

ARTICLE

Using of GGE biplot in determination of genetic structure and heterotic groups in wheat (*Triticum aestivum* L.)

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ABSTRACT The present study was undertaken to analyze diallel data using GGE biplot model to gather information about genetic interrelationships among parents and identification of heterotic combinations for yield and yield components in bread wheat varieties. For this purpose, 8 bread wheat genotypes tested across in half-diallel crosses design, GGE biplot technique was used. Parents included the genotypes of Kouhdasht, Karim, Ehsan, Mehregan, N-92-9, Line 17, N80-19 and Atrak. The hybrids obtained from the one-way cross (28 hybrids) in agricultural years of 2016-17 were evaluated as randomized complete block design in two replications on the research farm of Gonbad Kavous University. The evaluated traits included the grain yield, weight of spike grains, number of grains in spike and number of spikes. Additive main effects and genotype × environment interaction (GGE) were employed in the evaluation of genotypes; analyses showed significant ($P < 0.01$) $G \times E$, (genotype × environment interaction) with respect to plant seed yield. GGE biplot analysis showed that Karim was as the best general combiners for grain yield, number grain per spike and grain weight per spike, whereas Ehsan had the highest GCA effects for number of spikes. Ehsan and Karim had higher specific combining ability than other genotypes. The studied genotypes for this trait were divided into two heterotic groups where the first group included the genotypes of Kouhdasht, N-92-9, N80-19 and Atrak and the second group contained the genotypes of Line 17, Mehregan and Karim. Mehregan line had a weak combining ability with all testers and N-92-9 had also more power than others. Based on the biplot, the Karim genotype with high general adaptation was introduced as the ideal genotype in terms of grain yield, spike number, grain number per spike and grain weight, so the Karim genotype can be adapted to obtain high yield hybrids.

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KEY WORDS

GGE biplot
general combining ability
heterotic group
hybrid
specific combining ability
Triticum aestivum L

ABBREVIATIONS

GGE: Genotype, Genotype by Environment interactions
SCA: Specific Combining Ability
GCA: General Combining Ability
GNP: Number of grains in plant
GNS: Number of grains in spike
WSG: Weight of spike grains
YLD: grain yield

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Introduction

Grain yield is a complex trait outcome from several genes and their interaction with environment. Due to self-pollination nature of wheat and homozygosity of many loci, it is necessary to introduce different genes, which are known to be yield contributor (Ullah et al. 2010).

To breed the agricultural high-yielding genotypes like wheat, the comprehensive information on the confluence parents' genetic structure as well as the inheritance and desired combining ability of their traits. This is realized by using the quantitative genetic techniques including the diallel crosses (Biriay et al. 2017).

Heritability is among the most important properties of

a quantitative trait because phenotype in quantitative traits is the result of inheritance and environment. Importance of heritability of a trait lies behind the determination of techniques selected for population breeding, inbreeding and other aspects of selection; the heritability, hence, is among the primary goals of genetic study of a quantitative trait. Identifying the effective factors in heritability allows the breeders to design a breeding plan in such a way that the genetic improvement is maximized using the existing resources. Heritability is of two general and specific types. The latter is the ratio of total genotype variance to the phenotype variance and the former is defined as the ration of additive genetic variance to the phenotype variance. The specific heritability measures the relative importance which is transferred to the next generation of

progenies; therefore, it is a more appropriate criterion for predicting the expected efficiency from selection. Mass selection for the traits with higher specific heritability is more effective (Sabouri and Mohammadi-Nejad 2009).

Diallel crosses are used in genetic studies for determining the heritance of trait among a set of genotypes and for identifying the better parents in order to produce the hybrid genotypes or agricultural varieties. The findings of this breeding method help to breeders for generating superior hybrids (Dehghani et al. 2013). Common analysis of diallel data is limited to the division of changes in all crosses, general combining ability (GCA) of each parent and specific combining ability (SCA) of each cross. Specific effects are belonging to the crosses and do not give much information about the parents. Diallel crosses data can be analyzed by principal component (PC) biplot techniques following Yan and Hunt (2002). Biplot approach to diallel data analysis provides a much better understanding from the parents. For a set of definite data, they provide information such as GCA impact of each parent, SCA impact of each parent (not every cross), the best testers, heterotic groups and parents' genetic structure regarding the studied trait (Moghaddam et al. 2012).

Biplot technique was firstly proposed by Gabriel (1971) and a proper graphic method was introduced to analyze data by other scientists (Crossa et al. 2002; Gauch 2006). Biplot technique is usually designed for regional experiments, but it is also possible to use it based on reciprocal data of genotype-tester. This method is based on the values of main components corrected using the mean tester. This new approach provides a graphical demonstration of the data using principle components (PC1 and PC2) which are obtained through principle component analysis (Yan and Hunt 2002). Different investigators on different plants, investigated the results of diallel crosses by Biplot technique and determined the heterotic groups and then reported a good consistency between the results of Griffing method and Biplot graphic method (Khalil and Raziuddin 2017; Ali et al. 2017; Dogan 2016; Kendal et al. 2019; Adie et al. 2014; Khalil et al. 2010; Biriya et al. 2017; Sharifi and Safari Motlagh 2011; Sharifi 2013; Golkar et al. 2017; Ghotbi et al. 2018; Vanda and Houshmand 2011).

