

Genetic Analysis for Yield Potential and Quality Traits in Maize (*Zea mays* L.)

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Abstract: Grain yield is a complex phenomenon which results from the interaction of various contributing factors highly influenced by environmental variation. Phenotypic selection cannot directly improve the characters in heterozygous crops like maize unless dissected by genetic analysis. Gene action for various quantitative and qualitative traits was explored in a complete set of diallel involving seven elite inbred lines. Variance/Co-variance graphs revealed that the yield potential traits like number of days taken to tasseling, number of days taken to silking, plant height, number of ears per plant, number of kernel rows per ear, number of kernels per row, 100-kernel weight and grain yield per plant were controlled by over dominance type of gene action, while quality traits like protein and oil contents were under the control of partial dominance with additive type of gene action.

Key words: Gene action • Quantitative traits • Over dominance • Tasseling • Silking • *Zea mays* L • Quality traits • Inbred line

INTRODUCTION

Maize (*Zea mays* L.), the sole cultivated member of genus *Zea* and tribe Maydeae, ranks as one of the three important cereal crops in the world after wheat and rice. Maize being nutritionally an important crop has multiple functions in the traditional farming system, being used as food and fuel for human being and feed for livestock and poultry. It is a source of industrial raw material for the production of oil, starch, syrup, gluten, alcohol, glucose, custard powder, dextrose, flour, flakes, ethanol and many more products. The primary objective of most maize breeding programs is the evolution of high yielding and well adapted cultivars. Breeding for improving varieties is a continuous process and requires primarily a thorough knowledge of the genetic mechanism governing yield and yield components. Diallel cross technique developed by Hayman [1] and Jinks [2] provides information on the inheritance mechanism in the early generations and helps the breeder to make effective selection. Zia and Chaudhary [3] found that plant height was conditioned by partial dominance, while number of kernels per row, 100-grain weight and grain yield per plant showed over-dominance type of gene action. Kanaka [4], performed a 7 x 7 diallel cross analysis and reported partial dominance for plant height and number of leaves per plant, while

over-dominance was found for number of kernels per row, kernel rows per ear, 100-grain weight, number of days taken to tasseling and grain yield per plant. Saghir [5] showed that number of days taken to silking, plant height, 100-kernel weight and grain yield per plant were controlled by over-dominance type of gene action, while number of kernel rows per ear and number of kernels per row were controlled by additive type of gene action. Singh *et al.* [6] found that additive gene action was more important than dominance for grain yield. Bukhari [7] reported that plant height and number of kernels per row were controlled by additive type of gene action, while number of kernel rows per ear, 100-kernel weight and grain yield per plant were conditioned by over-dominance. Siddiqui [8], concluded that ear length and number of kernels per row were controlled by additive type of gene action with partial dominance, while plant height, number of ears per plant, kernel yield and 100-kernel weight were controlled by over-dominance type of gene action. Naveed [9] reported that kernel rows per ear and number of kernels per row were controlled by additive type of gene action, while number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant were conditioned by over-dominance type of gene action in maize. Tabassum [10] found, that number of days taken to tasseling and number of days

taken to silking were controlled by over-dominance type of gene action, while plant height, 100-grain weight and grain yield per plant were controlled by additive type of gene action. Rafiq *et al.* [11] observed plant height was controlled by over-dominance with complementary gene interaction. Dominant alleles were more than the recessive alleles and none of the parent was homozygous for plant height. Perez-Velasquez *et al.* [12] reported that plant height and number of kernels per row were controlled by additive type of gene action, while number of kernel rows per ear, 100-kernel weight and kernel yield per plant were conditioned by over-dominance. Shabbir and Saleem [13] conducted 6x6 complete diallel cross involving six maize inbred lines to find out the nature of gene action for protein content of maize kernel. The W_r/V_r graph indicated additive type of gene action. Inbred line Antigua-I possessed most dominant genes for protein percentage, whereas A-556 carried most recessive genes for the trait. The results suggest that mass selection could be practiced to alter the trait. Rosulj *et al.* [14] indicated that nine cycles of selection led to statistically significant increase in oil content and significant decrease for grain yield in both populations. Estimates of additive and dominance variances for grain oil content were highly significant for DS7u population. Mebrahtu and Mohamed [15] conducted a study to find out the mode of inheritance of protein in a 7x7 diallel analysis in beans and indicated that both additive and non-additive genetic variance were important for inheritance of protein contents. Srdic *et al.* [16] found that dominant gene effects were more significant in maize grain yield and number of kernels per row while additive gene effects were more important for kernel row number and 1000-kernel weight. The mode of inheritance of kernel row number was partial dominance, while over-dominance was of greater importance for grain yield, number of kernels per row and 1000-kernel weight.

