

## Biplot Analysis of diallel crosses for yield and some morphological traits in durum wheat

Davoud Sadeghzadeh-Ahari<sup>1</sup>, Peyman Sharifi<sup>2\*</sup>, Rahmatollah Karimizadeh<sup>3</sup>, Mohtasham Mohammadi<sup>4</sup>

<sup>1</sup>Dryland Agricultural Research Institute, Iran, y, P.O. Box 119.

<sup>2</sup>Department of Agronomy and Plant Breeding, Rasht Branch, Islamic Azad University, Rasht, Iran, Post code: 4147654919.

<sup>3</sup>Dryland Agricultural Research Institute, Gachsaran Station, Iran, Post code: 7581818449.

<sup>4</sup>Dryland Agricultural Research Institute, Gachsaran Station, Iran, Post code: 7581818449.

\*Corresponding author, E-mail: peyman.sharifi@gmail.com, Tel: 09112829197, Fax: 01333447060.

### Abstract

Six varieties of durum wheat were included in a full diallel mating design during 2003-2004 and 2004-2005 cropping seasons in the farm of Maragheh Dryland Agricultural Research Institute (DARI), Iran. Parental durum wheat genotypes and their complete diallel progenies were grown in a randomized complete block design with two replications in the growing seasons of 2005-06. The highest values of number of seeds per spike, one hundred seed weight and seed yield were obtained in Gerdish. The GCA effects indicated that Zardak was an ideal general combiner for one hundred seed weight, coleoptile length, number of germinated seeds, number of seeds per spike, growth vigor and radicle length. Crosses of Knd1149//68/ward × Waha and Zardak × Chehel daneh exhibited the highest value of seed yield and significant heterosis. Graphic analysis indicated that the hybrid between Knd1149//68/ward and Waha was the best hybrid for seed yield, because it integrated the four genes (A2, D1, D2 and probably D3) for seed yield. Zardak, Knd1149//68/ward and Gerdish can be used either as the best parents for selection programs based on their GCA effects, or as a superior parent in hybrid programs based on their SCA effects.

**Key words:** Biplot, Combining ability, Diallel, Heritability.

### INTRODUCTION

Durum wheat (*Triticum durum* Desf.) is grown on about 14 million hectares, or 6% of the world's total wheat growing area (USDA, 2009). It is the most important cereal crop for making macaroni and other types of foods. The production of durum wheat in Iran is relatively smaller than bread wheat production (Karimizadeh *et al.*, 2012)

Diallel mating designs widely used to obtain information on the inheritance of quantitative traits, to select the best parental combinations for crosses and to determine the heterotic responses and heterotic patterns, are important tools in plant breeding programs (Griffing, 1956). The technique helps breeders for generating superior hybrids (Yan and Kang, 2003). This method has been utilized remarkably in wheat breeding programs. The application of principal component (PC) biplot techniques for diallel crosses were suggested by Yan and Hunt (2002). Biplot approach based on diallel experimental data are used to estimate the general combining ability (GCA) and specific combining ability (SCA) and to identify potential heterotic relationships among different genotypes (Yan and Hunt, 2002). A high degree of heterosis occurs when the parents are genetically divergent or unrelated and result in a hybrid that presumably is heterozygous at numerous loci in the genome (Krishnamoorthy, 2005). Two advantages of biplot analysis compared to other biometric diallel analysis are its graphical presentation and better interpretability of data, which greatly enhances ability to understand the patterns of data. While the conventional method of diallel analysis was designed to describe the

phenotypic performance of the crosses, the biplot approach tries to explain the phenotypic variation of the crosses by understanding the parents (Yan and Hunt, 2002). The biplot approach of diallel data analysis allows a much better understanding of parents. For a given set of data, the following information can be easily visualized: the GCA effect of each parent; the SCA effect of each parent (not cross); the best crosses; the best testers; the heterotic groups; and genetic constitutions of parents with regard to the trait under investigation (Yan and Kang, 2003).

Some of researchers used biplot techniques for analysis of diallel data in cereals. Farshadfar and Hasheminasab (2012), Farshadfar *et al.* (2012) and Farshadfar and Hasheminasab (2013) studied the combining ability and genetic constitution of physiological indicators of drought tolerance in eight-parental diallel crosses of bread wheat using GGE biplot techniques. Malla *et al.* (2010) estimated combining ability for *Fusarium* head blight resistance in wheat by diallel mating design. Dehghani *et al.* (2005) and (2013) used biplot method for the analysis of diallel cross data for infection type of wheat stripe rust. Mostafavi and Zabet (2013) studied genetic behavior of yield and some agronomic traits in diallel data set of bread wheat by biplot and distinguished the best general and specific combiners. There are also some reports on the application of the GGE biplot in diallel data analysis in rice (Sharifi and Safari Motlagh, 2011; Sharifi, 2012, 2013), linseed (Rastogi *et al.*, 2011) and maize (Mostafavi *et al.*, 2012).

The objectives of this study were: i) to evaluate the performance of the six selected parents, ii) to determine their genetic potential as sources of potential breeding materials for a durum wheat breeding program, and iii) to identify heterotic groups among parents by principal component analysis.

## MATERIALS AND METHODS

### Genetic material and crosses

The experiment was carried out in the farm of Maragheh Dryland Agricultural Research Institute (DARI), located between 46°12'E longitude and 37°30'N latitude at an altitude of 1477 m from the mean sea level in northwest of Iran. Six durum wheat genotypes with three different growth habits including spring, winter and facultative (Chehel daneh, Gerdish, Zardak, Syrian-1, Waha and Knd1149//68/ward) were selected randomly among experimental lines and cultivars existing at Maragheh Agricultural Research Station for establishing of a complete diallel crosses. All possible crosses between genotypes were made during 2003-2004

and 2004-2005 cropping seasons. Six parental durum wheat genotypes and their complete diallel progenies were grown in a randomized complete block design with two replications in the growing seasons of 2005-2006. Due to the low number of hybrid seeds, the experiment was carried out only by two replications. Name and growth habits of genotypes were shown in Table 1. Plots of parents and F1 consisted of four rows of 4 m length with the spacing of 20 cm between rows and 5 cm between plants. To raise the crop, recommended doses of 120 N: 60 P<sub>2</sub>O<sub>5</sub>: 40 K<sub>2</sub>O kg ha<sup>-1</sup> were applied in the experimental plots. Half quantity of nitrogen and full quantities of P and K was applied before sowing. The remaining nitrogen was applied by top dressing at the first irrigation. Inter culture operation was done about one month and one and half month after sowing to prevent weeds. To remove border effects, the two middle rows in each plot were harvested for seed yield assessment; yield was adjusted for 10% seed moisture before converting it to kg ha<sup>-1</sup> for statistical analysis. The measured agronomic traits included number of seeds per spike (SS), one hundred seed weight (HSW) and seed yield (SY).

