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GENE ACTION STUDIES OF DIFFERENT QUANTITATIVE TRAITS IN MAIZE

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Abstract

The present study was carried out to determine the type of gene action, genetic parameters of yield and other quantitative traits by crossing 8 diverse maize inbred lines in complete diallel fashion. Seed of F_1 population along with their parents was planted in randomized complete block design replicated thrice. Analysis of variance showed that inbred lines differed significantly among each other for all traits. The estimates of components of genetic variation revealed that non additive genetic effects were more pronounced in the inheritance of plant height, days to 50% tasseling, days to 50% silking, ear height and grain yield per plant. Directional dominance was observed for all the characters under study. Asymmetrical gene distribution was observed for all the attributes except ear height for which parental lines contained equal number of dominant and recessive genes. The graphic analysis showed that all the characters were under the genetic control of over dominance type of gene action, therefore, the material can easily be exploited for heterotic effect.

Introduction

Maize is the most important cereal crop in the world after wheat and rice. It has great yield potential and attained the leading position among cereals in term of production as well as productivity (Anon., 2004). Maize has gained a special position in the crop husbandry of Pakistan. Currently the area under maize crop in Pakistan is 1022 thousand hectares with a total production of 3088 thousand tones having average yield of 3037 kg per hectare (Anon., 2007). Maize production in the country can be increased through hybridization and utilization of appropriate germplasm having sufficient diversity for different quantitative traits.

Planning and execution of a breeding programme requires information on the genetic systems controlling the character of the interest, so that the expected gain can be maximized with the selection process (Barelli *et al*., 1999; Viana *et al*., 1999). A technique frequently employed by plant breeders to ascertain genetic basis of variation in various attributes is diallel analysis. This technique has been effectively used by Amer (2004), Devi *et al*., (2004), Prakash *et al*., (2004), Kumar *et al*., (2005), Ali *at el*., (2007) and Singh & Roy (2007) in maize. The present study was conducted to get such information on grain yield per plant and other quantitative characters in the parental material used here.

Materials and Methods

The study was conducted in the research area of Maize, Sorghum and Millet Programme, National Agriculture Research Centre, Islamabad. The experimental material comprised of 8 maize inbred lines having sufficient genetic diversity. Four temperature tolerant inbred lines i.e., FR-37, MS-211, NYP-8 and NYP-8-1 were obtained from

Maize and Millets Research Institute, Yousafwala. While quality protein maize inbred lines NCQPM-1, NCQPM-2, NCQPM-3 and NCQPM-4 were received from National Agriculture Research Centre, Islamabad. Seeds of these inbred lines were planted during spring 2005 for hybridization using two rows of five meter length of each inbred line. At the time of flowering, crosses were made in all possible combinations.

Seed of F_1 hybrids along with their parents were planted during 1st week of July 2005 in randomized complete block design replicated thrice. Each treatment comprised of two rows of five meter length. Inter row and inter plant distance were kept at 75 cm and 25 cm respectively. Dose of fertilizer @ 206 kg N, 85 kg P and 62 kg K per hectare were applied. Data pertaining to plant height, days to 50% tasseling, days to 50% silking, ear height and grain yield per plant were recorded.

The data was statistically analyzed following Steel & Torrie (1980). Genetic analysis was done according to the diallel technique as described by Hayman (1954) and Jinks (1954). Genetic components of variation, D (additive effects of genes), H_1 and H_2 (dominance effects of genes) and F were computed from estimates of variances and covariances. These parameters provide estimates of the relative frequency of dominant to recessive alleles in the parental lines. The information on gene action and presence of dominant and recessive genes in the parents was also inferred by plotting the covariance (Wr) of each array against its variance (Vr).

Results and Discussions

Mean squares obtained from analysis of variance indicated significant differences among the parents and their F_1 hybrids for all the characters (Table 1) and thus allowed the use of Hayman-Jinks model for genetic analysis of these characters.

Plant height: The result of Hayman's analysis of variance showed significant differences for 'a' and 'b' which suggested the presence of additive and non additive genetic effects in the manifestation of plant height (Table 2). The significant 'b_1' item revealed the presence of directional dominant effects of genes. Among parents, asymmetrical gene distribution and specific gene effects for plant height were evident due to significant of 'b_2' and 'b_3' items respectively. Maternal effects were observed due to the significance of item 'c', which suggested retesting of 'a' against mean square of 'c' as proposed by Mather & Jinks (1982). Retesting of 'a' revealed that additive gene effects were masked by maternal effects.

Significant value of non additive genetic effects and non significant value of additive component revealed that plant height was under the influence of dominant gene effects (Table 5). The proportional value of $(H_1/D)^{1/2}$ indicated the control of over dominance gene action. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was found to be less than 0.25, denoting asymmetry at loci showing dominance, which evidenced the asymmetrical distribution of genes as depicted in Hayman's analysis of variance. The ratio h^2/H_2 indicated six groups of genes exhibiting some degree of dominance.

