# Comparison of genotype × trait and genotype × yield-trait biplots in Sunflower cultivars

Seyed Habib Shojaei<sup>1</sup> • Khodadad Mostafavi<sup>2</sup> • Isa Ansarifard<sup>1</sup> • Mohammad Reza Bihamta<sup>3</sup> • Hossein Zeinalzadeh-Tabrizi<sup>4</sup> • Ali Omrani<sup>5</sup> • Merve Gore<sup>6</sup> • Seyed Mohammad Nasir Mousavi<sup>7</sup> •

- <sup>1</sup> Department of Biotechnology and Plant Breeding, Islamic Azad University, Tehran, Iran
- <sup>2</sup> Department of Agronomy and Plant Breeding, Islamic Azad University, Karaj, Iran
- <sup>3</sup> College of Agriculture and Natural Resources (UCAN), University of Tehran, Karaj, Iran
- <sup>4</sup> Department of Horticulture and Agronomy, Faculty of Agriculture, Kyrgyz-Turkish Manas University, Bishkek, Kyrgyzstan
- <sup>5</sup> Crop and Horticultural Science Research Department, Ardabil Agricultural and Natural Resources Research and Education Center, Agricultural Research Education and Extension Organization (AREEO), Moghan, Iran
- <sup>6</sup> Department of Medicinal and Aromatic
- Plants, Ödemiş Vocational Training School, Ege University, Izmir, Türkiye
- <sup>7</sup> Institute of Land Use, Engineering and Precision Farming Technology, Faculty of Agricultural and Food Sciences and Environmental Management, Debrecen, Hungary

**Citation:** Shojaei, S.H., Mostafavi, K., Ansarifard, I., Bihamta, M.R., Zeinalzadeh-Tabrizi, H., Omrani, A., Gore, M., Mousavi, S.M.N. (2023). Comparison of genotype × trait and genotype × yield-trait biplots in Sunflower cultivars. International Journal of Agriculture, Environment and Food Sciences, 7 (1), 136-147

Received: 16 November 2022

Revised: 11 December 2022

Accepted: 14 December 2022

Published Online: 10 March 2023

Correspondence: Merve Gore

E-mail: merve.gore@ege.edu.tr



Available online at www.jaefs.com

#### CC O S BY NC

Content of this journal is licensed under a Creative Commons Attribution-NonCommercial 4.0 International License.

### Abstract

The selection of genotypes based on various characteristics is a critical challenge in plant breeding. An experiment was carried out in a randomized complete block design (RCBD) in three replications over two crop years, 2018-2019, to compare the effects of genotype  $\times$  trait (GT) and the genotype × yield-trait (GYT) methods as well as to investigate the relationships between grain yield and different agronomic traits. Plant materials included ten sunflowers (Helianthus annuus L.) genotypes. Based on the combined analysis of variance, there was a significant difference in all parameters except leaf length. The effect of year  $\times$  genotype was significant in all traits except plant height, stem diameter, and leaf length  $(P \le 0.01)$ . Gabur, Azargol and Favorite genotypes were ranked as highyielding genotypes in the years of the experiment. Based on the graphical analysis performed on the effect of genotype × trait (GT), Zaria genotype was selected as the best and stable genotype. The genotype  $\times$  yield-trait (GYT) biplot ranked genotypes by yield and other desired trait levels and depicts their trait profiles, or strengths and weaknesses. The correlation biplot revealed positive correlations between most traits with grain yield. This method is pictorial, objective, effective, and simple compared to the genotype  $\times$  trait (GT) method. The GYT biplot technique is based on the paradigm shift that genotypes should be assessed by their yield levels in combination with other variables rather than individually. The graphical analysis of the effect of genotype  $\times$  yield-trait (GYT) revealed that Gabur and Armavirski genotypes were selected as the best genotypes for all traits investigated and could be recommended for cultivation in the Karaj location.

**Keywords:** Sunflower, GT, GYT, Graphical analysis, Year × genotype, Multitraits

### **INTRODUCTION**

Sunflower (*Helianthus annuus* L.) is the major oilseed plant with the largest cultivation area after soybean, rapeseed and peanuts (Hu et al. 2010). Selection based on morphological traits and yield components with high heritability can be a fast and accurate way to screen plant populations to increase and improve crop yield (Gholizadeh and Dehghani 2016). Genetic control of yield is directly affected by parameters correlated with yield. Recognizing the correlation of yield and its components and finding the type of relationships between them can increase yield (Torres et al. 2004). The correlation study is significant in plant breeding to see the relationships between traits. The correlation coefficient indicates the intensity or weakness and direction of changes in two variables of plant traits, each of which is influenced by genetic and environmental structure (Malik et

al. 2010). GGE biplot can easily facilitate the selection of stable genotypes by graphical plotting (Yan 2001). Yan and Rajcan (2002) were the first researchers who studied the genotype by trait interaction (GT biplot), which is one of the GGE biplot methods. Genotype × trait (GT) biplots have also been used to identify reliable traits for indirect selection of a target main parameters (Akinwale et al. 2014). The GGE biplot method also has been used for evaluating the correlation of the characteristics by the genotype-trait biplot graphics (Akcura and Kokten 2017). In recent years, investigating the effect of genotype  $\times$ yield-trait (GYT) has become a new method for multitraits selection and screening of crop plants (Yan and Frégeau-Reid 2018). GYT biplot ranks genotypes based on the combination of grain yield with other evaluated traits and shows the strengths and weaknesses of genotypes with regards to trait weights (Yue et al. 2022). GYT method can be used to identify the best genotypes in the correlation between yield and other traits. As a result, the problem of genotype selection based on different traits can be overcome by the GYT method (Purwati et al. 2022). One of the superior of the GYT biplot is reducing the cost of measuring traits by identifying redundant traits (Mohammadi 2019). Gholizadeh and Ghaffari (2022) on 24 sunflower hybrids used GYT graphical analysis and reported a significant and positive correlation between the number of seeds per head and 100-grain weight combined with grain yield. This method has also been used in the study of various crop plants, including durum wheat (Kendal 2019), bread wheat (Hamid et al., 2019), sesame (Boureima and Abdoua 2019), maize (Mousavi et al. 2021) and oilseed rape (Zeinalzadeh-Tabrizi and Amiri Oghan 2021).

