

## ASSESSMENT OF GENETIC COMPONENTS FOR DIFFERENT TRAITS IN MAIZE (*ZEA MAYS* L.)

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### ABSTRACT

A complete 6 x 6 diallel mating design was followed to assess the genetic components for different traits in maize (*Zea mays* L.). Parents and F<sub>1</sub> generations were sown in RCBD with three replications in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during 2012. The data regarding plant height, leaf area, number of kernels per ear, stomatal size, stomatal frequency, leaf venation and 100-grain weight in maize were recorded at maturity to assess the genetic components and combining abilities. Analysis of variance was done to assess the significance of genetic differences among genotypes. Graphical approach used for diallel studies showed that most of the traits studied were under control of additive gene action. Plant height, leaf area, stomatal frequency and stomatal size were found under control of non-additive gene action. Whereas ear diameter, ear length, number of kernels per ear, number of kernels per row, leaf venation and 100-grain weight were under control of additive gene action.

**KEYWORDS:** *Zea mays*; maize; genotypes; cross breeding; F<sub>1</sub> generation; additive gene action; non-additive gene action; dominant gene action; diallel analysis, Pakistan.

### INTRODUCTION

Maize (*Zea mays* L.) is an important cereal crop that is third after wheat and rice (1) having high yield potential. Advances in maize production have a significant effect on the livings of large proportion of the world's population (8). In Pakistan 1083 thousand hectares area is under maize with a production of 4272 thousand tons (5). It is used as food, feed and forage.

Maize is naturally cross pollinated crop which is grown in two seasons i.e. autumn and spring. In case of spring maize, high temperature at flowering results in pollen desiccation which leads to reduction in yield per unit area in

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Pakistan. Different maize accessions differ in morphological and physiological basis and have complex interaction (16). Genetic components of maize were studied previously by different scientists i.e. additive effects for 1000-grain weight, grains per ear, ear diameter, number of leaves, leaf angle, shoot dry weight, anthesis date, anthesis silking interval and ear length whereas, non-additive effects for ear height, plant height, days to silking, days to maturing number of grains per row, days to emergences, days to physiological maturity (3, 4, 7, 10, 11, 14, 15, 17, 21, 22). The study of these traits like plant height, stem diameter, leaf area, ear length, ear diameter, number of rows per ear, number of grains per row, stomatal size, stomatal frequency and leaf venations are essential to assess their genetic background. Determination of inheritance pattern and type of gene action involved are very important factor for a breeder. This provides a base for deciding breeding methods, selection criteria and biometrical techniques. So the present study was planned to assess genetic components of different traits of maize using Hayman (9) diallel analysis.

## MATERIALS AND METHODS

Six maize accessions viz. A509, OH 54-3A, WA3748, B 34-2B, N 48-94 and 53AP1 were used as parents in diallel mating design to get all possible direct and reciprocal crosses during 2012. These crosses together with their parents were grown in RCBD alongwith three replications in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. All the recommended agronomic practices for crop production and protection were followed from sowing to harvesting. The data of five guarded plants for selected parameters from each entry. Plant height (cm), leaf area (cm<sup>2</sup>), number of kernels per ear, number of kernels per row, leaf venations, ear diameter (cm), ear length (cm), stomatal frequency, stomatal size (µm) and 100-grain weight (g) were recorded at maturity.

Stomatal size was measured with the help of ocular micrometer using microscope (NIKON-H3, JAPAN). Medium power 40X objective lens and 12.5X ocular piece were used for measurement of stomatal size. Leaf venation was also measured with the help of microscope. Upper surface of middle part of leaf blade was used to observe the stomatal frequency. Selected leaves were kept in Carnoy's solution (absolute alcohol 100 parts, chloroform pure 50 parts and glacial acetic acid 16 parts) for 24 hours to remove the chlorophyll and arrest the stomatal movement. Leaf samples were then examined by using 10X objective lens of microscope and number of stomata were counted. Data was subjected to analysis of variance (20), whereas, Huymen (9) graphical approach was used for genetic variability assessment.

**RESULTS AND DISCUSSION**

The results showed significant differences among genotypes for all the traits studied (Table 1).

