

GENETIC ANALYSIS FOR GRAIN YIELD AND VARIOUS MORPHOLOGICAL TRAITS IN MAIZE (*ZEA MAYS* L.) UNDER NORMAL AND WATER STRESS ENVIRONMENTS

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Correspondence Author E-mail: ghafoor59pk@yahoo.com**ABSTRACT**

A genetic analysis study was carried out for various morphological traits in a complete 8×8 diallel cross of maize inbred lines under normal irrigation and drought conditions. Estimation of genetic components of variation and graphical presentation deduced that most of the traits like days to pollen shed, anthesis-silking interval, ear height, kernel rows per ear, 100-kernel weight, shelling percentage, grain yield per plant showed over-dominance type of inheritance under both normal and drought conditions unlike leaf rolling which showed partial dominance under normal but over-dominance type of inheritance under drought conditions. It can be inferred that because of over-dominance nature of inheritance of most of the yield related traits, heterosis breeding can be pursued to exploit high yielding hybrids with considerable drought tolerance.

Key words: additive-dominance model, genetic analysis, Hayman's diallel approach, Maize.

INTRODUCTION

Together with rice and wheat, maize provides at least 30 per cent of the food calories to more than 4.5 billion people in 94 developing countries (von Braun *et al.*, 2010; CIMMYT, 2011), which highlights the importance of maize to ensure global food security. In tropical and subtropical regions maize crop is grown mainly on marginal lands and prone to face various extreme climatic conditions and different biotic and abiotic stresses (Edmeades *et al.*, 1992; Zaidi, 2002).

Drought is the major of three abiotic factors; waterlogging and low soil fertility being the other two, that are most responsible for restricting maize production and productivity in developing world. The trend of growing maize in poor and marginal areas subject to the abnormal rainfall distribution pattern is thought to be a major reason for slow dissemination of improved varieties and crop management practices. Global estimates about annual losses of maize production due to problem of drought in early 1990s across the non-temperate maize areas equaled about 19 million tons, representing about 15 per cent decrease in production (Edmeades *et al.*, 1992; Zaidi, 2002). Maize is the main staple in southern Africa where it is grown on over 34.5 million ha (FAOSTAT, 2011). Such losses can be far more dangerous; an overwhelming situation of drought stress in South Africa in 1991-92 reduced maize production by about 60 per cent (Rosen and Scott, 1992). Drought is assessed to cause average annual yield losses in maize of about 17 per cent in the tropics (Edmeades *et al.*, 1998). To control such heavy yield drawbacks an

integrated approach using available technological options, both crop management and genetic improvement is essential.

Genetic improvement of crops for drought adaptation is probably the greatest challenge in plant breeding due to the complexity of the drought environment. The use of genetics to improve drought tolerance and provide yield stability is an important part of the solution to stabilize global maize production. As grain yield and other morphological characters associated with drought tolerance are quantitative in nature, knowledge about their gene action permits maize breeders to optimize their breeding programs more efficiently. The diallel approach of analysis was developed to deduce information on the genetic makeup of populations as well as genetic mechanisms controlling various traits (Hayman, 1954a). Several scientists explored the mode of gene action in maize by the use of diallel technique. The prime aim of this study was to ascertain information on genetic regulation of grain yield and other drought prone morphological characters of maize under normal and water stressed conditions.

MATERIALS AND METHODS

Eight inbred lines of maize viz, NCMLQ₁, NCMLQ₂, NCMLQ₃, NCMLQ₄, NCMLD₁, NCMLD₂, NCMLD₃ and NCMLD₄ were crossed in all possible combinations. Seed of F₁ hybrid combinations along with their parental lines were sown on 3rd March during spring 2008 in the research field on Maize, Sorghum and Millet Program, N.A.R.C Islamabad, following a randomized

complete block design in a plot size of 6 m² having two rows of four meter length, in three replications. Planting geometry followed for evaluation purposes was 75 cm and 20 cm distance between rows and plants, respectively. All the agronomic practices like application of herbicide, insecticide, fertilizers etc. were applied similarly to both normal and drought induced trials. Drought imposed trial was planted in plastic tunnels. Water stress was imposed on the experiment under drought through withdrawal of irrigation at flowering and early phase of endosperm development and onwards; however, normal 16 to 17 irrigations were applied to stress-free trial.

Meteorological data on rainfall during the critical specified period i.e. of flowering and endosperm development was recorded (Fig 9). The plants were labelled randomly before recording data. Data on plant characteristics related to yield like leaf rolling (scale 1-4), days to 50% pollen shedding, anthesis-silking interval (ASI), ear height (cm), number of kernel rows per ear, 100-kernel weight (g), shelling percentage and grain yield per plant (g) were recorded on 10 guarded plants from each replication for analysis of variance (Steel *et al.*, 1997) and Hayman's diallel analysis (Hayman, 1954a, 1954b; Mather and Jinks, 1982).

Before conducting diallel analysis, two scaling tests i.e. regression analysis and analysis of $W_r + V_r$ and $W_r - V_r$ were carried out to determine the adequacy of the data sets for Additive – Dominance Model for a particular trait.

RESULTS AND DISCUSSION

Analysis of variance expressed highly significant differences among genotypes for all characters under both water regimes (Table 1). Therefore, estimation of 1st and 2nd degree genetic components was carried out for all the traits under normal and water deficient conditions and results are presented in Table 3 and Table 4. Hayman's analysis of variance (Table 2) showed significance of additive (a) and dominance (b) effects for almost every trait under study for both water regimes. All traits except ASI and kernel rows per ear showed directional dominance (b_1) under normal conditions whereas ASI and 100-kernel weight showed the same under drought conditions. Characters other than grain yield per plant under both water regimes and kernel rows per ear under water stressed trial, expressed significant (b_2) component, indicating asymmetry of gene distribution. Maternal effects (c) were significant for all traits under stress conditions but non-significant for ASI, kernel rows per ear, and grain yield per plant under normal conditions. When maternal effects are significant, item a (additive effects) is needed to be retested against c item. After retesting, 'a' items turned non-significant for leaf rolling and 100-kernel weight under both water

regimes, and for ear height and kernel rows per ear only under drought conditions. The reciprocal effects 'd' were significant under normal as well as drought conditions for traits like leaf rolling, days to pollen shedding, ear height, kernel rows per ear, 100-kernel weight, shelling percentage and grain yield per plant. Significance of d items for these traits made retesting of all b items, against d, necessary. As a result of retesting of b items (dominance effects) against d (reciprocal effects), b items for leaf rolling, days to pollen shedding, 100-kernel weight, and shelling percentage became non-significant under both water regimes. The results of 1st and 2nd degree genetic components are presented in Table 3 and 4.

