Multienvironment Analysis of Traits Relation and Hybrids Comparison of Maize Based on the Genotype by Trait Biplot

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Abstract: Problem statement: The Genotype by Trait (GT) biplot can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good in certain traits and therefore can be candidates for parents in plant breeding program. **Approach:** The objective of this study was to evaluate the maize hybrids based on Genotype by Traits (GT) biplot to examine its usefulness in visualizing maize trait relationship and its application in hybrids comparison. **Results:** Correlation coefficient between phenological-agronomic traits showed that there is a strong positive relationship between all of the measured traits, except Anthesis-Silking Interval (ASI). This pattern approximately repeated during three years. Also, correlation coefficient between grain yield components reveals a positive or negative relation between measured traits. These results reflect the complexity of the correlation among the grain yield components. The genotype by trait comparison indicated that KSC 700 had greater value for rows number per ear and kernel depth whereas OSSK 602 and ZP 684 had greater value for thousand kernel weight and grain number per row. **Conclusion:** Results indicate that the pattern of the polygon view traits varied across three years. Consequently, GT biplot describes the interrelationships among traits and it was used to identifying hybrids that are good for some particular traits.

Key words: *Zea mays* L., GGE biplot, Genotype × Environment, genotype by trait biplot, traits correlation

INTRODUCTION

Genotype × Environment (GE) interaction is commonly observed by crop producers and breeders as a differential ranking of genotype yields among locations and years. Plant breeders conduct Multiple-Environment Trials (MET) primarily to identify the superior cultivar and secondarily to determine if the target region can be subdivided into different mega environments (Yan *et al*., 2000). The GE interaction results from the differential responses of genotypes across a range of environments (Allard and Bradshaw, 1964; Kang, 1998; 2004). The GE interaction reduces the correlation between phenotypic and genotypic values (Comstock and Moll, 1963) and complicates the selection of the best genotypes (Ebdon and Gauch, 2002; Magari and Kang, 1993).

The GGE biplot, which is composed of two factors, effect of Genotype (G) and Genotype by Environment interaction (GE) and must be considered simultaneously, in cultivar evaluation (Yan and Tinker, 2005; Yan *et al*., 2000). The GGE biplot methodology was used to visually analyze the results of Sites Regression (SREG) analysis of MET data. This method uses a biplot to show the two factors (G plus GE) that are important in genotype evaluation and that are also the sources of variation in SREG model analysis of MET data (Yan *et al*., 2001).

The GGE biplot has been used to identify high yielding and adapted cultivars by many researchers such as Fan *et al*. (2007) and Setimela *et al*. (2007) for maize, Yan *et al*. (2000) and Morris *et al*. (2004) for wheat, Samonte *et al*. (2005) for rice, Dehghani *et al*.

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(2006) and Yan and Tinker (2005) for barley, Sabaghnia *et al.* (2006) for lentils and Kang *et al.* (2006) for common bean.

Furthermore, superior crop cultivars must be evaluated on the basis of multiple traits to ensure that the selected cultivars have acceptable performance in variable environments within the target region (Yan and Rajcan, 2002; Yan and Tinker, 2005).

The Genotype by Trait (GT) biplot can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good in certain traits and therefore can be candidates for parents in plant breeding program. The polygon view of GT biplot allows visualization of the which-won-where pattern that identifies genotypes that are best for certain traits and the traits vector allows visualization of the interrelationship among traits and it is also used as independent selection criteria based on several traits (Yan and Rajcan, 2002).

Iran is the world's largest importers of agricultural products, importing about 30% of its needs. Maize is an important field crop in the agricultural system in Iran. One way to increase maize production is to grow hybrids best adapted to different environments and growing conditions. To evaluate performances of maize hybrids, multi environment trials are frequently used in Iran. The objective of this study was to evaluate the hybrids based on Genotype by Traits (GT) biplot, to examine its usefulness in visualizing maize trait relationship and its application in hybrid comparison.

