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Araştırma Makalesi / Research Article

Investigation of Genotype × Environment Interaction in Some Sunflower (*Helianthus annuus* L.) Genotypes in Different Environmental Conditions

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Abstract

Trials in different environmental conditions have a fundamental role in selecting genotypes that perform best in different environments. Adana and Muş locations can be considered as a new test environment for sunflower breeders in terms of performance evaluation of some sunflower genotypes. This study was carried out in Adana and Muş ecological conditions in 2022 with 14 hybrid lines and 5 standard varieties according to Randomized Complete Block Design. According to the results of analysis of variance, genotype, location and genotype×location interaction were found statistically significant at 1% and 5% levels in terms of many traits. According to the average results of both locations in the study, plant height of genotypes is 139.0-179.0 cm, diameter 18.0-22.8 cm, 1000 seed weight 59.3-83.0 g, seed yield 2198- 4144 kg ha^{-1}, oil ratio 38.1-41.3 (%) and protein ratio ranged from 16.8 to 18.2 (%). In the GGE biplot technique, PC1 constituted 58.84% of the variation, PC2 constituted 41.16% and 100% of the variation in total. As a result, according to the findings obtained in the research; H1, H10 and H14 genotypes stand out in terms of oil ratio, H6, H18 and H3 genotypes in terms of seed yield and H9 and H11 genotypes in terms of both criteria. When the yield and quality traits of genotypes in Adana and Muş locations were evaluated together, it was concluded that H8 and H13 genotypes could be recommended for both locations.

Keywords: Sunflower, hibrid, seed yield, oil ratio, interaction

1. Introduction

Sunflower (*Helianthus annuus* L.) is the most important oil crop worldwide, generally used for oil production. With the Covid-19 pandemic, the need for oil production has gained more importance, especially in today's world where global food crises have come to the fore. Sunflower (*Helianthus annuus* L.) is grown in 72 countries in temperate and subtropical climates (Seiler et al., 2017). Sunflower is one of the most planted oilseed crops in the world after soybean, rapeseed and peanuts. While there are both oil and snack varieties of sunflower, cultivation of oil varieties for oil production has gained more importance. Sunflower has a higher oil content (48 %) than both rapeseed and soy, with about 70 % linoleic and 20 % oleic acid content of its oil content (Andrianasolo et al., 2016). According to FAOSTAT 2021 data, sunflower production is made in the world with a production of 58.2 million tons and a yield of 1.9 tons per hectare, while Turkey ranks 6th in sunflower production after Russia, Ukraine, Argentina, Romania and China. In 2021, the amount of oil sunflower production in Turkey increased by 16.5 % compared to the previous season and reached 2.2 million tons. In Turkey's 2021 production season, the provinces of Tekirdağ (399 thousand tons), Konya (324 thousand tons), Edirne (285 thousand tons), Kırklareli (226 thousand tons) and Adana (201 thousand tons) in oil sunflower production account for approximately 65 % of the total production (Anonim, 2022).

Due to the economic importance of sunflower, the determination of superior and effective hybrids in terms of quality characteristics to increase oil yield in sunflower breeding is one of the ultimate goals (Ghaffari et al., 2021). The ultimate goal of plant breeders is the development of new commercial genotypes that can adapt to different environmental conditions. Genotypes that are both stable and high yielding are considered to be the use of a wide range of genotype sets that can adapt to different environmental conditions (Lu'quez et al., 2002; Alizadeh et al., 2021; Ghaffari et al., 2021). For this reason, it is extremely important that the seed yield of the desired genotypes does not fluctuate much under different environmental conditions. G × E (Genotype × environment) interaction is defined as the performance of the cultivars developed as a result of many years of hard work, which differs according to changing environmental conditions. For this reason, the use of genotypes most suitable for the environment in order to achieve the desired yield and quality increases the chance of success. Sunflower studies should be given more importance both in Turkey and in the world, especially in order to combat the drought that emerged with global warming and to eliminate the vegetable oil deficit, which became more important in the food crisis. Varieties that adapt more easily to climatic conditions and show higher seed yield and oil yield performance are more preferred by producers in different regions. However, the main purpose of setting up yield trials is to predict the performance of the best variety in the future using available data.