a. Leaf rolling. Both additive as well as non-additive gene actions were present at the interplay of genetic control of leaf rolling parameter in maize as duly proved by the significance of D, H_1 and H_2 under normal conditions. However, insignificance of D and significance of H_1 and H_2 emphasized the predominant role of additive effects over dominance effects in the expression of this trait under water stressed conditions. Significance of F under both regimes yielded greater frequency of dominant alleles in the inheritance of this trait. Non-significance of h^2 diluted the role of heterozygous loci under normal as well as water stressed conditions. Effects because of E were non-significant under normal conditions but significant under drought conditions suggesting that the role of environment is unimportant under normal conditions but played important role in the expression of this character under water stressed conditions.

Over-dominance was observed to be involved for the control of leaf rolling in maize under normal irrigation as the mean degree of dominance ($(H_1/D)^{1/2}$) value remained above unity, whereas under drought conditions, this ratio fell below unity, hence showed partial dominance for drought imposed trails. These results differ with the findings of Chen *et al.* (1996) who reported non-allelic interactions for leaf rolling. Graphic elaboration made it very clear that inheritance of leaf rolling was being manifested by the over-dominance genetic effects under normal conditions, as revealed by negative intersect of the regression line upon W_r -axis in W_r - V_r graph (Fig. 1A). However, under water stress, the role of partial dominance was more pronounced as evident from positive intersect of regression line (Fig. 1B). Perusal of array point distribution inferred that under normal irrigation parental line NCMLQ₂ was beneficiary of sharing maximum of dominant alleles while inbreds NCMLQ₄ and NCMLQ₈ were laggards in this regard. While under water stress NCMLD₃ was the parent sharing maximum of the dominant genes compared to NCMLD₂ which shared maximum of the recessive alleles in controlling leaf rolling in maize.

b. Days to Pollen Shed. Results of genetic components of variation (Table 3) envisaged that D, H₁ and H₂ stood significant under both planting conditions, hence imparted both additive and dominance gene actions. Values of F although remained non-significant but bore a positive sign, thus emphasis was put on major role of dominance than additive effects. Dominance variance H (H₁ and H₂) experienced higher values than additive variance (D) inclined the position of the genetics of this trait towards dominance under both water regimes. Values of h^2 were observed significant under water stressed and non-significant under normal conditions yielding a mixed trend about significance of heterozygous loci. Role of environment E remained insignificant in the expression of this trait under both regimes. Over-dominance was made obvious as the average degree of dominance ratios were greater than one under both planting conditions. Saleem *et al.* (2002); Wattoo *et al.* (2009) and Irshad ul Haq *et al.* (2010) also reported over-dominance for days to pollen shed inheritance in maize. The same was visualized by the negative intercept of Wr-axis in Wr-Vr graph by the regression line (Fig. 2A, 2B). Distribution of array points along regression line yielded inference that under normal conditions, parents NCMLQ₂, NCMLQ₄, NCMLD₁, NCMLD₂ and NCMLD₄ being cluster in the first quadrante shared maximum dominant genes while NCMLQ₁ on the opposite side shared the maximum recessive alleles for anthesis in maize. Under drought, same situation of parents prevailed suggesting the narrow diversity prevails among parents for this trait.

c. Anthesis-Silking Interval (ASI). Both additive and non-additive gene actions were present for genetic control of ASI, as revealed by significance of D and H (H₁, H₂) under both irrigation levels. Comparative higher values of H (H₁, H₂) than D, imparted more prevalence of non-additive gene actions. $(H_1/D)^{1/2}$ values remained more than one, indicating that over-dominance was playing role behind the control of ASI. Wr-Vr graphic presentation (Fig. 3A, 3B) confirmed the role of over-dominance due to the fact that regression line cut Wr-axis well below the origin in both normal and water deficient trials. Among the parents, inbred line NCMLD₂ affixed itself near the origin in both trials hence carried maximum dominant gene in contrast to NCMLQ₃ which affixed itself at the farthest point along the regression line and possessed minimum dominant genes. Rest of the parental lines were distributed in the middle region of regression line thus, contained dominant and recessive alleles in relatively equal proportions. These findings are in line with those of Irshad ul Haq (2010) who presented that over-dominance gene action was operating ASI.

d. Ear Height. Both of the additive and non-additive gene actions were controlling ear height in maize as evident from the significance of D and H (H₁, H₂)

variances. Also the values of H components (H₁, H₂) remained greater than D showing preponderance of dominance as compared to additive genetic control of this trait. Significant values of F under normal water regime showed excessive presence of dominant alleles in parental lines. Average degree of dominance $(H_1/D)^{1/2}$ under both planting conditions showed that ear height was under the control of over-dominance type of gene action. Irshad ul Haq *et al.* (2010) also reported over-dominance type of gene action while results are not in agreement with the findings of Qadri *et al.* (1983) who reported additive type of gene action for ear height in maize. Regression line intercept was below the origin in Wr-Vr Graph (Fig. 4A, 4B) authenticating role of over-dominance in the inheritance of this character under drought and normal conditions. Array points of the parents arranged in the first quadrante along origin showed no diversity for this trait. However, inbred line NCMLD₁ falling in the close proximity of the origin shared more dominant alleles while NCMLD₂ was the inbred with minimum dominant alleles under both irrigation regimes.