MATERIALS AND METHODS

The studies were conducted at the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material comprised of seven inbred lines of maize i.e. A-239, AES-204, OH-28, B-34, Q-97 and PB-77 and 82 P1. The lines were crossed during spring, 2007 in a diallel fashion to obtain grains of all possible crosses including their reciprocals. The F_1 seed along with their parental inbred lines were sown in a triplicated randomized complete block design during autumn 2007, sowing was

done in 4.5 meters long rows, with dibble keeping plant to plant and row to row distance of 15 and 75cm, respectively. The grain was dibbled at the rate of two grains per hill and later thinned to one seedling per hill. Uniform agronomic practices were applied to all the entries. Ten guarded plants were selected from three replications of each entry to record the data for the following characters. Data pertaining to days taken to tasseling, days taken to silking, number of kernel rows per ear, plant height, number of ears per plant, number of kernel rows per ear, number of kernels per row, 100-kernel weight (g) and grain yield per plant (g) and protein and oil contents (%) in kernel were statistically analyzed [17]. Characters showing significant differences among the genotypes were further analyzed for gene action by using diallel technique developed by Hayman [1] and Jinks [2].

RESULTS AND DISCUSSION

Number of Days Taken to Tasselling: The differences in respect of number of days taken to tasseling among the genotypes were highly significant as indicated by the analysis of variance (Table 1). V_r/W_r graph (Figure 1). The regression line cuts the W_r -axis below the origin, which signifies the over-dominance type of gene action. From the relative position of the array points on the graph, it is evident that inbred line PB 77 being nearer to the origin possessed the maximum dominant genes, while inbred line AES 204 being away from the point of origin, carried the most recessive genes. The results are in agreement with the findings of Kanaka [4], Naveed [9] and Tabassum [10], who found that this character was under the control of over-dominance type of gene action.

Number of Days Taken to Silking: Analysis of variance for number of days taken to silking (Table 1) showed that the differences among the genotypes were highly significant. V_r/W_r graph (Figure 2), it is evident that the regression line intercepted the W_r -axis below the point of origin revealing over-dominance type of gene action for the inheritance of this character. As it is apparent from the graphical illustration that inbred line PB 77 possessed most dominant genes being in close vicinity to the point of origin, whereas inbred line OH 28, being away from the origin, had the most recessive genes. These results are in accordance with the findings of Saghir [5], Naveed [9] and Tabassum [10] who reported that number of days taken to silking was under the control of over-dominance type of gene action.

Table 1: Analysis of variance for grain yield and its components in 7x7 diallel crosses

SOV	d.f	Mean					Square				
		No. of days taken to tasselling	No. of days taken to silking	Plant height	No. of ear per plant	Kernel rows per ear	No. of kernels per row	100 kernel weight	Grain yield/plant	Protein contents	Oil contents
Replications	2	1.017	0.0272	11.26	0.00041	1.72	3.979	2.479	109.65	0.0501	0.0113
Genotypes	48	15.751**	12.397**	124.27**	0.0147**	2.31**	10.951**	13.397**	1075.70**	1.849**	5.63**
Error	96	3.673	3.326	16.13	0.00741	1.12	6.564	2.460	222.41	0.0576	0.132