The objectives of this research were: 1) to investigate the effect of genotype  $\times$  trait (GT) and select the best genotype based on this method, 2) to investigate the effect of genotype  $\times$  yield-trait (GYT), compare with (GT) method and select the most desirable genotype based on this method, 3) to determine grain yield relationships and related traits, 4) to classify of the genotypes in terms of all traits studied.

### **MATERIALS AND METHODS**

### **Experimental specifications**

In this research, ten sunflower genotypes were evaluated for the effect of genotype × trait (GT), genotype × yieldtrait (GYT) and also to investigate the relationship between yield and yield components in a randomized complete block design (RCBD) in three replications during two cropping years 2018-2019 in the research field of Islamic Azad University, Karaj Branch, Iran. According to meteorological statistics and the ombrothermic curve, this location has a Mediterranean arid-warm climate with 150-180 dry days per year. For its warm, dry summers and cold, rainy winters, it also has a dry moisture regime. The average annual precipitation in this area is 243 mm, according to Karaj's 30-year climatic data. Rainfall is most common in late autumn and early spring. The average temperature over the last 30 years has been 13.5 °C, while the soil temperature is 14.5 °C; hence, this location is categorized as having a thermic regime. According to the graphic derived for the number of freezing days/Year in Karaj agricultural weather station, the temperature decrease begins in October-November and lasts for the majority of the days in December, January, February, and March. Table 1 shows the genotype name, code and origin of the sunflower genotypes evaluated in this research. The Geographical and meteorological specifications of the experimental location are shown in Table 2.

The studied traits were: plant height (PH), flower diameter (FD), stem diameter (SD), leaf length (LL), leaf width (LW), grain width (GW), grain length (GL), grain diameter (GD), 100-grain weight (WHG) and grain yield (YLD).

Table 1. Origin, names and code of sunflower varieties st	tudied in the study
---	---------------------

Genotype code	Genotype name	Origin	Genotype code	Genotype name	Origin
G1	Progress	Russia	G6	Master	Russia
G2	Gabur	Russia	G7	SHF81-90	Russia
G3	Zargol	Iran	G8	Zaria	Iran
G4	Armavirski	Russia	G9	Favorite	Russia
G5	Azargol	Iran	G10	Record	Romania

Table 2.	Geographical	and meteoro	logical	specifications	of the	experimental	location
	5 1		2				

Location	Longitude	Latitude	Elevation (m)	Average r (mm)	rainfall
Karaj	50°54′E	35°55′N	1312	243	

Table 3. Soil characteristics of the cultivated area in the experiment

Location	EC(ds/m)	Acidity	Lime (%)	Organic carbon (%)	Organic materials (%)	Clay (%)	Silt (%)	Sand (%)
Karaj	0.20	8.2	7	32	45	32	25	22

Experimental plots were designed in four rows; each row was 5 m long with a row distance of 75 cm. Irrigation was done regularly during the growing seasons. All maintenance operations and harvesting were carried out on time. To eliminate marginal effects, sampling was done from the two middle rows. The soil property of the experimental location showed in Table 3.

### **Statistical analyses**

Before variance analysis, normality of data and homogeneity of error variances were checked using Grubbs's test and Bartlett's test, respectively. Combined analyses of variance were then performed to evaluate the genotype and genotype × years effects.

The mean values of all traits in the first, second and average two years of the experiment were subjected to the GT and GYT biplot analyses using polygon biplots, genotype rankings, genotype rankings based on ideal genotype, and correlation of traits. The following equation described by Yan and Rajcan (2002) was used to study the effect of genotype × trait:

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

In this equation, aij: mean of genotype i in the trait j,  $\beta$ j: mean of the trait j on all genotypes,  $\sigma$ j: standard deviation of the trait j between the mean of genotypes,  $\lambda$ n: singular value for principal component (PCn),  $\xi$ in: PCn value for genotype i, njn: PCn value for genotype j,  $\epsilon$ ij: residual value of genotype i for trait j in the model. Z score transformation was also used to eliminate the units of different traits as the following formula:

$$Z = \frac{X - \mu}{\sigma} \quad ^{(2)}$$

In this equation, Z: standard score, X: initial trait data,  $\mu$ : mean of the trait,  $\sigma$ : standard deviation of the trait.

GYT table was obtained based on multiplying/dividing each trait with YLD based on the desirableness/ undesirableness of each trait according to the method described by Yan and Frégeau-Reid (2018). Therefore, by this method, in the GYT table, a larger value is always more desirable. SAS v9.2 software was used for combined ANOVA. Genstat v12 software was used to perform GT and GYT analyses. Excel software was used for the mean comparison graph.

### **RESULTS AND DISCUSSION**

Based on the combined analysis of the evaluated traits, a significant difference was observed between

the genotypes in all characteristics except LL at the probability level of 0.01.