e. Number of kernel rows per ear. Additive gene action for this trait appeared to be expressed only under normal moisture level as revealed by the significance of D, while these effects were absent in moisture stress and only non-additive effects H₁ and H₂ were significant. Positive values of F and h^2 also emphasized the role of dominant factors. Over-dominance of this character was elaborated by the $(H_1/D)^{1/2}$ values which were more than one, and this was further authenticated by the negative intercept of regression line (Fig. 5A, 5B). Chen *et al.* (1996); Perez Velasquez (1996); Saleem *et al.* (2002); Wattoo *et al.* (2009) and Irshad ul Haq (2010) also reported over-dominance for this trait while Betran *et al.* (2003) and Khodarahmpour (2011) reported partial dominance for kernel rows per ear. Parental line NCMLD₄ laid near the origin under both normal and water stress conditions so contained maximum dominant alleles. Whereas NCMLQ₁ and NCMLD₂ arranged themselves at furthestmost point hence contained maximum of recessive alleles under normal and drought conditions respectively.

f. 100-kernel weight. Significant D, H₁ and H₂ genetic parameters across irrigation regimes were exhibited, which revealed that this trait was under control of both additive and dominance gene actions. The greater values of H components than D assessed that dominance effects were playing more vigorous role in control of 100-kernel weight. Positive values of F established symmetrical gene distribution. Environmental variance E was significant for the trial planted under normal irrigation and non-significant for trial under stress conditions suggesting that the environment played insignificant role in the expression of this trait under drought conditions. Average degree of dominance

$(H_1/D)^{1/2}$ value determined the involvement of over-dominance for the genetic control of this trait. Similarly, negative intercept of regression line in both trails in Wr-Vr graph (Fig. 6A, 6B) confirmed the over-dominance

genetic effect for 100-kernel weight. Parez Velasquez (1996); Chen *et al.* (1996); Saleem *et al.* (2002); Watto *et al.* (2002); Betran *et al.* (2003) and Khodarahmpour (2011) also reported over-dominance.

Table 1. Mean squares of various morphological traits in 8 × 8 diallel cross under normal and drought stress conditions.

SOV	df	LR	DtPS	ASI	EH	KRE ⁻¹	100-KW	Shell-P	GYP ⁻¹
DROUGHT									
Replications	2	1.12*	0.04 ^{ns}	6.27	107.60 ^{ns}	0.43 ^{ns}	70.60**	196.11**	215.40 ^{ns}
Genotypes	63	2.42**	34.12**	14.30**	159.39**	0.70**	43.33**	122.60**	466.84**
Error	126	0.23	3.68	1.78	31.80	0.27	2.28	23.31	62.31
NORMAL									
Replications	2	2.45**	16.03**	4.65 ^{ns}	107.60 ^{ns}	1.58*	29.87 ^{ns}	154.71**	327.78 ^{ns}
Genotypes	63	1.59**	40.47**	10.12**	155.01**	0.85**	203.90**	98.28**	254.96**
Error	126	0.21	0.83	4.71	31.80	0.38	30.23	15.08	114.86

LR = Leaf Rolling; DtPS = Days to 50% Pollen Shedding; ASI = Anthesis Silking Interval; EH = Ear Height; KRE⁻¹ = Kernel Rows Ear⁻¹; 100-KW = 100 Kernel Weight; Shell-P = Shelling Percentage; GYP⁻¹ = Grain Yield Plant⁻¹

Table 2. Hayman's analysis of variance for different morphological traits in 8 × 8 diallel cross under normal and drought stress conditions.

S.O.V (under normal conditions)	df	Means squares							
		LR	DtPS	ASI	EH	KRE ⁻¹	100-KW	Shell-P	GYP ⁻¹
Replications	2	3.14 ^{ns}	15.97**	4.65 ^{ns}	107.63*	1.58*	29.88 ^{ns}	154.09**	327.72 ^{ns}
a	7	2.61**†	119.76**	14.55**	290.76**	1.36**	257.47**†	226.58**	379.61**
b	28	1.74**	32.68**	13.32**	213.35**	0.84**	242.7**	92.27**	292.66**
b ₁	1	1.31**	26.58**	9.84 ^{ns}	2386.67**	1.3 ^{ns}	623.07**	371.18**	819.26**
b ₂	7	1.98**	13.8**	11.66*	195.87**	2.48**	83.56*	58.49**	179.24 ^{ns}
b ₃	20	1.68**	39.6**	14.08**	110.8**	0.24 ^{ns}	279.37**	90.15**	306.02**
c	7	2.15**	35.77**	2.9 ^{ns}	67.62*	0.64 ^{ns}	166.98**	59.47**	157.36 ^{ns}
d	21	1.16**	27.68**	6.78 ^{ns}	61.1*	0.77**	146.61**	76.13**	195.7*
Error	126	0.31	0.8	4.71	31.8	0.38	30.23	15.06	114.86
Total	191								
S.O.V (under drought conditions)									
Replications	2	1.21**	0.406 ^{ns}	6.27*	107.63*	0.43 ^{ns}	70.61**	196.09**	215.41*
a	7	6.13**†	88.74**	12.1**	198.59**†	0.5 ^{ns} †	63.26**†	294.25**	792.59**
b	28	1.44**	28.00**	15.21**	213.35**	0.96**	30.88**	119.78**	563.18**
b ₁	1	1.32**	81.02**	6.86 ^{ns}	2386.67**	17.26**	5.76 ^{ns}	611.62**	3631.64**
b ₂	7	1.58**	10.68**	8.26**	195.87**	0.35 ^{ns}	11.32**	90.25**	86.45 ^{ns}
b ₃	20	1.4**	31.42**	18.06**	110.8**	0.36 ^{ns}	38.98**	105.52**	576.61**
c	7	4.74**	36.65**	4.05*	166.98**	0.57*	32.59**	84.21**	244.68**
d	21	1.84**	24.09**	17.25**	61.1*	0.46*	56.89**	81.96**	303.86**
Error	126	0.22	3.70	1.78	31.8	0.27	2.28	23.31	62.31
Total	191								

†: a item turned non-significant after retesting against c items. : b items turned non-significant after retesting against d items.

