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Genetics of Physio-Agronomic Traits in Maize under Water Deficit Conditions

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Abstract: Fifty inbred lines of maize acquired from various sources, were screened in the warehouse for seedling traits under both normal and water deficit conditions and six diverse inbred lines were selected. The selected inbred lines were sown in the field for making all possible crosses in diallel mating fashion. The F_1 crosses and their reciprocals along with the parents were sown in the field under both regimes using a replicated Randomized Complete Block Design. Data for various agro-physiological traits were recorded at different growth stages of the crop and then subjected to statistical analysis. Significant genetic variability existed for most of the traits under normal and moisture deficit conditions. The results for scaling tests showed fully adequate for the traits like 100-kernel weight, grain yield per plant, cell membrane thermostability, stomatal conductance and canopy temperature under normal condition while plant height, 100-kernel weight, grain yield per plant, leaf temperature and canopy temperature depression under water stress condition. The data were partially adequate for the traits like anthesis-silking interval, cell membrane thermostability and stomatal conductance under moisture deficit condition. All traits exhibited additive gene action under both regimes. Heritability estimates for yield related traits revealed maximum ability to transfer the desirable genes to the next generation.

Key words: Maize, water stress, gene action, diallel analysis, cell membrane thermostability

INTRODUCTION

Maize (*Zea mays* L.), the sole cultivated specie belonging to genus *Zea*, is a multipurpose crop and ranks third important cereal crops in the world after wheat and rice. It is grown over a wide range of agro-ecological. Due to its multiple uses it is called as “Queen of cereals”. In Pakistan, direct use of maize is declining but it is extensively used in poultry and wet milling industry and constitutes about 60% of poultry feed of the country. In Pakistan it accounts for 1.083 million hectares with annual production of 4.271 million tones with average yield of 3.94 tons/hectare (Anonymous, 2011-12). The average yield of maize in Pakistan is low as compared to other leading maize growing countries. The country is faced with a serious water scarcity, a major constraint in food production.

Water stress is one of major abiotic factors which effects growth of the plant drastically and ultimately limit production potential. The global environmental changes suggested that there will be increase in aridity and in frequency of extreme events in most parts of the world. Due to water deficit conditions in maize about 24 million tons of maize lost annually and only high yielding genotypes could meet the projected increase in demand for next decades (Heisey and Edmeades, 1999). Abo-El-Kheir and Mekki (2007) observed reduction in kernel yield by 27.9 and 35.5% at silking and grain filling period in maize, respectively. Breeding for abiotic stress is a challenge due to complexity of the target environments (Reynolds *et al*., 2005). However, in spite of difficulties, genetic improvement of yield is possible and has been made in water deficit regions through dissection of genetic mechanism in certain physiological traits (Campos *et al*., 2004). Difference in grain yield between hybrids and inbred lines increased with the intensity of drought. Additive gene action was found to be of significantly important under drought prone environment (Betran *et al*., 2003).

Grain yield being a complex trait resulted from the interaction of various contributing factors which are highly influenced by environmental variation (Bruce *et al*., 2002). It cannot be directly improved by phenotypic selection of desirable plants, especially with heterozygous crops like maize. To overcome this tedious job, yield is partitioned into its components and thus the possible way to increase yielding ability is to study the inheritance mechanism governing various components of yield. Improvement of agronomic characters through genetic architecture has covered more than 30% gap between yield potential and actual yield under water deficit stress (Edmeades *et al*., 2004).

Understanding of genetic architecture for traits related to a fair degree of survival in water deficit condition is essential before to launch an efficient breeding program. It is difficult to breed for high yield under non favorable condition than favorable conditions. The present study is an attempt to estimate the genetic basis of variation and heritability among inbred lines and crosses to find the

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nature of genes involved in the inheritance of physiological and morphological traits to earmark parents for the synthesis of promising maize hybrids for drought stress environments.

MATERIALS AND METHODS

The experiment was conducted in the field area Department of Plant Breeding and Genetics, University of Agriculture Faisalabad during the years 2009-2011. A set of 50 diverse maize inbred lines collected from various national and international research organizations were evaluated in two phases i.e., preliminary in the green house and finally under field conditions. Six inbred lines viz: NCIL-20-20, D-157, OH-8, D-114, M-14 and D-109 selected on the basis of preliminary screening i.e., seedling stage screening using physiological and agronomic parameters under water deficit treatments were crossed in all possible combinations in the field during spring 2011 in a complete diallel mating. The F_1 and their reciprocal crosses along with the parents were planted in the research field during autumn 2011 using Randomized Complete Block Design (RCBD) with three replications under normal and water deficit stress environment. Except for irrigation schedule in both set, all recommended agronomic, cultural practices and plant protection measures were kept uniform. Normal experimental set received standard irrigation whereas 50% of normal irrigation was supplied to the water deficit set (Khan *et al*., 2004). On soil sampling 40% of water holding capacity of soil dry weight was recorded. The Meteorological data for the last five years (2006-2011) are presented. Ten equally competitive plants were ear-marked from each entry from both sets and data pertaining to various physio-agronomic traits were recorded as follows.

Agro-physiological parameters: On maturity data regarding agro-physiological traits for ten randomly tagged plants were recorded from each treatment and replication.

Cell membrane thermostability: Cell Membrane Thermostability (CMT) was determined according to Ibrahim and Quick (2001) under normal and water stress condition. The % age damage to leaf tissues due to water deficit was estimated from the first and second electrolyte measurements using the formula:

Cell membrane thermo stability (CMT) = (1-T1/T2) x 100

where, T1 represents EC value after water bath and T2 represents EC reading after autoclaving.

Stomatal conductance: Steady state porometer (Model L-1 1600 SSP1674 Li cor. Ink, USA) was used to record data for diffusible resistance after regulating it with the widespread environment with help of Null gain adjustment. Stomatal conductance is dependent on diffusible resistance. (Unit of measurement, mol m^{-2} s^{-1})

Leaf temperature: Leaf temperature of ten ear marked plants of each experiment entry per replication was recorded on sunny day at 13.00-15.00 from a fully exposed leaves and data were recorded from ear-marked plants in centigrade (°C) by using infrared thermometer (RAYPRM 30 CFRJ, RAYTEK, USA).