**Table1.** Information of used parents in diallel crosses.

No.	Genotype	Growth habit
1	Chehel daneh	Winter
2	Gerdish	Winter
3	Zardak	Facultative
4	Syrian-1	Spring
5	Waha	Spring
6	Knd1149//68/ward	Facultative

### Evaluation of seed germinated traits

In order to evaluate the response of genotypes to cold at the germination stage, parents and progenies of crosses were planted in the concrete boxes, which are specific to studies of cold. Cold tolerance experiment was carried out in a randomized complete block design with two replications. Each plot consisted of two rows of 1 m length. The number of germinated seeds from 20 cultured seeds was considered as cold tolerance. Radicle and coleoptile length of seedlings were also measured and growth vigor was scored from low to high.

### Statistical Analysis and Mathematical Model for GGE Biplot

GGE (genotype main effect plus genotype-by-environment interaction) biplots are commonly used to

analyze two-way data, where rows and columns represent different experimental units (Yan and Hunt, 2002). After obtaining the first two principal components of the adjusted data matrix, the biplot model can be written as:

$$\gamma_{ij} - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where,  $\gamma_{ij}$  is the genotypic value of the cross between entry  $i$  and tester  $j$  for the trait of interest;  $\beta_j$  is the mean of all combinations involving tester  $j$ ;  $\lambda_1$  and  $\lambda_2$  are the singular values for the first and second principal components (PC1 and PC2 respectively);  $\xi_{i1}$  and  $\xi_{i2}$  are the PC1 and PC2 eigenvectors, respectively, for entry  $i$ ;  $\eta_{j1}$  and  $\eta_{j2}$  are the PC1 and PC2 eigenvectors, respectively, for tester  $j$ ; and  $\varepsilon_{ij}$  is the residual of the model associated with the combination of entry  $i$  and tester  $j$ . Since in diallel cross data, each genotype is an entry and a tester,  $i$  and  $j$  can refer to the same or different genotypes. When  $i \neq j$ , the genotype is a population hybrid and when  $i = j$ , the genotype is a pure line.

All statistical analyses were performed with the Proc Princomp and Proc Mixed procedures of SAS software package (SAS, 2005). All biplots presented in this paper were generated using the software GGE biplot package that runs in a windows environment, an earlier version of which was described in Yan (2001). Up-to-date information on GGE biplot is available at <http://www.ggebiplot.com>.

Heterosis in  $F_1$  for all of the traits was calculated in percentage over mid-parent values, and t-test was employed by given formulae to determine whether  $F_1$  hybrid means were significantly different from mid-parental values compared to t table values at 0.05 and 0.01 probability levels, as discussed by Wynne *et al.* (1970). Deviation of  $F_1$  from its mid-parents or either of the parental values was interpreted by Mather and Jink (1977) depicting type of gene action operating for controlling the trait.

$$\text{Heterosis} = \left( \frac{F_{1ij} - MP_{ij}}{MP_{ij}} \right) \times 100$$

t values for Heterosis was calculated by:

$$t = \frac{F_{1ij} - MP_{ij}}{\sqrt{\frac{3}{8} EMS}}$$

Where:  $F_{1ij}$  = the mean of the  $ij^{\text{th}}$   $F_1$  crosses,  $MP_{ij}$  = the mid-parent value for the  $ij^{\text{th}}$   $F_1$  crosses,  $i$  = the female parent and  $j$  = the male parent,  $3/8$  is a constant presented by Wynne *et al.* (1970).

Baker genetic ratio was calculated using the following equation (Baker, 1978):

$$\frac{2\sigma_g^2}{2\sigma_g^2 + \sigma_s^2}$$

When,  $\sigma_g^2$  and  $\sigma_s^2$  are variance due to GCA and SCA.

## RESULTS

### Analysis of variance, Mean Performance and heterosis

Analysis of variance (Table 2) indicated significant effects of genotypes, general combining ability (GCA), specific combining ability (SCA) and reciprocal for the number of seed per spike, seed yield, number of germinated seeds and hundred seed weight. The significant effects of GCA and SCA indicated the importance of both additive and non-additive gene actions in inheritance of these traits (Table 2). According to Baker (1978) ratio, when combining ability ratio approaches unity, GCA alone can predict the performance of the parents. Thus, the GCA scores could not be used to predict the performance of the parents in the present study, because the value of Baker's ratio is much lower than the theoretical maximum of unity for all of the studied traits. Therefore, the low Baker's ratio emphasized the preponderant role of non-additive (dominance and/or epistatic) gene action in controlling the studied traits in durum wheat in comparison to additive one.

Among the parents, the highest values of number of seeds per spike, hundred seed weight and seed yield were obtained in Gerdish. The highest values of number of germinated seeds and radicle length were obtained in Knd1149//68/ward. The highest values of coleoptile length and growth vigor were observed in Chel daneh and Zardak, respectively. The lowest values of number of seeds per spike, one hundred seed weight, seed yield and radicle length were obtained in Zardak. The lowest values of coleoptiles length and number of germinated seeds were obtained in Syrian-1 and Gerdish, respectively. The lowest values of growth vigor were also revealed in Syrian-1, Waha and Knd1149//68/ward (Table 3). The highest number of seeds per spike in  $F_1$  hybrids presented in Gerdish  $\times$  Waha (36.50). The hybrid Waha  $\times$  Gerdish indicated the highest value of hundred seed weight (8.09 g). The range of seed yield per plant was from 1.25-12.13 (g/plant). The range of cold tolerance, coleoptile length (cm), radicle length (cm) and growth vigor were 2.5-20, 3-5.95, 5-22.5 and 1-5, respectively (Table 3). The

**Table 2.** Analysis of variance in a 6×6 complete diallel following Griffing' Method II Model I and estimation of genetic parameters.