A genotype with stable yields in different environments contributes little to the G×E interaction. Modeling of the G×E interaction in multimedia trials (METs) is required to identify genotypes with general and specific adaptations (Aarthi et al., 2020). Recently, GGE (genotype, genotype × environment) or GT (genotype × trait) biplot methods have been used in order to evaluate genotypes both in terms of their stability and in a versatile way. A GGE biplot (Yan et al., 2000), showing the genotype main effect (G) and the GE of a two-way table of a genotype environment simultaneously, can address relatively many questions to assess visual genotypes and environments (Yan, 2015; Kendal et al., 2022). The GGE biplot can be explained by a "which-where-won" model of MET (Mega × Environment × Trait) data for identification and variety recommendations important to each mega-environment.

Furthermore, a genotype × trait biplot (Yan and Rajcan, 2002) graphically approaches the genotype × trait interaction in two directions. The yield for each genotype in a genotype group is always affected by the interaction of genotypes, environment and G×E (Yan and Kang 2002; Gholizadeh et al., 2021). GEI (genotype×environment interaction) affects yield and production as it often prevents a genotype from maintaining its activity in different environments and identifying and selecting stable genotypes (Khomari et al., 2017; Ansarifard et al., 2020). If this interaction does not change the yield order of genotypes in different environments, a variety recommendation can be made (Kaya and Atakisi, 2002). The G×E interaction effect can cause yield variability that is often unexplained by the effect of genotypes and the environment, which is extremely important for breeders (Yan and Hunt, 2001). Such a biplot can be used to visualize genetic correlations between traits (breeding targets), making genotypes easier to understand by breeders. Understanding trait relationships also makes it easier to identify traits that can be used in indirect selection for a target trait and that can be extra-measured. A genotype × trait biplot can also be used to visualize the advantages and shortcomings of individual genotypes, which are important for both variety assessment and parent selection (Yan and Tinker, 2006; Kendal, 2022).

Many researchers used the GGE biplot (genotype main effect plus G×E interaction) graphical stable method for modeling the G×E interaction in different plant groups and multi-media experiments (Yan et al., 2000; Gauch 2006; Yan and Tinker 2006; Malla et al., 2010; Rakshit et al., 2012; Mohammadi and Amri 2013; Gholizadeh and Dehgani 2016; Sserumaga et al., 2016; Omoigui et al., 2017; Hassani et al., 2018; Dallo et al., 2019; Da Cruz et al., 2020; Ansarifad et al., 2020; Olanrewaju, 2021; Ghaffari, 2021; Kendal, 2022).

Sunflower is an important oil plant in Turkey and has half a century of cultivation history. Many researchers focused on the production of stable hybrids with higher oil yield in different environmental conditions in sunflower breeding studies. Therefore, in this study, the adaptability of hybrid sunflower lines with different characteristics in Adana and Muş locations was tested, and the interaction of GT (genotype × trait) and GL (genotype × location) was tried to be explained with graphics using the biplot technique.

2. Materials and Methods

The study was carried out with 14 hybrids (variety candidate) and 5 varieties in Adana and Muş locations in 2022. Some information about the hybrids and cultivars used in the study are given in Table 1, location information in Table 2, climate data in Table 3, and trial area soil structure data in Table 4.

Table 1. Some information about the hybrids and varieties used in the experiment

Code	Name	Pedigree	Breeding country	Seed yield	Oil ratio
H1	DA-VD 22-28	EH 935 x RYM13-61/1/2	Türkiye	3821	43.9
H2	DA-VD 22-29	EH 960 x RYH13-024/1/2 (1)	Türkiye	3666	40.3
H3	DA-VD 22-30	EH 960 x RYK17-10	Türkiye	3442	42.1
H4	DA-VD 22-31	EH 960 x RYK17-79 (2)	Türkiye	3427	44.3
H5	DA-VD 22-32	EH 960 x RYK18-08	Türkiye	3604	42.5
H6	DA-VD 22-33	EH 960 x RYM13-53/1	Türkiye	3748	42.9
H7	DA-VD 22-34	EH 960 x RYM13-59/2	Türkiye	2723	41.5
H8	DA-VD 22-35	EH 960 x RYM13-6/3	Türkiye	3729	43.1
H9	DA-VD 22-36	EH 500 SUL x RYM13-243/2	Türkiye	3216	46.5
H10	DA-VD 22-37	EH 933 İSO x DA-İMİ-R16-05	Türkiye	3591	42.2
H11	DA-VD 22-38	EH 935 x RYH13-029/2/2	Türkiye	3406	43.7
H12	DA-VD 22-39	EH 960 x RYK16-120	Türkiye	2823	42.7
H13	DA-VD 22-40	EH 960 x RYK17-47	Türkiye	3115	42.9
H14	DA-VD 22-41	EH 994 x MASR 2021	Türkiye	3241	38.0
H15	SUOMİ	not information available	Ukraine	2612*	45.3*
H16	P64LP140	not information available	Türkiye	2847*	47.9*
H17	P64LE141	not information available	Türkiye	2780*	44.1*
H18	LG50609 Sx	not information available	Spain	2624*	41.3*
H19	LG5485	not information available	Spain	3405*	46.5*