The present results for plant height are in accordance with those of Prakash *et al.*, (2004) and Kumar *et al.*, (2005) who reported over dominance type of gene action for the same trait. However, the finding of Singh & Roy (2007) revealed additive gene action involved in the inheritance of plant height, thereby differing with the present results. The difference might be due to variation in the genetic material and environmental condition to which genotypes were subjected.

Table 1. Mean square values of various plant characters in 8x8 diallel cross of maize.

Source of variation	d.f	Plant height (cm)	Days to 50% tasseling	Days to 50% silking	Ear height (cm)	Grain yield per plant (gm)
Genotype	63	823.34**	10.677**	12.449**	235.28**	1953.26**
Replication	2	34.88	0.349	0.661	2.82	17.92
Error	126	56.18	0.566	0.630	16.72	11.07

**, * = Significant at 1% and 5% probability level respectively.

The graphical presentation depicted that regression line passed below the point of origin (Fig. 1a) indicating over dominance type of gene action. Both estimates i.e., graphic analysis and genetic component analysis agreed on over dominance type of gene action as $(H_1/D)^{1/2}$ ratio is greater than unity and $D < H_1$. The distribution of array point on the regression line showed the concentration of dominant genes in the parents NYP-8-1 and NCQPM-2, while NYP-8, NCQPM-1 and NCQPM-3 possessed the maximum recessive alleles.

Days to 50% tasseling: The analysis of variance of F_1 data for days to 50% tasseling revealed the presence of both additive and non-additive genetic effects in the control of the trait due to the significance of ‘a’ and ‘b’ items (Table 2). The significance of ‘b_1’ item indicated the presence of directional dominance. Significance of ‘b_2’ and ‘b_3’ items suggested that the genes for days to tasseling were scattered asymmetrically among the parents and specific dominant gene effects were also present. Maternal and reciprocal effects were exhibited due to significance of items ‘c’ and‘d’. After retesting the mean square of ‘a’ and ‘b’ against the mean squares of ‘c’ and ‘d’ items respectively as suggested by Mather & Jinks (1982), the significance level of ‘a’ item remained unchanged. However significant ‘b_1’ ‘b_2’, ‘b_3’ and ‘b’ items changed to non significant indicating that the effect of dominant genes were masked by the genes with reciprocal effects.

Significant values of D, H_1, H_2 and h^2 showed that both additive and non additive gene effects were important in controlling this character (Table 5). The higher value of H_1 than D revealed that non additive effects were more pronounced as compared to additive gene effects. The positive value of ‘F’ indicated that dominant allele were more frequent than recessive one. The value of $(H_1/D)^{1/2}$ being greater than unity (1.23) indicated the involvement of over dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was found to be less than 0.25 denoting asymmetry at the loci showing dominance. The involvement of over dominance in the inheritance of days to 50% tasseling was reported by Kumar *et al.*, (2005) and Singh & Roy (2007). The character thus seems difficult to be fixed and progress through selection will be inherently slow.

The intersection of the regression line of Wr-Vr graph below the origin signified the importance of over dominance. The over dominance gene action controlling number of days to 50% tasseling is also supported by the $(H_1/D)^{1/2}$ ratio which is greater than unity. The relative distribution of inbred lines along the regression line revealed that inbreds NCQPM-3 and NYP-8 being closer to the origin carried the most dominant genes for the trait. While inbred lines MS-211, NCQPM-4 and FR-37 possessed the maximum recessive genes being away from the origin.