Source of variation <sup>1</sup>	d.f.	Mean Square						
		SS	SY	HSW	NGS	CoL	RL	GW (%)
Replication	1	1.53 <sup>ns</sup>	0.55	0.34	51.68	0.001	80.79	0.001
Genotype	35	67.74 <sup>**</sup>	19.41 <sup>**</sup>	4.39 <sup>*</sup>	51.19 <sup>**</sup>	0.83	28.45	0.08
GCA	5	80.06 <sup>*</sup>	29.55 <sup>**</sup>	4.78	82.02 <sup>*</sup>	0.71	11.74	3.37
SCA	15	62.05 <sup>*</sup>	14.81 <sup>*</sup>	4.42 <sup>*</sup>	43.79 <sup>*</sup>	1.17	23.81	2.85
REC	15	82.35 <sup>**</sup>	20.64 <sup>**</sup>	4.21	48.32 <sup>*</sup>	0.53	38.67	3.33
Error	35	30.53		2.25	22.28	0.67	32.11	1.94
Baker ratio	-	0.32		0.06	0.29	0.07	0.04	0.15

<sup>\*\*</sup> and <sup>\*</sup> indicate significant at 1% and 5% levels.

GCA, general combining ability; SCA, specific combining ability; REC: reciprocal effect.

SS: number of seeds per spike; HSW: hundred seed weight; SY: seed yield; NGS: number of germinated seeds; CL: coleoptile length; RL: radicle length; GV: growth vigor.

average values of these traits in durum wheat are very variable.

Mid-parent heterosis (MPH) was measured for all of the traits (Table 4). The positive value of heterosis indicated an ideal hybrid vigor. Some of hybrids including Chehel daneh×Zardak, Gerdish×Chehel daneh, Gerdish×Zardak, Zardak×Chehel daneh, Zardak×Knd1149//68/ward, Syrian-1×Chehel daneh and Waha×Knd1149//68/ward indicated the positive and significant heterosis for cold tolerance. The crosses including Chehel daneh×Zardak, Chehel daneh×Waha, Gerdish×Waha, Zardak×Chehel daneh, Zardak×Waha, Syrian-1×Zardak and Waha×Zardak indicated positive and significant heterosis for the number of seeds per spike. The hybrids that had positive and significant heterosis for hundred seed weight comprised Chehel daneh×Zardak, Chehel daneh×Waha, Zardak×Chehel daneh, Zardak×Gerdish, Zardak×Waha, Syrian-1×Zardak, Waha×Zardak and Waha×Knd1149//68/ward. The hybrids Syrian-1×Zardak and Zardak×Gerdish had the positive and significant MPH for coleoptile and radicle length, respectively. None of hybrids showed positive heterosis for growth vigor. The positive and highest values of MPH for seed yield were revealed in Zardak×Waha hybrid. The crosses containing Chehel daneh×Zardak, Chehel daneh×Waha, Gerdish×Zardak, Zardak×Chehel daneh, Syrian-1×Zardak, Waha×Zardak, Waha×Knd1149//68/ward and Knd1149//68/ward×Zardak also indicated positive and significant heterosis for seed yield.

### Biplot analysis

#### One Hundred seed weight

Principal component analysis of biplot for one hundred seed weight indicated that two first principal components explained 44.1% and 26.7% of the total variation, respectively (Figure 1a). Thus, the entry PC1 scores should approximate the GCA effects and displays the groups of parents relative to GCA. The PC2 indicates the non proportional interactions between entries and testers, as the testers assumed different signs. Specifically, PC2 displays positive interactions between heterotic groups. Less variation explained by the biplot implies that some predictions based on the biplot will be less accurate (Yan and Hunt 2002). Thus, the high values of PC1 and PC2 show a more accurate result than biplot. The average tester coordinate indicates that entries Zardak and Knd1149//68/ward had positive GCA effects (order also indicates ranking order), whereas entries Chehel daneh, Syrian-1, Gerdish and Waha had negative GCA effects (Figure 1a). Positive values for the GCA effects revealed a contribution to better parents for improving one hundred seed weight. Waha had the highest negative GCA effect for hundred seed weight, whereas Zardak had the highest positive GCA and was a better parent for improving one hundred seed weight. The GCA effects of the entries were in order of Zardak > Knd1149//68/ward > Chehel daneh > Syrian-1 > Gerdish > Waha. Entries Gerdish (according to the largest projection onto the ATC ordinate) and Knd1149//68/ward (regarding smallest projection onto the ATC ordinate) had the highest and lowest SCA effects, respectively. Three groups of entries obvious for hundred seed weight were: Gerdish which was above the PC2 guideline and Syrian-1, Waha and Chehel daneh which were below

**Table 3.** Average performance of some of traits in the six parents and their crosses.

Genotype	SS	HSW (g)	SY(g/plant)	NGS	CL(cn)	RL(cm)	GV(scale)
C	19.90	5.11	4.82	5.5	5.78	16.64	4.00
C*G	13.40	3.18	1.75	5	5.00	20.38	5.00
C*Z	23.05	5.66	7.35	13	5.40	14.13	5.00
C*S	17.85	4.75	3.82	3.5	5.09	14.98	4.00
C*W	28.60	6.47	7.95	5.5	5.80	21.45	4.00
C*K	19.91	5.07	4.05	3.5	4.66	17.07	5.00
G*C	22.00	5.67	6.22	20	5.32	12.88	4.00
G	30.15	6.80	10.33	2.5	5.04	13.65	4.00
G*Z	24.90	5.75	9.56	20	5.63	17.25	5.00
G*S	26.95	6.91	6.53	5	4.78	14.03	4.00
G*W	36.50	5.33	7.59	10.5	3.63	17.88	1.00
G*K	14.20	3.23	1.25	4	5.13	12.34	4.00
Z*C	31.24	6.56	9.21	14	4.82	12.60	4.00
Z*G	25.00	7.08	6.02	12.5	5.82	22.50	5.00
Z	10.81	2.18	0.98	6.5	5.35	9.92	5.00
Z*S	14.00	3.72	1.80	7	4.78	19.23	4.00
Z*W	24.90	6.70	6.83	6.5	5.28	18.75	3.00
Z*K	19.00	4.48	2.55	20	4.00	5.00	1.00
S*C	18.10	4.89	3.61	13.5	3.60	16.34	2.00
S*G	14.27	3.01	1.51	2.5	4.75	11.00	1.00
S*Z	24.10	5.45	4.97	8	5.95	12.39	3.00
S	16.87	3.44	2.13	3.5	4.30	14.72	3.00
S*W	20.93	3.28	1.72	2.5	4.97	17.40	4.00
S*K	19.90	3.97	2.22	5.5	4.62	18.15	3.00
W*C	18.71	5.32	2.29	5.5	4.76	14.85	3.00
W*G	18.43	4.79	2.99	7	3.00	11.00	2.00
W*Z	28.75	8.09	5.73	3.5	4.90	11.38	3.00
W*S	20.00	5.14	2.53	4.5	5.14	16.88	5.00
W	18.30	3.82	1.68	3	5.73	16.52	3.00
W*6	26.70	7.63	12.13	14	4.85	20.49	5.00
K*C	21.63	4.39	3.25	5.5	5.55	11.65	3.00
K*G	31.10	7.56	10.04	9	5.10	11.50	1.00
K*Z	23.75	6.01	7.11	6	5.13	19.05	4.00
K*S	14.70	3.58	1.57	3.5	4.75	16.60	3.00
K*W	19.43	4.88	2.94	5	5.25	12.69	2.00
K	24.40	6.65	8.90	7	4.78	19.88	3.00
Mean±SE	21.73±0.97	5.18±0.25	4.89±0.52	7.60±0.84	4.95±0.11	15.36±0.63	3.44±0.21
LSD5%	11.22	3.05	3.48	5.06	0.65	3.77	1.25