** Highly significant

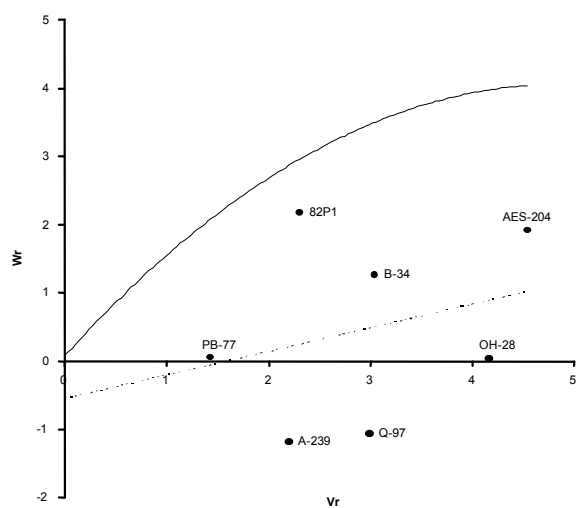


Fig.1: Vr/Wr graph for number of days taken to tasselling

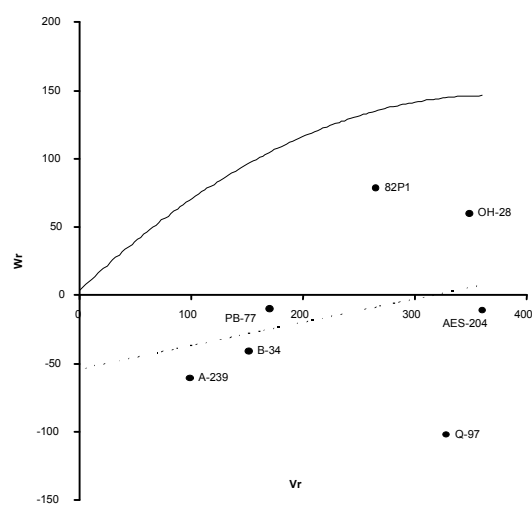


Fig.3: Vr/Wr graph for plant height (cm)

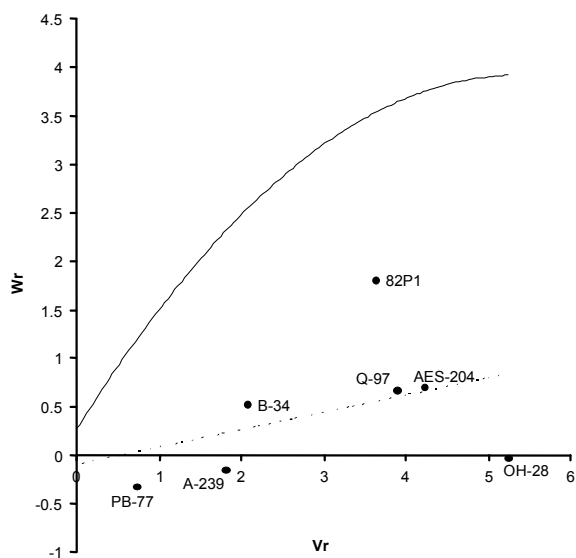


Fig.2: Vr/Wr graph for number of days taken to silking

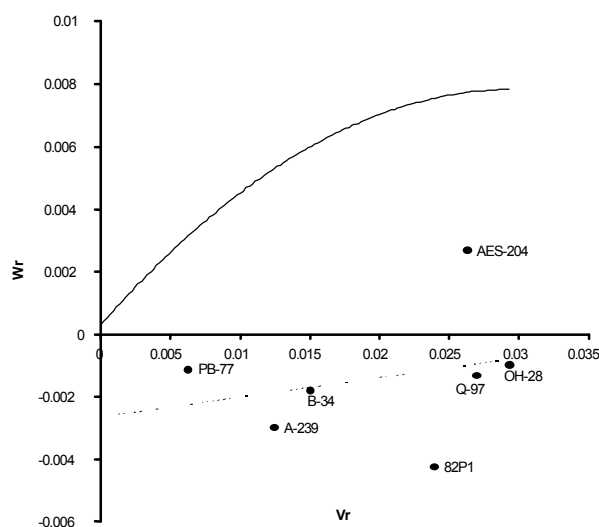


Fig. 4: Vr/Wr graph for number of ears per plant

Plant Height: The differences among the genotypes regarding plant height were highly significant (Table 1). From the graphical presentation (Figure 3), it is clear that the regression line passes below the point of origin which shows the over-dominance type of gene action.