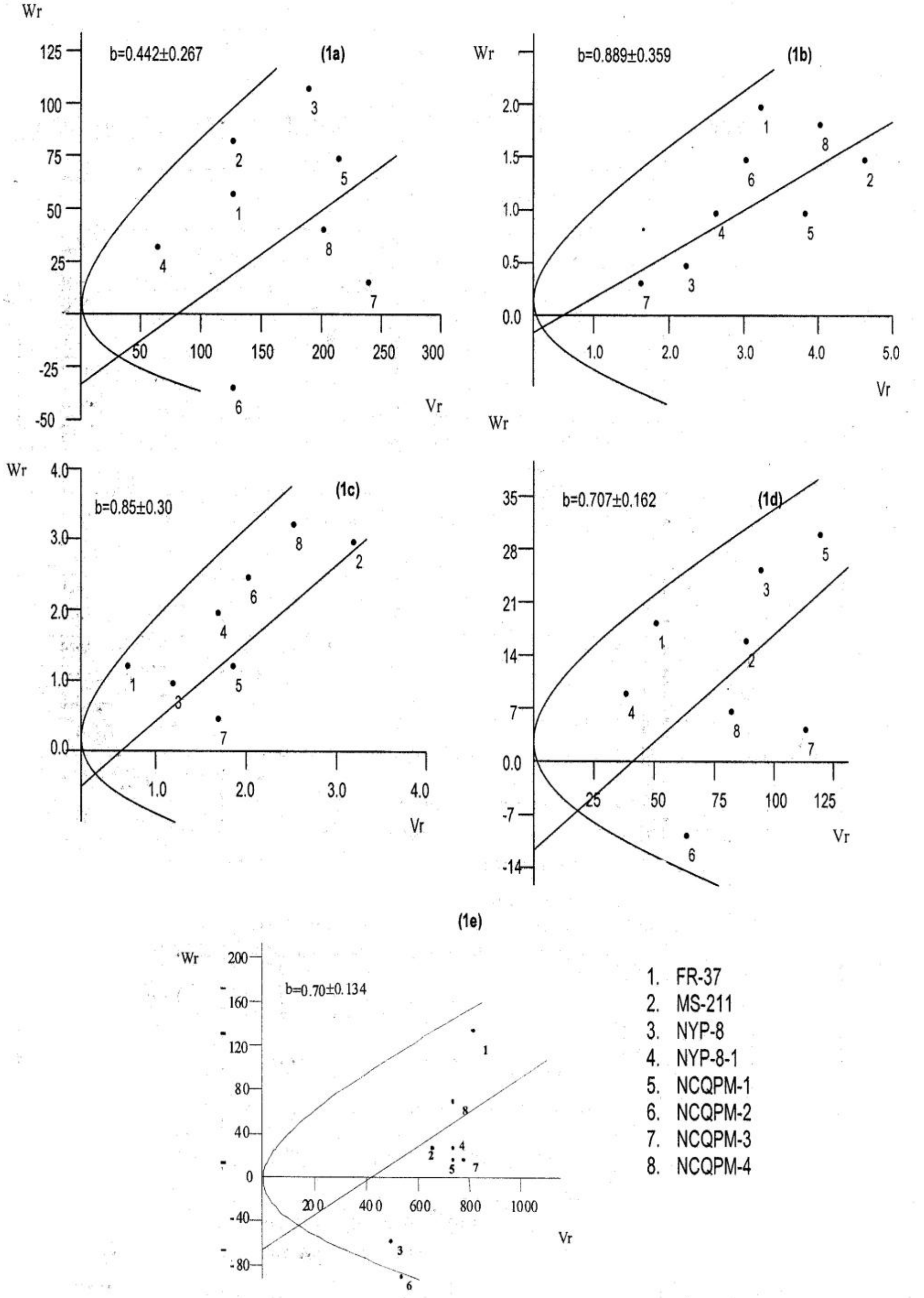

Fig. 1. Vr/Wr graph for number of plant height (a), number of days to 50% tasseling (b), number of days to 50% silking (c), ear height (d) and grain yield per plant (e).

Days to 50% silking: The results of Hayman's analysis of variance regarding days to 50% silking are given in the Table 3. The significance of 'a' and 'b' items revealed the importance of both additive and non additive type of genetic variance for the trait. The significance of 'b_1' item indicated the presence of directional dominance. Genes for silking period were distributed asymmetrically among the parents and specific dominance genetic effects were observed due to significance of 'b_2' and 'b_3' respectively. The 'c' and'd' items were significant indicating the presence of maternal and reciprocal effects. Retesting of 'a' and 'b' items was done against mean squares of 'c' and'd' respectively. After retesting, the significance of 'a' and 'b_1' items remained unchanged, whereas items 'b_2' 'b_3'and 'b' which were previously significant reduced to non significant.

Table 5 revealed the significance of genetic components D, H_1, H_2 and h^2 indicating the equal importance of additive as well as non additive genetic variances. However, higher magnitude of H_1 than D indicated more pronounced effects of non additive genes for days to 50 % silking. A positive value of 'F' revealed the presence of more dominant alleles as compared to recessive alleles. Over dominance was indicated for this trait on the basis of $(H_1/D)^{1/2}$ ratio. Asymmetrical gene distribution in the parents was apparent, as $H_2/4H_1$ ratio deviated from its expected value of 0.25. The findings of other researchers like Kumar *et al.*, (2005) and Singh & Roy (2007) are in accordance with the results of the present study.

The regression line intercepted the Wr-axis below the origin, thereby, indicating the over dominance type of gene action which is evidenced by the ratio $(H_1/D)^{1/2}$ being greater than unity. The position of the array points made it obvious that inbred lines FR-37, NYP-8 and NCQPM-3 had the maximum dominant genes due to their position closer to the origin, whereas inbreds MS-211 and NCQPM-4 possessed the recessive genes due to their distal position. Rest of the genotypes occupied central position and thus had almost equal frequencies of dominant and recessive genes (Fig. 1c).