Tulu and Wondimu (2019) used biplot to investigate Ethiopian bread wheat varieties for stability of yield and identification of suitable genotypes compatible with South-western Ethiopia environment. According to the GGE biplot analysis of the two main components PC1 and PC2, 63.88 and 15.71% of the total GGE sum of squares were justified, and two growth environments were identified for wheat and ideal genotypes.

Sharifi et al. (2019) using GGE biplot approach indicated high narrow and broad sense heritabilities and heterosis of crosses for yield and some of morphological

traits in wheat.

Pagliosa et al. (2017) indicated GGE biplot as an effective method for visual comparisons of GCA and SCA effects and identifying superior spring wheat genotypes.

Sadeghzadeh-Ahari et al. (2014) also used biplot analysis for evaluation of diallel crosses of six varied-ties of durum wheat for yield and identified the ideal general combiner, the best crosses and heterosis patterns for seed yield and yield components.

Dehghani et al. (2013) evaluated the diallel data obtained from the crosses of 5 wheat genotypes and its 10 hybrids in the greenhouse with three pathotype namely 7E18A-, 38E0A+ and 134E134A+. Results showed that two main components of biplot are responsible for 95%, 94% and 85% of variation for pathotypes.

Rastogi et al. (2013) followed the GGE biplot model using the 5×5 diallel data to identify the specific alkaloids in (*Papaver somniferum* L.). For further investigation and approval of GGE biplot model accuracy, results obtained from the diallel analysis were compared with Griffing results. Three parents A (papline), B (NB5KR40-7/2-3) and E (58/1) were detected as the good general compounds.

Mostafavi et al. (2012) evaluated the analysis of 14 corn inbreed genotypes using the diallel method. GGE biplot model was used to extract the interaction among the genotypes and hybrids. Results showed that the specific combining ability of grain yield was higher than the general combining ability that indicting the significant impact of dominant genes in genetic controlling of grain yield. Results of biplot diagrams were mostly consistent with the Griffing's results.

Alam et al. (2017) evaluated eight wheat genotypes under the thermal stress conditions. Results of diallel analysis showed a significant difference for grain yield in probability level of 1% and determined some dominant genotypes. GGE biplot results showed a good consistency between the Griffing technique results and biplot graphic method.

To study the yield in terms of genetics and some agricultural traits in six genotypes of bread wheat, (Mostafavi and Zabet 2013) used the biplot of diallel data. To evaluate the genotypes' potential, GGE biplot graphic technique was used. The studied traits included the grain yield, spike weight, hundred grain weight, number of fertile tillers, spike length, awn length, peduncle length and plant height. The general and specific combining ability for all traits was significant in 1% probability level. For grain yield of Gascogne genotype was the best general combination; Gascogne, Gaspard, Ghods and Pishtaz hybrids has the highest specific combination. These results were confirmed by biplot graphic method.

Ruswandi et al. (2015) evaluated 138 F1 hybrids, 46 parents and 3 tester genotypes in Indonesia to analyze

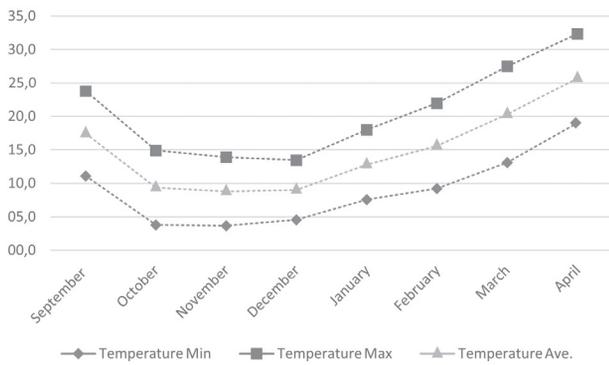


Figure 1. Temperature changes in the 2016-2017 crop season.

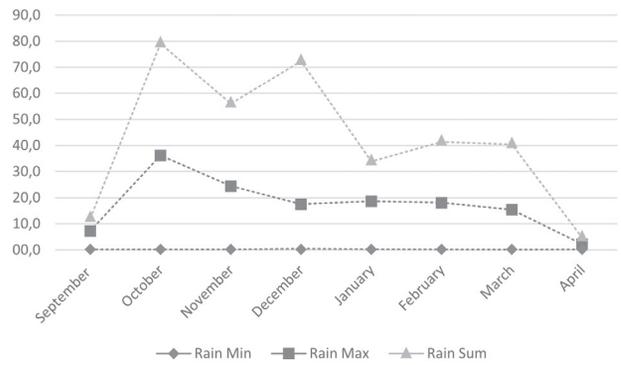


Figure 2. Raining changes in the 2016-2017 crop season.

the line × tester data and maturity time as well as grain yield using the GGE method to identify the genetic relations among the parents and the best combination in corn hybrid. High GCA effect was determined for maturity time and grain yield based on the average GGE biplot.

Graphic analysis of biplot shows the best input through the tester patterns and provides information such as GCA, SCA for each genotype, parents' heterotic groups, dominant hybrids and assumptions related to the genetics of genotypes; this is very important in terms of yield in increasing the products.

This study aims at the graphic determination of wheat diallel data to obtain the dominant hybrids using the biplot analysis for future research.