Canopy temperature depression (CTD): Portable hand held radiation thermometer (CHINO-IR-AHOT) was utilized to measure three readings from each experimental unit at anthesis stage of maize hybrids. Readings were taken between 12.00 to 15.00 hours on a cloudless, bright sunny day. Hand held infrared thermometer was held at 30-60° from the horizontal and also at a distance of 2m from the rows. The average of three values was used for analysis. Ambient air temperature was measured with hand held thermometer immediately after taking readings and then by using the formula given below.

CTD = AT - CT
CTD = Canopy temperature depression
AT = Ambient temperature
CT = Canopy temperature

Plant height: Plant height of each selected plant was measured at physiological maturity from the ground level to the apex of the tassel (Guzman and Lamkey, 2000) with measuring rod in centimeters (cm) from 10 randomly selected plants of each entry. The average was calculated for the analysis of data.

Anthesis-silking interval: Anthesis-silking interval (ASI) represents the period between the maturity of male and female inflorescence. It was estimated as the days to 50% silking minus days to 50% tasseling.

100-kernel weight: It was recorded in grams with an electronic balance from three samples obtained each from the bulk grain produce obtained from the ear-marked plants and average computed for statistical analysis.

Grain yield per plant: Grain yield per plant was calculated in grams by taking the total weight of shelled grains obtained from all the ears of each plot divided by the number of plants in that plot after drying to a constant moisture level (15%).

Statistical/biometrical analysis: Data relating to various physiological and agronomic traits were enumerated and compared using statistical analysis (Steel *et al*., 1997). The data were subjected to biometrical technique developed by Hayman (1954a, b) and Mather and Jinks (1982). Additive-dominance model (Hayman, 1954a; Jinks, 1954 and Mather and Jinks, 1982) was applied to check the validity of the data before proceeding for further analysis.

RESULTS AND DISCUSSION

Analysis of variance showed highly significant ($P \le 0.01$) differences for all traits except for anthesis-silking interval which was significant ($P \le 0.05$) among genotypes under normal condition while highly significant differences were observed for all traits under water deficit conditions (Table 1). Significant differences allowed to proceed for further genetic analysis (Hayman, 1954 a, b; Jinks, 1954). The data would be adequate if it passes two tests i.e., regression analysis and analysis of variance and co-variance. If data fulfill any one of the two tests, it will be considered to be partially adequate. Completely or partially adequate data were further processed to estimate genetic components of variation (Tabassum, 2004); Chohan *et al*., 2012 and Iqbal *et al*., 2012). Traits like plant height, anthesis-silking interval, 100-kernel weight, grain yield per plant, cell membrane thermostability, leaf temperature and stomatal conductance to be adequate by regression analysis whereas 100 kernel weight, grain yield per plant, cell membrane thermostability, stomatal conductance and canopy temperature depression were observed adequate for analysis of arrays under normal water condition whereas, plant height, 100-kernel weight, grain yield per plant and leaf temperature were fully adequate for analysis of array under water stress condition (Table 2).

Cell membrane thermostability: Genetic component of variation was computed using Hayman (1954b) presented in Table 3. Component D was found significant for cell membrane thermostability under normal and water deficit condition suggesting the presence of predominant role of additive genetic effects for inheritance of trait. The value for H_1 was much lower than D component confirming dominant role of additive genetic component for the expression of the trait under

Table 1: Mean square for physio-agronomic traits in diallel cross under both conditions

Source (Normal)	df	CMT	LT	SC	CTD	PH	ASI	100-KW	GYP
Replications	2	2.81	0.50	6.964	3.272	17.68	0.231	1.674	4.411
Genotypes	35	140.4**	10.3**	3.9**	11.86**	476.58**	0.925*	23.23**	990.4**
Error	70	2.11	0.81	1.05	1.29	12.36	0.56	2.05	7.55
Mean		72.2	33.37	0.159	4.88	140.8	4.57	27.8	131.4
CV%		2.01	2.71	2.05	23.33	2.50	16.43	5.14	1.98
Source (water stress)									
Replication	2	5.780	0.532	8.747	0.377	2.175	0.777	2.283	9.480
Genotypes	35	153.1**	12.4**	2.02**	22.5**	554**	3.8**	30.5**	2103**
Error	70	3.226	1.021	1.044	1.276	6.646	1.882	0.945	4.164
Mean		51.14	35.29	0.119	1.07	113.3	8.56	24.1	103.1
CV%		3.51	2.86	2.73	105.5	2.27	16.04	4.03	2.09

CV: Coefficient of variation, CMT: Cell membrane thermostability, LT: Leaf temperature, SC: Stomatal conductance, CTD: Canopy temperature depression, PH; Plant height, ASI: Anthesis-silking interval, KW: Kernel weight, GYP: Grain yield per plant.

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

	Regression analysis		Mean squares		
Trait normal	H0 b = 0	H0 b = 1	Wr+Vr	Wr-Vr	Remarks
Plant height	11.40**	1.250**	7657.57**	91.71^{NS}	Fully adequate
Anthesis-silking interval	5.09**	1.152^{NS}	6.37^{NS}	0.340^{NS}	Partially adequate
100-kernel weight	6.002**	1.168^{NS}	56.71**	1.717^{NS}	Fully adequate
Grain yield per plant	22.67**	1.525^{NS}	36696.8*	101.35^{NS}	Fully adequate
Cell membrane thermo-stability	4.89**	1.740^{NS}	611.04^{NS}	25.153^{NS}	Partially adequate
Leaf temperature	7.54**	1.643^{NS}	26.51*	0.528^{NS}	Fully adequate
Stomatal conductance	4.09**	1.007^{NS}	1.395^{NS}	7.244*	Partially adequate
Canopy temperature depression	8.34**	0.867^{NS}	16.54**	0.193^{NS}	Fully adequate
Trait (water stress)					
Plant Height	11.40**	1.250**	7657.57**	91.71^{NS}	Fully adequate
Anthesis-silking interval	5.09**	1.152^{NS}	6.37^{NS}	0.340^{NS}	Partially adequate
100-kernel weight	6.002**	1.168^{NS}	56.71**	1.717^{NS}	Fully adequate
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Stomatal conductance	4.09**	1.007^{NS}	1.395^{NS}	7.244*	Partially adequate
Canopy temperature depression	8.34**	0.867^{NS}	16.54**	0.193^{NS}	Fully adequate

NS: Non-significant *: Significant at $P \le 0.05$, **: Significant at $P \le 0.01$.

