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Genetic control of different traits in maize inbred lines (*Zea mays* L.) using graphical analysis

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This study was carried out in order to investigate the genetic structure of the twenty-eight maize hybrids established from eight maize inbred lines. The seed of the F_1 population along with their parents were planted in Iran in 2008, using RCBD with three replications. Estimation of gene effects and some of the genetic parameters and graphic plot drawing of Hayman-Jinks method were accomplished. Statistics a and b for all traits was significant. Considering the average degree of dominance, as well as the Hayman graphical plot, dominance effects were observed for grain yield and plant growth period traits over dominance, complete dominance for grain diameter and additive gene action with partial dominance for ASI, grain filling period, grain number in row, grain number in ear, grain row number in ear, ear diameter, grain depth, 1000 grain weight and hektolitr weight traits.

Key words: Maize, genetic parameters, graphic plot.

INTRODUCTION

Maize (*Zea mays* L.) is one of the important cereal crops of Iran and the world after wheat and rice. Recent projections by the International Food Policy Research Institute indicate that by 2020, the demand for maize in developing countries will overtake that for wheat and rice (Gerpacio and Pingali, 2007). In Iran, the average grain yield ha^{-1} in 2007 was 7.6 t ha^{-1}, whereas the soil and climatic conditions of Iran are suitable for maize production, but the yield is low when compared to the United States of America with 9.5 t ha^{-1} in 2007. Thus, it is prerequisite to select promising hybrids for different conditions in order to speed up economical crop production.

Maize breeders have successfully exploited heterosis for grain yield by crossing inbred lines to develop desirable hybrids. However, the nature of gene action involved in expression of heterosis for the grain yield and other traits of elite maize hybrids remains unresolved.

The choice of efficient breeding program depends on a large knowledge of the type of gene action involved in the expression of the character. Dominance gene action would favor the production of hybrids, whereas additive gene action indicates that standard selection procedures would be effective in breeding about changing the character (Edwards et al., 1976).

Betran et al. (2003) reported that the gene action for yield, ear diameter, number of grain in row, grain depth and 1000 grain weight, is over dominance, while the gene

action for number of grain rows is partial dominance. Barati et al. (2003) showed that gene action for yield, number of grain in row and 1000 grain weight is over dominance, but for number of grain rows, it is partial dominance. Also, Srdic et al. (2007) found that dominant gene effects were more significant in maize grain yield and number of grains per row, while additive gene effects were more important for grain row number and 1000 grain weight. The mode of inheritance of grain row number was partial dominance, while over dominance was of greater importance for grain yield, number of grains per row and 1000 grain weight. Wattoo et al. (2009) revealed that the yield potential like number of days taken for tasselling and number of days taken for silking, plant height, number of ears per plant, number of grain rows per ear, number of grains per row, 100 grain weight and grain yield per plant were controlled by the over dominance type of gene action.

Irshad-Ul-Haq et al. (2010) 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. The graphic analysis showed that all the characters were under the genetic control of the over dominance type of gene action. Also, for grain yield, 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 a maximum number of

Table 1. Analysis of variance mean squares obtained from 8×8 diallel crosses and analysis of the mean squares of diallel crosses of eight maize inbred lines.

Source of variance	df	ASI(day)	Grain filling period (day)	Grain filling period (day)	Plant growth period (day)	Grain number in ear	Grain row number in ear	Ear diameter (cm)	Grain diameter (cm)	Grain depth (cm)	1000 grain weight (gr)	Hektolitr weight (gr/lit)	Grain yield (kg/hac)	Grain yield (kg/hac)
Block	2	5.08ns	53.19*	53.19*	8.58**	244832**	14*	3.88**	0.003ns	0.17ns	4946ns	5998ns	2317944*	2317944*
Genotype	35	4.16*	68.5**	68.5**	6.18**	135981**	9.57**	1.74**	0.05**	0.35**	10738**	5170*	1316319**	1316319**
Error	70	2.31	13.86	13.86	1.53	120742	6	0.49	0.02	0.18	3669	2608	584733	584733
a	7	7.87**	222.5**	222.5**	327.9**	76050.9*	6.53**	0.78**	0.03**	0.09**	46883**	11128**	1944439**	1944439**
b	28	7.71**	103.64**	103.64**	93.16**	59029.1**	6.11**	0.66**	0.02**	0.07**	13836.8**	5208.6**	2775917**	2775917**
b1	1	4.88ns	370.9**	370.9**	23.05ns	305419**	5.84*	0ns	0.02*	0.04ns	10108.7ns	49859.8**	10723930**	10723930**
b2	7	7.32**	123.78**	123.78**	116.4**	26550.7ns	13.75**	0.7**	0.01*	0.04ns	13110**	2430.6*	2488819**	2488819**
b3	20	8**	83.23**	83.23**	88.5**	77580**	3.45**	0.67**	0.02**	0.08**	14277.6**	3209.8**	2479001**	2479001**
Error	126	2.1	12.19	12.19	9.43	27638.8	1.20	0.11	0	0.02	3320	983	535380	535380