Parental lines NCMLD₁ in stress free and NCMLQ₁ in drought stress trial, being in close proximity of origin carried dominant genes for this respectively. While NCMLD₃ falling farthest in all trials contained recessive alleles to the maximum for this trait.

Shelling percentage. To impart heredity for this biometrical trait, both additive D and dominance H (H₁, H₂) genetic effects were important. Dominance effects

were more pronounced as dominance variance H (H₁, H₂) occurred at higher numeric values than additive variance D. More number of alleles exerting dominance was apparent from the significance of F parameter. Graphic presentation (Fig. 7A, 7B) and values of $(H_1/D)^{1/2}$ revealed presence of over-dominance for the control of this trait. A perusal of array points affixed along the graph plot showed consistency of NCMLD₁ which contained maximum dominant alleles by virtue of falling

nearest to the origin in contrasting irrigation trials, while parents NCMLQ₃ and NCMLD₂ possessed maximum recessive alleles for inheritance of shelling percentage under normal and water deficient conditions respectively.

Grain yield per plant. Co-presence of both additive and dominant gene action in the control of this character was envisaged by the significance of both D and H (H_1 , H_2) components of genetic variation. Greater frequency of dominant genes was stressed upon by the positive and significant value of F at normal irrigation. However, the intensity of dominance involved in regulation of grain yield per plant became non-significant at water stress conditions, though positive values of F were supportive of the importance of dominance alleles involved in fixing this trait. Graphic Plot (Fig. 8A, 8B) and genetic parameter $(H_1/D)^{1/2}$ also displayed an over-dominant gene action under both planting conditions. The values of

$(H_1/D)^{1/2}$ were more than unity and regression line intersected the W_r -axis below the origin in both trials. Damborsky *et al.* (1994), Perez Velasquez (1996), Kumar (1998), Joshi *et al.* (1998), Dutu (1999), Mani *et al.* (2000), Saleem *et al.* (2002), Watto *et al.* (2002), Betran *et al.* (2003), Prakash and Ganguli (2004), Ali *et al.* (2007), Irshad-ul-Haq (2010) and Khodarahampour (2011) reported over-dominance type of gene action for grain yield, but Shabir and Saleem (2002) reported additive type of gene action with partial dominance. Arrangement of array points depicted that NCMLQ₂ and NCMLD₁ contained excess of dominant alleles under normal and drought conditions respectively, whereas NCMLD₃ being at the most distal position from origin contained maximum of recessive alleles for both levels of irrigation.

Table 3. First degree statistics of genetic variation for various morphological traits in 8x8 diallel cross in maize.

Plant Characters	Trials	Genetic Parameters											
		D		H ₁		H ₂		F		h ²		E	
Leaf Rolling	(Normal)	1.04	±0.18*	1.37	±0.46*	0.96	±0.35*	1.26	±0.40*	0.15	±0.27 ^{ns}	0.10	±0.08 ^{ns}
	(Drought)	1.03	±0.98 ^{ns}	0.98	±0.19*	0.73	±0.16*	0.79	±0.19*	0.07	±0.11 ^{ns}	0.08	±0.03*
Days to Pollen Shedding	(Normal)	12.63	±4.85*	24.50	±11.15*	21.26	±9.70*	5.97	±11.46 ^{ns}	3.76	±6.50 ^{ns}	0.27	±1.61 ^{ns}
	(Drought)	9.02	±3.38*	17.94	±7.77*	16.34	±6.76*	3.68	±7.98 ^{ns}	11.31	±4.53*	1.23	±1.12*
Anthesis-Silking Interval (ASI)	(Normal)	3.59	±0.86*	7.48	±1.98*	5.79	±1.72*	4.509	±2.03*	0.79	±1.15 ^{ns}	1.57	±0.28*
	(Drought)	2.36	±0.78*	10.57	±1.79*	8.97	±1.56*	3.12	±1.84 ^{ns}	0.76	±1.04 ^{ns}	0.59	±0.26*
Ear Height	(Normal)	51.52	±13.54*	162.05	±31.14*	121.34	±27.09*	70.96	±32.01*	343.71	±18.17*	10.6	±4.51*
	(Drought)	31.71	±13.59*	158.59	±31.26*	118.82	±27.19*	56.17	±32.13 ^{ns}	339.05	±18.24*	11.43	±4.53*
Number of Kernel Rows Per Ear	(Normal)	0.96	±0.05*	0.83	±0.12*	0.31	±0.11*	1.41	±0.13*	0.14	±0.07*	0.13	±0.02*
	(Drought)	0.03	±0.04 ^{ns}	0.48	±0.09*	0.46	±0.08*	0.03	±0.09 ^{ns}	2.48	±0.05*	0.09	±0.01*
100-Kernel Weight	(Normal)	53.70	±12.26*	154.98	±28.20*	141.96	±24.53*	48.10	±28.98 ^{ns}	86.73	±16.45*	10.73	±4.09*
	(Drought)	11.75	±2.20*	21.33	±5.06*	19.09	±4.49*	8.93	±5.20 ^{ns}	0.53	±2.95 ^{ns}	0.76	±0.73 ^{ns}
Shelling Percentage	(Normal)	33.97	±5.43*	62.33	±12.50*	51.63	±10.87*	27.20	±12.84*	52.07	±7.29*	5.02	±1.81*
	(Drought)	57.55	±7.81*	81.04	±17.95*	64.55	±15.62*	51.71	±18.46*	86.01	±10.47*	7.77	±2.60*
Grain Yield Per Plant	(Normal)	78.60	±13.02*	134.62	±29.93*	119.73	±26.04*	72.63	±30.76*	103.77	±17.46*	38.29	±4.34*
	(Drought)	82.99	±22.26*	339.95	±51.19*	334.56	±44.53*	28.18	±52.69 ^{ns}	521.09	±29.86*	20.77	±7.42*

D: Additive Variance H₂: Dominance Variance 2. h²: Dominance Effects (as the algebraic sum over all loci in heterozygous phase)
H₁: Dominance Variance 1 E: Environmental component of variation F: Frequency of gene distribution among parents.