Material and Methods

Plant material

The present study was conducted in the research farm of Agricultural University of Gonbad Kavous (37° 15' N and 45° 46' E) during the 2017-18 within as the randomized complete block design in desired irrigation conditions in two replications. Parents and F₁ seeds were sown

on 5 December 2017 as four rows with the spacing of 20 cm between rows and 5 cm between plants on rows. Plots were separated from each other by 1 m. A 1.5 m alley was kept between blocks. The studied parents included 8 genotypes as: Atrak, Ehsan, Karim, Kouhdasht, Line 17, N-80-19 and N-92-9, taken from the Agriculture and Natural Resources Research and Training Center of Golestan Province (Table 1). The local climate is temperate; summers are hot and dry and winters are mild and rainy. Climatically, the region has warm and semi-arid climate. The rainfall and temperature within 2017-18 changes represented in Figure 1 and 2. To determine the physicochemical characteristics of the experimental site before conducting the experiment, soil samples were taken from the depth of 0-30 cm. The testing soil was of loam silty with acidity of 7.8 and electric conductivity of 1 dS/m with 1.5% organic materials and 18-19% of lime. The optimum nitrogen levels determined as 150 kg/ha N fertilizer. Half of N was added at planting time and rest was added during seed filling stage. Weed control was done manually during the growing season. Tebuconazole 25% EW 25 was used to control the rusts. Also, tebuconazole 2% was used to control common bunt, loose smut and

Table 1. Characteristics and pedigree of parents.

Cultivar	Characteristics	Pedigree
N-80-19	Late-stage, spring, high yield, susceptible to drought	SW89.3064.STAR...
KOHDASHT	Early-stage, spring, drought resistant	TR8010200
ATRAK	Spring, short, high tillers	Kauz"s"
EHSAN	Late-stage, spring, high yield, susceptible to drought	SABUF.7.ALTA...
N-92-9	Spring, drought resistant	KLCQ.ER2000..WBLL1
MEHREGAN	Spring, high yield	OASIS.SKAUZ..4*BCN.3.2*PASTOR
KARIM	Spring, suitable for rainy season	Hamam-4
LINE17	Early-stage, short	Jup.alds..att"s".vee"s".3....

powdery mildew. TILT 25% EC was applied for bacterial leaf streak and chaff black control. The studied cultivars were harvested on May 26, 2018.

Evaluated traits

Fifty plants were selected randomly and the number of spikes (GNP), number of grains in spike (GNS), weight of spike grains (WSG), and grain yield (YLD) were evaluated.

Data analysis

Genotype main effect plus genotype-by-environment interaction (GGE) biplots are 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:

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

where γ_{ij} is the genotypic value of the cross between entry i and tester j for traits; β_j is the average of all combinations consisting tester j ; λ_1 and λ_2 are the singular values for the first and second principal components (PC1 and PC2, respectively); ξ_{i1} and ξ_{i2} are the PC1 and PC2 eigenvectors, respectively, for entry i ; η_{j1} and η_{j2} are the PC1 and PC2 eigenvectors, respectively, for tester j ; and ϵ_{ij} is the residual of the model associated with the combination of entry i and tester j . Each genotype in diallel cross data is an entry and a tester, So, i and j can represent 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 of the biplots were developed using the GGE biplot software (Yan 2001).

Results and Discussion

Grain yield

GGE biplot analysis has been importance for the plant breeders because it will present the relationship between traits as visually (Oral 2018). In biplot analysis of diallel data, every genotype was taken both as the line and tester. In these diagrams, genotypes and testers are shown in italic and capital letters. To determine the parents' general combining ability in biplot analysis, the smaller circle shows the average tester obtained from averaging the PC1 and PC2 values of all testers. The line crossing the biplot origin and average tester with an arrow to the average tester is called the average tester axis or ATC horizontal axis and the line passing the biplot origin and orthogonal to the average tester axis is called the vertical axis of average tester or ATC vertical axis (Yan and Hunt

2002; Moghaddam et al. 2012).

GGE biplot is responsible for 63% percent of data variation for the grain yield (42% and 21% by PC1 and PC2 from the total variation). The total variation in common analyses of diallel are divided into parents' GCA effects and crosses' SCA effects (Fig. 3a, b, c, d).

Ehsan and Karim have minimum and maximum general combining abilities, respectively (Fig. 1a). The distance of each genotype from the vector of average testers estimates the specific combining ability and shows each genotype's tendency to generate dominant hybrids with some testers, not all of them; therefore, the Karim and Atrak genotypes on the bottom of ATC horizontal genotypes have the biggest SCA impacts on the ATC vertical axis. N-92-9 on top of horizontal line followed by line 17 had larger SCA effects than the Mehregan line. Since the N80-19 and Kouhdasht genotypes have the smallest image on the ATC vertical axis, they have the least specific combining ability impact.

In order to group the testers into heterotic categories, graph (1-b) was used. In this figure, two groups of testers including Ehsan, Kouhdasht and Atrak testers were on top of the dotted line PC2 and N80-19, Mehregan, Line 17, N-92-9 and Karim testers was on below the line PC2. Upper testers have positive interaction with N-92-9, Mehregan and Line 17. Similarly, testers of N80-19, Mehregan, Line 17, N-92-9 and Karim have positive interaction with Ehsan, Atrak, Kouhdasht and N80-19. This interaction pattern shows clearly the heterosis in crosses (Atrak, Ehsan and Kouhdasht) \times (Karim, Line 17, Mehregan, N80-19 and N-92-9). Therefore, we will have two different heterotic groups. Based on a study, it was found that genotypes and environments included in the same sector had a positive relationship and genotypes emerging in different sectors had a negative relationship (Islam et al. 2014).