As the regression line does not deviate significantly from the unit slope, it indicated the absence of gene interaction. The relative position of the array points on the regression line depicts that inbred line A 239 carried most of the dominant genes and AES 204 contained

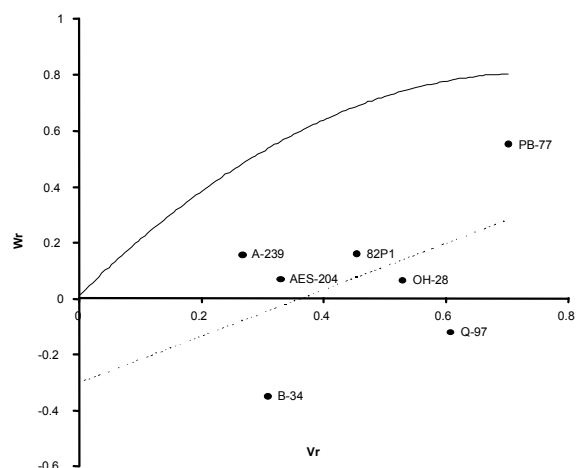


Fig. 5: Vr/Wr graph for Kernel rows per ear

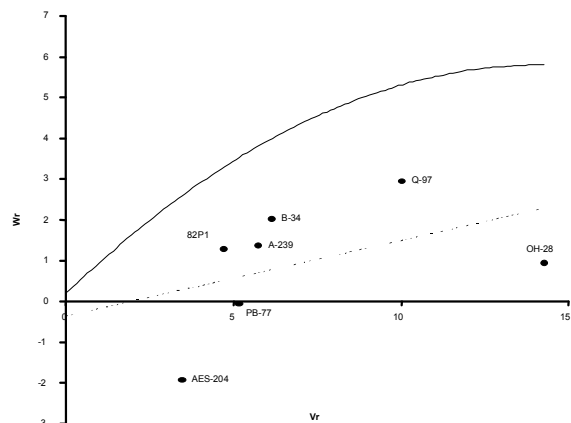


Fig.6: Vr/Wr graph for number of kernels per row

the maximum recessive genes being closest and farthest from the point of origin, respectively. The results are in accordance with those of Saghir [8], Siddiqui [8] and Rafiq *et al.*, [11], who reported that plant height was under the control of over-dominance type of gene action.

Number of Ears per Plant: Analysis of variance for number of ears per plant shows that the differences among the genotypes were highly significant (Table 1). Vr-Wr graph is shown as Figure 4. A perusal of Vr/ Wr graph (Figure 4) reveals that the regression line intercepts the Wr-axis below the point of origin, indicating over-dominance type of gene action for this character. As the regression line does not deviate significantly from the unit slope, it depicts the absence of gene interaction. It is obvious from the graphic illustration that inbred line PB 77 had the most dominant genes being in close vicinity to the point of origin, while inbred line OH 28 had most

recessive genes being away from the origin. Similar results have been reported by Siddiqui [8], Naveed [9] and Saeed [18], who reported that number of ears per plant was under the control of over-dominance type of gene action.

Number of Kernel Rows per Ear: Analysis of variance (Table 1) showed that the differences among the genotypes were highly significant. From the graphical presentation Vr/Wr (Figure 5), it is evident that the regression line passes below the point of origin which suggests the over-dominance type of gene action for this character. As the regression line deviates significantly from a unit slope, it shows the presence of gene interaction. From the distribution of the array points on the regression line, it is apparent that inbred line A 239 being nearer to the origin, possessed maximum dominant genes, while inbred line PB 77 being away from the origin, carried most recessive genes. The results are in line with those of Bukhari [7] and Perez-Velasquez *et al.* [12] who reported that number of kernel rows per ear was controlled by over dominance type of gene action.