Table 4. Combined analysis of variance in studied traits of 10 sunflower genotypes during two years of the experiment

The effect of year also demonstrated significant difference in SD, FD and YLD. The effect of genotype  $\times$  year was also significant in parameters except PH, SD and LL. The highest coefficient of variation was related to the SD (30.3), and the lowest was related to the FD (6.64) (Table 4).

Due to the importance of the YLD and also the significance of the genotype × year effect for this trait (Table 4), the average of the YLD was compared over the experimental years (Figure 1). Gabur, Azargol and Favorite genotypes had the best rank in the first year of the experiment. Gabur in the second year also had the highest rank among the genotypes studied. Accordingly, based on the data of the first year of the experiment, the highest mean YLD was related to Gabur with 4712 kg/ ha and then Azargol with 4585 kg/ha. The lowest mean YLD was related to Zargol genotype with 3589 kg/ha. In the second year of the experiment, the highest YLD was related to Gabur and Master Genotypes, with 3501 and 3102 kg/ha, respectively, while the lowest mean GY was related to Azargol genotype with 2191 kg/ha (Table 5).

The significant effect of the year × genotype interaction showed that grain yield cannot give a correct picture of cultivar stability across different environments. So, the GYT table is obtained based on the combination of each trait with YLD (Table 5). According to the GYT table, PH, FD, SD, LL, LW, GW, GD and WHG was multiplied by the YLD; therefore yield-trait data table for GYT analysis was obtained. Genotypes were evaluated based on genotype × grain yield-trait (GYT) interaction for two purposes: first, YLD is one of the most important traits, and other traits are important when combined with YLD. Second, the desirability of a genotype should be based on the levels of the combination of YLD with other traits (Yan and Frégeau-Reid 2018).

## Evaluation of genotypes based on genotype $\times$ trait (GT) biplot

### **Polygon biplot**

A polygon biplot was used to examine the genotypes and characteristics evaluated in the research's first, second, and average two crop years (Figure 2). This biplot is drawn by connecting the farthest genotypes from the plot's origin, and the other genotypes are located within this polygon. In each section, genotypes closer to certain traits are more desirable regarding that trait.

Accordingly, in the first year of the experiment, Record, Zargol, Master, Favorite, Gabur and Armavirski genotypes had the most significant distance from the plot's origin and were determined as desirable genotypes. In each



**Figure 1.** Comparison of the mean of genotype × year in grain yield on 10 sunflower genotypes in two cropping years (G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record).



**Figure 2.** Polygon biplot of genotypes based on the genotype × trait (GT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).



**Figure 3.** Ranking biplot of genotypes based on overall superiority and strengths and weaknesses in terms of genotype × trait (GT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record. (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).

Table 4. Combined analysis of variance in studied traits of 10 sunflower genotypes during two years of the experiment												
S.O.V	df	FD	PH	SD	LL	LW	GL	GW	GD	WHG	YLD	
Veer	1	1207*	175 Ans	0 2 4 2 *	0.01 ns	<b>F 70</b> ns	0.05*	0.00 ns	0 01 ns	007 04 ns	21420275**	

Year	1	13.87*	175.4 <sup>ns</sup>	0.342*	0.01 ns	5.79 <sup>ns</sup>	0.05*	0.28 ns	0.01 ns	887.04 <sup>ns</sup>	21420375**
Genotype	9	10.75**	1812.7**	0.14*	7.22 <sup>ns</sup>	10.7*	0.01**	3.5*	0.68**	7111.4**	465530.1*
Error1	4	657	649.17	0.02	6.11	5.59	0.0009	1.41	0.04	2244.1	397244.95
Year ×	9	10.46**	348.01 <sup>ns</sup>	0.06 <sup>ns</sup>	12.78	16.6*	0.01*	38.3*	0.46**	4475.7*	531180.3*
Genotype											
Error2	36	1.7	453.05	0.11	9.93	5.87	0.01	1.45	0.08	1885.2	76462.5
CV %	-	6.64	12.24	30.3	18.9	15.32	12.62	30.1	23.1	14.95	24.85
<u> </u>											2

\*,\*\* and ns: Significant at 5%, 1% and non-significant.

(FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: 100-grain weight, YLD: Grain Yield)

Tab	le 5.	Average grain	/ielo	d and ot	her agronomic	traits in t	he experimenta	l years of t	he studied	genotypes
							•	-		<u> </u>

