



Gene Action Studies for Yield and Yield Components in Maize (*Zea mays* L.)

T Sandeep Kumar, D Mohan Reddy and K Hariprasad Reddy

Department of Genetics and Plant Breeding, S V Agricultural College, Tirupati 517 502

ABSTRACT

The nature and magnitude of gene action was determined for various quantitative traits in a diallel set involving eight inbred lines of maize. Variance/covariance graphs revealed that number of kernels per row, cob length, cob girth, 100-seed weight and grain yield per plant were controlled by over dominance (non-additive gene effects), while number of kernel rows per ear showed partial dominance with additive gene effect. The parental lines possessed equal number of dominant and recessive genes for all the traits except number of kernels per row and cob length, for which the genes were distributed asymmetrically among the parents. From the distribution of the array points it appeared that inbred line BML 7 possessed maximum dominant genes for number of kernel rows per ear, cob length, 100-seed weight and grain yield per plant while the inbred line CM 133 possessed maximum dominant genes for number of kernels per row and cob girth. The graphic analysis revealed that most of the characters were under the genetic control of over dominance and therefore, the material can be effectively exploited for heterotic effects.

Key words : Gene action, Inbred lines, Maize, Over dominance.

Maize is one of the important cereal crops of India after rice and wheat. In India, maize ranks among the top four cereal crops occupying an area of 7.89 million ha with a production of 15.09 million tonnes and a productivity of 1904 kg ha⁻¹ and in Andhra Pradesh, it is grown in an area of 0.85 million hectares with a production of 4.15 million tonnes and productivity of 4073 kg ha⁻¹ (CMIE, 2010). Of late, the importance of maize has rapidly increased as industrial raw material and feed for livestock and poultry besides food and fuel for human being. Hence, keeping in view the present and future demand of maize production, maize breeding programmes should be strengthened to develop promising hybrids in order to speed up economical crop production in maize. Since yield is a complex trait, it is necessary to understand the genetic systems which control the growth of the plant and which regulate the most obvious components of yield. Also, planning and execution of a breeding programme requires information about the genetic systems controlling these quantitative characters. There are several genetic approaches to ascertain the genetic control of various attributes. However, the technique frequently employed by plant breeders is diallel analysis as described Hayman (1954) and Jinks (1954), which provides information on gene action of the traits in the early filial generations and

helps the breeder to make effective selection. Accordingly, the present investigation was carried out to study the genetic basis of variation for yield and yield related traits in the recycled and recently developed inbred lines using Hayman's graphical approach.

MATERIAL AND METHODS

The experimental material comprised of eight inbred lines of maize viz., CM 209, CM 132, CM 133, CM 148, CM 149, BML 6, BML 7 and BML 15, which were crossed in a half diallel fashion to obtain seeds of all possible 28 single crosses (excluding reciprocals) during *kharif*, 2010. The seeds of 28 crosses along with the parental inbred lines were sown in rows keeping 75 cm row to row and 20 cm plant to plant distances in a randomized complete block design with three replications during *rabi*, 2010-2011 in the wetland farm of S.V Agricultural College, Tirupati, Andhra Pradesh. Data pertaining to number of kernel rows per ear, number of kernels per row, cob length, cob girth, 100-grain weight and grain yield per plant were statistically analyzed by following the diallel analysis as described by Hayman (1954) and Jinks (1954) to estimate gene action involved in controlling the expression of these traits.

