

Study of Environmental Effects on Sunflower Oil Percent based on Graphical Method

Khodadad Mostafavi, Alireza Nabipour, Mohammad Norouzi

Abstract—Biplot can be used to evaluate cultivars for their oil percent potential and stability and to evaluate trial sites for their discriminating ability and representativeness. Multi-environmental trial (MET) data for oil percent of 10 open pollinating sunflower cultivars were analyzed to investigate the genotype-environment interactions. The genotypes were evaluated in four locations with different climatic conditions in Iran in 2010. In each location, a Randomized Complete Block design with four replications was used. According to both mean and stability, Zaria, Master and R453, had highest performances among all cultivars. The graphical analysis identified best cultivar for each environment. Cultivars Berezans and Record performed best in Khoy and Islamabad. Zaria and R453 were the best genotypes in Sari and Karaj followed by Master and Favorit. The GGE bi-plot indicated two mega-environments, group one contained Karaj, Khoy and Islamabad and the second group contained Sari. The best discriminating location was Karaj followed with Khoy, Islamabad and Sari. The best representative genotypes were Zaria, R453, Master and Favorit. Ranking of ten cultivars based their oil percent was as Zaria > R453 ≈ Master ≈ Favorit > Record ≈ Berezans > Sor > Lakumka > Bulg3 > Bulg5.

Keywords—Stability, Bi-plot, Genotype- environment interaction, Sunflower

I. INTRODUCTION

SUNFLOWER is a major oil crop in the world and is cultured in many different climatic conditions. Stability investigation and testing cultivars at multi-locations is very important to ensure that the selected cultivars have acceptable performance in variable environments [4], [7]. Effective interpretation and utilization of the MET data in making selection decisions, however, remain a major challenge to plant breeders. There are two major task works for researcher to be done in stability analysis. The first is to determine whether the target region is homogeneous or should be divided into different mega-environments; the second is to select superior cultivars for a given mega-environment. It is often difficult to determine the pattern of genetic response of different genotypes across the environments without the help of graphical methods [15], [6]). It is possible to describe the relationship between the genotypes and environments for each attribute graphically. Some authors proposed a GGE biplot that allows visual examination of the GE interaction pattern of MET data [8], [10], [11] [14]. GGE biplot refers to the genotype main effect (G) and the genotype × environment interaction (GE), which are the two sources of variation that are relevant to cultivar evaluation.

Mostafavi, K. is with Department of Agronomy and Plant Breeding, Karaj Branch, Islamic Azad University, Karaj, Iran (phone: +98-261-320-3575; fax: +98-261-320-3575; e-mail: mostafavi@kiaau.ac.ir).

Nabipour, A. is with Iranian Rice Research Institute, Deputy of Mazandaran, Amol, Iran

Norouzi, M. is with Iranian Rice Research Institute, Deputy of Mazandaran, Amol, Iran.

In this method, genotypes are depicted by numbers and environments by vectors from the origin. It can be used to identify superior cultivars and test environments that facilitate identification of such cultivars [3], [5].

This GGE biplot can effectively identify the GE interaction pattern of data. It clearly shows which cultivar won in which environments, and thus facilitates mega- environment identification. Therefore, multi-location trials conducted over years are essential for addressing the mega-environment issue. Ideal cultivars should have a large PC1 score (high yielding ability) and a small (absolute) PC2 score (high stability). Similarly, ideal test environments should have a large PC1 score (more discriminating of the genotypes in terms of the genotypic main effect) and small (absolute) PC2 score (more representative of the overall environment) [14], [11]).

The objectives of this study were to 1) graphically summarize the effects of G and GE interaction and examine the pattern of associations between attributes across environments 2) to reveal the possible existence of different mega-environments in the sunflower growing regions in Iran.

II. MATERIALS AND METHODS

Ten open-pollinating sunflower cultivars, Zaria, R453, Master, Favorit, Record, Berezans, Sor, Lakumka, Bulg3 and Bulg5 were evaluated in a Randomized Complete Block (RCB) design with four replications in four different locations in Iran, namely Karaj, Sari, Islamabad and Khoy (table 1). Each plot consisted of five 5-m-long rows, of which the three central lines were evaluated without the outer 0.50 m of each row. The rows were spaced 0.80 m apart, with a density of 5 viable plants per meter. The crop was treated with the normal cultural practices. These materials evaluated in the 2010-2011 growing season. To evaluate the phenotypic stability and adaptability, the GGE biplot analysis was employed, considering the simplified model for two main components. In this approach, the effects of genotype (G) and genotype by environment interaction (GE) were considered as random in the model. In this case, the best linear unbiased prediction (BLUP) of G and GE effects was calculated. The components of genotypic, GE interaction and residual variances were estimated by the method of restricted maximum likelihood (REML). For the analyses of variance, the SAS statistical software package was. We used GGE biplot software to explain the relationships between genotype and locations graphically [12].