LSD5%: Least Significant Differences at 5% probability Level.

C: Chehel daneh; G: Gerdish; Z: Zardak; S: Syrian-1; W: Waha; K: Knd1149//68/ward. SS: number of seeds per spike; HSW: hundred seed weight; SY: seed yield; NGS: number of germinated seeds; CL: coleoptile length; RL: radicle length; GV: growth vigor.

the PC2 guideline. Knd1149//68/ward and Zardak which were located in the positive section of two PCs, seem to belong to the third heterotic group (Figure 1a). The current grouping of varieties appears to be justified by the lowest heterotic effects of the within-group crosses. Therefore, crosses such as [Z] × [W, S] and [Ch] × [Z] are expected to indicate heterosis defined as better than mid-parents (Table 4). Waha were the best

testers in this dataset, as it was very close to the ideal tester. On the contrary, Zardak and Gerdish were the poorest testers (the biplot were not shown).

Entries Gerdish, Knd1149//68/ward, Zardak and Waha which were located farthest from the origin, defined a polygon that was divided into four sectors (Figures 2a). The best hybrid combination in a sector would be between the entry at the vertex of the polygon and

**Table 4.** Estimates of percentage of mid-parent heterosis.

I	J	(F1-MPV)/MPV						
		CTL	SS	HSW	CL	RL	GV	SY(plant)
C	G	25.00	-46.45**	-46.59**	-7.58	34.56	25.00	-76.91**
C	Z	116.67*	50.14*	58.46*	-2.96	6.40	11.11	153.24**
C	S	-22.22	-2.90	11.14	0.89	-4.43	14.29	9.98
C	W	29.41	49.74*	45.03*	0.78	29.41	14.29	144.39**
C	K	-44.00	-10.14	-13.76	-11.80	-6.52	42.86	-41.01*
G	C	400.00**	-12.09	-4.85	-1.76	-14.97	0.00	-17.95
G	Z	344.44**	21.60	30.24	8.28	46.40	11.11	69.08**
G	S	66.67	14.64	34.86	2.25	-1.11	14.29	4.81
G	W	281.82*	50.67**	0.33	-32.68**	18.51	-71.43**	26.33
G	K	-15.79	-49.77**	-55.02**	4.43	-26.41	14.29	-86.99**
Z	C	133.33**	103.48**	83.68**	-13.48	-5.08	-11.11	217.50**
Z	G	177.78**	22.09	60.36**	11.93	90.96**	11.11	6.49
Z	S	40.00	1.19	36.01	-1.04	56.11	0.00	15.44
Z	W	36.84	71.10**	129.08**	-4.78	41.88	-25.00	412.48**
Z	K	196.30**	7.94	3.23	-20.99*	-66.43**	-75.00**	-48.28*
S	C	200.00**	-1.54	14.42	-28.57**	4.21	-42.86	3.77
S	G	-16.67	-39.32**	-41.21*	1.71	-22.44	-71.43**	-75.73**
S	Z	60.00	74.20**	99.27**	23.32*	0.57	-25.00	219.10**
S	W	-23.08	19.04	-9.51	-1.00	11.43	33.33	-10.06
S	K	4.76	-3.55	-21.31	1.71	4.94	0.00	-59.72**
W	C	29.41	-2.04	19.14	-17.38	-10.41	-14.29	-29.57
W	G	154.55	-23.94	-9.77	-44.29*	-27.07	-42.86	-50.25**
W	Z	-26.32	97.56**	176.65**	-11.55	-13.92	-25.00	329.86**
W	S	38.46	13.75	41.56	2.49	8.07	66.67*	32.46
W	K	180.00**	25.06	45.82*	-7.66	12.59	66.67*	129.42**
K	C	-12.00	-2.37	-25.35	5.16	-36.18	-14.29	-52.58**
K	G	89.47	14.02	12.42	3.92	-31.39	-71.43**	4.39
K	Z	-11.11	34.92	38.42	1.23	27.90	0.00	43.92*
K	S	-33.33	-28.75	-29.14	4.68	-4.02	0.00	-71.55**
K	W	0.00	-8.99	-9.60	-0.14	-30.28	-33.33	-44.38**
	MAX	400.00	103.48	176.65	23.32	90.96	66.67	412.48
	MIN	-44.00	-49.77	-55.02	-44.29	-66.43	-75.00	-86.99
	MEAN	80.01	14.64	22.47	-4.50	3.11	-6.60	38.59
	SE	21.23	7.09	9.44	2.50	5.76	6.82	22.49

\*\* and \* indicate significant at 1% and 5% levels, respectively.

C: Chehel daneh; G: Gerdish; Z: Zardak; S: Syrian-1; W: Waha; K: Knd1149//68/ward. SS: number of seeds per spike; HSW: hundred seed weight; SY: seed yield; NGS: number of germinated seeds; CL: coleoptile length; RL: radicle length; GV: growth vigor; I: Female parent; J: Male parent.

the tester farthest from the origin. Entries and testers in the same sector represent good hybrid combinations and potential heterotic groups (Krishnamoorthy 2005). In sector Gerdish, the best hybrid combinations were the vertex Gerdish (entry) × Knd1149//68/ward (tester) and Gerdish (entry) × Zardak (tester). In sector Waha, the best hybrid was the vertex Waha × Gerdish. The best hybrid, in sector Zardak, was the Zardak × Waha and Zardak × Syrian-1 (Figure 2a).