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed highly significant differences among the genotypes for all the traits, indicating the existence of sufficient genetic variation in the present breeding material. Before proceeding to the genetic analysis, the test of epistasis was conducted through test of homogeneity (t^2) which was non-significant for all the traits, indicating that the diallel assumptions were fulfilled including the absence of epistasis, which might be due to independent distribution of genes in the parents of the diallel (Hayman, 1954). The estimates of genetic components of variance (Table 2) revealed that, both additive (D) and non-additive (H_1) types of gene effects were involved in the genetic control of the trait number of kernel rows per ear as indicated by significant additive and dominance variance. Partial dominance was indicated for this trait on the basis of $[H_1/D]^{0.5}$ ratio. As the ratio of $H_2/4H_1$ did not deviate from the expected value of 0.25, the gene distribution was symmetrical at the loci showing dominance. The estimates of F and also the ratio $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ revealed that dominant genes were excess over recessive genes. The ratio of h^2/H_2 indicated that two gene blocks influenced this trait. Vr/Wr (Fig. 1A) graph revealed that partial dominance type of gene action was predominant as the regression line passed above the point of origin. From the distribution of the array points on the regression line, it was evident that inbred line BML 7 being nearer to the origin, possessed maximum number of dominant genes, while inbred line BML 6 was located farthest from the origin, indicating that it carried mostly recessive genes. These results were in contrary to the findings of Perez-Velasquez *et al.*, (2002), who reported over dominance for number of kernel rows per ear.

The significance of components D and H_1 revealed the importance of both additive and non-additive gene effects in the genetic control of number of kernels per row. However, higher magnitude of H_1 than D indicated more pronounced non-additive gene effects for this trait. The estimated value of $H_2/4H_1$ (0.22) suggested unequal gene frequencies at all loci. The degree of dominance $[H_1/D]^{0.5}$ value (2.143) revealed over- dominance type of gene effects involved in this trait. F value was positive and the estimated value of the ratio $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ was more than unity, indicating that the proportion of dominant alleles were higher than recessive alleles. The ratio h^2/H_2 manifested that five gene groups controlled this character. The regression line in Vr/wr (Fig. 1B) graph passed below the graphic origin, which indicated over dominance

for this trait. From the relative position of the array points on regression line it was evident that inbred line CM 133 possessed maximum dominant genes while inbred line CM 148 possessed most of the recessive genes for this trait. Similarly, Zia and Chaudhary (1980) and Saleem *et al.*, (2002) also reported over dominance type of gene action for this trait.

Considering the trait cob length, the estimates of additive (D) and non-additive (H_1) genetic variances were significant, indicating involvement of both additive and non-additive gene effects. Due to higher magnitude of H_1 than D, non-additive gene effects seemed to be prominent over additive gene effects. Negative F value and the predicted value of $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ (0.848) indicated that recessive alleles were more frequent than dominant alleles. The proportion of positive and negative gene effects ($H_2/4H_1$) in the parents deviated from its expected value of 0.25, denoting asymmetry at the loci showing dominance. The ratio h^2/H_2 indicated that probably five gene groups exhibited some degree of dominance controlling the character. Over dominance was noticed as the regression line of unit slope intersected the Vr-axis below the point of origin as evident in Vr/Wr graph (Fig. 1C). The distribution of array points along the regression line showed the concentration of dominant genes in the parent BML 7, while CM 148 contained the maximum number of recessive genes.

The perusal of estimates of genetic ratios for the trait cob girth revealed significant values of D (additive) and H_1 (non-additive), indicating the importance of both additive and non-additive gene effects in the genetic control of this trait. However, the non-additive effect seemed more pronounced due to higher magnitude of H_1 than D. The $[H_1/D]^{0.5}$ ratio suggested over dominance for this trait. Positive value of F and the estimated value of the ratio $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ (1.354) indicated excess of dominant genes than recessive genes. As the ratio $H_2/4H_1$ did not deviate from its expected value of 0.25, the gene distribution was symmetrical. The estimated value of h^2/H_2 indicated that, about five numbers of groups of genes controlled the character. The results of Vr/Wr (Fig. 1D) graphic analysis suggested the existence of over dominance as the regression line with unit slope passed below the graphic origin. The position of array points on the graph indicated that the inbred line CM 133 was close to the origin and hence, had more number of dominant genes while the inbred line BML 6 occupied a far position, implying that it possessed more frequency of recessive genes.

Table 1. Analysis of variance for grain yield and its components in maize.