III. RESULTS AND DISCUSSION

Significant differences were found across-genotypes and environments for oil percent (data not shown). Similar results were reported by Salah and abdellah [2] for yield data in sunflower. The partitioning of the sums of squares indicated

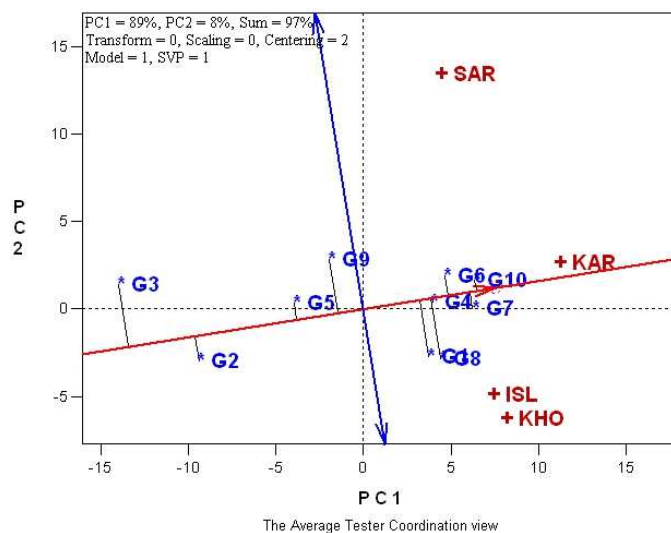
that environments accounted for 8.21% of the total sums of squares for oil percent. $G \times E$ interaction variance was 49.14% and G was 11.595 of total variation. Figure 1a shows the ranking of the genotypes based on their mean oil percent and stability. It was pointed out that if PC1 of a GGE bi-plot approximates the genotype main effects (mean performance) PC2 must approximate the GE effects associated with each genotype, which is a measure of instability [14], [13], [15]. The line passing through the bi-plot origin and the average environment indicated by circle is called the average environment coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all environments. Projection of genotype markers onto this axis should, therefore, approximate the mean yield of the genotypes. Thus, the genotypes Zaria, R453, Master, Favorit, Record and Berezans have the highest yield, followed by genotypes Sor, Lakumka, Bulg3 and Bulg5. The line which passes through the origin and is perpendicular to the AEC with double arrows represents the process of stability genotypes. Either direction away from the bi-plot origin, on this axis, indicates greater $G \times E$ interaction and reduced stability [13]. Therefore, genotypes Bulg5, and Sor near the top and Record near the bottom of the bi-plot are more variable and less stable than others genotypes. An ideal cultivar should have the highest mean performance and be absolutely stable. Such an ideal cultivar is defined by having the greatest vector length of the high-yielding genotypes and with lowest GE. In this study the nearest cultivar to ideal entry is Zaria. This cultivar can be used as a reference for cultivar evaluation. A genotype is more desirable if it is located closer to the ideal genotype, and therefore, most desirable of all the tested genotypes. For broad selection, the ideal genotypes are those that have both high mean yield and high stability. In the bi-plot, they are close to the positive end of AEC and have the shortest vector from the AEC. On the other hand, for specific selection, the ideal genotypes are that have high mean yield but low stability and respond well to particular environments. Two criteria are required to suggest existence of different mega-environments. First there are different winning genotypes in different test locations. Second, the between-group variation should be significantly greater than the within-group variation, a common criterion for clustering. Dividing the target environment into different mega-environments and deploying different genotypes in different mega-environments is the best way to utilize GEI. The polygon view of the GGE bi-plot (shown in figure 1b) indicates the best genotype(s) in each environment and groups of environments. The polygon is formed by connecting the markers of the genotypes that are furthest away from the bi-plot origin such that all other genotypes are contain in the polygon. The vertex cultivars (Zaria, Sor, Bulg5, Bulg3, Record and R453) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments. The vertex cultivars are, therefore, among the most responsive genotypes; all others are less responsive in their respective direction. The lines that

