

## Heterotic Grouping of Iranian Maize Inbred Lines Based on Yield - Specific Combining Ability in Diallel Crosses and GGE Biplot

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### ABSTRACT

This research was aimed to classify Iranian maize inbred lines in heterotic groups and to identify their heterotic patterns. Fourteen maize inbred lines were crossed in a diallel scheme without reciprocals. Parents and their 91 F<sub>1</sub> hybrids were evaluated in a randomized complete block design with three replications for two years (2007, 2008) in Karaj, Iran. Analysis of variance was performed following method 2 of Griffing's model 1. GGE biplot model was employed to extract the interaction among lines and testers. The estimates of specific combining ability (SCA) were bigger than the analogous estimates for the general combining ability (GCA), indicating the major influence of dominant genes on the expression of grain yield. Hybrids with higher grain yield represented successful combination of parental lines for the expression of heterosis. The best heterotic patterns were "Lancaster Sure Crop (LSC) × Lines", and "Reid Yellow Dent (RYD) × Lines, both extracted from CIMMYT originated materials" and "LSC × Lines extracted from Late Synthetic". The results in heterotic patterns obtained by biplot mostly are in accordance with those of using Griffing's method.

**Keywords:** *Zea mays* L., Combining ability, Griffing's model, Heterotic group, Heterotic pattern, GGE biplot

### INTRODUCTION

Maize (*Zea mays* L.) is a major crop in Iran, it's cultivated area and yield has increased rapidly during the last decade. Thus maize breeding and release of suitable hybrids are importance.

For a successful breeding program, exploitation of heterosis is important. According to Aguiar *et al.* (2008), the constitution of heterotic groups is one of the foundation pillars for exploitation of heterosis in maize breeding programs devoted to obtain superior hybrids. Therefore, selection of appropriate

parents is the first step in the hybrid breeding program.

Based on inbred lines abilities to produce superior hybrids, maize parental lines have been grouped into heterotic groups. For example, Chinese maize gene-pool has been classified into Dom, Reid and Lan heterotic groups (Zhang *et al.*, 2002); In Brazil, maize gene-pool have been classified into four distinct heterotic groups (Parentoni *et al.*, 2001). Reif *et al.* (2003) using SSR markers to evaluate the genetic divergence from CIMMYT's maize germplasm, performed two heterotic groups (flint and dent types) in concordance with the genealogy. Previous study on Iranian maize showed existence of four heterotic groups (Choukan *et al.*, 2006).

Diallel crossing is a common tool in plant breeding for studying the inheritance of traits (Silva *et al.*, 2004, Freitas Júnior *et al.*, 2006, Souza *et al.*, 2008); it is also using to identify heterotic groups (Amaral Júnior *et al.*, 1999, Marin *et al.*, 2006, Miranda *et al.*, 2008, Rangel *et al.*, 2008). Analysis of diallel data is usually done by Griffing methods (Griffing, 1956).

In addition, in diallel crosses, heterotic groups can also be identified by biplot analysis. Biplot graphically displays a two-way data matrix (Gabriel, 1971). A modified biplot called GGE biplot was proposed by Yan *et al.* (2000) for analysis of genotype by environment data matrix constructed from multi environment experiments. This method can also be used for all types of two-way data such as diallel data (Yan, 2001, 2002; Yan, and Hunt, 2001). Biplot analysis of diallel data has the following advantages: i) performs a ranking of the parents (as entries) based on combining abilities with a particular tester, ii) shows the parent's GCA, iii) identifies hybrid's SCA, iv) shows the best crosses, and (v) constitutes

efficiently heterotic groups and identifies the best testers (Yan and Hunt, 2002).

The objectives of this study were to classify Iranian maize inbred lines based on SCA and GCA in different heterotic groups, to predict hybrid yield based on parents' dissimilarity, and to identify the best testers for using in future maize breeding programs in Iran.