Table 4. Second degree statistics of genetic variation for various morphological traits in 8x8 diallel cross in maize

Plant Characters	Trials	Genetic Parameters							
		(H ₁ /D) ^{1/2}	KD/KR	h ² /H ₂	h	uv (H ₂ /4H ₁)	D/(D+E)	h ² b	h ² n
Leaf Rolling	(Normal)	1.15	0.76	0.18	-0.44	0.18	0.91	0.76	0.22
	(Drought)	0.97	0.69	0.11	0.33	0.18	0.93	0.85	0.48
Days to Pollen Shed	(Normal)	1.39	0.58	0.20	-1.97	0.22	0.98	0.98	0.47
	(Drought)	1.41	0.57	0.80	-3.44	0.23	0.88	0.86	0.40
Anthesis-Silking Interval (ASI)	(Normal)	1.44	0.72	0.16	1.20	0.19	0.70	0.54	0.11
	(Drought)	2.12	0.66	0.10	1.00	0.21	0.80	0.81	0.13
Ear Height	(Normal)	1.77	0.69	3.24	18.66	0.19	0.83	0.79	0.21
	(Drought)	2.28	0.71	3.24	18.66	0.88	0.75	0.78	0.14
Number of Kernel Rows Per Ear	(Normal)	2.93	0.89	0.51	0.44	0.09	0.88	0.48	0.16
	(Drought)	4.12	0.56	6.12	1.59	0.24	0.24	0.58	0.04
100-Kernal Weight	(Normal)	1.70	0.63	0.70	-9.53	0.23	0.84	0.82	0.17
	(Drought)	1.35	0.64	0.03	0.92	0.22	0.94	0.91	0.31
Shelling Percentage	(Normal)	1.35	0.65	1.15	-1.36	0.21	0.87	0.81	0.33
	(Drought)	1.19	0.69	1.52	-9.44	0.19	0.88	0.78	0.32
Grain Yield Per Plant	(Normal)	1.31	0.68	0.99	10.93	0.22	0.67	0.51	0.13
	(Drought)	2.02	0.54	1.78	23.01	0.24	0.80	0.85	0.22

(H₁/D)^{1/2}: Average degree of dominance. uv (H₂/4H₁): Balance of positive and negative genes. KD/KR: Proportion of dominant to recessive genes.
D/(D+E): True sense heritability. h²/H₂: Number of effective factors. h²b: Broad sense heritability. h: Average direction of dominance. h²n: Narrow sense heritability.

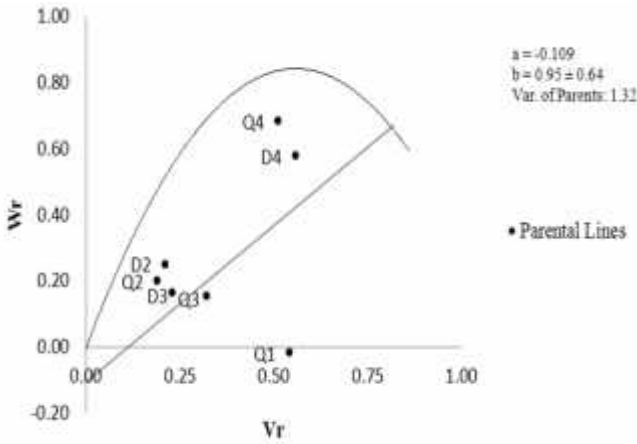


Fig.1A. Wr-Vr Graph for leaf rolling under normal water conditions

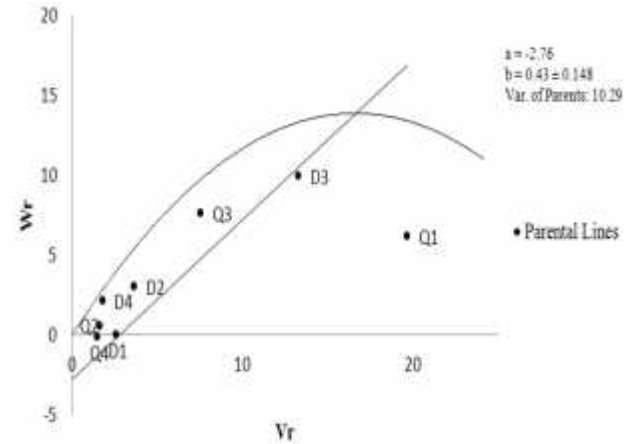


Fig. 2B Wr-Vr Graph for days to pollen shed under drought conditions.

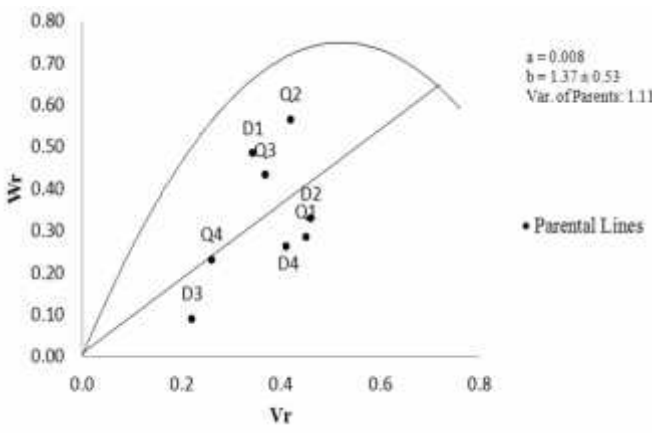


Fig. 1B. Wr-Vr Graph for leaf rolling under drought.