**Table 1. Mean square values of different parameters in maize under field condition.**

SOV	Df	PH	ED	EL	KE	KR	LA	LV	SF	SS	GW
Replications	2	24	0.06	0.04	813	6.84	118	6.25	2.57	2.09	2.38
Genotypes	35	166**	0.89**	6.66**	7433**	28**	697**	22**	65**	44**	11**
Error	70	10	0.07	1.22	254	1.79	34.56	3.40	4.52	2.77	1.06
Total	107										

PH = Plant height, ED = Ear diameter, EL = Ear length, KE = Kernels per ear, KR = Kernels per row, LA = Leaf area, LV = Leaf venation, SF = Stomatal frequency, SS = Stomatal size and GW = Grain weight.

**Genetic components**

The data (Table 2) showed that magnitude of additive components (D) is higher than both dominant components H<sub>1</sub> and H<sub>2</sub>. This provided evidence for the presence of additive type of gene action for ear diameter, ear length, kernels per row, kernels per ear and 100-grain weight while stomatal frequency, stomatal size, leaf area and plant height showed non-additive type of gene action. The degree of dominance was found to be partial as indicated by ratio (H<sub>1</sub>/D)<sup>0.5</sup> i.e. less than 1. The unequal magnitude of H<sub>1</sub> and H<sub>2</sub> suggested presence of unequal distribution of genes in parents for plant height, ear diameter, ear length, kernels per row, kernels per ear, leaf venations, stomatal size, stomatal frequency, 100-grain weight and leaf area.

**Table 2. Genetic components for different traits in maize.**

Components	PH	ED	EL	KR	KE	LV	SF	SS	GW	LA
D	98	0.30	6.81	7.39	4478	5.29	17.59	17	4.62	168
H <sub>1</sub>	199	0.11	3.64	3.82	3105	3.37	54	23	1.81	683
H <sub>2</sub>	142	0.16	3.80	6.21	2670	4.79	56	18	2.61	601
F	148	0.15	6.32	0.09	3462	-0.9	14	16	2.70	240
(H <sub>1</sub> /D) <sup>0.5</sup>	1.41	0.60	0.73	0.79	0.80	0.79	1.75	1.14	0.90	2.01
H <sub>2</sub> /4H <sub>1</sub>	0.17	0.36	0.26	0.24	0.21	0.21	0.25	0.20	0.24	0.22
(4DH <sub>1</sub> )+F/ (4DH <sub>1</sub> )-F	3.23	2.48	4.48	1.01	2.63	0.79	1.63	2.34	2.75	2.09
h <sup>2</sup> n.s	0.08	0.42	0.10	0.52	0.53	0.20	0.02	0.33	0.35	0.02
h <sup>2</sup> b.s	0.91	0.78	0.73	0.86	0.94	0.70	0.90	0.89	0.76	0.92

D = Variance due to additive effects, H<sub>1</sub> and H<sub>2</sub> = Variance due to dominance effects of genes, F = Relative frequency of dominant and the recessive alleles in the parent, (H<sub>1</sub>/D)<sup>0.5</sup> = Degree of dominance ratio or degree of dominance, H<sub>2</sub>/4H<sub>1</sub> = Proportion of genes with positive and negative effects in the parents, (4DH<sub>1</sub>)<sup>0.5</sup>+F/ (4DH<sub>1</sub>)<sup>-0.5</sup> F = Proportion of dominant and recessive genes in parents, h<sup>2</sup>(n.s) = Narrow sense heritability, h<sup>2</sup>(b.s) = Broad sense heritability, PH = Plant height, ED = Ear diameter, EL = Ear length, KE = Kernels per ear, KR = Kernels per row, LA = Leaf area, LV = Leaf venation, SF = Stomatal frequency, SS = Stomatal size and GW = Grain weight.

Positive value of F shows that number of dominant genes are more frequent than recessive ones. The situation evidenced by estimates of (4DH<sub>1</sub>)<sup>0.5</sup> +F/

$(4DH_1)^{0.5}-F$  which is higher than 1 as indicated by plant height, leaf area, ear diameter, ear length, kernels per row, kernels per ear, stomatal size, stomatal frequency, leaf venations and 100-grain weight. The estimates of broad sense heritability for the characters are higher than narrow sense heritability estimates. Higher magnitude of broad sense heritability than the variation in parameters is less heritable in nature. The process of selection is helpful for better phenotypic manifestation of these traits.