## MATERIALS AND METHODS

The experiment was carried out at the Seed and Plant Improvement Institute in Karaj in 2007/2008. Fourteen maize inbred lines (Table 1) were crossed in a diallel scheme (without reciprocals). Parents along with their 91 F<sub>1</sub> hybrids were evaluated in a randomized complete block design with three replications. Each replication was broken into two blocks to improve uniformity.

Fertilizer was applied at 140 kg ha<sup>-1</sup> of N and 160 kg. ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>, and an additional N 50 days after sowing. There were 20 hills per row with 4 kernels per hill. Rows were spaced 0.75 m apart and hills were spaced at 0.35 m. The experiment had two surrounding border rows. When the plants had four to five leaves the plots were thinned to two plants per hill for a final plant density of 76000 plants ha<sup>-1</sup>. Grain yield (ton. ha<sup>-1</sup>) for each genotype was evaluated and adjusted to 14 percentage grain moisture at harvest. Before analyzing the data, Bartlett's test for homogeneity of parents and hybrids variance and normality test were performed by Mini-tab software. Analysis of variance was performed using SAS, and the partition of genotypes sum of squares to GCA and SCA was performed according method 2 of Griffing (1956) methodology, by using procedure D2 on SAS program (Zhang *et al.*, 2005).

Principal Component analysis was performed using SAS by PROC PRINCOMP procedure and symmetrical scaling. The GGE biplot method was used to study the entry effect plus entry by tester interaction effect of yield. This method has been described in detail by Yan and Hunt, (2002).

### RESULTS AND DISCUSSION

Combined analysis of variance showed a significant difference ( $p < 0.01$ ) for all sources of variation except genotype  $\times$  year and SCA  $\times$  year (Table 2). Significance of GCA and SCA

effects indicated that both additive and non-additive gene effects act on control of expression for grain yield. This result differs with Melani and Carena (2005) results that indicated GCA effects were significant ( $p < 0.01$ ) whereas SCA effects were not. In popcorn, Miranda *et al.* (2008) evaluated five genitors and ten hybrids by diallel crossing scheme – including five controls – in two localities of Minas Gerais State, Brazil, by using the Griffing (1956) methodology and obtained significance for both GCA and SCA effects in relation to grain yield.

Table 1. Fourteen maize inbred lines, their pedigree data including heterotic groups and respective codes of the medium to late maturing.

Number	Inbred lines	Pedigree sources (origin)	Genotype code
Lancaster Sure Crop (LSC) related lines			
1	MO17	CL. 187-2 $\times$ C103	A
2	K18	Derived from MO17 changes	C
3	K19/1	Derived from K19 changes	D
Reid Yellow Dent (RYD) related lines			
4	B73	BSSS C5(Iowa Stiff Stalk Synthetic)	B
5	A679	A B73 back-cross derived line[(A662 $\times$ B73)(3)]	F
Lines extracted from late synthetic			
6	K3615/2	SYN-Late	G
7	K3640/5	SYN-Late	H
8	K3653/2	SYN-Late	J
9	K3651/1	SYN-Late	K
Lines extracted from CIMMYT originated materials			
10	K166B	--	E
11	K3547/5	Srinagar 8848	L
12	K3544/1	--	M
13	K3545/6	Telaltizapan-8946	N
14	K3493/1	Unknown from EVT 16A	Q

Table 2. Grain yield mean squares from Griffing analysis (1956) for 14 maize inbred lines and their 91 hybrids grown at two years (2007-2008)

Source of variation	df	Sum of squares	Mean squares
Year	1	1563.35	1563.35**
Replication (Year)	4	368.72	92.18**
Genotype	104	1626.56	15.64**
GCA	13	307.45	23.65**
SCA	91	1318.59	14.49**
Genotype × Year	104	510.64	4.91 <sup>ns</sup>
GCA × Year	13	134.16	10.32**
SCA × Year	91	376.74	4.14 <sup>ns</sup>
Error	416	1605.76	3.86
Coefficient of Variation (CV)			25.6

<sup>ns</sup> and \*\*: Non- significant and significant at  $p < 0.01$ , respectively.