MATERIALS AND METHODS

Experimental locations and maize hybrids: Data used in this study were obtained from the national maize multi-environment yield trials. These trials were conducted in three years (2006-2008) by the Seed and Plant Improvement Institute in Iran. Each year, 14 maize hybrids (Table 1) were grown and tested in 9 field stations (Table 2) in different regions in Iran. These stations were the Moghan (MGN) field station in the northwestern, Karaj (KRJ) field station in the northern, Esfahan (ESF) field station in the center, Shiraz (two sowing dates, SHZ A and SHZ B) field station, Darab (DRB) field station and Kerman (KRM) field station in the southern, Khoramabad (KHM) and Kermanshah (KSH) field stations in the western and Dezfol (two sowing dates, DZF A and DZF B) field station in the southwestern part of the country. The name of the hybrids, their code and their origins are given in Table 1.

Experimental design and culture: In each location a randomized complete block design with four replicates was used. Plots consisting of two rows (9 m² with row spacing at 75 cm and plant spacing at 35 cm) were hand planted and harvested. Plots were initially over-planted and later thinned to two plants per hill. Plant density is 76000 plants ha^{-1} in all environments. Irrigation system was similar for all experimental locations and they were irrigated once per week. Nitrogen (200 kg ha^{-1} before sowing and 200 kg ha^{-1} after thinning) and phosphorus (300 kg ha^{-1} before sowing) fertilizers were applied according to the recommendations of the Soil and Water Research Institute for each location.

Data collection: Several phenological traits such as days to tasseling (days between emergence and mid tasseling), days to anthesis (days between emergence and mid pollination), days to maturity (days between emergence and black layer) and anthesis-silking interval (difference between days to mid silking and days to mid pollination), agronomic traits (plant height and ear height), grain yield components (thousand kernel weight, grain number per row, kernel depth and row number per ear) were recorded for all locations and years. In order to obtain appropriate results, these traits were divided into two groups (phenological-agronomic traits and grain yield components) and were analyzed, separately.

Table 1: Names, codes, and origin of 14 maize hybrids

Name of hybrids	Hybrids code	FAO group	Origin of hybrids
ZP 677	G1	600	Serbia
ZP 434	G2	400	Serbia
ZP 684	G3	600	Serbia
BC 572	G4	500	Croatia
BC 678	G5	670	Croatia
BC 666	G6	660	Croatia
BC 582	G7	580	Croatia
BC 5982	G8	510	Croatia
BC 682	G9	680	Croatia
OSSK 602	G10	600	Croatia
G-3261	G11	500	Greece
ZP 599	G12	500	Serbia
KSC 700	G13	700	Iran
KSC 704	G14	700	Iran

Table 2: Geographic coordinates of test locations

Location	Longitude	Latitude	Evaluation (m)
Karaj (KRJ)	51°00'	35°49'	1360
Esfahan (ESF)	51°39'	32°38'	1575
Moghan (MGN)	48°03'	39°01'	1100
Dezfol (DZF)	48°24'	32°24'	143
Shiraz (SHZ)	52°33'	29°36'	1491
Darab (DRB)	54°34'	28°46'	1150
Kerman (KRM)	57°05'	30°17'	1748
Kermanshah (KSH)	47°07'	34°19'	1322
Khoramabad (KHM)	48°21'	33°32'	1171

The genotype by trait biplot: The Genotype by Trait (GT) biplot approach (Yan and Rajcan, 2002) was used to display the genotype by trait data in a biplot and is based on the following formula:

$$\frac{\alpha_{ij} - \beta_j}{\sigma_j} = \sum_{n=1}^{2} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{2} \xi_{in}^* \eta_{jn}^* + \varepsilon_{ij}$$

Where:
α_{ij} = The mean value of genotype i for trait j
β_j = The mean value of all genotypes for trait j
σ_j = The standard deviation of trait j among genotype means
λ_n = The singular value for Principal Component (PCn)
ξ_{in} = The PCn score for genotype i
η_{jn} = The PCn score for trait j
ε_{ij} = The residual associated with genotype i in trait j

To achieve trait-focused scaling between genotype and trait scores the singular value λ_n has to be absorbed by the singular vector for genotype ξ_{in} and for traits η_{jn}. That is, $\xi_{in}^* = \xi_{in} \lambda_n^0 = \xi_{in}$ and $\eta_{jn}^* = \eta_{jn} \lambda_n^1 = \eta_{jn} \lambda_n$. Because n=2 in a biplot, only PC1 and PC2 are retained in the model and such a model tends to be best for extracting patterns and rejecting noise from the data. A Genotype by Trait (GT) biplot is constructed by plotting PC1 scores against PC2 scores for each genotype and each trait (Yan and Rajcan, 2002).