Table 3: Components of genetic variation under both regimes

								(*4DH$_1$+F/			
	Condition	D	H_1	H_2	F	(h^2)	E	(H_1/D)$^{0.5}$	*4DH$_1$-F)	(H_2/4H_1)	h^2(n.s)
CMT	Normal	98.17±0.90*	4.96±2.296*	4.64±2.05*	-7.08±2.21^{NS}	-0.39±1.380^{NS}	0.77±0.34	0.225	0.234	0.723	0.87
	W/ Stress	97.70±2.45*	11.33±6.2^{NS}	9.34±5.57^{NS}	-13.09±6.0^{NS}	1.50±3.75^{NS}	1.20±0.93	0.340	0.206	0.671	0.85
LT	Normal	5.88±8.56*	0.67±0.22*	0.53±0.19*	-1.007±0.209^{NS}	-5.20±0.13^{NS}	0.29±3.23^{NS}	0.34	0.198	0.596	0.82
	W/ Stress	6.05±0.33*	2.89±0.853*	2.71±0.762*	-1.61±0.82	-0.195±0.513^{NS}	0.366±0.12^{NS}	0.69	0.234	0.677	0.73
SC	Normal	2.57±1.88*	2.21±4.784*	2.23±4.27*	-2.55±4.60^{NS}	1.044±2.87*	3.80±7.12	0.29	0.253	0.709	0.85
	W/ Stress	1.41±1.19*	8.52±3.0458*	7.85±2.720*	-1.12±2.93^{NS}	2.048±1.83^{NS}	3.78±4.53	0.24	0.230	0.72	0.88
CTD	Normal	4.45±0.24*	3.15±0.618*	2.45±0.552*	-2.02±0.594^{NS}	-0.24±0.371^{NS}	0.49±9.20^{NS}	0.841	0.194	0.575	0.76
	W/ Stress	12.47±0.52*	2.563±1.33NS	2.36±1.19*	-3.09±1.285^{NS}	-0.229±0.80^{NS}	0.455±0.198	0.453	0.230	0.570	0.87
PH	Normal	359.91±8.64*	-10.664±0.22^{NS}	-7.88±0.19^{NS}	-10.631±0.21^{NS}	-2.522±0.132^{NS}	4.549±0.032*	0.172	0.184	0.842	0.91
	W/ Stress	408.423±3.0*	17.667±9.41^{NS}	13.4±8.41^{NS}	-8.405±9.06^{NS}	-0.132±5.66^{NS}	2.371±1.40^{NS}	0.208	0.190	0.905	0.89
ASI	Normal	0.19±0.0016*	-0.36±0.004^{NS}	-0.2±0.003^{NS}	-0.21±0.004^{NS}	-0.05±0.002^{NS}	0.2±0.0006^{NS}	1.35	0.180	0.44	0.38
	W/ Stress	1.65±0.14*	-0.99±0.36^{NS}	-0.61±0.3^{NS}	-0.78±0.35^{NS}	-0.361±0.22^{NS}	0.67±5.39^{NS}	0.773	0.154	0.53	0.66
100-KW	Normal	11.08±0.54*	5.30±1.365*	4.92±1.2199*	-3.15±1.3142^{NS}	0.42±0.8211^{NS}	0.74±0.20^{NS}	0.691	0.232	0.658	0.78
	W/ Stress	20.19±0.58*	2.09±1.469^{NS}	1.36±1.31^{NS}	-1.66±1.414^{NS}	-0.198±0.883^{NS}	0.357±0.22^{NS}	0.321	0.162	0.773	0.88
GYP	Normal	878±17.1*	136.9±43.50*	105.53±38.8*	197.41±41.87*	64.97±26.16*	2.71±6.47^{NS}	0.394	0.192	1.795	0.86
	W/ Stress	15.62±4.51*	39.22±11.46*	33.07±10.23*	-9.96±11.02^{NS}	3.79±6.89^{NS}	1.56±1.71^{NS}	0.156	0.211	0.960	0.90

Additive variance (D), Dominance variance (H_1), Proportion of positive and negative genes in the parent (H_2), Relative frequency of dominant and recessive alleles in the parents (F), Dominance effect (over all loci in heterozygous phase) (h^2), Environnemental variance (E), Mean degree of dominance (H_1 /D)$^{0.5}$; Proportion of genes with positive and negative effects in the parents (H_2/ 4H_1), Proportion of dominant and recessive genes in the parents (v4DH$_1$ + F /v4DH$_1$ – F), Heritability (Narrow sense). (Note: The value of variance is significant (*) when the value exceeds 1.9996 after dividing it with its S.E.).

both conditions. Significant estimates for H component under normal condition showed importance of dominant variation while non-significant value was observed under water stress condition showing less important dominant effects for trait inheritance. H_1 and H_2 represented similar distribution of dominant genes. Negative and non-significant value for F component revealed that recessive alleles were not frequent under both conditions. Non-significant value of h^2 represents no major effect of heterozygous alleles for expression of trait under normal as well as water stress condition. Mean degree of dominance $(H_1/D)^{0.5}$ was found less than one under both normal (0.225) and water deficit condition (0.34) indicating additive type of gene action. $H_2/4H_1$ was recorded less than 0.25 which represented unequal distribution of genes among parents. Significant role of environmental variance (E) indicated the role of environment for expression of cell membrane thermostability. Heritability for narrow sense was observed 89 and 87% under normal and stress condition. The results corroborate the findings of Chohan *et al*. (2012) who suggested additive type of gene action for this trait. However, Hussain *et al*. (2009) reported over-dominance type of gene action for the inheritance of the trait. The distribution of array points over regression (Fig. 1a) line for under normal water application showed that parent D-157 closest to the origin possessed maximum dominant genes followed by M-14 and NCIL-20-20, while inbred D-114 showed maximum recessive genes. Under water deficit condition (Fig. 1b), NCIL-20-20 displayed maximum dominant genes followed by D-114 and OH-8, respectively whereas inbred M-14 showed minimum dominant genes.