GCA: General combining ability.

SCA: Specific combining ability.

In another study by using circulate diallel in popcorn, Rangel *et al.* (2008) evaluated ten genitors and fifteen hybrids in two localities for two growing seasons in Rio de Janeiro State, Brazil, and detected significance mean squares for parents  $\times$  years and hybrids  $\times$  year for four important economically traits, including grain yield. Besides, the effects of GCA and SCA for grain yield were highly significant (Rangel *et al.*, 2007). Similar results of significance for GCA and SCA for grain yield by diallel analyses were further verified by Viana and Matta (2003), Freitas Júnior *et al.* (2006) and Scapim *et al.* (2006) in popcorn, as well as by Balestre *et al.* (2008) in maize.

Of the total sum of squares attributed to the crosses, 19% was due to GCA effects, indicating the presence of genes with additive effects, and 81% due to SCA effects, indicating the presence of genes with non-additive effects. The average grain yield for parents was 5.05 ton ha<sup>-1</sup>, and ranged from 2.45 ton ha<sup>-1</sup> for K3493/1 to 8.32 ton ha<sup>-1</sup> for K166B. The average grain yield for hybrids was 8.08 ton ha<sup>-1</sup>, and ranged from 4.90 ton. ha<sup>-1</sup> for B73 $\times$ A679 to 10.75 ton ha<sup>-1</sup> for K19/1 $\times$ K166B. Hybrids of K18 $\times$ K166B, K3615/2 $\times$ K166B, K3615/2 $\times$ K3653/2 and MO17 $\times$ K3547/5 had high grain yield (Table 3). Therefore, high grain yield values are valuable measure of the potential of the hybrids and their parents as sources of inbred lines for hybrid development.

Eighty-three of the crosses showed a significant and positive mid-parent heterosis (MPH) at  $p < 0.05$  (Table 3). The two lower values of estimates of MPH occurred for K3545/6  $\times$  K3547/5 and K18  $\times$  K19/1 crosses, corresponding to -0.66 and -0.46 respectively. These hybrids also expressed low values estimates for grain yield. The higher estimates of heterosis for MPH were observed in the combinations K679  $\times$  K3544/1, A679  $\times$  K3493/1 and

K3545/6  $\times$  K3493/1, corresponding to 5.45, 5.28 and 5.23 respectively (Table 3). These hybrids had high grain yield, but other hybrids with high performance for estimates of grain yield (K19/1  $\times$  K166B, K3615/2  $\times$  K166B and K3615/2  $\times$  K3653/2) also revealed positive estimates of heterosis for MPH. Therefore, the presence of heterosis is one of the best measures of genetic diversity of the parents (Hallauer and Miranda, 1988; Mungoma and Pollak, 1988). Thus, parents in top performing crosses are expected to be genetically more divergent than the parents in the opposite situation.

The best heterotic responses were presented by A679  $\times$  K3544/1 and A679  $\times$  K3493/1 crosses. A679 line is from the US RYD group, K3544/1 and K3493/1 are from CIMMYT originated materials. Therefore, the presence of these two most-divergenbackground explains the high levels of heterosis verified in these crosses and the heterotic pattern of 'RYD $\times$ CIMMYT originated materials'. In other crosses, the presence of two CIMMYT's parents K3544/6 $\times$ K3493/1 showed a high MPH, therefore this lead to this finding that high diversity exists in CIMMYT maize germplasms. Other hybrids having diverse genetic background in their parents also exhibited a similar performance.

The K19/1  $\times$  K166B hybrid had the highest grain yield, and a positive MPH ( $p < 0.01$ ). The lines K19/1 and K166B are from LSC groups and CIMMYT originated materials, respectively. Similar situation also occurred for: i) K18 $\times$ K3653/2, that showed significant heterosis and being that K18 line (from LSC group) and K3653/2 line (from SYN-Late); ii) crosses involving lines from RYD and LSC heterotic groups, for example, B73 $\times$ K19/1 was heterotic, where B73 is from RYD and K19/1 is from LSC.