Number of Kernels per Row: Analysis of variance for number of kernels per row (Table 1) indicated that the differences among the genotypes were significant. A perusal of Vr/Wr graph (Figure 6) showed that the regression line cuts the Wr axis below the point of origin, which demonstrated that over-dominance type of gene action for this character. As the regression line did not deviate significantly from a unit slope, it indicated the absence of gene interaction. From the relative position of the array points on the regression line, it is evident that inbred line 82 P1 possessed most dominant genes being in close vicinity to the point of origin, while inbred line OH 28 being away from the point of origin, carried most recessive genes. These results are compatible with those of Zia and Chaudhary [3], Kanaka [4], Singh *et al.* [6] and Srdic *et al.* [16] who reported that number of kernels per row was conditioned by over-dominance type of gene action.

100-Kernel Weight: Analysis of variance (Table 1) for 100-kernel weight revealed that the differences among the genotypes were highly significant. From the graphical presentation Vr/Wr (Figure 7), it is evident that the regression line passes below the point of origin, which suggests the over-dominance type of gene action controlling this character. As the regression line shows no significant deviation from the unit slope, it indicates the absence of gene interaction. The relative position of

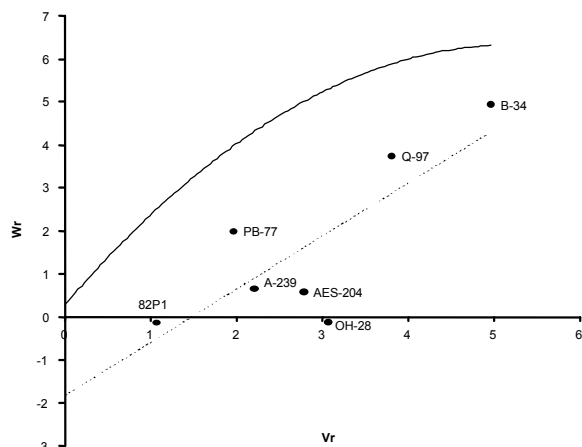


Fig.7: Vr/Wr graph for 100-Kernel Weight (gm)

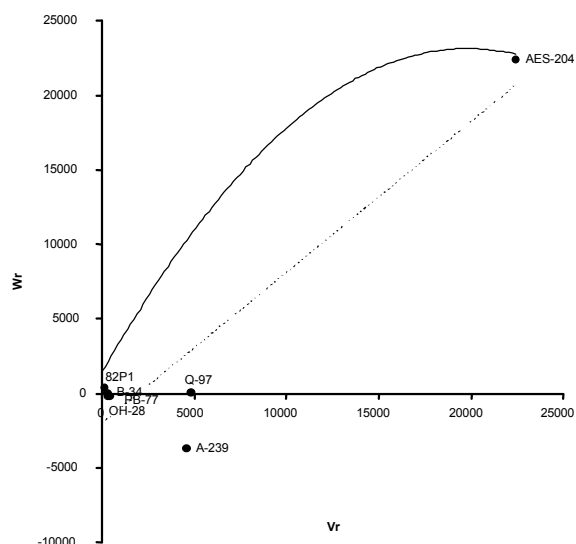


Fig.8: Vr/Wr graph for grain yield per plant (gm)

the array points on the regression line shows that inbred line 82 P 1 being nearer to the point of origin, possessed maximum dominant genes, while inbred line B 34 being away from the origin, carried most recessive genes. Bukhari [7], Siddiqui [8], Naveed [9] and Perez-Velasquez *et al.* [12] reported similar results about the character that it was controlled by over-dominance type of gene action.

Grain Yield per Plant: The differences among the genotypes were highly significant (Table 1). It is apparent from the graphic presentation Vr/Wr (Figure 8) that the regression line passes below the point of origin, which shows over-dominance type of gene action in the inheritance of grain yield per plant. As the regression line did not show any significant deviation from the unit