#### Coleoptile length

Biplot analysis of coleoptile length indicated that entries Zardak, Gerdish, Chehel daneh and Waha had positive GCA effects, While Knd1149//68/ward and Syrian-1 had negative GCA effects (Figure 1b). An entry with positive GCA effect is a sign of its contribution to an increase in coleoptile length in its offspring. Waha exhibited the highest GCA effect. The relative ranking of entries based on GCA effects were Waha ≈ Chehel daneh > Gerdish = Zardak > Syrian-1 > Knd1149//68/ward (Figure 1b). Furthermore, the biplot explained

64.7% (PC1 = 36.7% and PC2 = 28%) of total variation that would be partitioned into GCA effects of the parents and SCA effects of the crosses in conventional analyses (Figure 1b). Based on the guidelines advertised by Yan and Kang (2003), Chehel daneh was the best entry in the data set because it lies closest to the ATC axis, and is the most discriminating. Knd1149//68/ward was the poorest entry for coleoptile length as it falls farthest from the ideal center of the concentric circles. The distance between the x axis and a genotype in the biplot is an estimation of its SCA effect (Yan and Hunt 2002). All entries clustered near the x axis, indicating that SCA effects were not important. Entries and testers that located in same side of the x axis were positive SCA effects and the entries and testers in different side of the x axis, indicating negative SCA effects. Entries contain Gerdish and Waha had large SCA effects relative to the other entries. The other entries including Chehel daneh, Zardak; Syrian-1 and Knd1149//68/ward had the smallest SCA effect since it had the smallest projection onto the ATC ordinate (Figure 1b). Three potential heterotic groups were identified in the biplot for coleoptile length. The first group included Chehel daneh and Waha, the second group included Gerdish and Zardak, and the third group included Syrian-1 and Knd1149//68/ward.

Entries Knd1149//68/ward, Waha and Gerdish defined a polygon that was divided into three sectors (Figure 2b). In sector Waha, the vertex entry Waha showed a high response in hybrids with Chehel daneh and Knd1149//68/ward as a tester. The vertex entry Gerdish showed a high response in hybrids with tester Zardak. In other sectors the vertex entries did not show responses with any of testers (Figure 2b).

#### Number of germinated seeds

A principal component analysis of biplot for the number of germinated seeds influenced by cold, indicated that 78.9% of variation was explained with PC1 = 49.8% and PC2 = 29.1% (Figure 1c). Figure 1c shows that entries Zardak, Knd1149//68/ward and Chehel daneh had the positive GCA effects, whereas entries Syrian-1, Waha and Gerdish had the negative GCA effect. The GCA effects of the entries are in order of Chehel daneh > Knd1149//68/ward > Zardak > Gerdish  $\approx$  Waha > Syrian-1 (Figure 1c). Chehel daneh had the highest positive GCA effect and Syrian-1 had the highest negative GCA effects. Entries Zardak and Knd1149//68/ward had the highest SCA effects, and Syrian-1 and Waha had the smallest SCA. Entry Zardak interacted positively with Chehel daneh, Gerd-

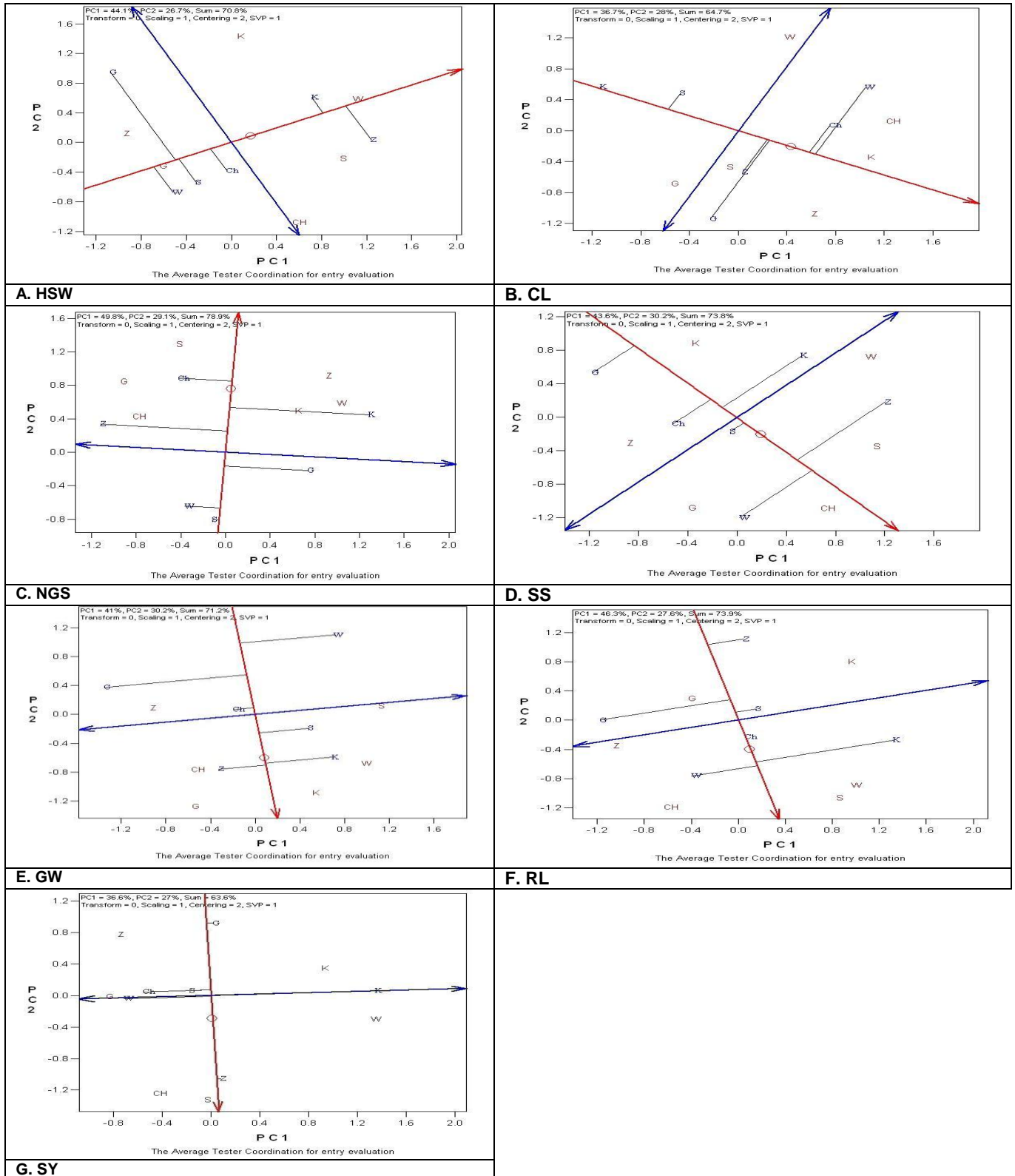
ish and Syrian-1, but negatively with other entries. Based on the proximity of Chehel daneh to the ATC abscissa and its vector length, it is the best entry for the number of germinated seeds (Figure 1c).