In contrast, some hybrids having similar genetic background, showed low yield.

K3547/5 × K3545/6 cross had the lowest MPH and also presented low value for grain yield. This performance was not surprise since both parents were from CIMMYT originated materials with low genetic distance. The K18 × K19/1 cross showed a similar pattern, both parents of this hybrid belongs to LSC group and have a low genetic distance. B73 × A679 cross had the lowest yield and its MPH was not significant, both parents of this cross are from RYD group and therefore their narrow genetic distance explains their poor yield.

There was a high genetic diversity among SYN-Late lines. For instance, the cross K3615/2 × K3653/2 had positive and significant ( $p < 0.01$ ) MPH, and had the second highest grain yield among the hybrids.

Regarding the GCA of parents, the estimates ranged from -0.73 for K3493/1 to 0.98 for K166B (Table 4). These results are in agreement with Melani and Carena (2005) who reported GCA ranging of -0.74 to 1.07 in maize open pollinated populations. Four parental lines showed significant estimates of GCA, where two (K166B and K3615/2) presented positive values and the others (K3651/1 and K3493/1) had negative GCA values. Therefore, these lines could be useful in producing recombinant populations to apply half-sib and full-sib recurrent selection schemes, for obtaining recombinant inbred lines.

There was a positive correlation between grain yield of the parents *per se* and their corresponding GCA values ( $r = 0.92$ ). The lines K166B and K3615/2 had the highest GCA as well as the highest mean of grain yield, whereas K3493/1 had the lowest GCA and the lowest mean of grain yield.

In relation to the hybrids, the pairs B73 × K19/1, MO17 × K3547/5, K18 × K3545/6, K3547/5 × K3493/1 and K3545/6 × K3493/1 had positive and

significant SCA (Table 4). These combinations also had high means for grain yield. Three crosses had the lowest SCA value: B73 × A679 (both from RYD group), K18 × K19/1 (both from LSC group) and K3547/5 × K3545/6 (both from CIMMYT originated materials). These hybrids also had the lowest estimates of mean for grain yield. But the cross A679 × K3544/1 had the highest SCA estimate, where the line A679 is from RYD group and K3544/1 is from CIMMYT originated materials, ratifying the great importance of the genetic distance between genitors.

The biplot axis for the mean grain yield data of the lines explained 55% (33 and 22% by PC1 and PC2, respectively) of the total variation (Figure 1). The GCA effects of the entries were determined by mean tester coordinate (ATC) axis. The ATC is established by its passing through the origin and the mean testers (mean testers indicated by circle in Figure 1-a). The positive end of the ATC is on the side of the biplot origin where the mean testers is located and pointed out by arrow in graphic (Figure 1).

Table 3. Mean of grain yield performance for fourteen maize inbred lines (diagonal), their 91 hybrids (above diagonal), and the corresponding mid-parent heterosis value (below diagonal) for two growing seasons.