	Genotype	FD	PH	SD	LL	LW	GL	GW	GD	WHG	YLD
	G1	24.3	171.4	1.1	16.8	15.1	0.9	5.2	1.3	310.9	3969.3
	G2	20.6	132.4	0.9	15.7	14.2	0.9	3.9	1.2	303.0	4712.3
	G3	21.1	176.3	1.4	19.1	16.5	0.8	4.1	2.2	308.8	3589.3
	G4	21.9	163.0	0.9	14.3	15.1	1.0	4.3	1.4	279.1	4101.0
Year 1	G5	18.1	193.5	1.1	21.3	16.5	0.8	3.6	0.9	259.5	4585.3
	G6	16.2	180.3	1.2	16.5	14.7	0.8	1.1	0.4	344.8	3595.7
	G7	19.1	183.7	1.4	14.2	16.9	0.9	3.8	1.3	383.1	4045.3
	G8	17.6	191.0	1.4	18.4	15.8	0.9	3.9	2.1	317.5	4252.0
	G9	20.1	159.3	0.9	13.6	13.2	0.9	1.3	0.6	218.3	4425.3
	G10	21.8	170.7	1.3	16.5	17.1	1.0	4.2	1.1	215.8	3849.3
	G1	19.5	150.1	0.8	16.4	18.1	0.8	3.9	1.1	345.0	2672.3
	G2	20.0	148.1	0.9	16.6	13.4	0.9	3.3	1.6	264.0	3501.0
	G3	18.3	175.6	1.3	15.7	14.7	0.8	3.1	1.3	251.6	3011.3
	G4	17.0	179.5	0.9	16.9	15.3	0.9	5.2	1.6	323.6	3347.0
Voar 2	G5	18.9	196.1	1.2	16.0	16.8	0.8	4.6	1.6	287.0	2191.7
	G6	19.0	199.4	0.7	14.7	16.5	0.9	3.7	1.3	318.6	3102.7
	G7	18.3	184.8	0.9	17.2	20.3	0.8	2.82	1.2	286.3	3282.0
	G8	19.1	195.3	1.2	17.5	14.3	0.8	4.0	1.4	257.3	3056.3
	G9	21.4	177.9	1.0	17.6	16.1	0.7	3.8	0.9	281.3	2566.0
	G10	19.8	148.7	1.1	17.1	15.5	0.8	2.7	0.9	249.0	2444.6
	G1	21.9	160.8	0.9	16.5	16.6	0.8	4.6	1.2	327.9	3320.8
	G2	20.3	140.3	0.9	16.3	13.8	0.9	3.6	1.4	283.5	4106.7
	G3	19.7	175.9	1.3	16.8	15.5	0.8	3.6	1.6	280.2	3291.3
Mean	G4	19.4	171.3	0.9	16.0	15.2	0.9	4.8	1.5	301.3	3724.0
OT TWO	G5	18.5	194.8	1.1	17.8	16.6	0.8	4.1	1.4	273.2	3388.5
years	G6	17.6	190.0	0.9	15.3	15.6	0.8	2.4	1.0	331.7	3361.2
	G7	18.7	184.2	1.1	16.1	18.6	0.9	3.3	1.3	334.7	3663.7
	G8	18.3	193.1	1.3	17.7	15.0	0.8	3.9	1.7	287.4	3654.3
	G9	20.7	168.6	0.9	16.2	14.6	0.8	2.6	0.8	249.8	3501.7
	G10	20.8	159.7	1.2	16.9	16.3	0.9	3.4	0.9	232.4	3153.0

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7:SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW, Grain Width, GD: Grain Diameter, WHG: 100-grain weight, YLD: Grain Yield).

section, genotype Record in terms of GW, genotype Zargol with regards to LW and SD and Gabur genotype in terms of YLD were more desirable than other genotypes (Figure 2. A). Based on the polygon biplot obtained from the data of the second year of the experiment, the genotypes Armavirski, Master, Progress, Favorite,

Record and Zaria were identified as the best genotypes, considering that they were the most distant from the origin of the biplot. Also, Zaria genotype in terms of SD, Armavirski genotype in terms of FD and GL, Master genotype in terms of WHG, Progress genotype with regards to LW and Favorite genotype in terms of flower

	Genotype	Y*FD	Y*PH	Y*SD	Y*LL	Y*LW	Y*GL	Y*GW	Y*GD	Y*WHG	Y*FD
	G1	96547.4	680343.7	4366.3	66817.1	60069.2	3667.6	20762.2	5004.0	1234066	96547.4
	G2	97231.1	623912.9	4445.3	73826.6	66852.3	4291.3	18786.5	5500.8	1427837	97231.1
	G3	75871.3	632679.8	5120.8	68675.9	59104.4	3093.5	14685.1	7061.4	1108506	75871.3
Year 1	G4	89680.7	668463.0	3909.6	58781.0	61925.1	4199.4	17850.2	6717.4	1144452	89680.6
	G5	83174.9	887414.8	4982.7	97667.6	75658.0	4074.8	16650.8	4826.8	1189894	83174.8
	G6	58398.4	648418.6	4218.9	59208.6	52856.3	2886.1	4118.2	2327.5	1239786	58398.4
	G7	77478.9	742992.9	5717.4	57308.9	68500.9	3932.0	15550.3	4288.0	1549902	77478.9
	G8	74772.8	812132.0	5782.7	78095.1	67039.9	4067.7	16449.5	7934.2	1350152	74772.8
	G9	89005.2	705103.1	4041.8	60037.0	58414.4	4263.0	6003.7	4977.0	9661970	89005.2
	G10	84069.4	657209.5	5106.8	63385.7	65951.9	4016.1	16103.0	3823.6	8306860	84069.4
	G1	52110.5	401170.7	2271.5	43870.8	48378.1	2262.5	10573.5	2654.5	921955	52110.5
	G2	70113.3	518568.1	3092.5	58233.3	46971.7	3220.9	11459.9	4924.7	924264	70113.3
	G3	55137.5	528890.5	3844.5	47303.0	44326.8	2670.0	9294.9	4828.1	757852	55137.5
Year 2	G4	56954.7	600842.3	3280.1	56720.5	51209.1	3257.7	17404.4	4451.5	108331	56954.7
icui 2	G5	41429.8	429676.3	2564.2	35212.8	36929.6	1877.5	10001.3	3324.0	629008	41429.8
	G6	59105.8	619706.0	2306.3	45764.3	51328.4	2833.7	11459.2	5181.4	988716	59105.8
	G7	60038.7	606458.9	2910.1	56450.4	66777.7	2910.0	9277.1	3916.5	939746	60038.7
	G8	58335.2	597003.8	3647.2	53526.6	43776.9	2516.3	12225.3	4278.8	786496	58335.2
	G9	54809.7	456431.5	2694.3	45170.1	41432.3	1984.3	9746.5	2762.7	721901	54809.7
	G10	48575.5	363530.1	2819.5	41958.6	38096.1	2077.9	6555.7	2159.4	608722	48575.5
	G1	72764.9	533857.2	3237.8	54978.2	55186.7	2940.0	15254.8	3594.6	1089067	72764.9
	G2	83488.5	576001.1	3750.7	66984.3	56678.8	3758.9	14907.2	5449.0	1164240	83488.5
Moan	G3	64918.2	579110.1	4448.7	55458.9	51322.8	2877.5	11812.6	5676.4	922396	64918.2
of two	G4	72403.2	637766.0	3599.8	59865.4	56604.8	3719.0	17787.0	5335.2	1122289	72403.2
years	G5	62759.5	660051.6	3823.3	60352.9	56503.2	2957.0	13883.8	4615.1	925907	62759.5
-	G6	59310.0	638733.7	3221.1	51500.5	52507.0	2883.8	8131.7	4467.3	1115011	59310.0
	G7	68594.8	674939.0	4213.2	59310.6	68290.7	3404.7	12219.5	4209.1	1226351	68594.8
	G8	67005.8	705895.4	4665.3	65039.0	54979.4	3252.3	14377.3	5683.7	1050377	67005.8
	G9	72611.7	590398.5	3437.4	56929.3	51381.1	3040.6	9025.5	3826.1	874833	72611.7
(C1) Drog	G10	65755.8	503591.9	3909.7	53383.8	51577.8	2984.8	10822.6	2900.7	732757	65755.8