An ideal tester should have two criteria: firstly, it should discriminate the genotypes better, secondly, it should have good yield. Based on this definition, an ideal tester should be located on ATC axis of which the vector should be higher than other testers so that it is considered as the most discriminating tester; such tester is observed in concentric circles and the more it is close to the center, the more it would be desired. N-92-9 is known as the best tester (Fig. 3c). In contrast, Karim tester is the most undesired tester and has the lowest value in terms of representativeness. The best testers are N-92-9, Line 17, Mehregan, N80-19, Ehsan, Kouhdasht, Atrak and Karim, respectively.

Polygon scheme of biplot helps the identification of best crosses between the genotypes and testers. Polygon includes straight genotypes which connect the farthest lies from biplot origin such that other genotypes are located

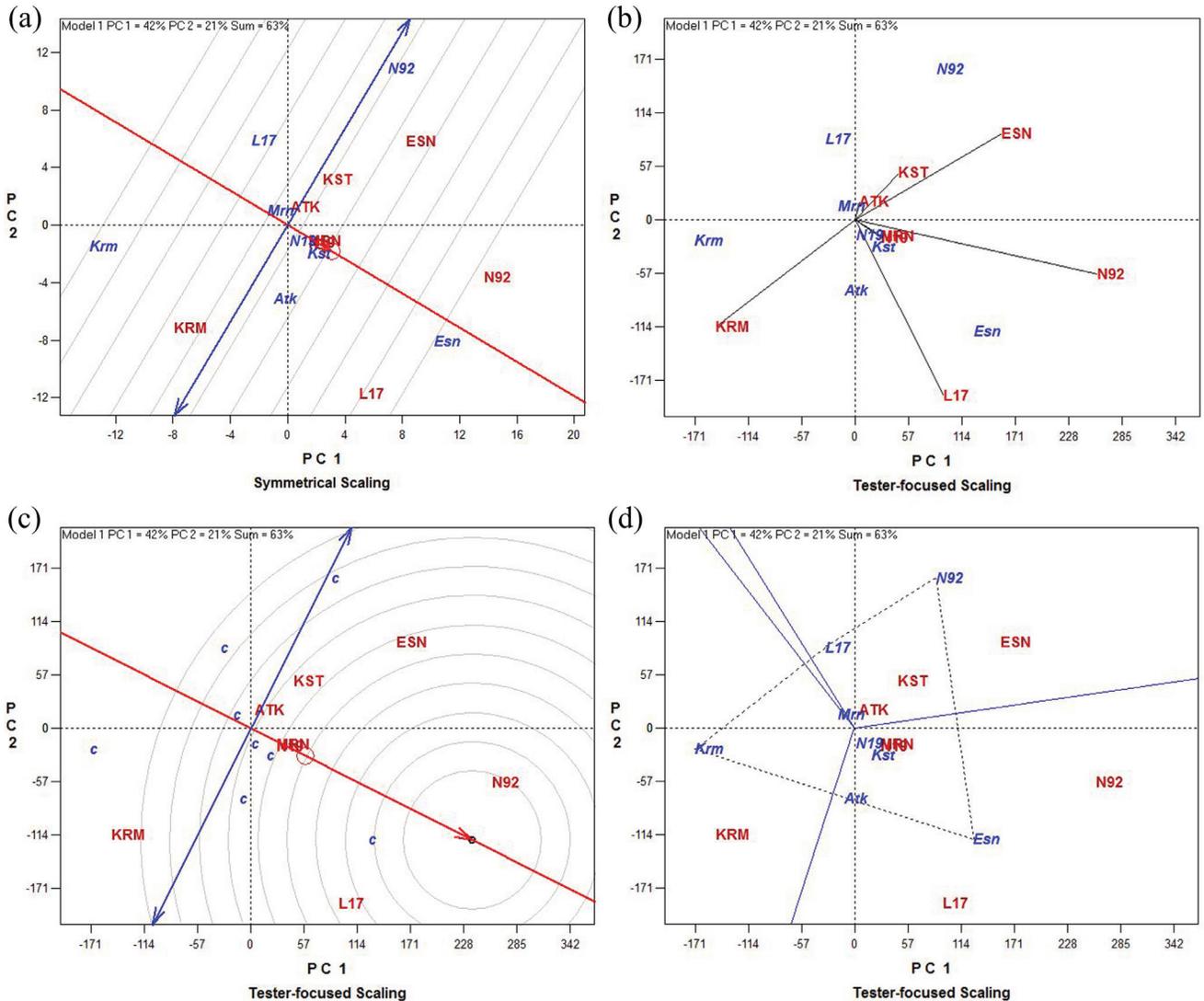


Figure 3. 2D diagram of diallel data for grain yield per m² for 8 genotypes of bread wheat. (a) position of genotypes, testers and average testers; (b) axis of average genotypes to determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. Small letters determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. The lowercase letters indicate the genotypes and the capital letter indicate the testers. Circle shows the position of average testers.

inside the polygon. Vertical genotypes on each polygon drawn from the biplot origin and expanding out of the polygon divide the biplot into several sections. Therefore, definition of (Fig. 3d) was divided into three sections in which the Karim, Ehsan and N-92-9 genotypes are on the vertex. N-92-9 line and Ehsan tester are on one angle and Ehsan line and N-92-9 tester on the other angle. This means that there are many combining abilities between genotypes of N-92-9 and Ehsan and their hybrid is so heterotic. Karim tester was besides the Karim line indicating this pure genotype should be better than all crosses related to Karim and as a result, heterosis between Karim

and any other parent would not be possible. Kouhdasht and Atrak testers, on one side, and Kouhdasht and Atrak genotypes, on the other side, are observable indicating the low combining ability of these genotypes together. Other researchers have confirmed the effectiveness of the biplot method in interpreting diallel data in wheat (Mostafavi and Zabet 2013; Motamedi and Safari 2017).