<i>Genotype code</i>	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>	<i>E</i>	<i>F</i>	<i>G</i>	<i>H</i>	<i>J</i>	<i>K</i>	<i>L</i>	<i>M</i>	<i>N</i>	<i>Q</i>
A	4.57	8.97	7.78	8.88	8.84	8.67	7.99	8.88	9.14	7.39	10.03	6.96	9.31	6.72
B	4.80**	3.78	8.35	9.77	8.74	4.90	8.92	8.11	7.59	6.60	8.43	8.64	8.24	6.28
C	2.99**	3.97**	5.00	4.94	10.07	6.64	8.81	8.30	9.62	8.14	8.30	6.50	9.79	5.97
D	3.70**	4.98**	-0.46 <sup>ns</sup>	5.80	10.75	8.02	7.00	8.73	8.12	7.99	8.01	8.88	7.89	8.58
E	2.39*	2.69**	3.41**	3.69**	8.32	8.18	10.23	7.48	9.46	8.22	8.20	8.43	8.56	7.08
F	4.72**	1.34 <sup>ns</sup>	2.47*	3.45**	2.34*	3.34	7.90	7.08	7.92	7.51	8.56	9.55	9.08	8.17
G	1.63 <sup>ns</sup>	2.97**	2.24*	0.03 <sup>ns</sup>	2.00*	2.16*	8.14	7.23	10.37	8.49	9.49	7.85	8.52	8.14
H	4.23**	3.86**	3.44**	3.46**	0.95 <sup>ns</sup>	3.05**	0.79 <sup>ns</sup>	4.73	8.29	6.29	6.71	7.40	6.07	7.87
J	4.27**	3.12**	4.53**	2.63**	2.71**	3.66**	3.72**	3.34**	5.17	7.68	7.46	9.19	7.21	8.63
K	3.32**	2.93**	3.86**	3.30**	2.28*	4.06**	2.64**	2.14*	3.32**	3.56	8.34	6.83	8.08	6.52
L	4.82**	3.63**	2.88**	2.19*	1.12 <sup>ns</sup>	3.97**	2.50**	1.42 <sup>ns</sup>	1.96*	3.64**	5.84	8.08	4.94	8.98
M	2.34*	4.41**	1.67 <sup>ns</sup>	3.64**	1.93*	5.54**	1.45 <sup>ns</sup>	2.70**	4.27**	2.72**	2.83**	4.68	8.08	6.38
N	4.35**	3.68**	4.62**	2.32*	1.73 <sup>ns</sup>	4.73**	1.78 <sup>ns</sup>	1.03 <sup>ns</sup>	1.95*	3.63**	-0.66 <sup>ns</sup>	3.07**	5.35	9.13
Q	3.21**	3.16**	2.25*	4.45**	1.75 <sup>ns</sup>	5.28**	2.85**	4.28**	4.83**	3.51**	4.84**	2.82**	5.23**	2.45

*ns*, \* and \*\*: Non- significant, significant at P < 0.05 and significant at p < 0.01, respectively.

S.E. (mid-parent heterosis) = 0.96.

Genotypes code: *A*- MO17, *B*- B73, *C*- K18, *D*- K19/1, *E*- K166B, *F*- A679, *G*- K3615/2, *H*- K3640/5, *J*- K3653/2, *K*- K3651/1, *L*- K3547/5, *M*- K3544/1, *N*- K3545/6, *Q*- K3493/1.

Table 4. General combining ability values for fourteen maize inbred lines (diagonal) and specific combining ability of their 91 hybrids (above diagonal) for grain yield in two growing seasons.

