N. Tahir, 2004. Selection criteria based on seedling growth parameter in maize varies under normal and water stress conditions. Int. J. Agric. Biol., 6: 252-256.
- Khan, I.A., S. Habib, H.A. Sadaqat and M.H.N. Tahir, 2004. Selection criteria based on seedling growth parameter in maize varies under normal and water stress conditions. Int. J. Agric. Biol., 6: 252-256.
- Khodarahmpour, Z., 2011. Genetic control of different traits in maize inbred lines (*Zea mays* L.) using graphical analysis. Afr. J. Agric. Res., 6: 1661-1666.
- Khotyleva, L. and V.A. Lemesh, 1994. Genetic control of morphological and physiological characters of the seedlings in maize. Tsitologiya Genetika, 28: 55-59.
- Kumar, P. and S. Gupta, 2004. Genetic analysis in maize (*Zea mays* L.). J. Res. Birsa Agric. Univ., 16: 113-117.
- Kuriata, R., W. Kaubiec, J. Adamczyk and H. Cygiert, 2003. Diallel analysis of single hybrids of maize. Biuletyn Institutu Hodowli i Aklimatyzacii Roslin., 230: 417-422.
- Mather, K. and J.L. Jinks, 1982. Introduction to Biometrical Genetics. Chapman and Hill Ltd., London.
- McKee, G.W., 1964. A coefficient for computing leaf area in hybrid corn. Agron. J., 56: 240-241.
- Mendes, A.A., C.G.L. Aparecida, S.A. Resende da, S.M. Figueiredo, G.A.A. Franco and S.J.C. Lopes-de, 2003. Combining abilityof inbred lines of maize and stability of their respective single-crosses. J. Scientia Agricola, 60: 83-89.
- Mitra, J., 2001. Genetics and genetic improvement of drought resistance in crop plants Curr. Sci., 80: 758-763.
- Moussa, I. and S.M. Abdel-Aziz, 2008. Comparative response of drought tolerant and drought sensitive maize genotypes to water stress. Aust. J. Crop Sci., 1: 31-36.

- Muraya, M.M., C.M. Ndirangu and E.O. Omolo, 2006. Heterosis and combining ability in diallel crosses involving maize (*Zea mays* L.) S<sub>1</sub> lines. Aus. J. Exp. Agric., 46: 387-394.
- Ojo, G.O.S., D.K. Adedzwa and L.L. Bello, 2007. Combining ability estimates and heterosis for grain yield and yield components in maize (*Zea mays L.*). J. Sustainable Dev. Agric. Environ., 3: 49-57.
- Paterniani, E., 1990. Maize breeding in the tropics. CRC Critical Rev. Plant Sci., 9: 125-54.
- Pingali, P.I., 2001. CIMMYT 1999-2000 facts and trends. Meeting the World Maize Needs: Technological Opportunities and Prioritiesfor the Public Sector. CIMMYT, Mexico City.
- Rauf, S. and H.A. Sadaqat, 2008. Identification of physiological traits and genotypes combined to high achene yield in sunflower (*Helianthus annuus* L.) under contrasting water regimes. Aust. J. Crop. Sci., 1: 23-30.
- Richards, R.A., 2004. Defining selection criteria to improve yield under drought. Plant Growth Regul., 20: 157-166.
- Shabbir, G. and M. Saleem, 2002. Gene action for protein content of maize grain in diallel cross. Pak. J. Seed Technol., 1: 53-58.

- Shao, H.B., L.Y. Chu, M.A. Shao, C. Abdul Jaleel and M. Hong-Mei, 2009. Higher plant antioxidants and redox signaling under environmental stresses. Comp. Rend. Biol., 331: 433-441.
- Srdic, J., Z. Pajic and S. Drinic-Mladenovic, 2007. Inheritance of maize grain yield components. Maydica, 52: 261-264.
- Steel, R.G.D., J.H. Torrie and D.A. Discky, 1997. Principles and procedures of statistics: A Biometrical approach, 3rd Edn., McGraw Hill Book Co., New York.
- Sullivan, C.Y., 1972. Mechanisms of heat and drought resistance in grain sorghum and methods of measurement. In N.G.P. Rao and L.R. House (Eds.) Sorghum in the seventies. Oxford and IPH publishing Co., New Delhi, India.
- Tabassum, M.I., 2004. Genetics of physio-morphological traits in *Zea mays* L. under normal and water stress conditions. Ph.D. Thesis, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.
- Tabassum, M.I., M. Saleem, M. Akbar, M.Y. Ashraf and N. Mehmood, 2007. Combining ability studies in maize under normal and drought conditions. J. Agic. Res., 45: 261-268.