Leaf temperature: Estimation of genetic component of variation (Table 3) indicated a significant value for both D and H component suggesting presence of both additive and dominant gene action for the inheritance of trait under both normal and water deficit conditions. Different values of H_1 and H_2 under both conditions represented unequal distribution of dominant and recessive genes among parents. Negative and non-significant value of F component indicated more recessive alleles than dominant alleles under both environments.

Non-significant estimates for h^2 indicated no major role of heterozygous loci for leaf temperature under both conditions. Value of mean degree of dominance under both conditions was less than one reflecting additive type of gene action. Estimates for $H_2/4H_1$ was observed less than 0.25 thus indicating unequal distribution of genes among parents under both conditions. Narrow sense heritability was recorded 82 and 73% under normal and water deficit condition. Significant value for Environmental variance (E) suggested a role of environment for expression of trait.

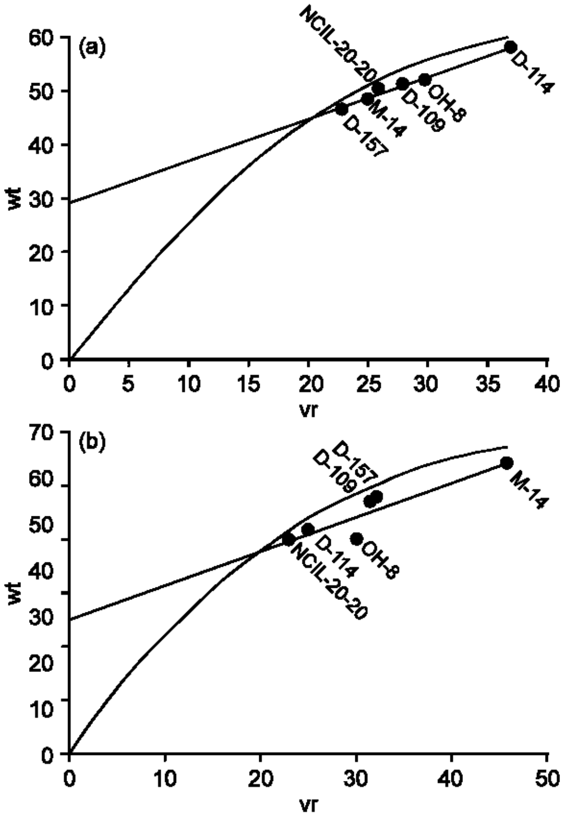

Fig. 1(a-b): Wr/Vr graph for cell membrane thermostability. (a) Normal condition and (b) Water stress condition

Results are in accord with Hussain *et al*. (2009) and Chohan *et al*. (2012) who reported additive type of gene action for the inheritance of trait. Array distribution (Fig. 2a) under normal water application revealed that parent D-114 possessed maximum dominant genes regarding leaf temperature character among the genotypes followed by NCIL-20-20 and D-109, respectively while minimum dominant genes were shown by inbred D-157. Inbred D-114 and D-157 displayed maximum and minimum dominant genes (Fig. 2b) also under water deficit condition for the trait under consideration, respectively.

Stomatal conductance: Genetic components of variation were calculated applying Hayman (1954b) approach and are presented (Table 3). Significant component D and H under both conditions indicated the presence of additive and dominant effects for the inheritance for stomatal conductance. Significant H component (H_1 and H_2) under both condition indicated significance of dominance variance. Negative and non-significant value of F component depicted the presence of more recessive alleles than dominant alleles under both conditions.

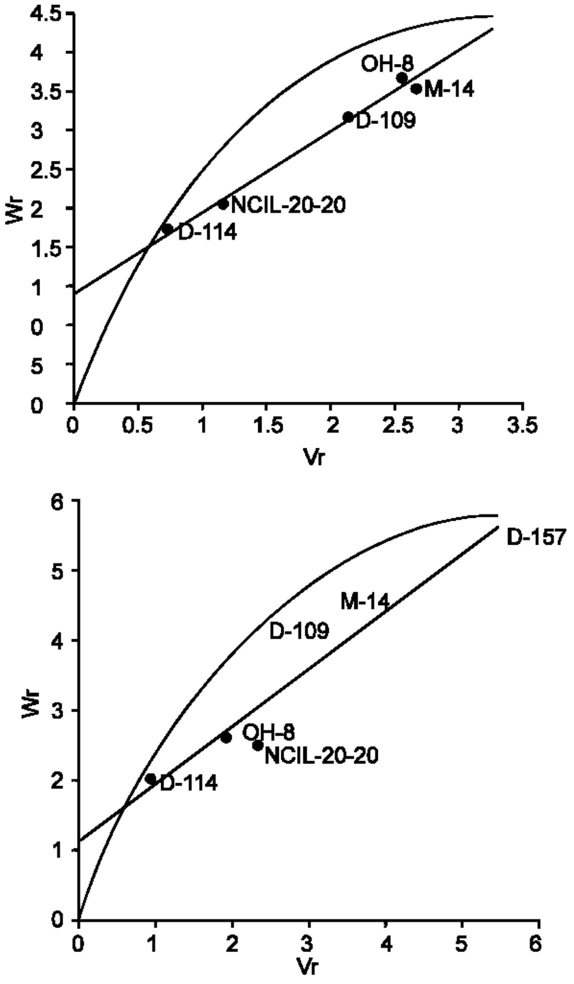

Fig. 2(a-b): Wr/Vr graph for leaf temperature. (a) Normal condition and (b) Water stress condition