Source of Variation	Degrees of freedom	No. of Kernel rows per ear	No. of Kernels per ear	Cob length	Cob girth	100-seed weight	Grain yield per plant
Replication	2	21.93	2.76	0.55	24.74	5.53	500.31
Genotype	27	98.04**	22.77**	5.84**	83.41**	42.53**	3884.18**
Error	70	8.96	1.53	0.39	9.91	2.69	206.91

** significance at 1 % level

Table 2. Estimates of genetic components of variation for yield and yield components in an 8 x 8 diallel set of maize (Hayman's approach)

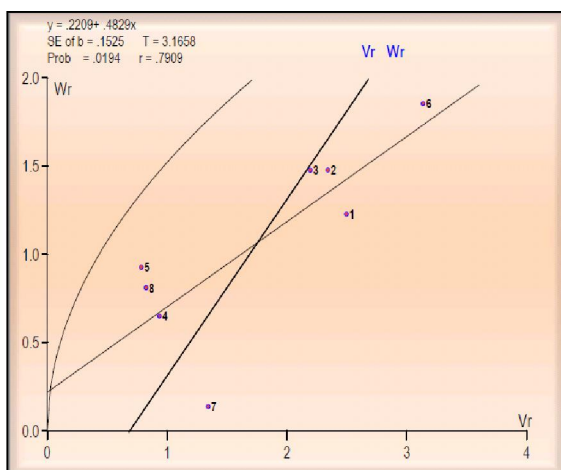
Components	No. of Kernel rows per ear	No. of Kernels per ear	Cob length	Cob girth	100-seed weight	Grain yield per plant
D	4.991**	17.025**	2.758**	0.925**	5.904**	263.048**
H ₁	4.590**	78.153**	15.889**	5.057**	35.179**	3770.031**
H ₂	4.012**	70.179**	14.326**	4.922**	32.146**	3517.127**
h ²	8.091**	378.753**	77.331**	24.332**	124.198**	18042.452**
F	0.090	11.782	-1.086	0.651	1.208	363.003
E	0.172	3.330**	0.522	0.310	1.492	74.613**
[H ₁ /D] ^{0.5}	0.910	2.143	2.401	2.338	2.441	3.786
H ₂ /4H ₁	0.248	0.224	0.225	0.248	0.239	0.249
[4DH ₁] ^{0.5} + F	1.018	1.385	0.848	1.354	1.088	1.446
[4DH ₁] ^{0.5} - F						
h ² /H ₂	2.014	5.397	5.396	4.94	3.864	5.130
t ²	1.485	4.227	1.317	2.039	1.694	2.823

** significance at 1 % level

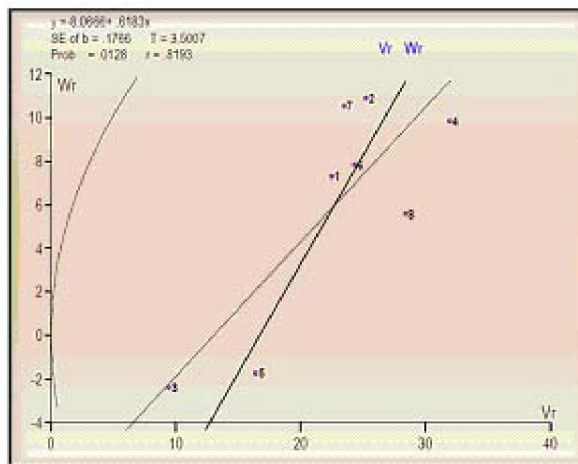
The estimates of additive (D) and non-additive (H₁) genetic variances for 100-seed weight were significant, indicating the importance of both additive and non-additive gene effects. The dominant gene effects however, seemed to be more prominent as the H₁ was higher in magnitude than D. Over dominance was indicated for this trait on the basis of [H₁/D]^{0.5} ratio. The ratio of H₂/4H₁ did not deviate much from the expected value (0.25), indicating symmetry at the loci showing dominant genes. The estimates of both F value and [4DH₁]^{0.5} + F / [4DH₁]^{0.5} - F confirmed that dominant alleles were predominant