ns, * and **: nonsignificant, significant at 5 and 1% probability level, respectively.

recessive alleles.

Hussain et al. (2009) reported that plant height, leaf area, grain yield per plant and harvest index, under normal and water stress conditions, indicated additive gene action with partial dominance. Also, over dominance type of gene action was recorded for grains per row and 100 grain weight. Heritability estimates ranged from moderate to high (54 to 85%) for various traits.

Rezaei et al. (2005) reported that high broadsence heritability estimates (0.85 to 0.95) were observed; but for most traits, the estimates for narrowsence heritability were relatively low, while the lowest values belonged to number of grain row and grain yield (0.23 and 0.38), respectively.

Heritability degrees varied from low to moderate for grain yield (Singh et al., 2002; Kalla et al., 2001).

The diallel analysis study of the genetic traits would certainly be a valuable aid in the selection and breeding for better maize hybrids and synthetics. The information derived may be helpful in developing the selection criterion and selection of most promising inbred lines for further future breeding programs.

MATERIALS AND METHODS

The study was conducted at Shushtar City located in Khuzestan province, Iran (32°2 N and 48°50′ E, 150 m asl) in the year 2008. The type of soil found at this location is clay loam, and its pH = 7.6 with EC = 0.5 mmhos/cm.

The experimental material comprised eight inbred lines of maize (A679, K3651/1, K3640/5, K47/2-2-1-21-2-1-1-1, K19, K18, K166A and K166B). The lines were crossed during spring, in 2008 in a partial diallel fashion to obtain grains of direct crosses. The F_1 seed along with their parental inbred lines were sown in a triplicated randomized complete block design in 27 July (which was the planting date). Each plot contained 3 rows that are 75 cm apart and 9 m in length and they consisted of 45 hills, two seeds of which were sown and one seedling of which was removed at the 4 leaves stage. The experiment was irrigated every 5 days, while fertilizers were applied prior to sowing at a rate of 120 kg N ha^{-1} and 140 kg P ha^{-1}, and an additional side

dressing of 120 kg N ha^{-1} was applied at the six leaves stage of maize plants. Data pertaining to anthesis silking interval (ASI), grain filling period, plant growth period, grain row number in ear, grain number in row, grain number in ear, ear diameter, grain diameter, grain depth, 1000 grain weight, hektolitr weight and grain yield traits were analyzed using SPSS software. Genetic analysis was done according to the diallel technique as described by Hayman (1954) and Jinks (1954). 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 DISCUSSION

The analysis of variance (Table 1) showed that mean square due to inbred lines and hybrids for all traits was significant, indicating the existence of variability among genotypes for all traits and thus the use of Hayman-Jinks model was allowed for genetic analysis of these characters.

The results of the analysis of variance of F_1 data showed significant differences for a and b,

Table 2. Estimation of the statistical indices and genetics parameters for different traits in eight maize inbred lines of diallel crosses.