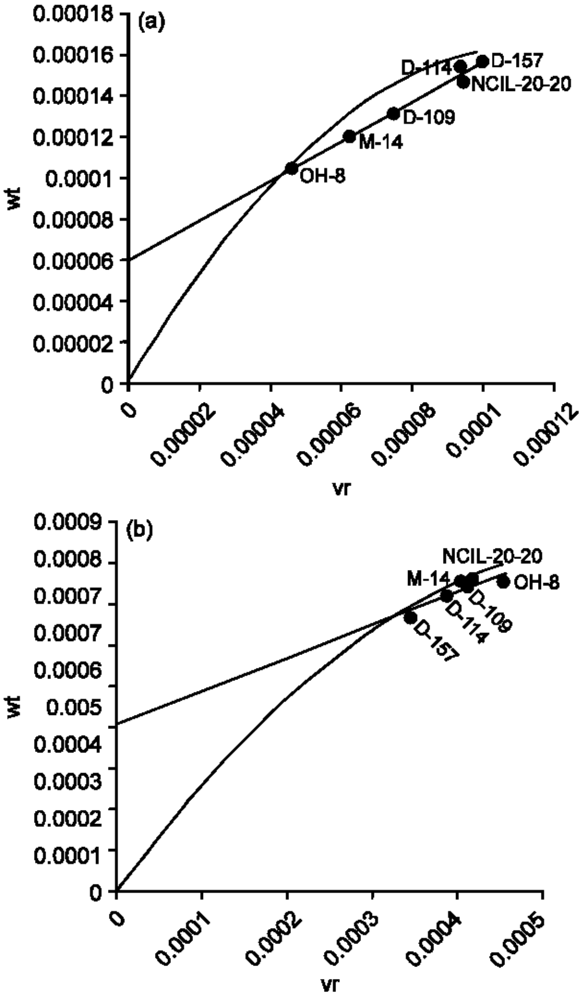

Fig. 3(a-b): Wr/Vr graph for stomatal conductance. (a) Normal condition and (b) Water deficit condition

Significance of h^2 under normal condition showed important role of heterozygous loci while non-significant h^2 value observed under water stress condition. Mean degree of dominance displayed less value under both condition than one indicating additive genetic effects. The value of $H_2/4H_1$ more (0.253) under normal condition showed equal distribution of genes for trait while under stress condition $H_2/4H_1$ possess less (0.23) value than 0.25 thus suggesting unequal distribution of genes among the parents. Environmental variance (E) was also observed significant revealing the importance of environment for expression of stomatal conductance. Narrow sense heritability observed for normal and stress condition were 85 and 88%, respectively showing high genetic variation for trait, however it was increased under water stress condition.

Graphical representation of Wr/Vr depicted that inbred OH-8 carried maximum dominant genes for stomatal conductance under normal water application (Fig. 3a) followed by M-14 and D-109, respectively whereas D-57 displayed minimum dominant genes for the trait. In case of water deficit condition D-157 exhibited maximum dominant gene for the trait and inbred OH-8 showed maximum dominant gene as it occupied farthest position to the origin (Fig. 3b). The results are comparable with Rebetzke (2003) who reported both additive and non-additive gene action for the control of the trait while Akbar (2008) reported additive type of gene action.

Canopy temperature depression: Estimation of component of variation disclosed the significant value for D component depicting the presence of additive genetic effects for the inheritance of canopy temperature depression under normal as well as stress condition (Table 3). The value of D component is more than H component thus suggesting additive genetic effects.

Unequal value of H_1 and H_2 represent unequal distribution of genes among parents.

Non-significant h^2 value showed no important effects of heterozygous loci for trait under both conditions. Negative and non-significant value for component F indicated more recessive alleles than dominant alleles under both conditions. Mean degree of dominance $(H_1/D)^{0.5}$) was observed less than one under both normal and stress condition for canopy temperature depression. Value $H_2/4H_1$ found less than 0.25 thus suggesting unequal distribution of genes among parents for character. Environmental variance (E) observed significant under both conditions thus suggesting a role for expression of trait. Estimates for narrow sense heritability were observed 76 and 88% for normal and water stress conditions, respectively.

Distribution of array means over regression line (Fig. 4a) indicated that parent D-114 possessed maximum dominant genes for canopy temperature depression trait under normal water application and D-157 displayed maximum recessive genes for trait under consideration while on the other hand under water deficit condition (Fig. 4b) inbred M-14 displayed maximum dominant genes followed by NCIL-20-20 and D-114, respectively whereas maximum recessive genes for canopy temperature depression were noted for inbred D-109. Results are in accordance with Punia (2011) who reported the significance of both additive and non-additive gene action for the trait.

Plant height: Components of genetic variation were assessed according to Hayman (1954b) and are presented in Table 3. Significant D value under normal as well as water deficit condition depicted the importance of additive genetic effects which remained same under normal as well as water stress environment. Non-significant value was observed for H_1 and H_2 under normal and water deficit condition indicating unimportant role of dominant genes. Low value of H_1 and H_2 than D component suggested that additive effects were more important than dominant effects in controlling plant height. Unequal estimates for H_1 and H_2 under both conditions showed unequal distribution of dominant genes among the parents. Non-significant value of F component under both condition showed that frequency of dominant and recessive genes among the parents were not frequent. It is inferred that positive and negative genes were almost in similar distribution among the parents. Non-significant negative value for h^2 showed that heterozygous loci effects were not significant for plant height under normal and water stress condition.

Mean degree of dominance $(H_1/D)^{0.5}$ observed (<1.96) under normal (0.172) and stress condition (0.208) showed no dominant effects regarding plant height under both conditions. The value of $(H_2/4H_1)$ was observed less than 0.25 representing unequal distribution of genes under both normal (0.185) and water deficit condition (0.190). Significant value for E component under both conditions suggested important role for the expression of the trait.