Weight of spike grain

The biplot diagram related to the spike grain weight was responsible for 82% of data variations. Therefore, by locating the genotypes in the positive and negative

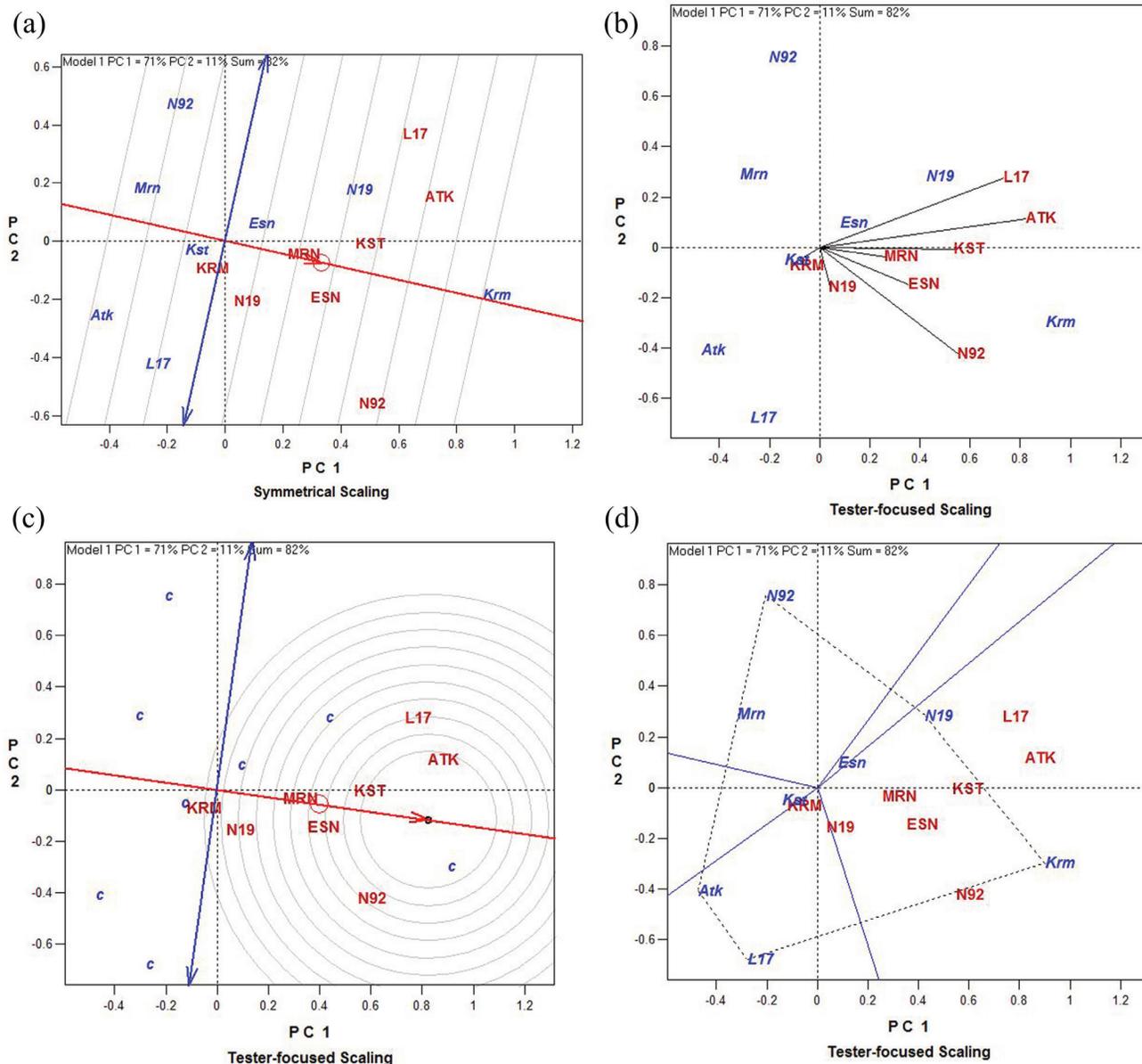


Figure 4. 2D diagram of diallel data for grain yield per m² for 8 genotypes of bread wheat. (a) position of genotypes, testers and average testers; (b) axis of average genotypes to determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. Small letters determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. The lowercase letters indicate the genotypes and the capital letter indicate the testers. Circle shows the position of average testers.