located at the origin would rank the same in all environments and are not at all responsive to the environments. We can compare two adjacent vertex genotypes with polygon. For example comparison of cultivars number R453 with Record indicates that R453 had higher yields in Karaj because genotype R453 located on Karaj sector. Similarly genotype G8 is better in Khoy and Islamabad because this cultivar and Khoy and Islamabad located in one sector. The rays are lines that are perpendicular to the sides of the polygon or their extension [13]. These rays divide the bi-plot into six sections, and ten genotypes and four sites fall into one of them. The vertex lines for each sector are the ones that gave the highest yield for the environments that fall within that sector. Vertex genotypes are the most responsive genotypes; they are the best or else the poorest genotypes in some or all of the test environments. Figure 1c provides the summary of the interrelationships among the environments. The lines that connect the bi-plot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them [9], [13]. Based on the angles of environment vectors, the four sites are grouped into two groups. Group one includes Karaj, Khoy and Islamabad. Group two involves Sari. For example the small angle between Khoy and Islamabad implies that there is a high correlation between them. Another interesting observation from the vector view of the bi-plot is that the length of the environment vectors approximates the standard deviation within each environment, which is a measure of their discriminating ability [12]. Thus, Karaj is most discriminating. Figure 1d shows the ranking of different genotypes based ideal genotype. Ideal genotype in this figure located in center of concentric circles that shows with arrow in picture. Genotypes near this point are better than others. Therefore ranking of genotypes is Zaria > R453 \approx Master \approx Favorit > Record \approx Berezans > Sor > Lakumka > Bulg3 > Bulg5. Entries that are close together are similar in performance across environments, while adjacent environments are similar in the way they discriminate among genotypes. High yielding and stable genotypes usually tend to be on the bottom right quadrant of the joint plot. Results shows that genotypes Berezans, Favorit, Master, R453, Record and Zaria, being in the right quadrant, gave the highest average oil percent (highest primary scores) and were defined as widely adapted over the sites (small secondary scores) as described by de la Vega and Chapman [1]. Genotypes Master, Favorit, R453 and Zaria are closely related in their oil percent potential as well as their response to varying environments as indicated by acute angle formed between these genotypes from origin as reported by Kroonenberg [10]. Genotype Zaria can also be termed as high yielding and stable because of its large primary effect scores and almost near zero secondary scores. Entries Bulg3 and Bulg5 had the yields which were below the average and were highly unstable (large absolute secondary value).

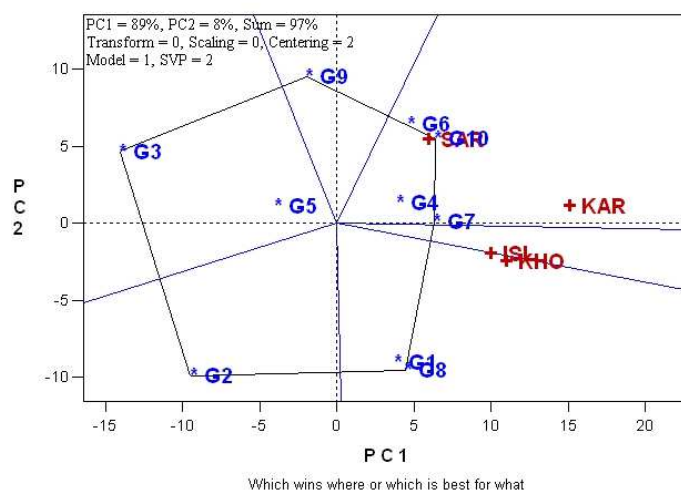
TABLE I

SUMMARY INFORMATION OF FIVE SITES AND MEAN OIL PERCENT OF
SUNFLOWER GENOTYPES

Trial	Karaj	Sari	Islamabad	Khoy
Latitude	35° 46′	36° 33′	34° 06′	38° 33′
Longitude	50° 54′	53° 03′	46° 31′	44° 56′
Elevation (m)	1250	40.55	1333.54	1148.17
Mean oil percent (%)	46.54	43.11	44.84	45.99



a



b

Fig. 1 The GGE bi-plot based on the 10 sunflower genotypes oil percent for 4 environments. The 10 genotypes are displayed by G and numbers (G1 – G10) and the 4 environments in letter (KAR: Karaj, SAR: Sari, KHO: Khoy and ISL: Islam Abad). a, Average-environment coordinate (AEC) view of the GGE bi-plot for Ranking of 10 genotypes based on mean and stability; b, Polygon view of the GGE bi-plot show the "which-won-where pattern". G1: Berezans, G2: Bulg3, G3: Bulg5, G4: Favorit, G5: Lakumka, G6: Master, G7: R453, G8: Record, G9: Sor, G10: Zaria