<i>Genotype code</i>	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>	<i>E</i>	<i>F</i>	<i>G</i>	<i>H</i>	<i>J</i>	<i>K</i>	<i>L</i>	<i>M</i>	<i>N</i>	<i>Q</i>
A	0.22 <sup>ns</sup>	1.32 <sup>ns</sup>	0.00 <sup>ns</sup>	0.73 <sup>ns</sup>	-0.05 <sup>ns</sup>	1.17 <sup>ns</sup>	-0.66 <sup>ns</sup>	1.43 <sup>ns</sup>	0.87 <sup>ns</sup>	0.11 <sup>ns</sup>	1.99 <sup>*</sup>	-0.75 <sup>ns</sup>	1.38 <sup>ns</sup>	-0.44 <sup>ns</sup>
B		-0.25 <sup>ns</sup>	1.05 <sup>ns</sup>	2.09 <sup>*</sup>	0.33 <sup>ns</sup>	-2.14 <sup>*</sup>	0.74 <sup>ns</sup>	1.14 <sup>ns</sup>	-0.21 <sup>ns</sup>	-0.20 <sup>ns</sup>	0.88 <sup>ns</sup>	1.40 <sup>ns</sup>	0.78 <sup>ns</sup>	-0.41 <sup>ns</sup>
C			-0.12 <sup>ns</sup>	-2.86 <sup>**</sup>	1.53 <sup>ns</sup>	-0.52 <sup>ns</sup>	0.50 <sup>ns</sup>	1.20 <sup>ns</sup>	1.69 <sup>ns</sup>	1.20 <sup>ns</sup>	0.61 <sup>ns</sup>	-0.87 <sup>ns</sup>	2.21 <sup>*</sup>	0.85 <sup>ns</sup>
D				0.25 <sup>ns</sup>	1.83 <sup>ns</sup>	0.48 <sup>ns</sup>	-1.68 <sup>ns</sup>	1.25 <sup>ns</sup>	-0.18 <sup>ns</sup>	0.68 <sup>ns</sup>	0.05 <sup>ns</sup>	1.14 <sup>ns</sup>	-0.06 <sup>ns</sup>	1.38 <sup>ns</sup>
E					0.98 <sup>**</sup>	-0.06 <sup>ns</sup>	0.81 <sup>ns</sup>	-0.73 <sup>ns</sup>	0.43 <sup>ns</sup>	0.18 <sup>ns</sup>	-0.59 <sup>ns</sup>	-0.04 <sup>ns</sup>	-0.13 <sup>ns</sup>	-0.84 <sup>ns</sup>
F						-0.39 <sup>ns</sup>	-0.14 <sup>ns</sup>	0.25 <sup>ns</sup>	0.26 <sup>ns</sup>	0.85 <sup>ns</sup>	1.15 <sup>ns</sup>	2.45 <sup>*</sup>	1.76 <sup>ns</sup>	1.62 <sup>ns</sup>
G							0.76 <sup>**</sup>	-0.75 <sup>ns</sup>	1.57 <sup>ns</sup>	0.68 <sup>ns</sup>	0.99 <sup>ns</sup>	0.39 <sup>ns</sup>	0.06 <sup>ns</sup>	0.44 <sup>ns</sup>
H								-0.45 <sup>ns</sup>	0.70 <sup>ns</sup>	-0.31 <sup>ns</sup>	-0.65 <sup>ns</sup>	0.36 <sup>ns</sup>	-1.18 <sup>ns</sup>	1.38 <sup>ns</sup>
J									0.37 <sup>ns</sup>	0.25 <sup>ns</sup>	-0.72 <sup>ns</sup>	1.33 <sup>ns</sup>	-0.86 <sup>ns</sup>	1.33 <sup>ns</sup>
K										-0.62 <sup>*</sup>	1.15 <sup>ns</sup>	-0.04 <sup>ns</sup>	0.99 <sup>ns</sup>	0.19 <sup>ns</sup>
L											0.13 <sup>ns</sup>	0.46 <sup>ns</sup>	-2.89 <sup>**</sup>	1.92 <sup>*</sup>
M												-0.19 <sup>ns</sup>	0.56 <sup>ns</sup>	-0.37 <sup>ns</sup>
N													0.03 <sup>ns</sup>	2.16 <sup>*</sup>
Q														-0.73 <sup>**</sup>

*ns*, \* and \*\*: Non- significant, significant at P < 0.05 and significant at p < 0.01, respectively.

S.E. (GCA) = 0.273. S.E. (SCA) = 1.06.

Genotypes code: A- MO17, B- B73, C- K18, D- K19/1, E- K166B, F- A679, G- K3615/2, H- K3640/5, J- K3653/2, K- K3651/1, L- K3547/5, M- K3544/1, N- K3545/6, Q- K3493/1.



The GCA effect of an entry may be defined by the value of its hybrid with the mean testers. Thus the GCA effects of the entries are approximated by their projection on to the ATC. The genotypes that situated in the positive end of ATC had a higher GCA. On the other hand, genotypes located in the negative end of ATC had a lower GCA. Thus, the entry n (K3545/6) had the highest GCA, whereas b (B73) had the lowest. The GCA of the entries are in order of  $n > l > d > g > j > m > h > e > c \approx a > k > q > f > b$  (Figure 1- a). In this method genotypes are labeled with uppercase letters when viewed as testers and with lowercase letters when viewed as entries.