**Table 6.** Value of genotype × yield-trait in 10 sunflower genotypes in the first, second and average of two cropping years

diameter had better performance than other genotypes (Figure 2. B). The polygon biplot drawn based on the average data of the two crop years of the experiment showed that Zaria, Azargol, Master, Favorite, Gabur and Armavirski genotypes had the longest distance from the origin. Zaria genotype with regards to LL, Azargol genotype with regards to SD and Armavirski genotype were better and more desirable in terms of GL and yield than other genotypes (Figure 2. C). According to the polygon biplots drawn in the first, second and average two crop years, it can be concluded that in terms of all traits, Master, Favorite and Armavirski genotypes are selected and determined as the most desirable genotypes compared to the others. Rahmati and Ahmadi (2020) used this method in their analysis of wheat and obtained similar results.

Ranking of genotypes based on overall superiority in terms of all traits

In this biplot, which is connected to the mean of the traits from the origin of linear coordinates, the genotypes that are at the positive beginning of this axis have higher performance and desirability, thus the genotypes that are close to this axis have a higher value in terms of the trait studied. Based on the ranking biplot of genotypes in terms of all traits (Figure 3), in the first year, Zargol, Record, Zaria and SHF81-90 genotypes were determined as the best genotypes. Favourite and Master genotypes were also selected as undesirable genotypes. The order of genotypes from most desirable to most undesirable is as follows: (Figure 3. A)

Zargol> Record> Zaria> SHF81-90> Progress> Armavirski> Azargol > Gabur> Master> Favorite.

Based on the biplot obtained from the second year of the experiment, the Armavirski genotype was pointed out as the preferred genotype. Favourite and Record genotypes



Figure 4. Genotype ranking biplot based on the ideal genotype in terms of genotype  $\times$  trait (GT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).



Figure 5. Correlation biplot between the traits evaluated in the experiment, A: the first year of the experiment, B: the second year of the experiment, C: the average of the first and second year of the experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield)



**Figure 6.** Polygon biplot based on genotype × yield-trait (GYT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).

were selected as undesirable genotypes. The order of genotypes from most desirable to most undesirable is as follows: (Figure 3. B)

Armavirski> Master> Azargol> Gabur> SHF81-90> Zargol> Zaria> Progress> Record> Favorite.

Based on the data of the average of the first and second year of the experiment, Zaria and Azargol genotypes were determined as superior genotypes Master and Favorite genotypes were pointed out as undesirable genotypes. The order of genotypes from the best genotype to the most unfavorable genotype is as follows up: (Figure 3.C)

Zaria> Azargol> Armavirski> Zargol> SHF81-90> Record> Gabur> Progress> Favorite> Master.

### Selection of the best genotype based on the ideal genotype biplot

The ranking biplot of genotypes was drawn based on the ideal genotype to select the best genotype (Figure 4). In this biplot, the best point is the center of the concentric circle, which is marked with an arrow, and other genotypes are ranked based on this point. The hypothetical ideal genotype is described based on the most stable and high-yielding genotype (Yan and Kang 2002). According to this biplot, in the first year of the experiment, Zargol, SHF81-90 and Zaria genotypes were selected as superior genotypes and Master and Favorite genotypes were selected as unfavorable genotypes. The ranking of genotypes from the best to the most unfavorable genotypes is as follows: (Figure 4.A)

Zargol> SHF81-90> Zaria> Record> Progress> Armavirski> Azargol> Gabur> Favorite> Master.

Based on the biplot of the second year of the experiment, the Armavirski genotype was determined as the most desirable genotype compared to other cultivars, and Favorite and Record genotypes were stated as undesirable genotypes. The order of genotypes in the second year of the experiment is as follows: (Figure 4.B)

Armavirski> Master> Azargol> Gabur> SHF81-90> Zargol> Zaria> Progress> Record> Favorite.

The biplot on the average of the data of the first and second years of the experiment indicated that the Zaria genotype was specified as the preferred genotype and Master and Favorite genotypes as the undesirable genotype. The order of genotypes from the most desirable to the most undesirable genotype is as follows: (Figure 4.C)

Zaria> Azargol> Zargol> Armavirski> SHF81-90> Record> Progress> Gabur> Favorite> Master.