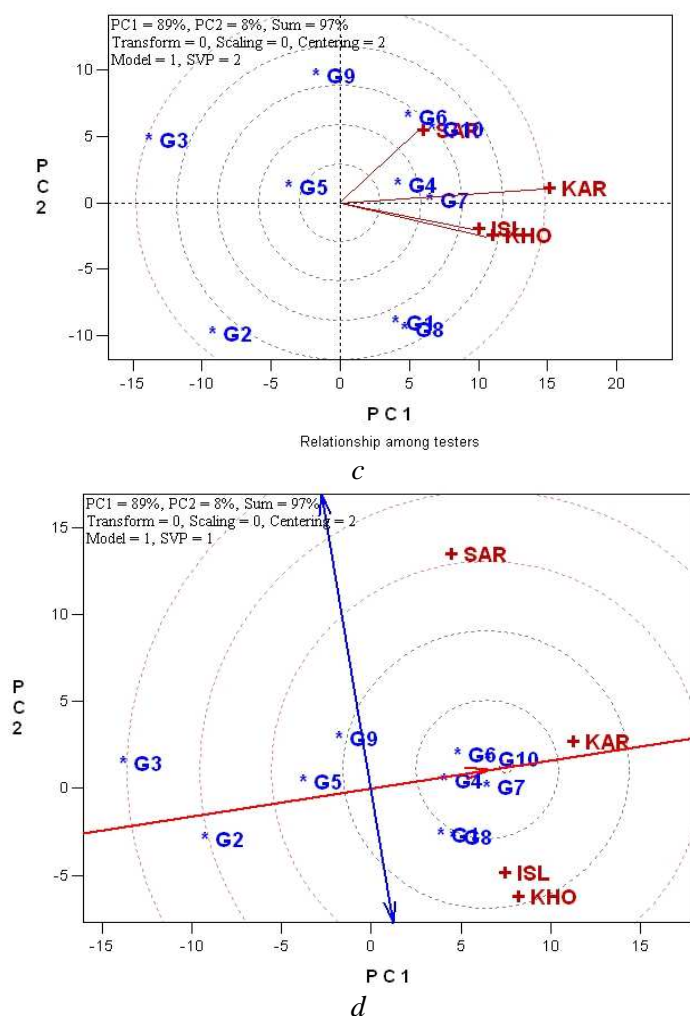


Fig. 1 Continue. *c*, The vector view of the GGE bi-plot to show relationship among environments. *d*, Ranking genotypes based on ideal genotype

REFERENCES

- [1] A. J. De la Vega, and S. C. Chapman. 2001. Genotype by environment interaction and indirect selection for yield in sunflower. II. Three mode principal component analysis of oil and biomass yield across environments in Argentina. *Field Crops Res.*, 72: 39-50.
- [2] B. M. A. Salah and A. W. H. Abdella. 2009. Genetic yield stability in some sunflower (*Helianthus annuus* L) hybrids under different environmental conditions of Sudan. *J. of Plant Breeding and Crop Sci.* 1(1): pp. 016-021
- [3] C. Gwanama., M. T. Labuschagne and A. M. Botha. 2000. Analysis of genetic variation in *Cucurbita moschata* by random amplified polymorphic DNA markers. *Euphytica*, 113: 19-24.
- [4] I. A. Khan., B. A. Malik and M. Bashir. 1988. Investigation of genotype X environment interaction for seed yield in chickpea (*Cicer arietinum* L.). *Pak. J. Bot.*, 20(2): 201-204.
- [5] J. Anothai., A. Patanothai. K. Pannangpetch. S. Jogloy. K. J. Boote. G. Hoogenboom. 2009. Multi-environment evaluation of peanut lines by model simulation with the cultivar coefficients derived from a reduced set of observed field data. *Field Crops Research* 110: 111 – 122.
- [6] J. Crossa., P. L. Cornelius, and W. Yan. 2002. Biplots of linear -bilinear models for studying crossover genotype \times environment interaction. *Crop Science* 42:136-144.
- [7] K. Mostafavi, S. Hosseini Imeni, M. Zare. 2011. Stability Analysis of Rice Genotypes Based GGE biplot Method in North of Iran. *Journal of Applied Sciences Research*, 7(11): 1690-1694.
- [8] K. R. Gabriel, 1971. The biplot graphical display of matrices with applications to principal component analysis. *Biometrika*, 58: 453-467.
- [9] P. M. Kroonenberg. 1995. Introduction to biplots for G \times E tables, University of Queensland, Brisbane.
- [10] P. M. Kroonenberg. 1997. Introduction to biplots for GXE tables. Research Report No. 51. Centre for statistics, the Uni. of Queensland, Brisbane, Qld.
- [11] W. Yan and L. A. Hunt. 2001. Biplot analysis of multi-environment trial data, In M. S. Kang, ed. *Quantitative Genetics, Genomics and Plant Breeding*. CAB International, Willingford.
- [12] W. Yan and M. S. Kang. 2003. GGE biplot analysis: a graphical tool for breeders, In M. S. Kang, ed. *Geneticists, and Agronomist*. CRC Press, Boca Raton, FL.
- [13] W. Yan. 2002. Singular-value partitioning in biplot analysis of multi-environment trial data. *Agron. J.* 94:990-996.
- [14] W. Yan., L. A. Hunt, Q. Sheng, and Z. Szlavics. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science* 40:597-605.
- [15] W. Yan., P. L. Cornelius., J. Crossa and L. A. Hunt. 2001. Two types of GGE Biplots for Analysis Multi – Environment Trial Data. *Crop Sci.* 41: 565 – 663.