The tester vector view helps visualize the heterotic groups. The testers seem to fall into six groups. In the first group, Zardak had the significant heterosis with Chehel daneh and Gerdish. In the second group, Chehel daneh had the highest heterosis with Syrian-1. In the third group, Knd1149//68/ward had the significant heterosis with Zardak and Waha (Figure 2c and Table 4). Entries contain all of the genotypes defined a polygon that was divided into six sectors (Figure 2c). In the first sector, the best hybrid combinations were the vertex Zardak (entry)  $\times$  [Chehel daneh and Gerdish (as testers)]. Chehel daneh had the best mating partner with Syrian-1. In the third sector, the best hybrids were obtained from crosses between Knd1149//68/ward  $\times$  [Zardak and Waha]. This is consistent with the data provided by the table of heterosis (Table 4).

#### Number of seeds per spike

Both principal components 1 and 2 explained 73.6% of the observed variation for the number of seeds per spike (43.6% and 30.2%, respectively, for PC1 and PC2). These values revealed that biplot is effective for considering genotype structure of this trait. The corresponding biplot (Figure 1d) indicated that entries Syrian-1, Zardak and Waha had positive GCA effects. The other entries containing Chehel daneh, Knd1149//68/ward and Gerdish had negative GCA effects. The relative ranking of GCA effects provided by biplot analysis is Waha > Zardak > Syrian-1 > Knd1149//68/ward > Chehel daneh > Gerdish. The distance between the ATC abscissa and a genotype is an estimation of its SCA effect. Entry Zardak had the highest SCA effects followed by Knd1149//68/ward and Waha. It interacted positively with Syrian-1, Waha and Knd1149//68/ward, but negatively with the other testers. Based on its proximity to the ideal tester center and the length of its vector, Waha appears to be the best general combiner, while Knd1149//68/ward is considered to be the poorest general combiner based on its proximity to the ATC abscissa (Figure 1d).

The polygon view of the biplot for the number of seeds per spike provided four sectors (Figure 2d). In the sector of Gerdish, the testers contain Knd1149//68/ward and Zardak produced the best combinations with Gerdish. The Zardak sector contained testers Waha and Syrian-1. In the Waha sector, Chehel daneh and Gerdish were as the best testers. According



**Figure 1.** Biplot graphs based on diallel data in six durum wheat varieties for average tester ordination view (SCA and GCA of parents).  
 C: Chehel daneh; G: Gerdish; Z: Zardak; S: Syrian-1; W: Waha; K: Knd1149//68/ward. SS: number of seeds per spike; HSW: hundred seed weight; SY: seed yield; NGS: number of germinated seeds; CL: coleoptile length; RL: radicle length; GV: growth vigor.



to the polygon view, Waha  $\times$  Chehel daneh is predicted to be the best combination. While in the Zardak sector, crosses Zardak  $\times$  [Waha and Syrian-1] showed significant MPH values (Table 4).

### Growth vigor

The first two principal components together explained 71.2% (41 and 30.2%, respectively) of the variation for growth Vigor. The biplot revealed entries containing Syrian-1, Knd1149//68/ward and Zardak had positive GCA effects. Negative GCA effects were observed in Waha, Gerdish and Chehel daneh (Figure 1e). The relative ranking of GCA effects provided by the biplot is Knd1149//68/ward  $\approx$  Zardak  $>$  Syrian-1  $>$  Chehel daneh  $>$  Gerdish  $>$  Waha. Entries Chehel daneh had the smallest SCA effect, since it had the smallest projection onto the ATC ordinate. Waha and Gerdish had the highest SCA according to their projection onto the ATC ordinate and vector length (Figure 1e). The tester vector view, identified three groups including Syrian-1, Waha and Knd1149//68/ward as the first group; Chehel daneh and Gerdish as the second group; and Zardak as the third group.

Entries Gerdish, Waha, Knd1149//68/ward and Zardak defined a polygon that was divided into three sectors (Figure 2e). In the first sector, the vertex entry Gerdish indicated a high response in hybrids with Zardak. The vertex entry Waha showed a high response in hybrids with Syrian-1 as a tester. In the third sector, the vertex entry Knd1149//68/ward revealed high responses with Waha. In the other sector, Zardak had the best combination with Gerdish and Chehel daneh (Figure 2b).