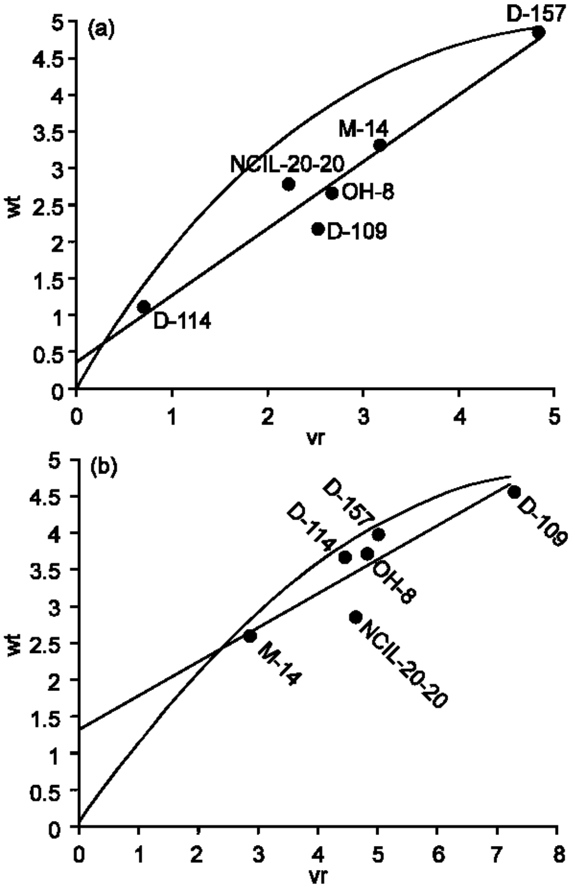

Fig. 4(a-b): Wr/Vr graph for canopy temperature depression. (a) Normal condition and (b) Water stress condition

The proportion of dominant and recessive genes in the parents (F_1) were found less than one indicating partial dominance under both conditions suggesting important role of additive gene action for the inheritance of this trait. Narrow sense heritability for was 91% under normal and 89% under water stress condition indicating highly heritable trend for the trait as well as suggesting additive genetic effects for inheritance. Graphical presentation of the data (Fig. 5) also suggested additive gene action for inheritance of this trait.

The results are in accordance with the findings of Shabbir and Saleem (2002), Kuriata *et al.* (2003), Mendes *et al.* (2003), Kumar and Gupta (2004), Malik *et al.* (2004), Tabassum (2004), Tabassum *et al.* (2007), Hussain *et al.* (2009), Chohan *et al.* (2012) and Iqbal *et al.* (2012) who inferred additive type of gene action for the character.

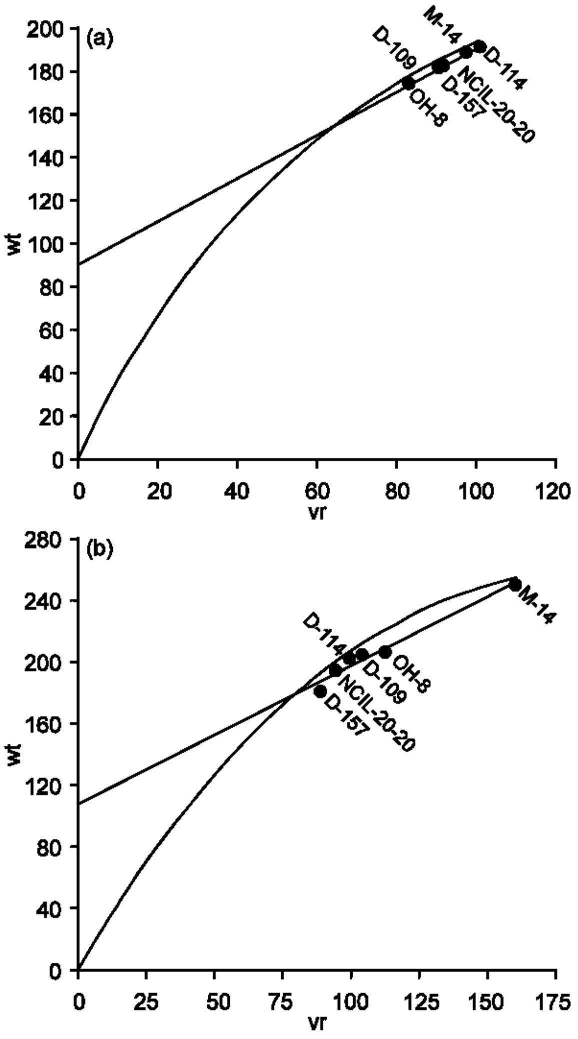

Fig. 5(a-b): Wr/Vr graph for Plant Height. (a) Normal Condition and (b) Water deficit condition

Graphical presentation of the data for plant height under normal condition (Fig. 5a) revealed that inbred OH-8 possessed most frequent dominant genes followed by D-109, D-157 and NCIL-20-20 while maximum recessive genes were displayed by inbred D-114. On the other hand, distribution of array point over regression line under water deficit condition (Fig. 5b) indicated inbred D-157 as the top most for carrying maximum dominant genes followed by NCIL-20-20, D-114 whereas minimum dominant genes were recorded for M-14.

Anthesis-silking interval: Significant and positive estimates for D component under normal and water stress condition indicated the presence of additive genetic effects for expression of anthesis-silking interval (Table 3). Cumulative value of H_1 and H_2 is less than D component confirmed the role of additive gene action for trait under both normal and water stress condition. Unequal value of H_1 and H_2 under both condition showed unequal distribution of positive and negative gene for the expression of anthesis-silking interval.

Negative and non-significant estimates for F component showed less frequent dominant alleles under both conditions. Negative and non-significant value recorded for h^2 represented no role of heterozygous loci for trait. Mean degree of dominance $(H_1/D)^{0.5}$ was greater than one under normal condition (1.39) indicating over dominance type of gene action while under water stress condition (0.77) it was less than one highlighting the importance of additive gene action. Narrow sense heritability was observed 38 and 66% under normal and water deficit conditions respectively. Environmental variance (E) was also observed significant displaying the role of environment for expression of trait. The value for $H_2/4H_1$ was recorded less than 0.25 which confirmed unequal distribution of positive and negative genes for trait among the parents.

These results are in line with Farooq (2008), Bello and Olaoye (2009), Khodarahmpour (2011), Chohan *et al.* (2012) and Iqbal *et al.* (2012) who found additive type of gene action for anthesis-silking interval. Afarinesh *et al.* (2005) found dominance variance for controlling anthesis-silking interval.

The graphical presentation (Fig. 6a) regarding anthesis silking interval displayed inbred OH-8 carrying maximum dominant genes under normal condition followed by D-109 and D-114 while D-157 exhibited maximum recessive genes. In case of water deficit condition (Fig. 6b) maximum dominant genes were produced by inbred D-114 followed by NCIL-20-20 and D-109. D-157 showed maximum recessive genes for anthesis-silking interval.