The axis that pass through the origin and perpendicular to the ATC, can help to estimate the SCA of the lines (the line SCA represents the tendency of the line to produce superior hybrids with specific testers). The direction of arrows in this axis indicates the increasing direction of SCA. The lines close to the origin had lower SCA, and the lines situated at the end of this axis had a higher SCA. In other word, the projection or straight distance of each genotype from ATC is the degree of SCA. Thus, according to Figure 1, the entry k had the smallest SCA (smallest projection on to the ATC). In the opposite, entries n, j, l, b, f, m, a, c and q had the highest SCA effects (largest projection on to the ATC).

Two heterotic groups were identified in this experiment, the first group included genotypes codified by n, l, j, h, e, f and b, and the second group contained genotypes designed by codes d, g, m, a, c and q. Genotype k located on the ATC did not seem to belong to any of two the groups. Therefore, the 42 crosses i.e.  $[n, l, j, h, e, f, b] \times [d, g, m, a, c, q]$  are expected to show heterosis defined as better than both parents.

The best tester should be highly discriminating between the entries, and

be highly representative of all the testers. It also should have a high performance for grain yield. According to biplot analysis the best tester would be that allocated at the positive end of ATC. In the graphic, this genotype represents the position where the estimate of GCA is the highest and the lowest for the SCA. Thus, the genotype K was the best tester in this data set, and we speculate the GCA effects of the genotypes should be reasonably assessed by the performance of their hybrid with genotype K. The order of lines based estimates of mean grain yield values in the crosses with the tester K (Table 3) were  $G > L > E > C > N > D > J > F > A > M > B > Q > H > K$ , whereas on the basis of their GCA (Table 4) the order was  $E > G > J > D > A > L > N > C > M > B > F > H > K > Q$ . Although these two rankings show a good degree of conformity, they differ, and this difference is explained by the fact that biplot displays only 55% of data variation.

The polygon of a biplot provides the best way to interpret the results based on interaction of genotypes by testers. This polygon is drawn by connecting the entries furthest from the origin such that all other entries remain within the polygon. From the plot's origin, lines perpendicular to each side of the polygon are drawn; this divides the biplot into several sectors. Testers falling in the same sector share the same best-mating partner and this would be the entry at the vertex of the polygon in that sector. This entry has the highest distance from origin among other entry in this sector (Yan *et al.*, 2001; Yan and Hunt, 2002).

The value of the hybrid between an entry and a tester is visualized by measuring the perpendicular distance between the vector of the tester and the entry's marker position (a vector of a tester is the line from the biplot origin towards the marker of the tester). The

entries located on vertex of polygon are the best-mating partners with the same sector's testers, and the poorest-mating partners with other sector's testers. Entries located near the biplot origin are less responsive to the change of testers.

Lines n, l, j, h and e allocated in one sector. In this sector there are five testers (A, C, K, M, Q), indicating high GCA effects for these lines (Figure 1-B). The line n and the tester Q were situated in one sector; vice versa the line q with the tester N are together in one sector, indicating the hybrid  $N \times Q$  has potential to express high effect of heterosis. Similar conditions observed for  $L \times Q$  hybrid. In fact, these hybrids had a high estimate of grain yield (higher than the mean of all combinations) and had the high MPH values (Table 3) and SCA values (Table 4). Both lines N (K3545/6) and Q (K3493/1) are from CIMMYT originated materials. Another hybrids with high heterosis were: crosses [B, F, E]  $\times$  [D, G, M, A, C, Q, K], crosses [A, C, M]  $\times$  [J, N, L, H, E].

Lines h, l and n were situated in one sector together. In contrast their testers (H, L and N) were allocated another sector together, indicating low combining ability among those lines. Similar results were obtained for the B and F lines. These results are in accordance with former reports on heterotic groups (Choukan *et al.*, 2006).

### CONCLUSIONS

The results indicated that there is a genetic variability among Iranian maize inbred lines that allows the exploitation of additive and non-additive effects for grain yield. Maize breeding programs in Iran can be successfully by intra or interpopulational methods and the biplot method although explained only 55% of the total variation, easily showed the best combinations between lines and those with the best testers.