Trait	ASI (day)	Grain filling period (day)	Plant growth period (day)	Grain row number in ear	Grain number in row	Grain number in ear	Ear diameter (cm)	Grain diameter (cm)	Grain depth (cm)	1000 grain weight (gr)	Hektolitr weight (gr/lit)	Grain yield (kg/hac)
D	1.25^{ns}	114.5*	39.7**	7.4**	133.4ns	-22034ns	0.58**	0.01ns	0.05ns	9876.99*	4274.35*	275424^{ns}
H1	1.2**	88.8**	82.5**	6.42**	120.1*	20654.8**	0.52**	0.01*	0.04*	9458.5**	3162.03*	1982055**
H^2	1**	61.07**	55.9**	3.29**	127.6*	21214.8**	0.37**	0.01*	0.03**	7045.6**	2830.8*	1499272**
F	2.11^{ns}	24.88*	39.9**	6.1**	-32.5ns	-6340.4^{ns}	0.27**	0.003^{ns}	0.02*	3694.2*	653.02ns	646364^{ns}
h^2	0.42^{ns}	52.4**	2.07^{ns}	0.689^{ns}	231.08ns	40761.6**	-0.01**	0.003^{ns}	0.002^{ns}	1020.25^{ns}	7991.36**	1490713^{ns}
E	0.7**	4.08**	3.15**	0.396**	35.8**	9212.9**	0.04**	0.001**	0.008^{ns}	1106.7**	327.6**	178460**
$\sqrt{\dfrac{H1}{D}}$	0.98	0.88	1.44	0.93	0.95	0.97	0.95	1	0.89	0.98	0.86	2.68
$\dfrac{H2}{4H1}$	0.21	0.17	0.17	0.13	0.27	0.26	0.18	0.25	0.19	0.19	0.22	0.19
h^2b	0.63	0.86	0.90	0.72	0.56	0.44	0.77	0.70	0.58	0.76	0.78	0.71
h^2n	0.12	0.31	0.44	0.15	0.17	0.11	0.18	0.23	0.15	0.39	0.32	0.09

ns, * and **: nonsignificant, significant at 5 and 1% probability level, respectively.

suggesting the presence of both additive and dominance genetic effects in the expression of all traits (Table 1). The significant b1 item revealed the presence of directional dominant effects of genes. However, the b1 item for grain filling period, grain number in ear, grain row number in ear, grain number in row, hektolitr weight, grain diameter and grain yield traits was significant. Among inbred lines, asymmetrical gene distribution for ASI, grain filling period, plant growth period, grain row number, 1000 grain weight, hektolitr weight, ear diameter, grain diameter and grain yield were evident due to the significance of the b2 item. Also, among parents, specific gene effects for all traits were evident due to the significance of the b3 item. Irshad-Ul-Haq et al. (2010) reported that a, b, b1, b2 and b3 items for all traits were significant.

In Table 2, the genetic component of variation and the significant value of D for grain filling period, plant growth period, grain row number in ear, ear diameter, 1000 grain weight and hektolitr weight indicated the importance of additive genetic effects. Significant H components (H_1 and H_2) revealed the importantce of dominant variation, while different distribution of dominant genes was displayed by an unequal value of H_1 and H_2.

The additive and dominance effects covariance (F) used as a criterion of dominance and additive allele frequency for grain filling period, grain row number in ear, 1000 grain weight, ear diameter and grain depth, resulted to a significant and positive value which indicated that the positive genes were more frequent.

The important effect of heterozygous loci for plants, which was indicated by a significant value of h^2 for grain filling period, plant growth period, grain number in ear, hektolitr weight and ear diameter traits was significant.