ends of testers average vector, maximum and minimum general combining abilities of genotypes would be Karim and Atrak, respectively. Concerning the distance of each line to the vector of average testers, genotypes of Line 17 and Atrak on the lower part of ATC horizontal axis and N-92-9 Line on top of horizontal line followed by N80-19 have larger SCA impact than others. Since the Karim has the smallest image on the ATC vertical axis,

they have the lowest specific combining ability (Fig. 4a). Concerning the testers of Line 17 and Atrak on top of dotted lone PC2 and testers of N80-19, Mehregan, Ehsan and Karim below the PC2 line, it seems that the despite locating on the line, Kouhdasht tester does not belong to these two heterotic groups (Fig. 4b). Upper testers have positive interaction with N-92-9, Mehregan, Ehsan and N80-19. Similarly, N80-19, Mehregan, N-92-9, Ehsan

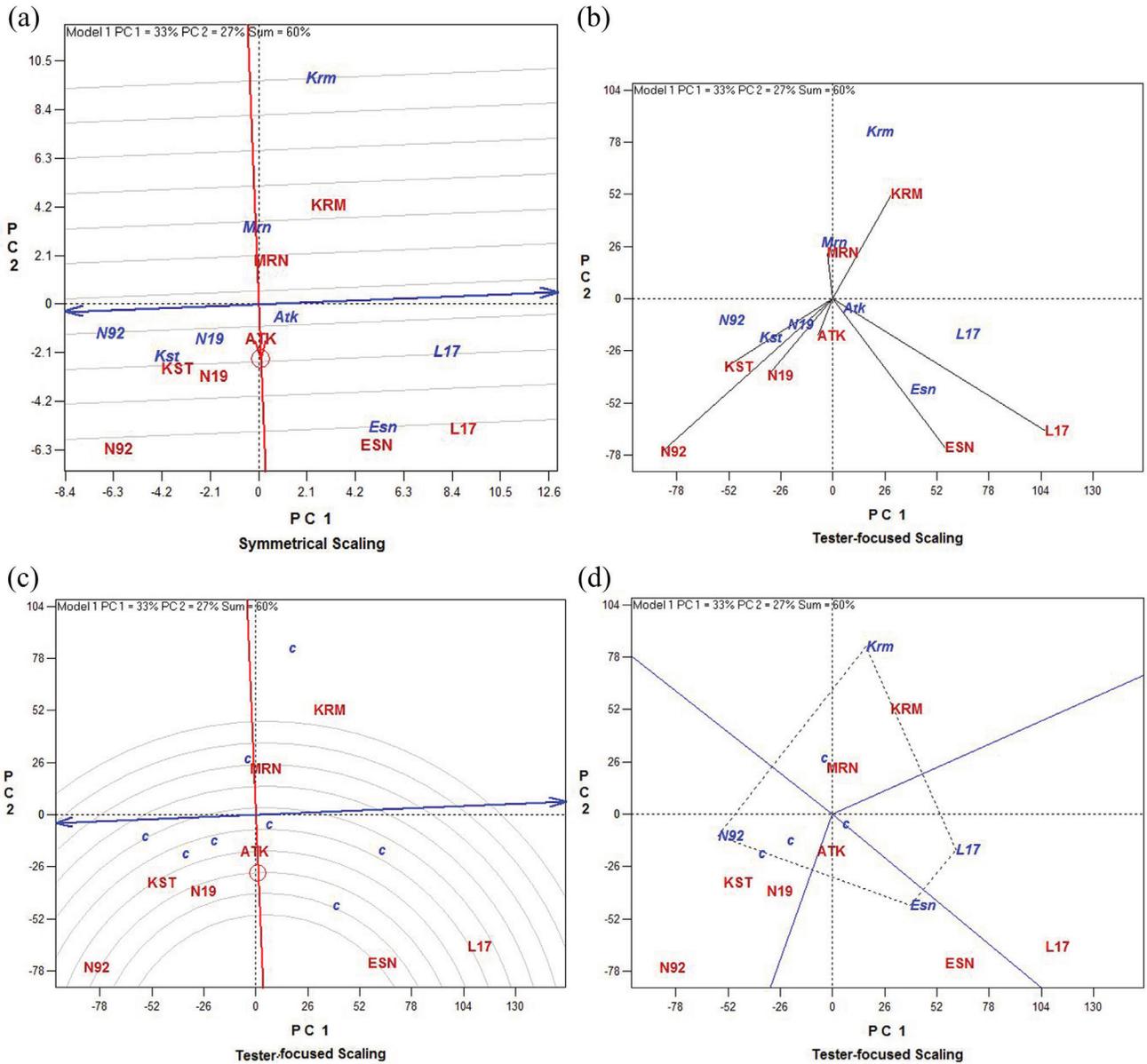


Figure 5. 2D diagram of diallel data for grain yield per m² for 8 genotypes of bread wheat. (a) position of genotypes, testers and average testers; (b) axis of average genotypes to determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. Small letters determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. The lowercase letters indicate the genotypes and the capital letter indicate the testers. Circle shows the position of average testers.

and Karim testers have also positive interactions with Karim, Kouhdasht, Atrak and Line 17. This interaction line clearly shows the heterosis in crosses (Atrak & Line 17) × (N-92-9, Ehsan, Karim, N80-19 and Mehregan). Therefore, we have two different heterotic groups.

Atrak tester is known as the best tester (Fig. 4c). In contrast, Karim tester is the most undesired tester and has the lowest value in terms of representativeness. The

testers are ranked as: Atrak, Kouhdasht, Line 17, N-92-9, Ehsan, Mehregan, N80-19 and Karim, respectively.