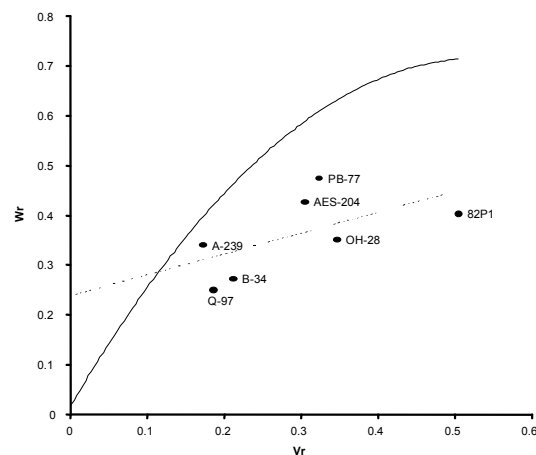


Fig. 9: Vr/Wr graph for protein contents in kernel

slope, it showed the absence of gene interaction. It is evident from the relative position of the array points on the regression line that inbred line B 34 being nearer to the point of origin possessed maximum dominant genes, while inbred line AES 204 being away from the origin, carried most recessive genes. The results corroborate the findings of Siddiqui [8], Naveed [9], Bukhari [7] and Perez-Velasquez *et al.* [12], who reported that grain yield per plant was under the control of over-dominance type of gene action.

Protein Contents: Analysis of variance (Table1) indicated that the differences among the genotypes were highly significant. Vr/Wr is shown in Figure 9. From the graphical presentation (Figure 9), it is evident that the regression line passes above the point of origin which suggests the partial dominance with additive type of gene action for this character. As the regression line does not deviate significantly from a unit slope, it indicated the absence of gene interaction. From the relative position of the array points on the regression line, it is predictable that inbred line Q 97 possessed most dominant genes being in close vicinity to the point of origin, while inbred line 82 P1 being away from the point of origin, carried most recessive genes. The present study gets support from those of Shabbir and Saleem [13] and Mebrahtu and Mohamed [15] demonstrated that protein contents in kernel was controlled by additive type of gene action. The results suggest that mass selection could be practiced to alter the trait. Most of the traits are independently associated with protein contents and it can be increased or decreased without adversely affecting the characters like plant height, ear height, 100-kernel weight, kernel density and days taken to 50% silking.

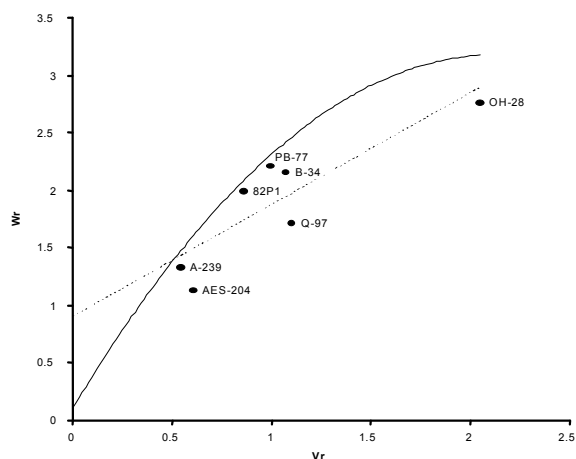


Fig. 10: Vr/Wr graph for oil contents in kernel

Oil Content: The differences among the genotypes regarding oil contents are highly significant (Table 1). From the graphical presentation Vr-Wr (Figure 10), it is clear that the regression line with a unit slope intercepted the Wr-axis above the point of origin revealing that the additive type of gene action was involved in the inheritance of this character. As regression line shows no significant deviation from a unit slope, it indicates the absence of gene interaction. It is also apparent from the graphic illustration that inbred line AES 204 possessed most dominant genes being in close vicinity to the point of origin, whereas inbred line OH 28 being away from the origin, had most recessive genes. These results are in accordance with the findings of Rosulj *et al.* [14], who reported additive type of gene action controlling oil contents in kernel. The results suggest that this trait can be altered by cycles of mass selection.

CONCLUSION

Prediction in the case of additive gene action would be expected to be more reliable as compared to the characters which are controlled by non-additive type of gene action. A preponderance of non-additive effects would not favor mass selection in altering any traits but pedigree test, sib test, progeny test or various combinations among them, will certainly be required to improve grain yield through various yield components.

Inheritance of yield components appeared to involve varying degree of over-dominance type of gene action except for protein and oil contents in kernel. To conclude, most of the yield components are non-additively controlled and selection for these populations must be practiced with great care to develop pure breeding line.

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