The environmental variation (E) was significant for all traits, except for grain depth trait, indicating important environmental effects on traits. Degree of dominance $\sqrt{\dfrac{H1}{D}}$ indicated over dominance gene action for grain yield and plant growth period, but for grain diameter, it showed complete dominance, while for other traits, it showed partial dominance gene action. Betran et al. (2003) reported that the gene action for yield, ear diameter, number of grain in row, grain depth and 1000 grain weight traits is over dominance, but for number of grain rows, it is partial dominance.
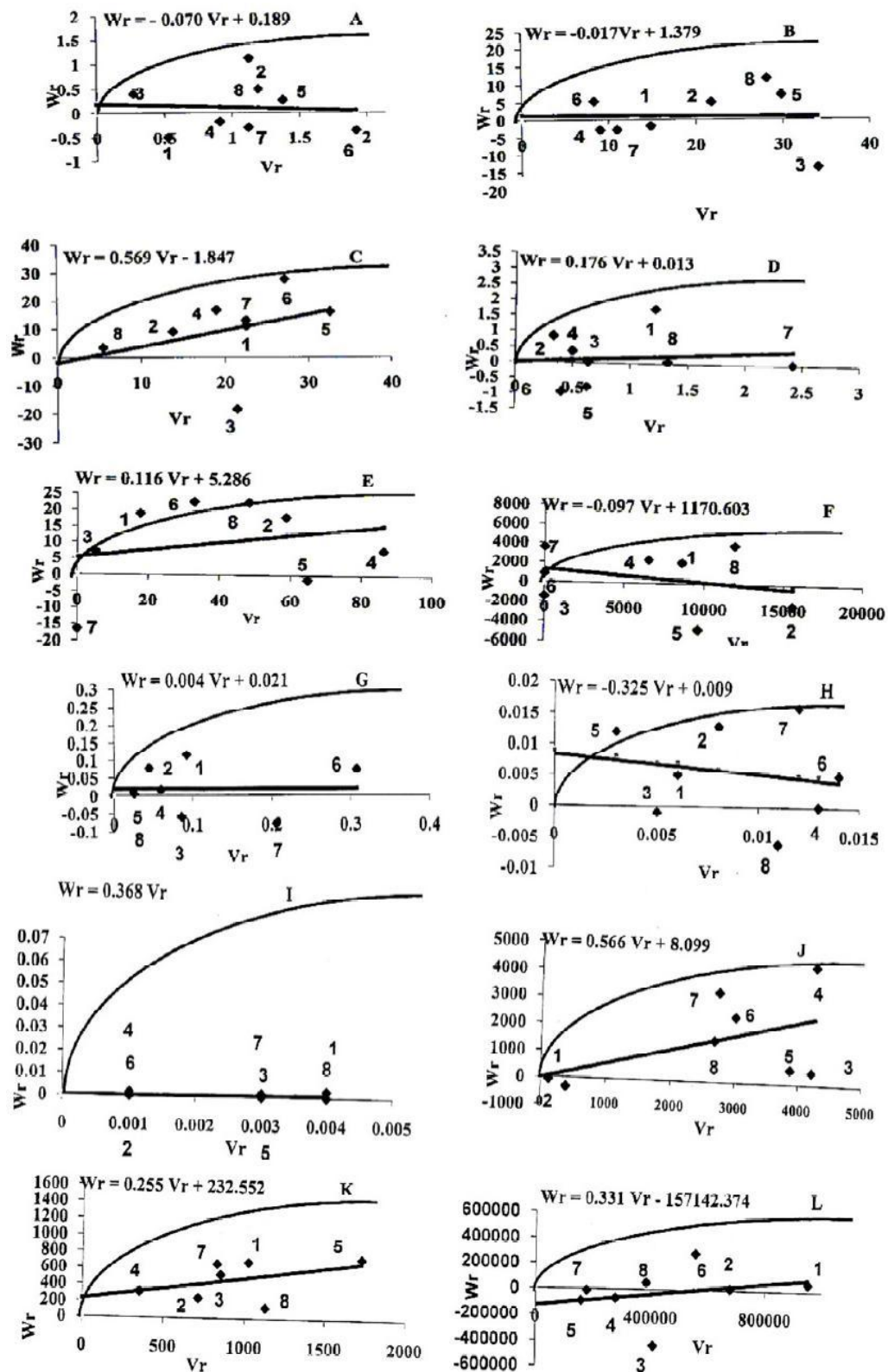
Figure 1. Vr/Wr graph of (A) ASI (day), (B) grain filling period (day), (C) plant growth period (day), (D) grain row number in ear, (E) grain number in row, (F) grain number in ear, (G) ear diameter (cm), (H) grain depth (cm), (I) grain diameter (cm), (J) 1000 grain weight (gr), (K) hektolitr weight (gr/L) and (L) grain yield (kg/plot). 1: K18; 2: K3651/1; 3: A679; 4: K166A; 5: K166B; 6; K3640/5; 7: K47/2-2-1-21-2-1-1-1 and 8: K19.