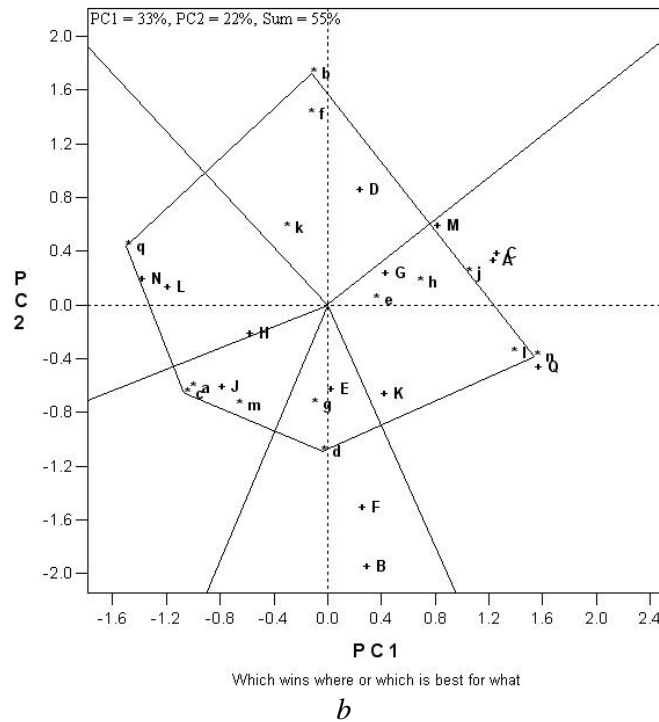
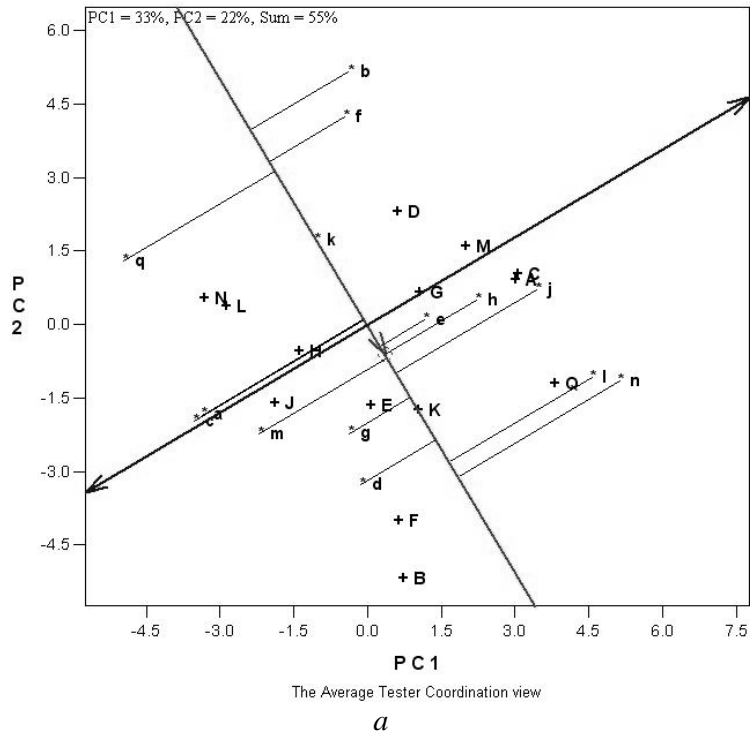


Figure 1. Biplot based on diallel data of fourteen maize inbred lines with different grain yield; *a*, mean tester ordination, and *b*, polygon graphic. Genotypes are labeled with uppercase letters when viewed as testers and with lowercase letters when viewed as entries. Codes of genotypes are: A- MO17, B- B73, C- K18, D- K19/1, E- K166B, F- A679, G- K3615/2, H- K3640/5, J- K3653/2, K-K3651/1, L- K3547/5, M- K3544/1, N- K3545/6, and Q- K3493/1

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