All analyses reported in this study were conducted by using the GGE biplot software (Yan, 2001; Yan and Kang, 2003) (www.ggebiplot.com).

RESULTS

Trait relations: The GT biplot reveals the interrelationships between traits and it is also used as independent selection criteria based on several traits and in yield trials for grain yield evaluation (Yan and Rajcan, 2002). The correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors. Two traits are positively correlated if the angle between their vectors is <90°, negatively correlated if the angle is >90°, independent if the angle is 90°.

The GT biplot for each of the three years explained high proportion of the total variation of the data. Provided that the biplot explained a high amount of the total variation, the correlation coefficient between each two traits is approximated by the cosine of the angle between the vectors (Yan and Rajcan, 2002). Phenological traits such as days to Tasseling (TSL), days to anthesis (PLD), Days to Maturity (DMA) and Anthesis-Silking Interval (ASI) and agronomic traits such as plant Height (HGT) and ear Height (HGX)

were analyzed. The correlation coefficient between each two traits calculated and examined by the cosine of the angle between the vectors (Fig. 1).
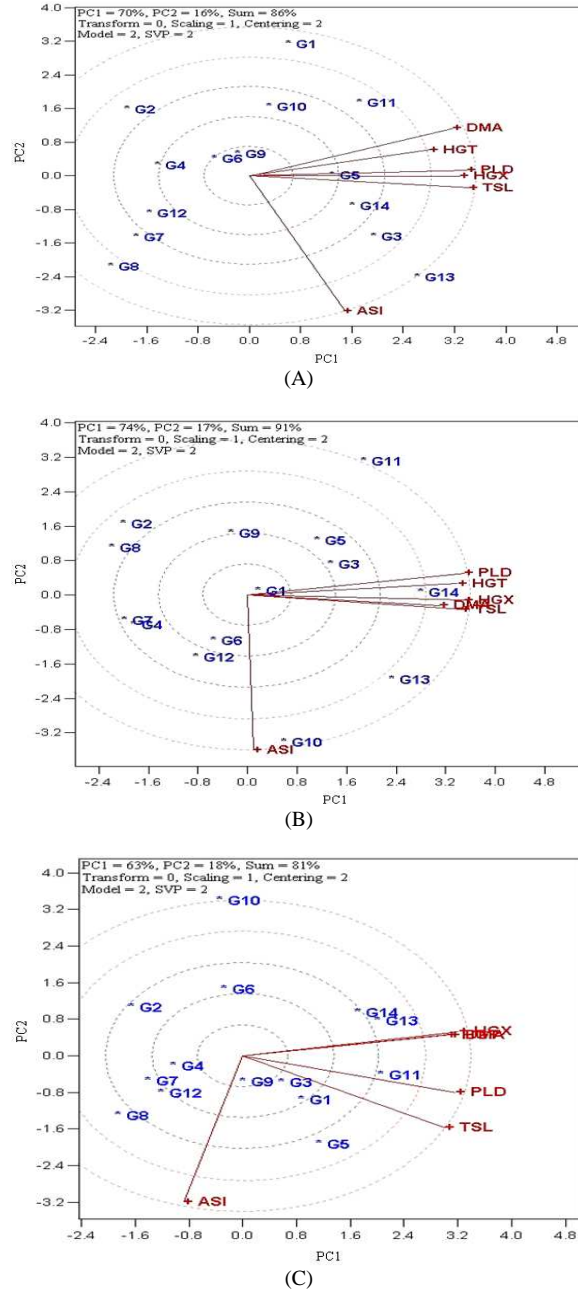

(A)

(B)

(C)

Fig. 1: The yearly correlation between different traits: (A) 2006; (B) 2007; (C) 2008. Days to Maturity (DMA), days to Tasseling (TSL), days to anthesis (PLD), Anthesis-Silking Interval (ASI), plant Height (HGT) and ear Height (HGX)

Therefore, there is a strong positive relationship between all of the measured traits, except Anthesis-Silking Interval (ASI) as indicated by the small acute angles between their vectors (Fig. 1). This pattern approximately was repeated during 3 years.