Ear height: The analysis of variance of diallel data for ear height showed that 'a' and 'b' items were significant suggesting the role of both additive and dominant gene effects (Table 3). The significance of 'b_1' item indicated the presence of directional dominance effects. The parents contained uniform distribution of dominant genes for ear height as item 'b_2' was non significant. Significant 'b_3' item revealed the presence of specific gene effects other than attributed to 'b_1 and 'b_2'. Maternal effects were also present due to significant 'c' item. Non-significant 'd' item revealed the absence of reciprocal effects. Since 'c' item was significant, therefore,'a' item was to be retested against the mean square of 'c'. After retesting, 'a' item changed to non significant indicating that maternal effects has masked the effects of genes which were acting additively.

Dominance (H_1, H_2, h^2) genetic variances were found to play an important role in the expression of this character as indicated by the significance and non significance of dominance and additive genetic components respectively (Table 5). Over dominance was observed for this trait on the basis of $(H_1/D)^{1/2}$ ratio. As indicated by the ratio $H_2/4H_1$, positive and negative alleles were present asymmetrically at loci showing dominance. The ratio of h^2/H_2 indicated that probably 5 groups of genes were involved in the inheritance mechanism of this character. The findings of Prakash *et al.*, (2004) did not support the present results indicating the involvement of additive type of gene action for ear height.

Table 4. Hayman's analysis of variance for grain yield per plant in 8x8 diallel of maize.

Item	DF	SS	MS	F. ratio	Retested against	
					c	d
a	7	4144.867	592.12	85.48**	5.23 **	
b_1	1	116946.7	116946.7	60429.2**		6090**
b_2	7	352.73	50.39	8.88**		2.62**
b_3	20	478.28	23.91	1.35		1.24
B	28	117777.7	4206.35	298.10**		219**
C	7	792.63	113.23	10.49**		
D	21	403.21	19.20	2.26**		
T	63	123118.4	1954.26	176.53**		
A x B	14	98.98	6.93			
b_1 x B	2	3.87	1.94			
b_2 x B	14	79.47	5.68			
b_3 x B	40	706.84	17.67			
b x B	56	790.18	14.11			
x B	14	151.00	10.79			
d x B	42	356.67	8.49			
Error	126	1394.82	11.07			

**, * = Significant at 1% and 5% probability level, respectively.

The point of interception of regression line on Wr-axis was below the origin showing over dominance type of gene action for this trait. The results of graphic analysis and that of genetic component analysis agreed as the ratio $(H_1/D)^{1/2}$ also suggested the presence of over dominance. On the basis of location of genotypes on graph, inbred lines NCQPM-2, NYP-8-1 and FR-37 were found to have maximum dominant genes being closer to the origin. (Fig. 1d) whereas inbred lines NCQPM-1 and NYP-8 being the farthest position from the origin contained the most recessive genes.

Grain yield per plant: The results of analysis of variance of F_1 data showed significant differences for items 'a' and 'b' suggesting the presence of both additive and dominance genetic effects in the expression of grain yield per plant. The significant 'b_1' item indicated the directional dominance effect of genes (Table 4). Asymmetrical gene distribution among the parents was observed due to significant 'b_2' item. The non significant 'b_3' item revealed the absence of specific gene effects. The 'c' and 'd' items were significant, indicating the presence of maternal as well as reciprocal effects. After retesting of 'a' and 'b' against the mean squares of 'c' and 'd' items respectively, the situation for 'a', 'b_1', 'b_2' and 'b' remained unchanged. However, significant 'b_3' item reduced to non significance indicating that dominant gene effects were masked by reciprocal effects.

Significant value of D, H_1, H_2 and h^2 indicated the importance of both additive and non-additive types of gene action involved in the inheritance of this character (Table 5). However, non-additive gene effects seemed to be more important than additive ones. This was supported by higher magnitude of components of H_1 than D. The degree of dominance $(H_1/D)^{1/2}$ value (7.75) exhibited over dominance. Over dominance types of gene action for grain yield per plant in maize was also reported by Prakash *et al.,* (2004) and Ali *at el.,* (2007). 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**.** The ratio of KD/KR suggested that dominant and recessive alleles controlling the character were equal. The ratio of h^2/H_2 indicated that probably seven groups of genes were controlling the grain yield per plant.

Graphical configuration regarding grain yield is depicted in Fig. 1e. The regression line of unit slope intercepted the Wr-axis below the point of origin indicating over dominance for this character. The distribution of array points along and around the regression line of unity indicated that the parents NYP-8 and NCQPM-2 were close to the point of origin and had an excess of dominant genes whereas FR-37 being farthest from the origin was carrying maximum number of recessive alleles. Equal distribution of dominant and recessive genes was noted among all the parents under study.

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