### Plant height

From graphical illustration (Fig.1) it is evident that regression line intercepted below the point of origin, which shows the non-additive type of gene action (over-dominance). Plant height is controlled by non-additive gene action. As regression line deviate non-significantly from the unit slope, it indicates the absence of epistasis. The relative position of array point in the graph on regression line shows that genotype OH 54-3A has more dominant genes whereas, WA 3748 has more recessive genes as these are closest and farthest from point of origin, respectively. The results are similar to those of Alam *et al.* (3), Kanagarasu *et al.* (11), Zare *et al.* (22) and Mhike *et al.* (14) who reported that plant height was under the control of non-additive genes. However, the results are contrary to the finding of Mahmood *et al.* (13) and Bello *et al.* (6) who reported the involvement of additive type of gene action for plant height. It showed that plant height is under dominant gene effects and can be exploited through hybrid production. OH 54-3A can be used as parent in crosses to increase the plant height.

### Leaf area

According to graphical presentation (Fig.2) regression line (b) cuts Wr-axis below point of origin which indicates that over dominance type of gene action was involved in controlling of this trait. As regression line deviates non-significantly from the unit slope, therefore gene interaction (epistasis) was not involved. The distribution of array points on the regression line in graph shows that genotype 53AP1 has mostly dominant genes and the genotype A 509 has mostly recessive genes being nearest and farthest from point of origin, respectively. The results are in contrary to Zare *et al.* (22) who reported partial dominance type of gene action for this trait. The difference in results could be due to the difference in environmental conditions under which experiment was conducted and breeding material was used. As leaf area is correlated to photosynthesis, the more the leaf area, more will be photosynthesis, so it plays an important role in plant productivity. This trait

was controlled by genes showing over dominance, which means that hybrids can be obtained with high leaf area using 53AP1 as parent.

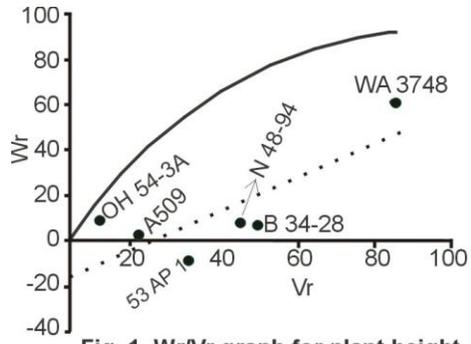


Fig. 1. Wr/Vr graph for plant height.

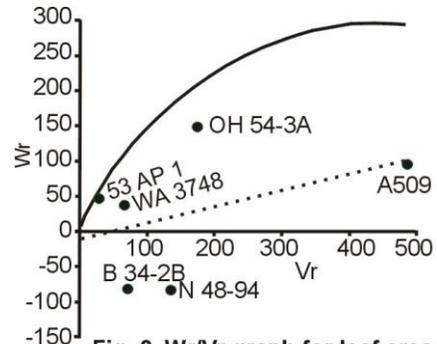


Fig. 2. Wr/Vr graph for leaf area.

### Ear diameter

The graph (Fig.3) indicated that regression line cuts Wr-axis above the origin which shows that additive genes control ear diameter. The distribution of array points on graph showed that genotype WA3748 had maximum dominant genes and OH54-3A possessed mostly recessive genes being nearer and farther from point of origin, respectively. The additive genetic effects in case of ear was reported by Shieh (19).

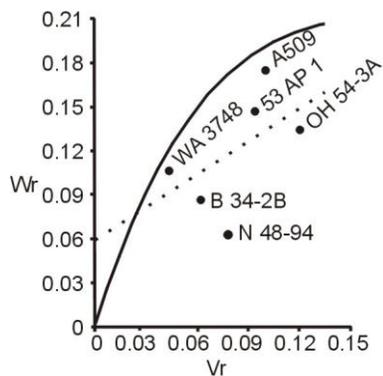


Fig. 3. Wr/Vr graph for ear diameter

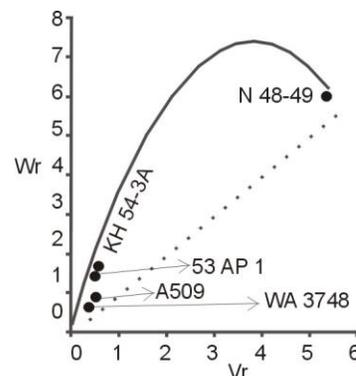


Fig. 4. Wr/Vr graph for ear length.