### **Correlation between evaluated traits**

According to this biplot, the cosine of the angle between the vectors of traits represents an estimate of the correlation coefficient between them. The acute angle between vectors represents a positive correlation, and the obtuse angle between vectors represents a negative correlation. If the angle between the vectors of the attributes is 90 degrees, it represents no correlation between them (Yan and Kang 2002). According to the correlation biplot drawn in the first crop year, GW, LW and SD, LL, PH, WHG and YLD, GL and FD were positively correlated. Considering the vector angle between the two traits of YLD and LL, which shows an angle of 180 degrees, a negative and significant correlation was evident between these two traits. The correlation between LL and GW traits was also estimated to be zero (Figure 5. A). The results of the correlation biplot in the second-year data also showed a positive correlation between GD, PH, YLD, GW and GL. Also, a positive correlation was observed between WHG and LW traits and between SD and LL traits. WHG was negatively correlated with SD, FD with PH. According to the angle between the two vectors, WHG traits with FD and SD traits with GD were estimated to be zero (Figure 5. B). The results of correlation between the evaluated traits in the mean of the first and second-year crop data are also a positive correlation between GW, GD, LL, SD, PH, LW and WHG, and GL, YLD and FD were observed together. Also, the degree of correlation between FD and PH traits was negative. The correlation between trait GD with the FD and PH traits was zero (Figure 5. C). Sincik and Goksoy (2014) reported a positive correlation between FD and YLD.

## Evaluation of genotypes based on genotype $\times$ yield-trait (GYT) biplot

### **Polygon diagrams**

Figure 6 shows the polygon biplot of genotypes in terms of genotype × yield-trait (GYT). As in Figure 2, the genotypes with the greatest distance from the origin of the biplot are specified as the most desirable trait. In each section, genotypes close to certain traits are more desirable than that trait (Figure 6). Based on the graph drawn in the first year of the experiment (Figure 6. A), the first two principal components explained 40.07% and 22.06%, respectively, and a total of more than 62% of the data variance. The high percentage of the first two principal components indicates the high validity of the GYT biplot in justifying the percentage of the data variance (Hamid et al. 2019). This biplot identified Armavirski, Gabur, Azargol, Zaria, Master and Favorite genotypes as the most desirable genotypes. In each section, Gabur genotype had the highest value of Y imesFD,  $Y \times GL$ , indicating that this was more desirable than other genotypes in combining YLD with a FD and GL. Azargol and Zaria genotypes also had the highest values in Y  $\times$  LW, Y  $\times$  LL, Y  $\times$  PH and Y  $\times$  SD and were superior in terms of YLD combination with PH, LW, LL and SD. In the second year of the research, the first and second major components covered 62.79 and 14.09, respectively, and 76.98% of the variance of the data. Zargol, Zaria, Gabur, Armavirski, SHF81-90, Master, Progress, Azargol and

Record genotypes were selected as the best genotypes according to the distance from the origin of the biplot. In each section, Gabur and Armavirski genotypes in terms of Y  $\times$  GD, Y  $\times$  LL, Y  $\times$  PH, Y  $\times$  FD, Y  $\times$  GL and Y  $\times$ GW show the combination of YLD with traits of SD, LL, PH, FD, GL and GW, the best genotypes were identified. Zargol and Zaria genotypes were also more desirable than other genotypes in terms of  $Y \times SD$ , which shows the combination of YLD with SD (Figure 6. B). Gabur, Zaria, Zargol, Master, Record and Progress genotypes were determined as the best genotypes in studying the average data of two crop years. In each part, Gabur genotype in terms of  $Y \times FD$  (combination of YLD in FD) and Zaria genotype in terms of Y  $\times$  SD, Y  $\times$  PH and Y  $\times$ GD (combination of yield in SD, PH and SD were pointed out as the best genotypes (Figure 6. C). According to the graphs of the first, second and average years of the experiment, the Zaria genotype was identified as the upper genotype in all years and also this genotype was the best known compared to other genotypes in terms of  $Y \times SD$  (combination of YLD with SD) in all years.

### Ranking of genotypes based on genotype effect × yield-trait (GYT)

In this biplot, the genotypes at the positive end of the mean axis are identified as superior genotypes in terms of all traits (Figure 7). Based on the ranking biplot of genotypes in the first year of the experiment (Figure 7. A), Azargol, Zaria and Gabur genotypes were identified as the best genotypes in terms of a combination of traits, while Master Favorite genotypes were identified as undesirable genotypes. Based on this biplot, Azargol and Zaria genotypes were identified as desirable genotypes in combining YLD with LW, LL, WHG, PH and SD. The order of genotypes in the first year of the experiment from the most desirable genotype to the most undesirable genotype is as follows:

Azargol> Zaria> Gabur> SHF81-90> Progress> Armavirski> Record> Zargol> Favorite> Master.

Based on the second-year biplot, Armavirski and Gabur genotypes were identified as superior genotypes, whereas Azargol and Record genotypes were identified as undesirable genotypes. Armavirski genotype was ranked high compared to other genotypes in combining YLD with GW. The order of genotypes from the most desirable genotype to the most undesirable genotype is as follows: (Figure 7. B)

Armavirski> Gabur> SHF81-90> Master> Zaria> Zargol> Progress> Favorite> Azargol> Record.