Also, grain yield components (Thousand Kernel Weight (TKW), grain number per row (SNO), kernel depth (SDP) and Row Number per ear (RNO)) were analyzed separately. The GT biplot for each of the three years explained 77, 82 and 84% of the total variation of the standardized data (Fig. 2). Therefore, according to these results, can be fundamental patterns among the traits which were captured by the GT biplots. The most prominent relations showed by these biplots are: (i) a close correlation between row number per ear and kernel depth (Fig. 2A and B) as indicated by the near perpendicular vectors, (ii) a positive relation between thousand kernel weight and grain number per row (Fig. 2A and C) and between kernel depth and grain number per row (Fig. 2B) in addition between thousand kernel weight and kernel depth (Fig. 2C), (iii) a negative association between row number per ear and grain number per row (Fig. 2A and C) and between row number per ear and thousand kernel weight (Fig. 2A and 2B). These results reflect the complexity of the correlation among the measured traits.

Hybrids comparison: The Genotype by Trait (GT) biplot is used to identify genotypes that are best for certain traits. The GT biplot is also used as independent selection criteria based on several traits and in yield trials for grain yield evaluation (Yan and Rajcan, 2002). Fig. 3 is a GT biplot with a polygon view that presents the data of 14 maize hybrids on three years with four traits. The vertex hybrids for the first year (Fig. 3A) are G13, G10, G3, G2, G7 and G8 and the traits fell into the sectors of G13 and G10 hybrids. Therefore, it seems that G13 hybrid had the highest values of kernel depth (SDP) and Rows Number per ear (RNO); G10 hybrid had the highest values of Thousand Kernel Weight (TKW) and grain number per row (SNO). Figure 3B indicates that G13 was highest in rows number per ear and G11 was highest in kernel depth and grain number per row whereas G3 had the highest values in thousand kernel weight. Also, the third year (Fig. 3C) showed that G3 was best for grain number per row and G1 and G10 were best for kernel depth whereas G8 had greater value for rows number per ear.

Based on the three years data (Fig. 3D), it is resulted that G13 had greater value for rows number per ear and kernel depth whereas G3 were best for thousand kernel weight and grain number per row. No traits fell into sectors with G2, G7 and G8 hybrids as the vertices,

indicating that they had not great values for the expression of any of the concerned traits. These results indicate that the pattern of the polygon view varied across years (Fig. 3).
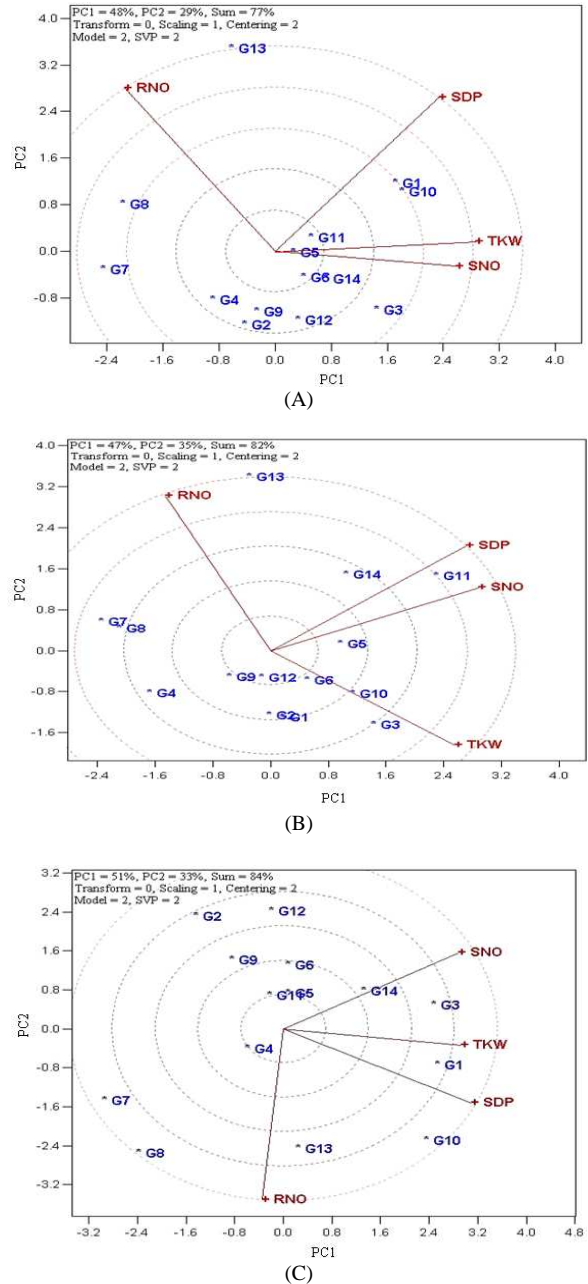