### Ear length

The graphical illustration (Fig. 4) showed that regression line cuts Wr-axis above point of origin revealing that the additive type of genes action was involved in inheritance of this trait. As regression line deviates non-

significantly from unit slope, it shows the absence of genes interaction. It is evident from graphical presentation that inbred line N48-94 had maximum dominant genes as it is nearest to the point of origin and the genotype B34-2B has most of recessive genes being farthest from point of origin. Additive gene effects were found predominant in ear length in a previous study (4). Rezaei and Roohi (17) found that non-additive gene action is dominant in ear length.

### Number of kernels per ear

From the graphical illustration (Fig.5) it is clear that regression line intercepts  $W_r$ -axis above point of origin which shows that number of kernels per ear is under control of additive gene action. As regression line deviate non-significantly from unit slope, it indicated non-involvement of epistasis. The distribution of array points on regression line in graph showed that genotype N48-94 had maximum dominant genes being nearest to point of origin and the genotype B34-2B has maximum recessive genes as it is farthest from the point of origin. The results are in accordance with the findings of Alam *et al.* (3) and Zivanovic *et al.* (23) who reported partial dominance type of gene action for this trait. However, the results are in contrast with the findings of Iqbal *et al.* (10) and Pavan *et al.* (15) who reported the involvement of over dominance type of gene action for this character.

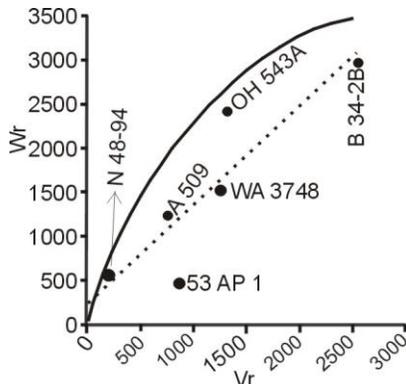


Fig. 5.  $W_r/V_r$  graph for kernels/ear.

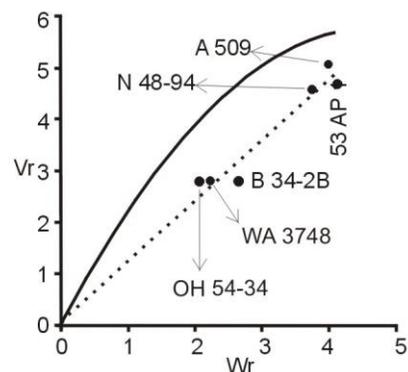


Fig. 6.  $W_r/V_r$  graph for kernels/row

### Number of kernels per row

The graphical illustration (Fig.6) shows that additive type of gene action was involved in inheritance of this character as the regression line (b) intercepts  $W_r$ -axis above point of origin. The regression line did not deviate significantly

from unit slope, therefore epistasis was not involved. The genotype OH54-3A has more dominant genes as it is nearest to the point of origin and the genotype A-509 has more recessive genes being farthest from the point of origin. Saeed *et al.* (18) reported that additive genetic effects are overwhelming in case of number of kernels per row in maize. It has also been reported that additive and non-additive genetic effects are predominant in case of number of kernels per row (12).

### **Leaf venations**

The graphical illustration (Fig.7) shows partial dominance type of gene action because the regression line passes above the point of origin. It shows the additive genes were involved in the control of this trait. The regression line deviate non-significantly from the unit slope, it shows that gene interaction is not involved. The position of array point in graph on regression line shows that genotype OH 54-3A possesses mostly dominant genes and 53AP1 has recessive genes as it is closest and farthest from point of origin, respectively. Similar results were also reported by Ahsan *et al.* (2).