According to the average data of the first and second years, Gabur, SHF81-90 and Armavirski genotypes were identified as the best genotypes while, Record, Master and Favorite genotypes were identified as unfavorable genotypes. Gabur and Armavirski genotypes were more desirable by combining YLD with FD, GL, GW, WHG and LL traits. Zaria genotype can also be selected as more desirable than other genotypes in combining YLD with PH and SD traits. The order of genotypes from the most desirable genotype to the most undesirable genotype is as follows: (Figure 7. C)

Gabur> Zaria> Armavirski> SHF81-90> Azargol> Zargol> Progress> Favorite> Master> Record.

According to the biplots of different years of the experiment, Gabur and Armavirski genotypes can be identified as desirable genotypes.

### Selection of the best genotype based on the ideal genotype

The genotypes were ranked based on the ideal genotype ranking biplot, which is similar to Figure 4 (Figure 8). In the first year of the experiment, Azargol and Zaria genotypes were determined as the best genotypes while, Master genotype was ranked as undesirable. According to this biplot, the order of genotypes from the best genotype to the most unfavorable genotype is as follows: (Figure 8. A)

Azargol> Zaria> Gabur> SHF81-90> Progress> Record> Armavirski> Zargol> Favorite> Master.

Based on the biplot of the second year of the experiment, Armavirski and Gabur genotypes were identified as desirable genotypes while, Record was ranked as undesirable genotype. The ranking of genotypes from favorable genotype to unfavorable genotype is as follows: (Figure 8. B)

Armavirski> Gabur> SHF81-90> Master> Zaria> Zargol> Favorite> Progress> Azargol> Record.

Based on the biplot of the average of two years of the experiment, Armavirski, SHF81-90, Gabur and Zaria genotypes were identified as desirable genotypes while, Record genotype remained undesirable genotype, respectively. The ranking of genotypes based on the average biplot of the first and second year of the experiment from the best genotype to the most unfavorable genotype is as follows: (Figure 8. C)

Armavirski> SHF81-90> Gabur> Zaria> Azargol> Zargol> Progress> Favorite> Master> Record.

### **Correlation biplot of Yield × Trait data**

In this biplot, the vector length indicates the discrimination of genotypes (Figure 9). In other words, traits with longer vector lengths have more discrimination power. This biplot, like Figure 5, can show the correlation between the traits based on the angles of the vectors. Since yield performance as a component is present in all yield×trait combinations, different yield×trait combinations tend to be positively correlated. According to the biplot in the first year of the experiment, there was a positive correlation between  $Y \times FD$ ,  $Y \times GL$ ,  $Y \times GW$  and  $Y \times GD$ , indicating the high utility of combining FD, GL, GW and GD with YLD. Also, a positive correlation was observed between  $Y \times LW$ ,  $Y \times LL$ ,  $Y \times WHG$ ,  $Y \times PH$  and  $Y \times SD$ , which



**Figure 7.** Genotype ranking biplot based on overall superiority and strengths and weaknesses in terms of genotype × yield-trait (GYT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).



**Figure 8.** Genotype ranking biplot based on ideal genotype in terms of genotype × yield-trait (GYT), A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).



**Figure 9.** Correlation biplot between grain yield compounds in the traits evaluated in the experiment, A: first year of the experiment, B: second year of the experiment, C: average of the first and second year of the experiment.

(G1: Progress, G2: Gabur, G3: Zargol, G4: Armavirski, G5: Azargol, G6: Master, G7: SHF89-90, G8: Zaria, G9: Favorite, G10: Record). (FD: Flower Diameter, PH: Plant Height, SD: Stem Diameter, LL: Leaf Length, LW: Leaf Width, GL: Grain Length, GW: Grain Width, GD: Grain Diameter, WHG: Weight of 100 Grain, YLD: Grain Yield).

indicated the high usefulness of the combination of LW, LL, WHG, PH and SD with YLD. (Figure 9. A). In the biplot of the second year of the experiment, there is a positive correlation between  $Y \times SD$ ,  $Y \times GD$ ,  $Y \times LL$ ,  $Y \times PH$ ,  $Y \times FD$ ,  $Y \times GL$  and  $Y \times GW$  together. Positive correlations were observed between  $Y \times WHG$  and  $Y \times LW$  (Figure 9. B). The positive correlation between  $Y \times FD$ ,  $Y \times GL$ ,  $Y \times GW$ ,  $Y \times WHG$ ,  $Y \times LL$  and between  $Y \times LW$ ,  $Y \times GD$ ,  $Y \times SD$  and  $Y \times PH$ ,  $Y \to PH$ ,

### CONCLUSION

The selection of genotypes based on various characteristics is a critical challenge in plant breeding. Combined analysis of variance indicated a significant effect among genotypes in terms of all traits except LL. Comparison of the mean interaction effect of genotype × year in the YLD trait also identified Gabur, Azargol and Favorite genotypes as high-yielding genotypes in the years of the experiment. Based on the graphical analysis performed on the effect of genotype  $\times$  trait (GT), Zaria genotype was selected as the best and stable genotype. The genotype × yield-trait (GYT) biplot ranked genotypes by yield and other desired trait levels and depicts their trait profiles, or strengths and weaknesses. This method is pictorial, objective, effective, and simple compared to the genotype × trait (GT) method. The GYT biplot technique is based on the paradigm shift that genotypes should be assessed by their yield levels in combination with other variables rather than individually. The graphical analysis of the effect of genotype  $\times$  yield-trait (GYT) revealed that Gabur and Armavirski genotypes were selected as the best genotype for all traits investigated and could be recommended for cultivation in the Karaj location.

### COMPLIANCE WITH ETHICAL STANDARDS Conflict of interest

The authors declared that for this research article, they have no actual, potential or perceived conflict of interest. **Author contribution** 

The contribution of the authors to the present study is equal. All the authors read and approved the final manuscript. All the authors verify that the Text, Figures, and Tables are original and that they have not been published before.