### Radicle length

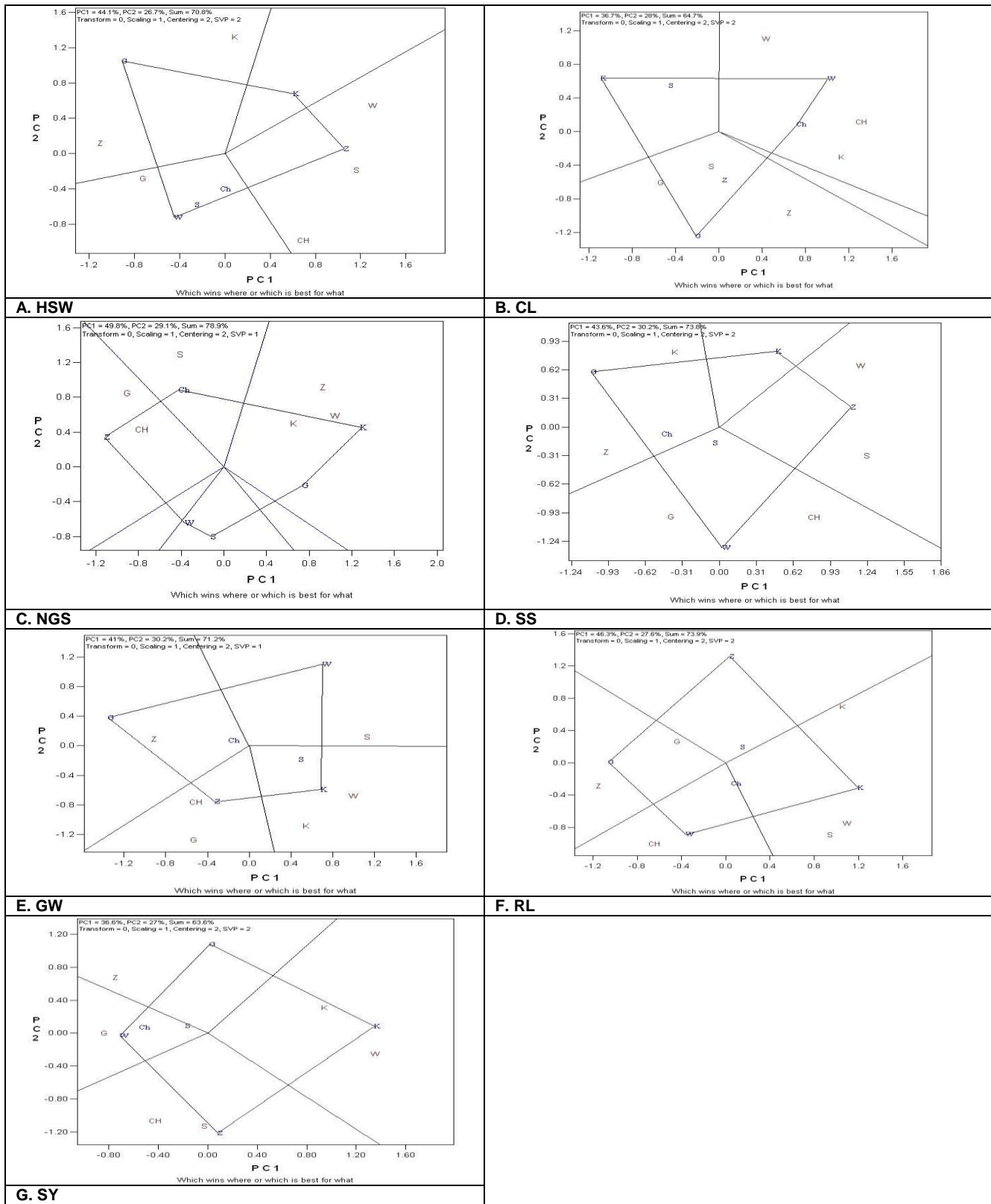
The first two principal components explained 73.9% (46.3 and 27.6% by PC1 and PC2, respectively) of the variation of radicle length. The average tester coordinate biplot indicates that entries Waha, Knd1149//68/ward and Chehel daneh had positive GCA effects, whereas Syrian-1, Gerdish and Zardak had negative GCA effects (Figure 1f). The relative ranking of GCA effects provided by the biplot analysis is Waha  $\approx$  Knd1149//68/ward  $>$  Chehel daneh  $>$  Syrian-1  $>$  Gerdish  $>$  Zardak. Entries Knd1149//68/ward, Gerdish and Waha had the highest SCA effects; while Chehel daneh and Syrian-1 had the lowest SCA effect. Parents including Zardak, Gerdish and Syrian-1 were particularly poor testers. The testers seem to fall into four groups according to the tester vector view: Zardak and Chehel daneh in group 1; Syrian-1 and Waha in group 2; and Gerdish and Knd1149//68/ward in the other two groups, separately.

The biplot in Figure 2f is divided into five sectors, with entries Gerdish, Zardak, Knd1149//68/ward and Waha as the vertex. Testers Gerdish and Zardak fell into Gerdish sector, indicating that its crosses with Zardak generated good hybrid combinations. High values of MPH for these crosses were observed (Table 4). The vertex entry Knd1149//68/ward showed a high response with Knd1149//68/ward, Waha and Syrian-1 as testers. Sector Waha contained good hybrid combinations with Chehel daneh.

### Seed yield

The first two principal component axes in the biplot for seed yield explained 36.6% and 27% of total variation, respectively (Figure 1g). Less variation explained by the biplot implies that some predictions based on the biplot will be less accurate. Therefore, it would be a good strategy to try to reduce the data size by removing redundant parents. Due to the low number of parents in the present study, removing some of them for increasing accuracy, can result in the loss of critical information. Therefore, with these values of cumulative percent of the first two PCs, the results were interpreted. The average tester coordinate biplot indicates that entry Zardak had positive GCA effects whereas Gerdish had negative GCA effects. The other genotypes had low GCA effect. A greater projection toward either direction means greater SCA effects. Thus, entries Waha and Chehel daneh, above the ATC abscissa, had the greatest SCA effects or largest projections onto the ATC ordinate. Below the ATC abscissa, entry Knd1149//68/ward had large SCA effects. Entries Zardak, Gerdish and Syrian-1 had the smallest SCA effect since had smallest projection onto the ATC ordinate (Figure 1g).

The testers are grouped by PC1 and PC2 scores. Three groups of testers are obvious: Chehel daneh and Syrian-1 with negative value of two PCs; Zardak with negative PC1 and above the PC2 guideline; Knd1149//68/ward with positive PC1 and above the PC2 guideline and Waha with positive PC1 and below the PC2 guideline. Moreover, above the guideline, testers Knd1149//68/ward and Waha interacted positively with entries Gerdish, Zardak, Knd1149//68/ward and Waha. Similarly, below the guideline, testers Gerdish, Zardak, Chehel daneh and Syrian-1 interacted positively with entries Waha, Chehel daneh and Syrian-1. Entries Waha, Gerdish, Knd1149//68/ward and Zardak which are located farthest from the origin, defined a polygon that was divided into five sectors (Figure 2g). In sector Waha, the best hybrid combination was the vertex Waha (entry)  $\times$  Gerdish (tester). In the second sector, the best hybrid was the vertex Gerdish (entry)  $\times$



**Figure 2.** Biplot graphs based on diallel data in six durum wheat varieties for polygene view (best partier of parents). C: Chehel daneh; G: Gerdish; Z: Zardak; S: Syrian-1; W: Waha; K: Knd1149//68/ward. SS: number of seeds per spike; HSW: hundred seed weight; SY: seed yield; NGS: number of germinated seeds; CL: coleoptile length; RL: radicle length; GV: growth vigor.