### **Stomatal frequency**

From graph (Fig.8), it is clear that regression line intercepts Wr-axis below the point of origin which shows the over-dominance type of genes action. It means non-additive genes were involved in this trait. As regression line did not show significant deviation from the unit slope, it indicates the absence of epistasis. The position of array point in the graph on regression line shows that genotype OH 54-3A has more dominant genes and B34-2B has more recessive genes as it is closest and farthest from the point of origin, respectively. Ahsan *et al.* (2) also reported non-additive type of gene action for this trait. As stomatal frequency was under over dominance gene action so simple selection cannot be used to adjust stomatal frequency. Only crosses of specific lines will result in desired stomatal frequency.

### **Stomatal size**

From graphical presentation (Fig.9) regression line passes below the point of origin which shows the over-dominance type of genes action. It means non-additive genes were involved in this trait. As regression line did not show significant deviation from the unit slope, it indicated that gene interaction is not involved. The position of array points in the graph on regression line shows that genotype B34-2B has most of the dominant

genes and OH54-3A has mostly recessive genes as these are closest and farthest from the point of origin, respectively. The results are similar with the findings of Ahsan *et al.* (2). Stomatal size is an important parameter regarding drought tolerance. Lower the stomatal size lower will be the water losses and as a result plant will be able to perform well under drought stress. It was found that this trait is controlled by non-additive gene action. It cannot be improved through successive selections but only specific crosses can be selected.

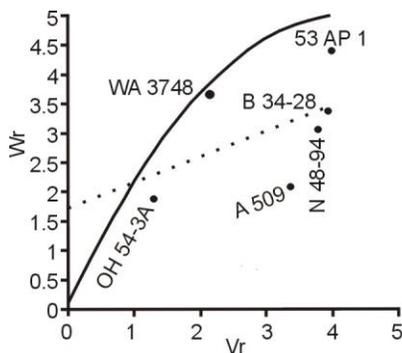


Fig. 7.  $W_r/V_r$  graph for leaf venations.

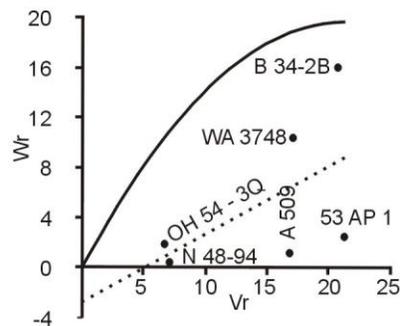


Fig. 8.  $W_r/V_r$  graph for stomatal frequency.

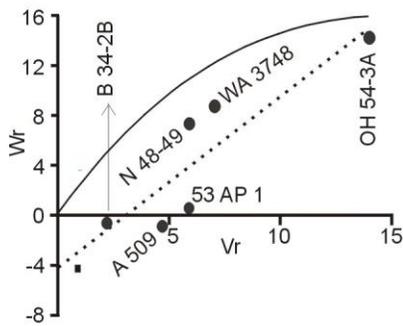


Fig. 9.  $W_r/V_r$  graph for stomatal size

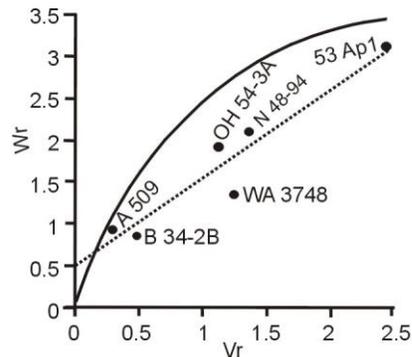


Fig. 10.  $W_r/V_r$  graph for 100 grain weight

### 100-grain weight

It is clear from graph (Fig.10), that regression line (b) intercepts  $W_r$ -axis above the point of origin, which suggested the partial dominance type of gene action controlling this trait. As regression line did not show significant deviation from the unit slope, it indicates the non-involvement of epistasis. The graphical distribution of array points on the regression line indicates that genotype A509 has mostly dominant genes as it is nearest to the point of origin while the genotype 53AP1 had mostly recessive genes being the

farthest from point of origin. Chen *et al.* (7) and Mahmood *et al.* (13) also reported additive type of gene action for this trait. However the results are in contrast to the findings of Kanagarasu *et al.* (11) and Wali *et al.* (21), who reported non-additive type of gene action for this trait. As this trait is under additive gene action so lines with high 100-grain weight can be used in synthetic cultivar production and selection of this trait improvement of germplasm.

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