#### **Ethical approval**

Ethics committee approval is not required. **Funding** 

No financial support was received for this study. **Data availability** 

All data associated with this research were indicated and used in the manuscript submitted.

#### **Consent for publication**

All authors consented to the publication of this manuscript.

#### REFERENCES

- Akcura, M., Kokten, K. (2017). Variations in grain mineral concentrations of Turkish wheat landraces germplasm. Quality Assurance and Safety of Crops & Foods, 9(2): 153-159. https://doi.org/10.3920/QAS2016.0886
- Akinwale, R., Fakorede, M., Badu-Apraku, B., Oluwaranti, A. (2014). Assessing the usefulness of GGE biplot as a statistical tool for plant breeders and agronomists. Cereal Research Communications, 42(3): 534-546. https://doi. org/10.1556/crc.42.2014.3.16
- Boureima, S., Abdoua, Y. (2019). Genotype by yield\* trait combination biplot approach to evaluate sesame genotypes on multiple traits basis. Turkish Journal of Field Crops, 24(2): 237-244. https://doi.org/10.17557/tjfc.655165
- Gholizadeh, A., Dehghani, H. (2016). Graphic analysis of trait relations of Iranian bread wheat germplasm under nonsaline and saline conditions using the biplot method. Genetika, 48(2): 473-486. https://doi.org/10.2298/ GENSR1602473G
- Gholizadeh, A., Ghaffari, M. (2022). Simultaneous selection for seed yield and agronomic traits in sunflower. Isfahan University of Technology-Journal of Crop Production and Processing, 11(4): 1-15. https://doi.org/10.47176/ jcpp.11.4.36103
- Hamid, A.E., Aglan, M., Hussein, E. (2019). Modified method for the analysis of genotype by trait (Gt) biplot as a selection criterion in wheat under water stress conditions. Egyptian Journal of Agronomy, 41(3): 293-312. https://doi. org/10.21608/AGRO.2019.16580.1177
- Hu, J., Seiler, G., Kole, C. (2010). Genetics, genomics and breeding of sunflower. CRC Press, Routledge, USA.
- Kendal, E. (2019). Comparing durum wheat cultivars by genotype× yield× trait and genotype× trait biplot method. Chilean Journal of Agricultural Research, 79(4): 512-522. http://dx.doi.org/10.4067/S0718-58392019000400512
- Malik, S.R., Bakhsh, A., Asif, M.A., Iqbal, U., Iqbal, S. (2010). Assessment of genetic variability and interrelationship among some agronomic traits in chickpea. International Journal of Agriculture and Biology, 12(1): 81-85.
- Mohammadi, R. (2019). Genotype by yield\* trait biplot for genotype evaluation and trait profiles in durum wheat. Cereal Research Communications, 47(3): 541-551. https://doi.org/10.1556/0806.47.2019.32
- Mousavi, S.M.N., Bojtor, C., Illés, Á., Nagy, J. (2021). Genotype by trait interaction (GT) in Maize hybrids on complete fertilizer. Plants, 10(11): 2388. https://doi.org/10.3390/ plants10112388
- Purwati, R., Anggraeni, T., Machfud, M. (2022). Genotype by yield\* trait biplot analysis to evaluate Jatropha curcas genotypes based on multiple traits. IOP Conference Series: Earth and Environmental Science, 974:012013. https://doi. org/10.1088/1755-1315/974/1/012013
- Rahmati, M., Ahmadi, A. (2020). Assessment of interrelationship between agronomic traits of wheat genotypes under rainfed conditions using double and triple biplots of genotype, trait and yield. Iranian Dryland Agronomy Journal, 9(1): 1-20. https://doi.org/10.22092/IDAJ.2020.122220.284

- Sincik, M., Goksoy, A.T. (2014). Investigation of correlation between traits and path analysis of confectionary sunflower genotypes. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 42(1): 227-231. https://doi.org/10.15835/ nbha4219429
- Torres, V., Davila, J., Mendoza, A., Godina, F., Maiti, R. (2004). Importance of agronomic characteristics in the grain yield of maize under irrigated and rainfed conditions. Crop Research, 27(2): 169-176.
- Yan, W. (2001). GGEbiplot-a windows application for graphical analysis of multienvironment trial data and other types of two-way data. Agronomy Journal, 93(5): 1111-1118. https://doi.org/10.2134/agronj2001.9351111x
- Yan, W., Frégeau-Reid, J. (2018). Genotype by Yield\* Trait (GYT) Biplot: a Novel approach for genotype selection based on multiple traits. Scientific Reports, 8(8242): 1-10. https://doi. org/10.1038/s41598-018-26688-8

- Yan, W., Kang, M.S. (2002). GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC press. DOI: https://doi.org/10.1201/9781420040371
- Yan, W., Rajcan, I. (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science, 42(1): 11-20. https://doi.org/10.2135/cropsci2002.1100
- Yue, H., Wei, J., Xie, J., Chen, S., Peng, H., Cao, H., Bu, J., Jiang, X. (2022). A study on genotype-by-environment interaction analysis for agronomic traits of maize genotypes across Huang-Huai-Hai Region in China. Phyton,91(1): 57. DOI: https://doi.org/10.32604/phyton.2022.017308
- Zeinalzadeh-Tabrizi, H., Amiri Oghan, H. (2021). Selection of superior spring rapeseed genotypes using new approach: Genotype by Yield×Trait biplot (GYT). Proceedings of the 7th Iranian Plant Physiology Conference. Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran. September 1-2, 2021. Pp 170-173.