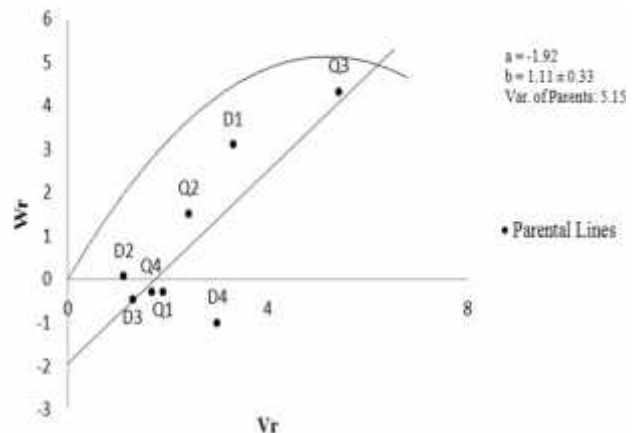


Fig. 3A. Wr-Vr Graph for anthesis-silking interval under normal conditions.

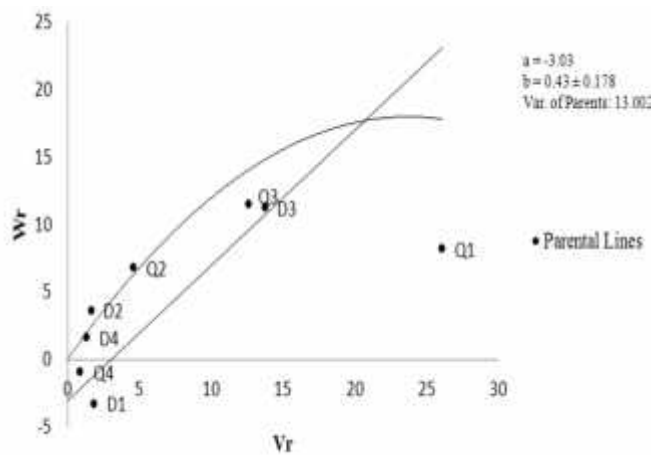


Fig. 2A. Wr-Vr Graph for days to pollen shed under normal conditions.

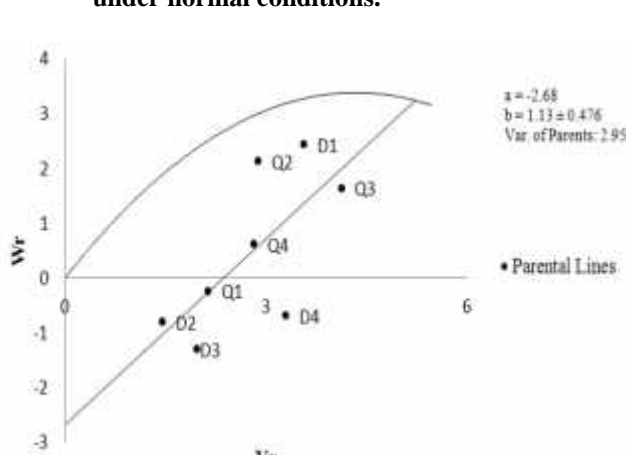


Fig. 3B. Wr-Vr Graph for anthesis-silking interval under drought stress.

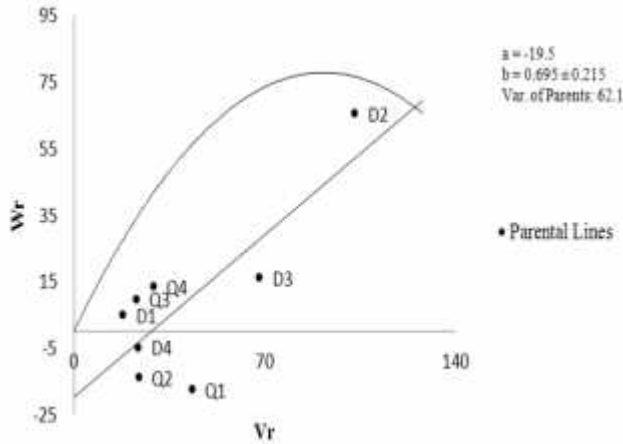


Fig 4A. Wr-Vr Graph for ear height under normal conditions.

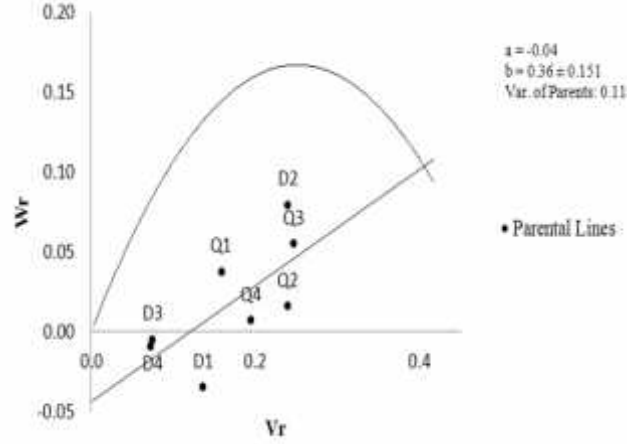


Fig 5B. Wr-Vr Graph for kernel rows per ear under drought conditions.

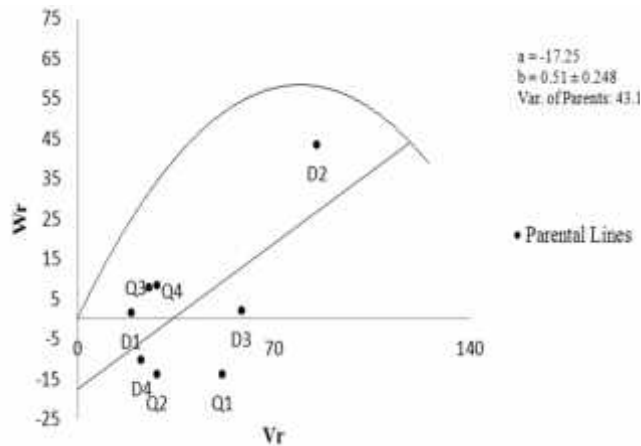


Fig 4B. Wr-Vr Graph for ear height under drought stress conditions.