Hussain et al. (2009) reported that plant height, leaf area, grain yield, per plant and harvest index, under normal and water stress conditions, indicated additive gene action with partial dominance. Shiri et al. (2010) reported that the type of gene action for grain yield was additive and non additive. Also, over dominance type of gene action was recorded for grains per row and 100 grain weight. However, over dominance type of gene action in maize was reported by Prakash et al. (2004) and Ali et al. (2007) for grain yield and for all traits by Wattoo et al. (2009) and Irshad-Ul-Haq et al. (2010).

The proportion of genes for traits with positive and negative effects $\dfrac{H2}{4H1}$ in the parents was found to be higher than 0.25 for grain number in row and grain number in ear, while for grain diameter, it was 0.25 and for other traits, it was less than 0.25, denoting asymmetry at the loci showing dominance.

Broad sense heritability varied from 0.44 for grain number in ear to 0.90 for plant growth period, while narrow sense heritability was of non-additive nature and displayed a lower percentage than 44% of the genetic variation transferred from the parents. Heritability degrees were reported from low to moderate for grain yield (Singh et al., 2002; Kalla et al., 2001). Rezaei et al. (2005) reported high broadsence heritability estimates (0.85 to 0.95) for most traits, while the estimates for narrowsence heritability were relatively low, with the lowest values belonging to number of grain row and grain yield (0.23 and 0.38), respectively. However, Hussain et al. (2009) reported that heritability estimates ranged from moderate to high (54 to 85%) for various traits.

Graphical representation revealed that the regression line intercepted the Wr axis just below the point of origin which indicated the presence of over dominance type of gene action for plant growth period (Figure 1C) and grain yield (Figure 1L) traits and complete dominance for grain diameter (Figure 1F), while for ASI, grain filling period, grain number in row, grain number in ear, grain row number in ear, ear diameter, grain depth, 1000 grain weight and hektolitr weight (Figures 1A, B, D, E, G, H, I, J and K) traits, the regression line intercepted the Wr axis just above the point of origin which indicated the presence of partial dominance (additive) type of gene action. Nonetheless, these results were in agreement with the results received for the degree of dominance $\sqrt{\dfrac{H1}{D}}$.

Inbred line A679 for ASI trait (Figure 1A), being closer to the origin, possessed maximum dominant genes, while inbred line K3640/5 had mostly, recessive alleles. However, lines K3640/5 and A679 for grain filling period (Figure 1B), lines K19 and K166B for plant growth period (Figure 1C), lines K3651/1 and K47/2-2-1-21-2-1-1-1 for grain row number in ear (Figure 1D) trait, inbred lines A679 and K166A for grain number in row (Figure 1E) trait, inbred lines K3640/5 and K3651/1 fo r grain number

in ear (Figure 1F) trait, lines K166B and K3640/5 for ear diameter (Figure 1G), lines K166B and K3640/5 for grain depth (Figure 1H), K18 and K166A for 1000 grain weight (Figure 1J), lines K166A and K166B for hektolitr weight trait (Figure 1K) and lines K166B and K18 for grain yield (Figure 1L) had respectively, maximum dominant and recessive genes. For grain diameter (Figure 1I) trait, lines K3651/1, K166A and K3640/5 had maximum dominant genes, while line K18 had maximum recessive genes. Saleem et al. (2007) indicated that inbred lines B-46 and line EX-285 possessed maximum dominant genes for 100 grain weight and grain yield per plant, respectively. For number of days taken to tasseling, number of days taken to silking and number of grain row per ear, inbred line SYP-24 had maximum dominant genes. Irshad-Ul-Haq et al. (2010) indicated that for grain yield, 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 a maximum number of recessive alleles.

In this study, all traits except grain yield, plant growth period and grain diameter were controlled by additive type of gene action. Prediction in the case of additive gene action would be expected to be more reliable as compared to the characters which are controlled by the 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. However, inheritance of grain yield and plant growth period appeared in the over dominance type of gene action. Conclusively, grain yield and plant growth period are non-additively controlled and selection for these population must be practiced with great care to develop pure breeding line.

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