than recessive alleles. The estimates of h²/H₂ suggested that four gene blocks exhibited some degree of dominance for this trait. The regression line intercepted the Wr-axis below the graphic origin (Fig. 1E) suggesting over dominance for this trait. Among the parents, the inbred BML 7 and BML 6 possessed most of the dominant and recessive genes, respectively as evident from the distribution of array points along the regression line. Similarly, Kanaka (1982), Perez-Velasquez *et al.*, (1996) and Saleem *et al.*, (2002) also reported over dominance for this trait.

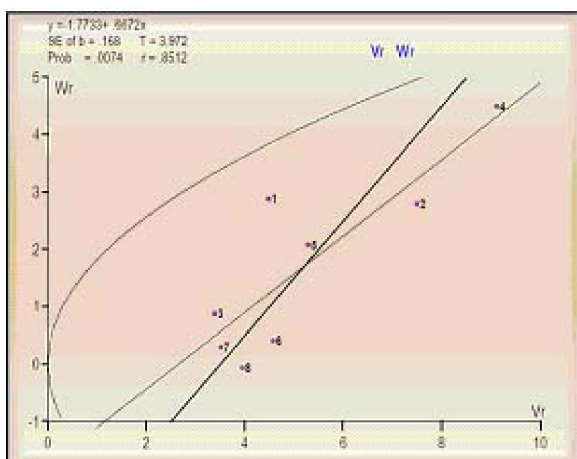
Fig. 1. Vr/Wr graphical configuration for yield and yield components in maize