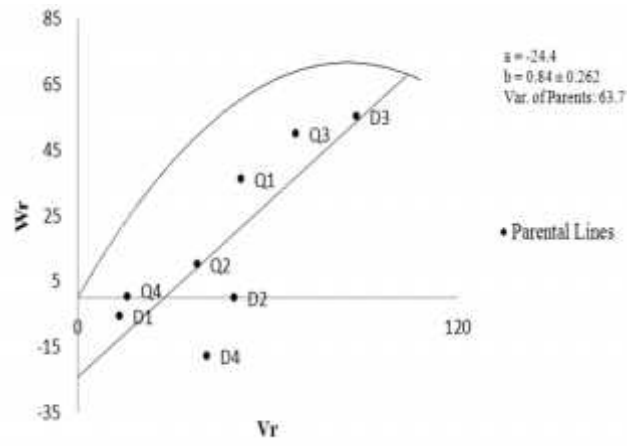


Fig 6A. Wr-Vr Graph for 100-kernel weight under normal conditions.

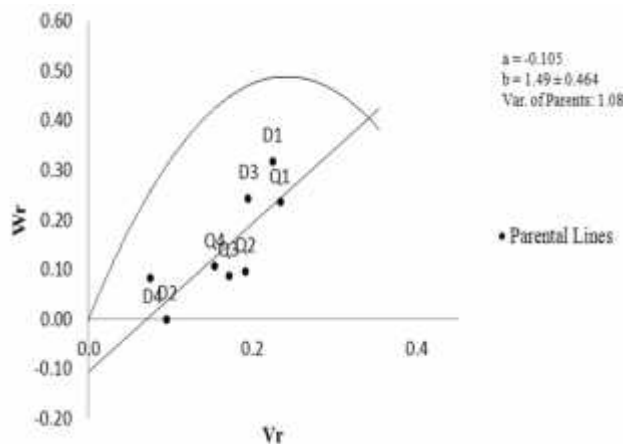


Fig 5A. Wr-Vr Graph for kernel rows per ear under normal conditions.

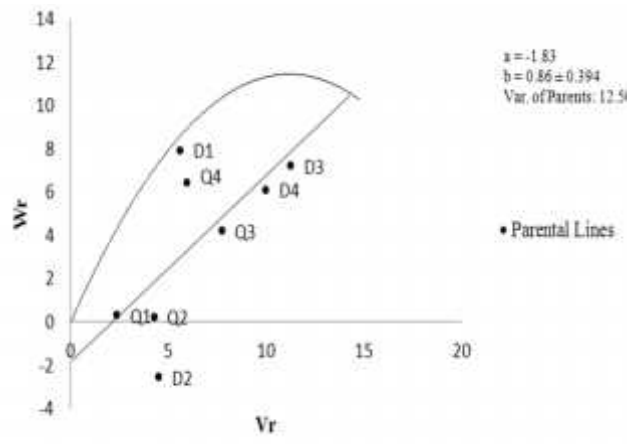


Fig 6B. Wr-Vr Graph for 100-kernel weight under drought stress conditions.

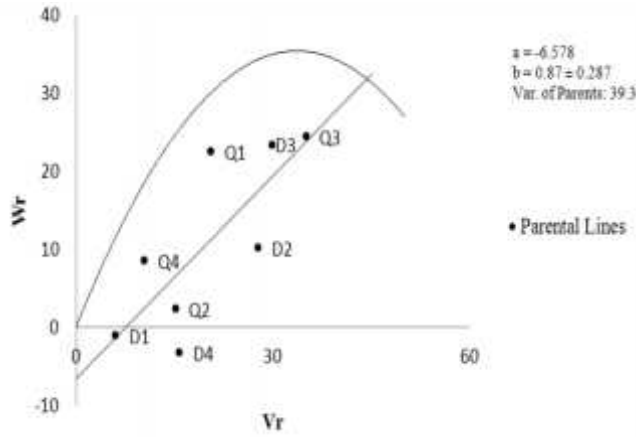


Fig. 7A. Wr-Vr Graph for shelling percentage under normal conditions

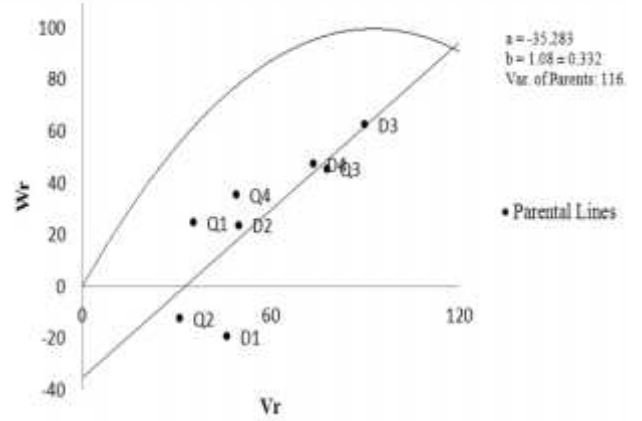


Fig 8A. Wr-Vr Graph for grain yield per plant under normal conditions.

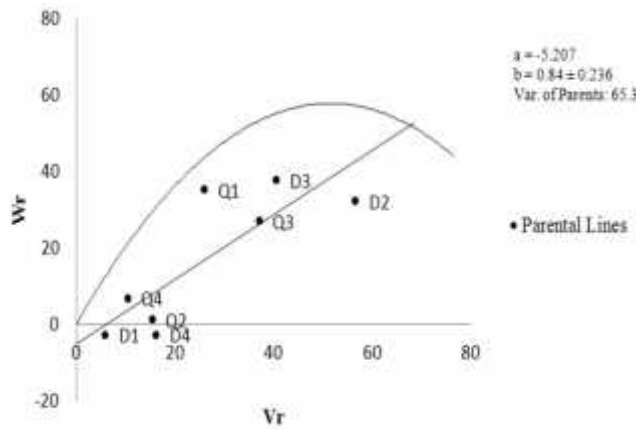


Fig. 7B. Wr-Vr Graph for shelling percentage under drought conditions.