(A)

(B)

(C)

Fig. 2: The yearly correlation between different traits: (A) 2006; (B) 2007; (C) 2008. Thousand kernel weight (TKW), grain number per row (SNO), kernel depth (SDP) and Rows Number per ear (RNO)
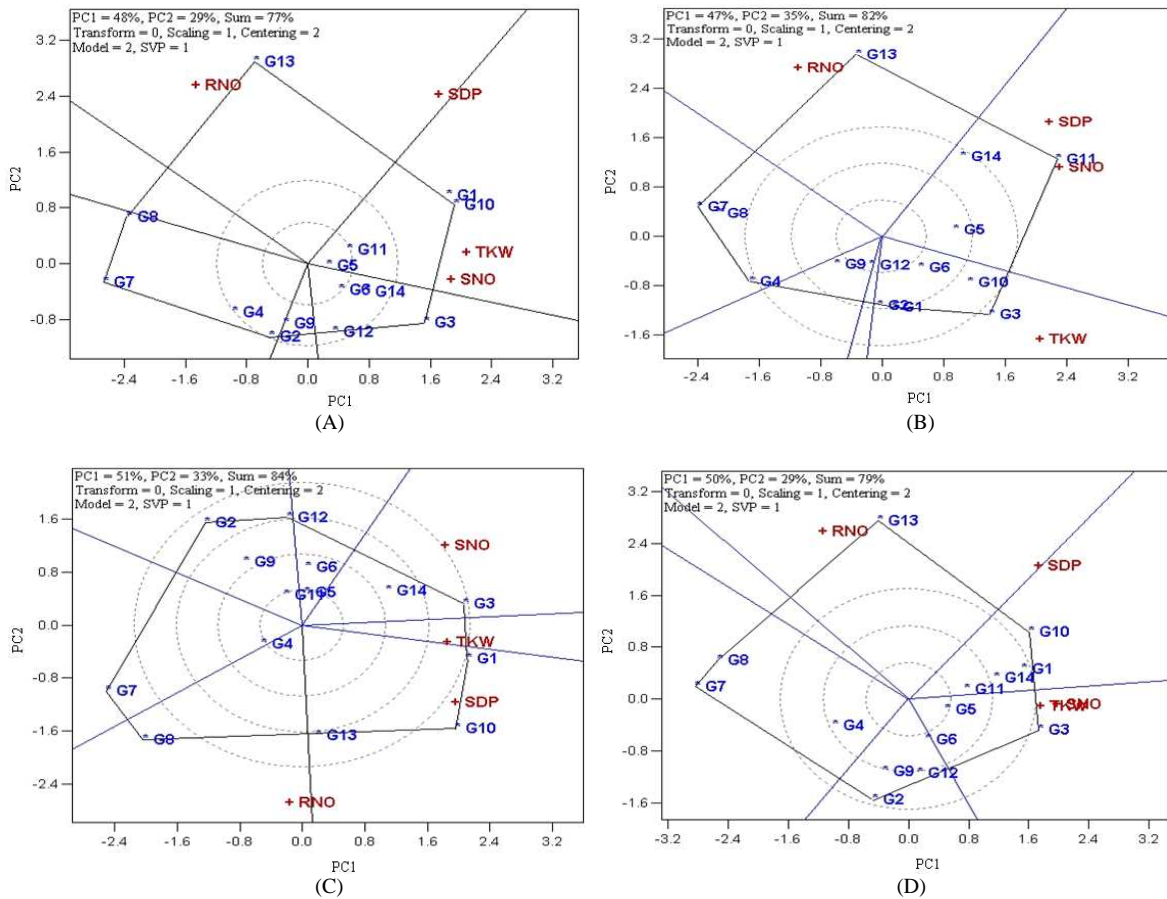
Fig. 3: The polygon view of the hybrid by traits. (A) 2006; (B) 2007; (C) 2008; (D) three years. Thousand Kernel Weight (TKW), grain number per row (SNO), kernel depth (SDP) and Rows Number per ear (RNO)

