

Gene Action for Yield and Morpho-Physiological Traits in Maize (*Zea mays* L.) Inbred Lines

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Abstract

The present study was carried out to investigate the genetic structure of 28 hybrids generated by crossing 8 diverse and new maize inbred lines in a half diallel fashion. The estimated value of average degree of dominance $(H_1/D)^{0.5}$ revealed that non-additive genetic effects was more pronounced in the inheritance of days to 50 per cent maturity, anthesis-silking interval and grain yield per plant. On contrary, additive genetic effects was evident for days to 50 per cent tasseling and days to 50 per cent silking. The distribution of positive and negative genes were not too distant for the traits viz., days to 50 per cent tasseling, days to 50 per cent silking and grain yield per plant. Dominance to recessive genes ratio $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ ranged from one to two, indicating that excess of dominant genes against one recessive genes were not much higher. The results indicated that most traits were under the genetic control of non-additive (over dominance) type of gene action, therefore the material can easily be exploited for heterotic effect.

Keywords: Gene effects, Grain yield, Hayman's ratios, Maize

1. Introduction

Maize (*Zea mays* L.) is an important kharif cereal crop, ranks third among cereal crops in the world after rice and wheat. Worldwide maize is cultivated in an area of 159 million hectares with a production of 796.46 million tonnes (USDA, 2010) and 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. Presently, the demand for maize is also growing as poultry feed and in several industrial applications and moreover there is a very need to meet the future food demands of the rapidly increasing population. Therefore, keeping in mind the future demand of maize as a food for human and as a feed for livestock, there is a continuous need to evolve new hybrids, which should surpass the yield of the existing hybrids and give sustainable yields. To achieve this target, yield improvement through genetic approaches which determines the gene action would become highly essential and moreover formulation of comprehensive breeding strategies is to be done for the yield improvement of any crop which depends mostly on understanding the nature of gene action involved for a specific trait to be improved. Further, the choice of efficient breeding programme depends on the large knowledge of the type of gene action for components of productivity. Dominance gene action is desirable for developing hybrids and additive gene action implies that standard selection protocols would be effective enough in breeding about improving the character (Edwards *et al.*, 1976). For such studies diallel analysis is a useful biometrical approach to understand the nature of gene action. By understanding these components of variance a plant breeder can identify the parents which combine well and produce productive progenies and moreover suitable breeding strategies can be drawn up on the basis of expected performance of the progenies. Therefore, the present investigation was undertaken to understand the nature and magnitude of gene action involved in the inheritance of yield and its attributes and thereby suitable breeding strategies can be made.

2. Research Methods

The experimental material comprised genetically diverse 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 seed of all possible 28 single crosses (excluding reciprocals) during *kharif*, 2010. Both parents and F₁ seeds were grown 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. The parents and F_1 s were planted in single rows of 4m length and the distance between rows and plants was kept at 75 cm and 20 cm, respectively. Observations were recorded on five randomly selected competitive plants from each replication for the characters *viz.*, days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval, days to 50 per cent maturity and grain yield per plant. The data were subjected to preliminary statistical analysis of variance (Panse and Sukhatme, 1957) and then genetic component analysis was performed according to the procedure suggested by Hayman (1954) and Jinks (1954) to estimate gene action involved in controlling the expression of these traits.

3. Analysis Results

The analysis of variance revealed that there was a significant variation for all the characters studied (Table 1). The genetic parameter estimates and their ratios for yield and yield related components are furnished in Table 2. It is evident that non-additive gene effects were predominantly involved in the inheritance of all the traits under study.