Zardak (tester). Knd1149//68/ward  $\times$  Waha was the best hybrid in the third sector. This hybrid had the highest seed yield (Table 3) and positive heterosis (Table 4). In the other sector, the best hybrid was the crosses between Zardak (entry)  $\times$  [Syrian-1 and Chehel daneh (as testers)]. Potential heterotic groups for seed yield could involve crosses between cultivars consisting of Waha and Knd1149//68/ward as the first; Zardak as the second; Gerdish as the third and Syrian-1 and Chehel daneh as the 4<sup>th</sup> group. These are the best hybrids based on the data per se. The current grouping of varieties appears to be justified by the lowered heterotic effects of the within-group crosses (Table 4).

## DISCUSSION

Since yield and yield components are quantitative in nature, the estimation of the general and specific combining abilities and heterosis patterns contributes to a better understanding and enables rational and targeted combination of desirable genes into future cultivars (Butorac *et al.*, 2004). Baker's ratios for seed yield and other studied traits, suggests that non-additive genes were more important than additive for the control of yield. Preponderance of non-additive effects contributed to genetic control of grain yield has been reported by Chalish *et al.* (2011), Dere *et al.* (2006) and Mousavi *et al.* (2006). In this study, the parents with positive GCA are superior, whereas inferior varieties had negative GCA effects. The SCA effects that indicated in some crosses, involve both dominance and epistasis which together constitute the non additive type of gene action, whereas the GCA effects is a reflection of additive and additive  $\times$  additive type of gene action (Yan and Kang, 2003). The biplot approach allows a much better understanding of genetic constitution of parents for the analysis of diallel data and easily visualizes the GCA and SCA effects of each parent, the best crosses, the best testers, the heterotic groups and genetic constitutions of the parents (Yan and Kang, 2003). In this study, the GCA and SCA effects were significant in controlling the number of seeds per spike, seed yield, hundred seed weight and cold tolerance, and some of entries had significant GCA and SCA according to their graphical view. These results are in agreement with the report of Dere and Yildirim (2006), Barnard *et al.* (2002) and Joshi *et al.* (2004) which indicated both general and specific combining ability was significant for yield and yield components of wheat. Since the biplot displays a complete picture of interrelationships among parents, it provides a unique opportunity or possibility to peek into the genetic constitutions of the parents using the  $F_1$  rather than the  $F_2$  generation. In conventional analyses

of diallel data, interpretation of the genetic constitutions of parents with regard to the trait under investigation is not attempted until the  $F_2$  generation. The biplot provides a unique means to visualize the interrelationships among parents, and thus allows hypotheses to be formulated on the genetic constitution of parents (Yan and Kang, 2003). Sharifi and Safari Motlagh (2011) used biplot analysis method for studying cold tolerance at the germination stage in diallel crosses of rice and indicated the genetic constitutions of parents. Sharifi (2012) used graphic analysis to study the salinity tolerance traits of rice and indicated that parents with negative GCA were superior for salinity tolerance. Malla *et al.* (2010) also studied the combining ability for fusarium head blight resistance in wheat (*Triticum aestivum* L.) through the biplot method and showed that the ND2710/BacUp combination had the best healthy index and undamaged kernels.

Four groups were revealed relative to general combining ability (GCA) of genotypes for seed yield; group 1 contained entry Gerdish with negative GCA effect and group 2 included entries Chehel daneh, Syrian-1 and Waha, with the lowest GCA, minor differences among them and negative PC1; group 3 included entry Knd1149//68/ward, with the lowest GCA but positive PC1 and group 4 included entry Zardak, with the largest GCA. The GCA of the second and third groups was very close together, but was different to that of the first and fourth groups. Therefore, to explain the differences in GCA, we hypothesized that group 2 and 3, according to their differences compared to group 1, had two additive genes (A1 and A2) with additive epistatic effects (A1A2) relative to group 1; and group 4 had an additional gene (A3) relative to group 2 and 3. PC2 displays the non-proportional interactions between entries and testers, as the testers assumed different signs (Crossa and Cornelius, 1997; Yan *et al.*, 2000). Specifically, PC2 indicates positive interactions between three heterotic groups: Zardak as the first group; Knd1149//68/ward, Chehel daneh, Syrian-1 and Waha as the second group and Gerdish as the other. If we suppose that heterosis arises from the accumulation of different dominant genes, then Zardak and Gerdish must have different genes that are designated as D1 and D2. Entries Knd1149//68/ward, Chehel daneh, Syrian-1 and Waha, as the second group, with low PC2, implying that there was no non-proportionate interaction between this group and either of the other two groups. The entries in the second group carries an additive gene that is different to both D1 and D2, or both D1 and D2. This grouping can explain the observed heterosis between Zardak and Gerdish due to the presence of D1 and D2 genes in

this hybrid. The integrated findings of GCA and SCA grouping of the six parents explains their performance as pure lines and the performances of their hybrids. The hybrid between Knd1149//68/ward and Waha was the best hybrid for seed yield, because it integrated the four resistance genes (A2, D1, D2 and probably D3). The superior hybrids combine all or most of genes through one of the two pathways: 1) both parents exhibit high GCA but belong to different heterotic groups, and 2) one high GCA parent and one superior tester. The GCA effects indicate that Zardak was an ideal general combiner for hundred seed weight, coleoptile length, cold tolerance, number of seeds per spike, growth vigor and radicle length.

## CONCLUSION

The information obtained from this experiment can facilitate the identification of the best parents and crosses by GCA and SCA effects. The heterosis values observed and the performance of crosses, suggested that some varieties have potential as breeding material to select genotypes with improved durum wheat yield and yield components. Crosses including Knd1149//68/ward × Waha and Zardak × Chehel daneh exhibited the highest level of seed yield and significant heterosis for this trait. Cross Waha × Zardak was superior for hundred seed weight. The best crosses for improving number of germinated seeds were Zardak × Chehel daneh and Zardak × Gerdish. Zardak × Waha was the best cross for improving the number of seeds per spike. Zardak, Knd1149//68/ward and Gerdish can be used either as the best parents for selection programs based on their GCA effects, or as a superior parent hybrid programs on their SCA effects.

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