Karim, Atrak, Line 17, N-92-9 genotypes were located on the vertex (Fig. 4d). Hence, we have 4 groups of genotypes. No tester was seen in Line 17, Atrak and N-92-9. Consequently, these genotypes are not the best cross pairs with no genotypes and generate the worst hybrids by some testers or all of them. One N-92-9 tester was besides the

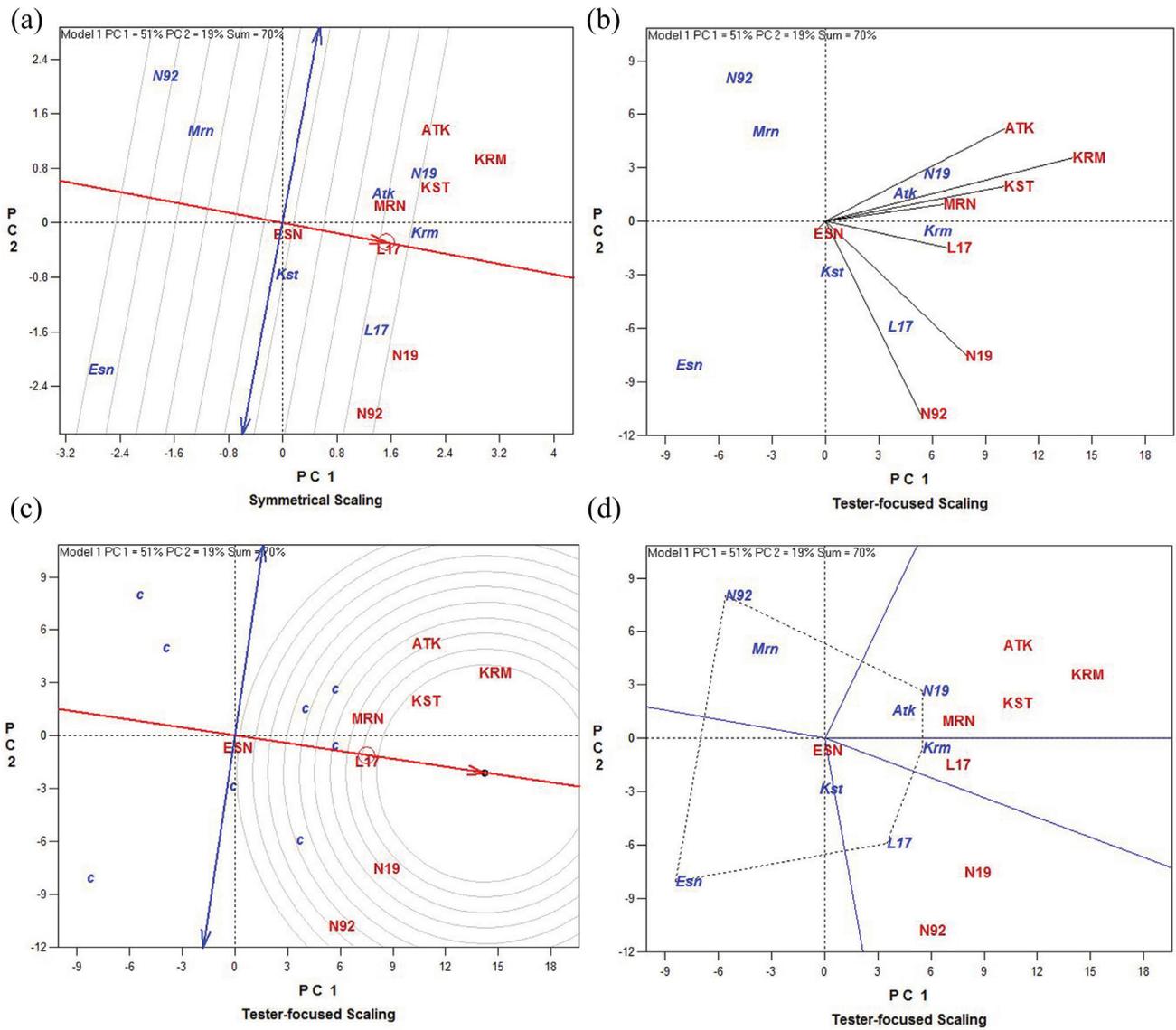


Figure 6. 2D diagram of diallel data for grain yield per m² for 8 genotypes of bread wheat. (a) position of genotypes, testers and average testers; (b) axis of average genotypes to determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. Small letters determine the relationships among them, (c) rating the testers based on the best tester, (d) polygon display and genotypes and testers positions. The lowercase letters indicate the genotypes and the capital letter indicate the testers. Circle shows the position of average testers.

Karim indicating this genotype is the best cross pair with this tester; i.e. Karim × N-92-9 cross means the prediction of best cross among the ones related to the N-92-9 tester. Since the Karim parent was not on the similar section as a tester, Karim × N-92-9 cross should be heterotic; i.e. it should be better than its both parents (Karim × Karim and N-92-9 × N-92-9). Kouhdasht, Mehregan, Ehsan and N80-19 testers are seen in one section, i.e. besides the Karim indicating the Karim would be the best cross pair for these testers. Since the Karim tester was not on this

section, all Karim crosses with these testers are heterotic. Kouhdasht and Mehregan testers are approximately on the same line separating the sections of Karim and N80-19. Therefore, N80-19 should be a good pair for cross with Mehregan and Kouhdasht. The Line 17 and Atrak testers are on the N80-19 section, hence this line is an appropriate pair for cross with the aforementioned testers and since the inverse does not occur in another section, this cross, Line 17 × N80-19 and N80-19 × Atrak, is heterotic.