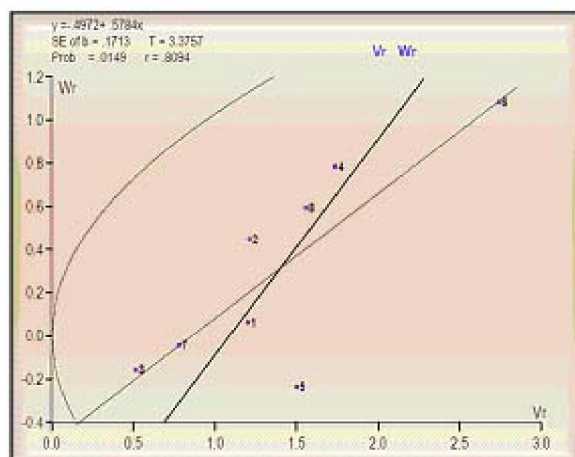
A. No. of Kernel rows per ear



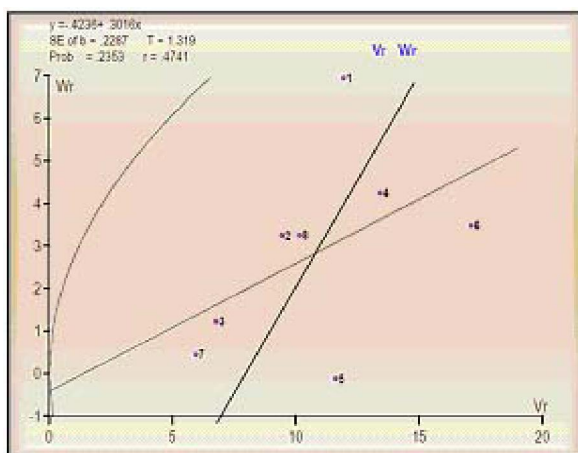
B. No. of Kernel rows per ear



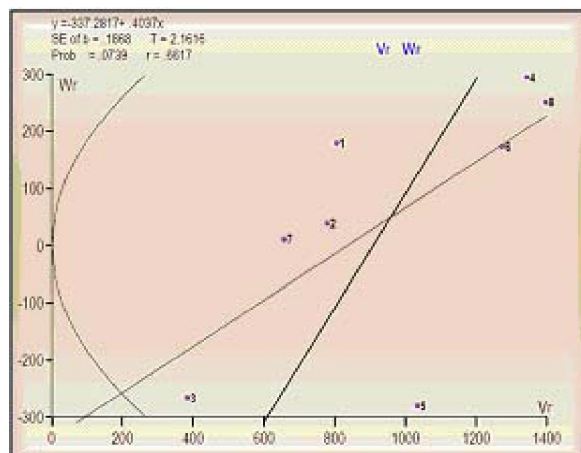
C. No. of Kernel rows per ear



D. No. of Kernel rows per ear



E. No. of Kernel rows per ear



F. No. of Kernel rows per ear

Inbred Lines:

1 = CM 209; 2= CM 132; 3= CM 133; 4= CM 148; 5= CM 149; 6= BML 6; 7= BML 7 and 8= BML 15

Grain yield is the economic trait and the interest of any breeding programme. Significant values of D and H_1 indicated the involvement of both additive and non-additive gene effects for this trait. However, the non-additive gene effects were more predominant than additive ones. This was supported by higher magnitude of components of H_1 than D. The degree of dominance $[H_1/D]^{0.5}$ value (3.786) indicated that this trait exhibited over dominance. As the $H_2/4H_1$ did not deviate from its expected value of 0.25, it indicated that the positive and negative alleles were distributed equally at the loci exhibiting dominance in the parental genotypes. A positive value of F depicted that dominant alleles were more frequent than recessive ones. This finding was further confirmed by the estimated ratio of $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$, which was more than unity. The ratio h^2/H_2 denoted that five gene groups were involved in the genetic control of grain yield per plant. The regression line of unit slope intercepted the W_r -axis below the point of origin (Fig. 1F), indicating over dominance for this trait. A perusal of distribution of array points along and around the regression line of unity indicated that the parent BML 7 was close to the point of origin and possessed excess of dominant genes, whereas BML 15 situated farthest from the origin carried maximum number of recessive genes. These results were in conformity with the findings of Siddiqui (1988) and Joshi et al., (1998), who also reported over dominance for this trait.

By and large, the components of genetic variance showed the presence of additive and non-additive gene effects for number of kernel rows per ear, number of kernels per row, cob length, cob girth, 100-seed weight and grain yield per plant. However, non-additive variance was predominant for all these traits except number of kernel rows per ear. This information would also be useful to classify the parents on the basis of the alleles regarding their utilization in future maize breeding programme. Further, the exploitation of heterosis in the present material could also yield better dividends for developing superior hybrids.

LITERATURE CITED

- CMIE 2010** Centre of Monitoring India Economy Pvt. Limited, Mumbai.
- Hayman B I 1954** The theory and analysis of diallel crosses. *Genetics*, 39: 789-809.
- Jinks J L 1954** The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics*, 39: 767-788.
- Joshi V N, Pandiya N K and Dubey R B 1998** Heterosis and combining ability for quality and yield in early maturing single cross hybrids of maize. *Indian Journal of Genetics and Plant Breeding*, 58: 519-24.
- Kanaka S K 1982** Genetic analysis of ten quantitative characters in grain sorghum. *Indian Thesis Abstracts*, 8: 72-73.
- Perez-Velasquez J C, Celallos H, Pandey S and Amaris C D 1996** A diallel cross analysis of some quantitative characters in maize. *Crop Science*, 36: 572.
- Saleem M, Shahzad K, Javid M and Ahmed A 2002** Genetic analysis for various quantitative traits in maize (*Zea mays* L.) inbred lines. *International Journal of Agriculture and Biology*, 4(3): 380-384.
- Siddiqui N A 1988** Genetic analysis of grain yield and its components in maize diallel crosses. M.Sc Thesis, Dept. Plant Breeding and Genetics, University of Agriculture, Faisalabad.
- Zia M K and Chaudhary A R 1980** Gene action for yield and yield components in maize. *Pakistan Journal of Agricultural Science*, 17(2): 87-92.

(Received on 01.11.2011 and revised on 16.01.2012)