DISCUSSION

Genotype by Trait (GT) biplot is effective tool for revealing the interrelationships among the maize traits and it provides a tool for visual comparison among genotypes on the basis of multiple traits. Also, it can be used in independent culling based on multiple traits and in comparing selection strategies (Yan and Rajcan, 2002).

Many researchers such as Shakoor *et al*. (2007); Chapman and Edmeades (1999); Turi *et al*. (2007) and Andrea *et al*. (2006) examined the relation between different traits of maize. As an example, Shakoor *et al*. (2007) reported the relation between ear height and plant height and between days 50% silking and plant height are positive and the relation between ear height and ears plant^{-1} is negative, as well as in this present study it has been resulted that the relation between plant Height (HGT) and ear Height (HGX) is positive (Fig. 1)

and the between grain number per row (SNO) and Rows Number per ear (RNO) is negative (Fig. 2). These results are relatively similar to the reports mentioned above. In this study the method of calculation to find the relation between traits in GT biplot is different from simple correlation coefficient because the GT biplot approach is constructed by the first two principal components (PC1 and PC2), so in this approach, the total yield variation could not be explained (Fig. 1 and 2). In addition, GT biplot graphically describes the interrelationships among all measured traits on the basis of overall pattern of the data in different environments and years, whereas simple correlation coefficients only describe the relationships between two traits (Yan and Rajcan, 2002). Therefore, simple correlation between traits does not agree with those of relation between traits in GT biplot completely. Also, GT biplot can be used to visualize the relation among traits (breeding objectives)

which facilitates a systems understanding of the crop and facilitates identification of traits that can be used in indirect selection for a target trait (Yan and Tinker, 2005). Considering what mentioned above, interrelationships among measured traits on the basis of overall pattern of the data (GT biplot) are better than the simple correlation coefficients that only describe the relationships between two traits.

Genotype by Trait (GT) biplot provides a tool for visual comparison among genotypes on the basis of multiple traits. Also, it can be used in independent culling based on multiple traits and in comparing selection strategies, which is important for both cultivar evaluation and parent selection (Yan and Rajcan, 2002; Yan and Tinker, 2005) . Based on this study for example G1 and G10 were best for Thousand Kernel Weight (TKW) and grain number (SNO) and G13 was best for kernel depth (SDP) and rows number per ear (RNO) witch these traits are favorable characteristics for hybrids (Fig. 3A). Also, Thousand Kernel Weight (TKW), grain number per row (SNO), kernel depth (SDP) and Rows Number per ear (RNO) which are major yield components and greatly affect grain yield should be considered in the maize breeding programs for improvement of these traits and yield. Independent culling based on the traits can also be used to aid genotype selection (Yan and Rajcan, 2002).

CONCLUSION

Results indicate that the GT biplot for each of the three years explained high proportion of the total variation of the data and the pattern of the polygon view traits varied across three years. Consequently, Provided that the biplot explained a high amount of the total variation, GT biplot describes the interrelationships among traits and it was used to identifying hybrids that are good for some particular traits.

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