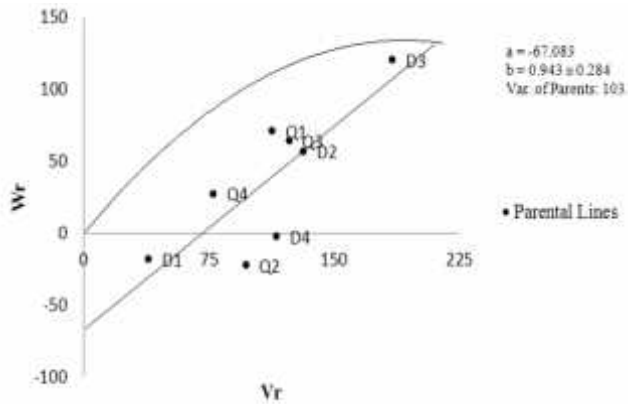
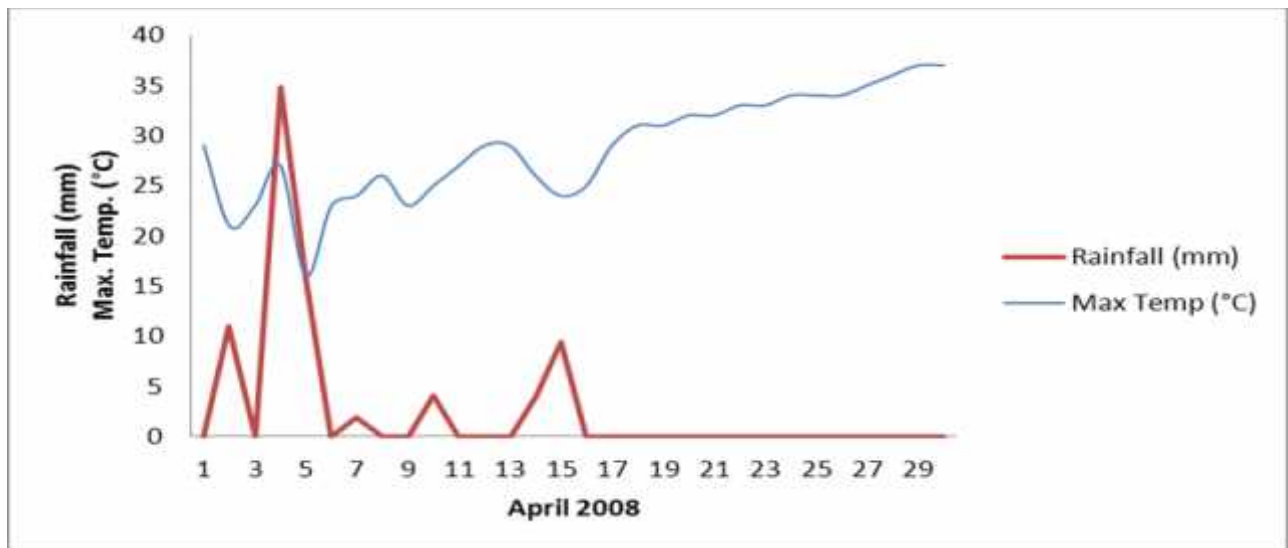


Fig. 8B. Wr-Vr Graph for grain yield per plant under drought stress conditions.

Parents: 1. NCMLQ₁, 2. NCMLQ₂, 3. NCMLQ₃, 4. NCMLQ₄, 5. NCMLD₁, 6. NCMLD₂, 7. NCMLD₃ and 8. NCMLD₄



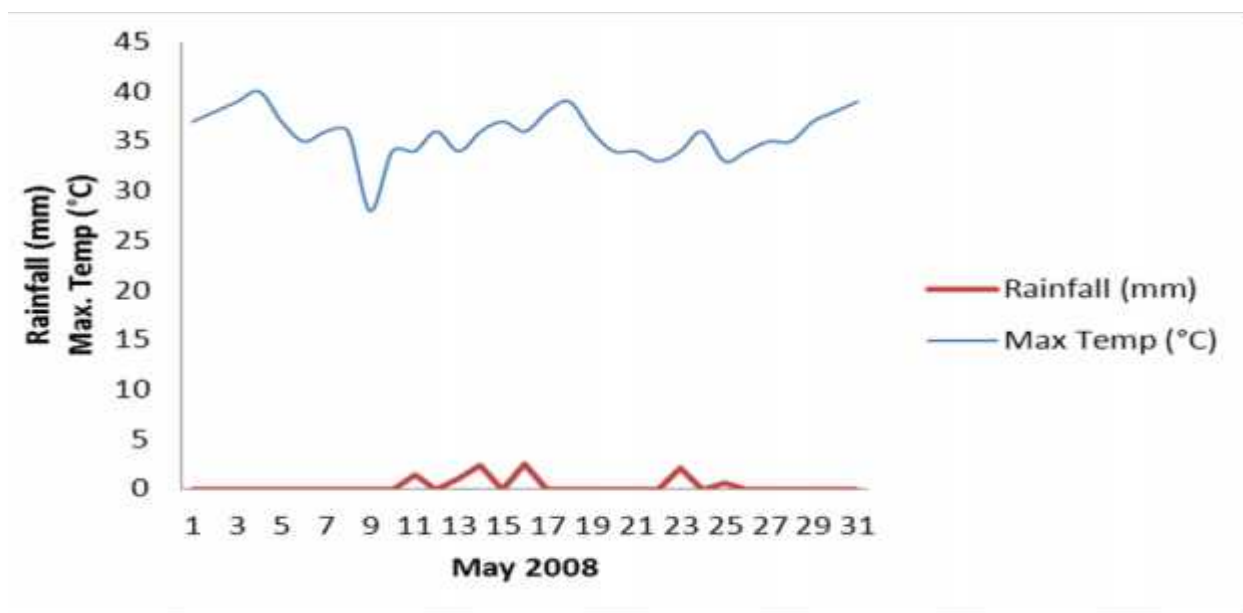


Fig. 9. Meteorological data for the month of April and May 2008.

Conclusion. From this study about genetic analysis of different traits in maize under normal and drought stress conditions, it can be deduced that since most of the yield related traits showed over-dominance type of inheritance, heterosis breeding can be pursued and hybrid combinations can be developed with considerable tolerance to drought stress.

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