Number of spikes

Biplot diagram related to the number of spikes is responsible for 60% of data variations. The maximum and minimum general combining abilities were for Ehsan and Karim, respectively. N-92-9, Kouhdasht, Line 17 and Ehsan have higher specific combining ability than others (Fig. 5a). For number of spikes, two heterotic groups were observed where the first group included Mehregan and Karim testers and the second included N80-19, Kouhdasht, N-92-9, Ehsan, Karim and Line 17 testers (Fig. 5b). Ehsan and Karim testers were the best and worst tester for number of spike (Fig. 5c). Biplot was divided into four sections in which Karim, Line 17, Ehsan and N-92-9 were on the vertex (Fig. 5d). Concerning the figure, the testers related to each figure were besides them; i.e. combination of Ehsan tester \times Ehsan genotype, Line 17 tester \times Line 17 genotype, Karim tester \times Karim genotype, and N-92-9 tester \times N-92-9 genotype indicated that these genotypes should be better than all their related crosses, as a result, heterosis between these genotypes and each parent would not possible. Because faster and easier interpretation is one of the advantages of the biplot method, its use was recommended for researchers to show the differences between the genotypes selected (Pržulj and Momčilović 2012; Motamedi and Safari 2017; Karaman 2020).

Number of grains in spike

In connection to the trait of number of grains in spike, 70% of data variance were justified and Karim and Ehsan genotypes showed the maximum and minimum general combining abilities (Fig. 6a). Genotypes of N-92-9 and Atrak had the highest specific combining ability. Order of testers for this trait based on the most valuable and least valuable was Karim and Ehsan (Fig. 4c). The heterotic groups include Atrak, Karim, Kouhdasht and Mehregan testers in the first group and Line 17, N80-19, genotype N-92-9 and Ehsan testers on the second group (Fig. 6b). N80-19 genotype showed a high combining ability with Mehregan, Kouhdasht, Atrak and Karim testers. On the other hand, on the other part of Karim genotype with Line 17 tester and Kouhdasht genotype with Ehsan tester were appropriate pairs for cross. As the N80-19 and genotype N-92-9 testers were on the Line 17 part, this genotype was introduced as the best cross pairs with these testers. In general, hybrids N80-19 \times Mehregan, N80-19 \times Kouhdasht, N80-19 \times Karim, N80-19 \times Atrak, Karim \times Line 17, Ehsan \times Kouhdasht, Line 17 \times N-92-9 and Line 17 \times N80-19 were highly heterotic. On the vertexes of genotype N-92-9 and Ehsan, no tester was found. As a result, these lines are not the best cross pairs with none of genotypes and they generate the worst hybrids with some or all testers (Fig. 6d).

According to the above results, Karim genotype for

grain yield, weight of spike grains and number of grains in spike and Ehsan genotype for the number of spikes by being located at the positive end of the average vector line of testers with high general combining ability and increasing gene action, can be used as a general parent in breeding programs or in the preparation of artificial or hybrid varieties and conversely, genotype N-92-9 for all four traits studied, including grain yield, weight of spike grains, number of spikes and number of grains in spike and genotype Line 17 for grain yield traits, weight of spike grains and number of spikes and Atrak genotype for grain yield traits, spike weight and number of grains in spike, which have a high degree of combining ability due to the non-additive effects of gene action on inheritance of these traits, should be used as hybrid parents.

Also, the best genotypes obtained based on high GCA and low SCA as the best testers include N-92-9 for grain yield, Atrak for weight of spike grains, Ehsan genotype for number of spikes and Kouhdasht for number of grains in spike compared to other testers, in order for distinction of the lines, were introduced.

Therefore, the graphs provided by biplot analysis can double their validity by simultaneously examining GCA and SCA hybrids.

Conclusion

Based on graphic results, Karim was the best general combining abilities for grain yield, number of grains in spike and weight of spike grains as well as Ehsan for number of spikes. The maximum value of heterosis was in (Atrak, Ehsan and Kouhdasht) \times (Karim, Line 17, Mehregan, N80-19, N-92-9) crosses for grain yield; (Atrak and Line 17) \times (Mehregan, Karim, Ehsan, N-92-9 and N80-19) crosses for weight of spike grains; (Mehregan and Karim) \times (Kouhdasht, Mehregan, Ehsan, Karim, Line 17, N-92-9 and N80-19) crosses for number of spike and (Atrak, Karim, Kouhdasht, Mehregan) \times (Line 17, Ehsan, N-92-9 and N80-19) crosses for number of grain in spike which is highly suitable in breeding plans to obtain the hybrids with high yield at the same weather conditions. Concerning the dominance of graphic techniques in easier and faster interpretation of results and consistency of results of numerical analyses with graphic results, these analytical techniques can be described for convenience in studies. Based on the results of present study, GGE biplot indicated good potential for identifying suitable parents and heterotic crosses and the best hybrids according to diallel mating design.

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