100-Kernel weight: Genetic components estimated are given in (Table 3) Component D found to be significant under normal as well as water stress condition indicated the predominance of additive genetic effects for the inheritance of 100-kernel weight. Component D possessed more value than H component suggesting the role of additive genetic effects. Different value of H_1 and H_2 indicated unequal distribution of dominant genes among the parents. F component displayed negative and non-significant value under normal and water stress condition which revealed that recessive alleles were not frequent. Non-significant value was observed for h^2 under both normal and water deficit condition. Mean degree of dominance $(H_1/D)^{0.5}$ revealed additive type of gene action as the value for normal (0.692) and water stress condition (0.322) was less than one. Estimate for $H_2/4H_1$ was found less than 0.25 thus representing partial dominance due to unequal distribution of genes among parents for 100-kernel weight trait.

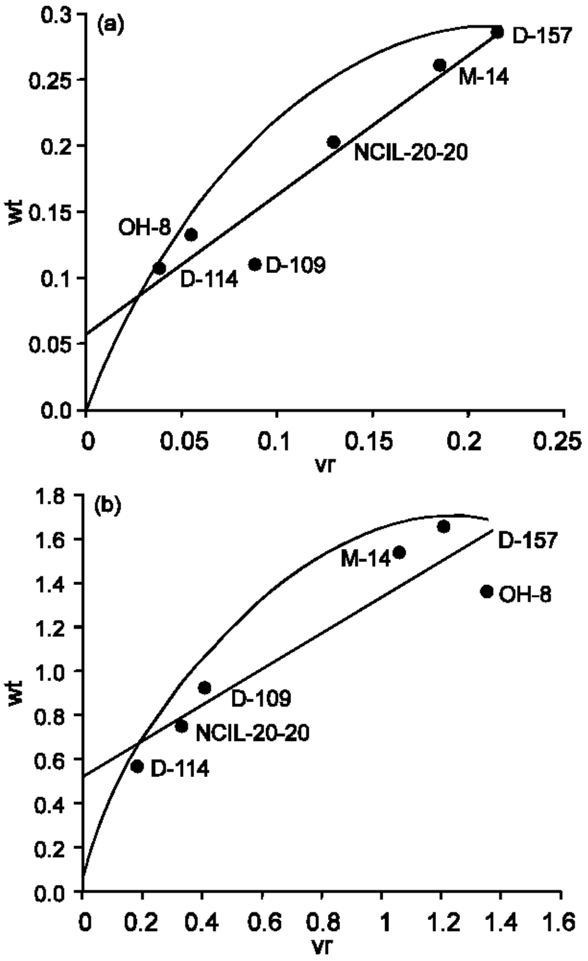

Fig. 6(a-b): Wr/Vr graph for anthesis-silking interval. (a) Normal condition and (b) Water deficit condition

Environmental variance (E) was also observed significant. Narrow sense heritability observed for normal and stress condition were 78 and 88%, respectively showing high genetic variation for trait, however it was reduced under water stress condition.

Mani *et al.* (2000), Farshadfar *et al.* (2002), Tabassum (2004), Kumar and Gupta (2004), Katna *et al.* (2005), Muraya *et al.* (2006), Srdic *et al.* (2007), Tabassum *et al.* (2007), Asefa *et al.* (2008), Farooq (2008), Jehanzeb (2010), Khodarahmpour (2011) reported 100-grain weight under the control of additive and non additive type of gene action. The results differ from those of Shakil (1992), Shabbir and Saleem (2002), Afarinesh *et al.* (2005), Akbar *et al.* (2008) and Hussain *et al.* (2009) who reported dominance and over dominance type of gene action. This difference in result may be due to different germplasm or the environment.

Graphical presentation indicating the array points suggested that parent D-157 carried maximum dominant genes followed by NCIL-20-20 and parent M-14, displayed maximum recessive genes for 100-kernel weight under normal condition (Fig. 7a). The array position under water deficit condition (Fig. 7b) suggested NCIL-20-20 with maximum dominant genes and D-157 exhibited minimum dominant genes for the trait.

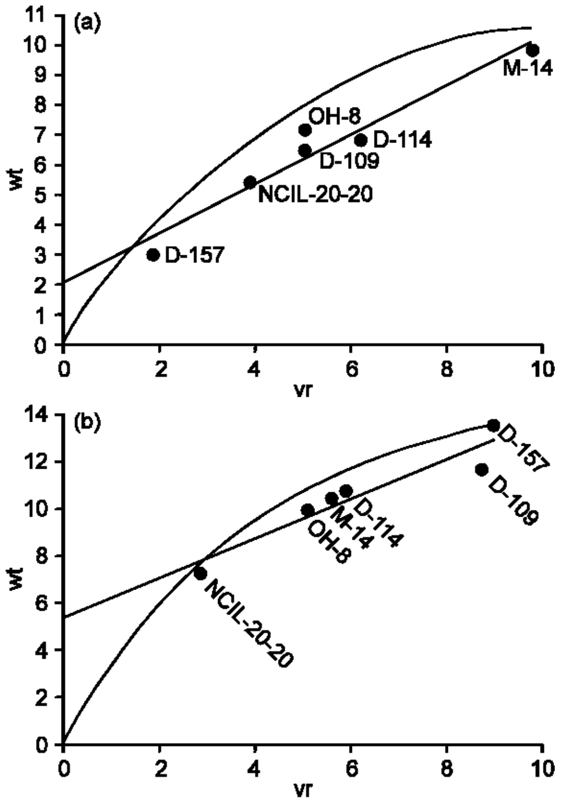

Fig. 7(a-b): Wr/Vr graph for 100-kernel weight. (a) Normal condition and (b) Water deficit condition

Grain yield per plant: Both Genetic components (D and H) were observed significant (Table 3) under both normal and water stress condition indicating the role of additive as well as dominant genetic effects for grain yield per plant. H_1 and H_2 components were also recorded significant under both environments. Different value for H_1 and H_2 represents unequal distribution of dominant genes among parents. F value was found significant under normal condition indicating more frequent dominant genes while non-significant value of F under water stress indicating less frequent dominant and recessive genes.