The magnitude of dominance gene effects (H_1) was preponderance over its respective additive gene effects (D) for all the traits except days to 50 per cent tasseling and days to 50 per cent silking. Further confirmation of the preponderance of non-additive variance was available from the average degree of dominance $[H_1/D]^{0.5}$. This estimate showed that there was over dominance for most traits *viz.*, anthesis-silking interval (Zahra, 2011), days to 50 per cent maturity and (El-Hosary *et al.*, 1994) grain yield per plant (Irshad-Ul-Haq *et al.*, 2010), contrarily partial dominance was evident for days to 50 per cent tasseling (Paul and Debnath, 1999) and days to 50 per cent silking (Tallei and Kochaksaraei, 1999), wherein the ratio was less than unity. In maize non-additive genetic variance is more often evident in controlling the inheritance of traits than additive components (Wright *et al.*, 1971). In this experiment also non-additive genetic component (H_1) was the major part of genetic variance for most of the yield and yield related traits. Another estimate of dominance variance (H_2) was found to be significant for all the traits, indicating overwhelming dominance effect of genes even after correction to gene distribution. The estimates of F (mean F_r over arrays) were positive for all the traits except for days to 50 per cent maturity, indicating that dominant genes were majorly involved in the control of these traits. The results were confirmed by the ratio $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$, which depicts the relative value of dominance and recessive genes among parents. This ratio was greater than unity for days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval and grain yield per plant. On contrary, the trait days to 50 per cent maturity was controlled by excess of recessive genes as the ratio was less than unity. The estimated values of $H_2/4H_1$ (genes with +/- effects) in parents were less than 0.25 implying asymmetric distribution of positive and negative alleles for all the traits. Similarly, Kumar *et al* (1999) also reported asymmetrical distribution of positive and negatives genes for grain yield per plant and for anthesis-silking interval by Zahra (2011). The estimates of $H_2/4H_1$ and $[4DH_1]^{0.5} + F / [4DH_1]^{0.5} - F$ thus gave inconsistent results regarding symmetrical distribution of alleles with positive and negative effects and were not always showing equal spread of dominance and recessive alleles, respectively. This implies that, dominant alleles may or may not be associated with positive effect. Similarly, a recessive allele may or may not be associated with a negative effect. More will be the gain in selection if proportion of dominant genes is high. From the results it was evident that, the numerical values ranged from 0.83 for days to 50 per cent maturity to 1.917 for anthesis-silking interval, indicating that the recessive and dominant genes were not in high disproportion and most of the allele pairs might be existing in heterozygous form. The estimates value of h^2/H_2 for flowering indicated that inheritance of anthesis-silking interval and days to 50 per cent maturity was governed by one to two groups of genes. Days to 50 per cent tasseling and days to 50 per cent were governed by three groups of genes. The value of h^2/H_2 indicated that five dominant gene blocks were influencing the trait grain yield per plant. This finding was similar to the findings of Turgut *et al* (1995). This ratio underestimates the number of genes and gives no exact information about group of genes exhibiting a little or no dominance hence, greater dependency cannot be placed on this ratio. The component of variance due to dominance effect H_2 and h^2 was found significant for all the expect for anthesis-silking interval. It was evident that the analysis of test of homogeneity (t^2) was non-significant for all the traits, indicating that the diallel assumptions were fulfilled including the absence of epistasis. In such conditions, there might be a very low chance of obtaining additive genetic variance. However, expression of non-additive component could be more because most of the genes were expected to exist in heterozygous form for many loci. The results revealed non-additive gene action to be predominant in the inheritance of the most traits under study and hence, there is a little scope for improvement in these traits by selection. Further, over dominance (non-additive gene action) for most traits reveals that selection in later generations may be more effective and the selection in early generations will be more effective for the traits which are additively controlled. Heterosis could be exploited in developing inbreds and hybrids. Moreover, results indicate that rapid gain under recurrent selection cycles doesn't seem to be very high. Maximum gain could be achieved by maintaining considerable heterozygosity coupled with selection in the segregating generation to enhance recombination which might result in breaking of

undesirable linkage, ensure transgressive segregation to accumulate, reassemble and express maximum number of potentially functional genes for the improvement of the trait, leading to production of stable and widely adapted genotypes.

To conclude that in the present material, selection can be made for the parents which possessed most dominant genes with positive effects for respective traits. The parents with dominant positive genes for earliness and high yields could be advanced for heterosis breeding programme to produce hybrids with high yield and earliness. The parents with most positive dominant genes causing short anthesis-silking interval might be exploited in drought resistance maize breeding programmes aimed at high yield in water stress conditions, as anthesis-silking interval has been correlated with drought tolerance mechanism in maize (Balanos and Edmeades, 1993). By and large, the present material can be effectively exploited in the hybrid breeding programme to evolve high yielding stable genotypes in maize.

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Table 1. Preliminary Analysis of variance for grain yield and its components in 8 x 8 diallel crosses

Source of Variation	Degrees of freedom	Days to 50 % tasseling	Days to 50 % silking	Anthesis-silking interval	Days to 50 % maturity	Grain yield per plant
Replication	2	3.01	4.39	1.01	5.11	500.31
Genotype	27	68.42**	62.87**	2.88**	75.04**	3884.18**
Error	70	1.65	1.73	0.53	2.63	206.91

** Significance at 1 % level

Table 2. Hayman's ratio of genetic parameters for different traits in maize

Source	Days to 50 % tasseling	Days to 50 % silking	Anthesis-silking interval	Days to 50 % maturity	Grain yield per plant
D	37.03*	32.05*	1.09*	22.32*	263.048*
H ₁	28.86*	28.60*	2.42*	40.83*	3770.031*
H ₂	25.54*	25.46*	1.55*	32.99*	3517.127*
h ²	89.19*	83.35*	1.020	51.24*	18042.452*
F	12.8	10.42	1.027	-5.59	363.003
E	0.61	0.67	0.269	0.948	74.613
[H ₁ /D] ^{0.5}	0.88	0.93	1.487	1.352	3.786
H ₂ /4H ₁	0.221	0.223	0.16	0.202	0.223
$\frac{[4DH_1]^{0.5} + F}{[4DH_1]^{0.5} - F}$	1.481	1.412	1.917	0.830	1.446
h ² /H ₂	3.492	3.274	0.66	1.553	5.130
t ²	0.489	1.501	0.001	1.296	2.823

* Significance at 5 % level