Effect of heterozygous loci (h^2) among the parents was found significant under normal condition while it was non-significant under water stress condition. Mean degree of dominance $(H_1/D)^{0.5}$ was reported less than one indicating additive genetic effects for the inheritance of trait both under normal as well as stress condition.

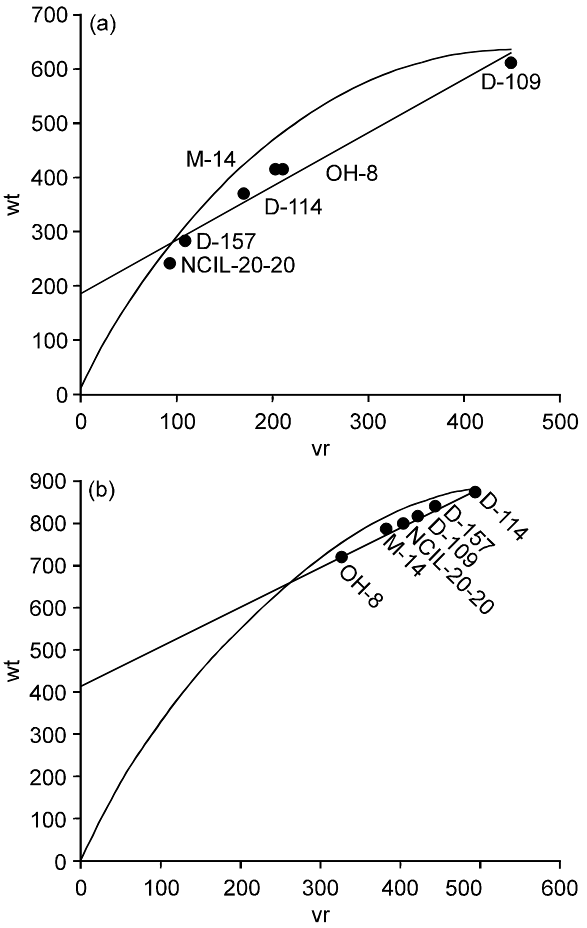

Fig. 8(a-b): Wr/Vr graph for grain yield per plant. (A) Normal condition and (b) Water stress condition

Less value of $H_2/4H_1$ ratio suggested different distribution of genes among the parents under both conditions. Environmental variance (E) was found significant indicating a role for expression of trait under both conditions. The value of narrow sense heritability 86 and 90% were recorded under normal and water stress condition, respectively.

The results are in line with the finding of Mani *et al.* (2000), Farshadfar *et al.* (2002), Betran *et al.* (2003), Afarinesh *et al.* (2005), Ojo *et al.* (2007), Farooq (2008), Hussain *et al.* (2009), Chohan *et al.* (2012) and Iqbal *et al.* (2012) who reported additive gene action for grain yield. Whereas, Bukhari (1986), Siddiqui (1988), Naved (1989), Yousaf (1992), Shabbir and Saleem (2002) and Akbar (2008) who reported over-dominance type of gene action for the inheritance of grain yield trait. The graphical presentation of data (Fig. 8a) revealed NCIL-20-20 containing highest dominant genes chased by D-157 and D-114 while D-109 showed minimum dominant genes under normal condition for grain yield per plant. Regarding array distribution under water deficit condition

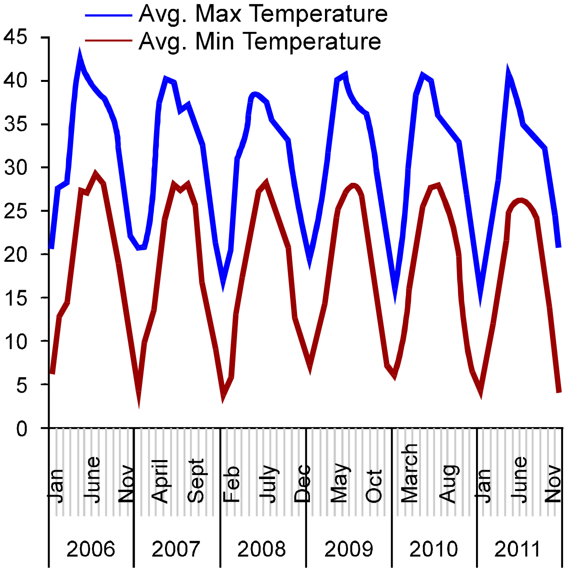

Fig. 9: Average maximum and minimum temperature of five years

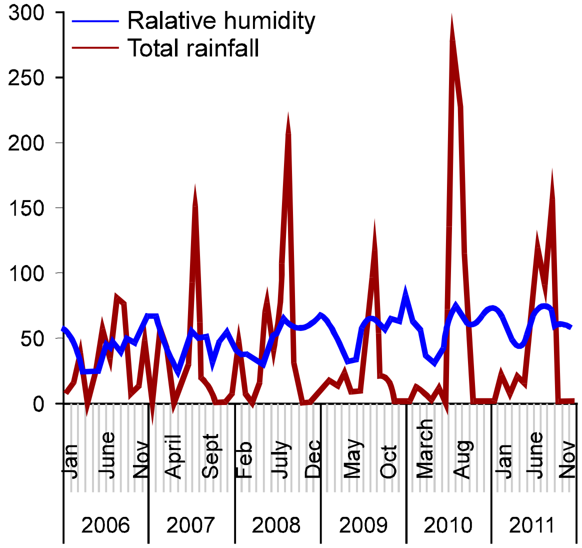

Fig. 10: Rainfall and relative humidity of five years (2006-2011)

indicated OH-8 with maximum dominant genes being closest to the origin while D-109 farthest from the origin displayed maximum recessive genes (Fig. 8b).

Conclusion: Genetic variation existed in the germplasm which could be used to explore the required targeted genotype. Moderate to high heritability pattern for all the studied traits showed influence of additive gene action thus suggested early stage selection. The results will be helpful for understanding the inheritance pattern of traits in the development of water stress tolerant genotypes.

The inbred line NCIL-20-20, D-157 and OH-8 recorded as the best parents on the basis of performance regarding grain yield per plant under both conditions. These inbred lines can be further explored and utilized in future breeding program.

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