Source: Eastern Mediterranean Agricultural Research Institute Directorate, Adana, Türkiye.-2022, *****Varıety Registration and Seed Certıfıcatıon Center averages in registration trials

Table 2. Location information

Location	Altitude	Latitude	Longitude
Muş/TİGEM	1271	38°48'47.00"K	41°34'0.88"D
Adana/Ceyhan/Mercimek	25	37° 6'9.77"K	35°48'25.77"D

Table 3. Location climate data

Months	Average Precipitation (mm)				Average Temperature (°C)				Average Relative Humidity (%)			
	Location/Years				Location/Years				Location/Years			
	Adana		Muş		Adana		Muş		Adana		Muş	
	2010-2021 (l.term)	2022	2010-2021 (l.term)	2022	2010-2021 (l.term)	2022	2010-2021 (l.term)	2022	2010-2021 (l.term)	2022	2010-2021 (l.term)	2022
March	70.0	79.2	113.4	162.6	12.9	9.8	3.3	-0.1	71.2	63.0	66.3	89.1
April	51.7	1.0	67.8	32.0	17.1	19.4	10.9	11.3	70.3	54.5	66.0	54.9
May	56.6	1.6	77.1	91.6	21.2	21.5	15.7	13.5	65.9	63.3	57.4	64.1
June	26.4	29.2	14.9	16.0	24.9	25.4	21.3	21.1	69.9	73.3	59.4	43.4
July	11.8	0.0	5.5	0.0	28.1	28.5	25.7	25.5	75.3	65.8	57.3	23.2
August	4.5	4.6	2.3	0.0	28.7	29.2	26.0	26.6	75.0	68.3	53.9	17.3
September	20.6	10.0	6.4	17.2	26.0	26.4	21.5	21.4	71.3	60.9	55.8	25.6
October	33.5	0.0	32.8	21.4	21.0	22.4	14.7	15.1	64.1	52.7	54.9	45.4

Source: General Directorate of Meteorology -2022

Table 4. Soil structure data of the trial area

Soil analysis results											
	Physical Analysis					Chemical Analysis					
Locations	**Depth (cm)**	**Sand (%)**	**Silt (%)**	**Clay (%)**	**Ph**	**Calcification (%)**	**Salinity %**	**Organic Matter (%)**	**P_2O_2 kg ha^{-1}**	**K_2O kg ha^{-1}**	**Texture Class**
Muş/TİGEM	0-30	36.6	17.4	45.9	7.6	19.6	0.9	2.15	222	140	clayed
Adana/Ceyhan/Mercimek	0-30	34.2	12.7	41.5	7.7	20.07	0.04	1.61	63	128	clayed

Source: TİGEM laboratories-2022

This study was set up in a Randomized Complete Block Design with three replications. Trial sowing was done on 02 June 2022 in Muş location and on 07 April 2022 in Adana location. In the trials, the sowing depth was 6-8 cm, the distance between the rows was 70 cm, the distance between the rows was 30 cm, the number of plants in each row was 25, the plot length was 7.5 m and the sowing was done in 4 rows. In the trials, the middle 2 rows were harvested. In the trials, 80 kg ha^{-1} pure N and 50 kg ha^{-1} P_2O_5 fertilizer were used. When the plant height reached 10-15 cm, hand hoe and machine hoe between rows were made. Plants were harvested when they reached physiological maturity. Harvest was done on 12 October 2022 at the Mus location and on 19 August 2022 at the Adana location. Seed yield values obtained without correcting the harvest moisture of each plot were adjusted according to 10 % humidity in accordance with the technical instructions of the Variety Registration and Seed Certification Center Directorate (TTSM, 2001). Oil ratio was calculated by Soxhelet automatic oil extraction device (Gerhardt, Soxtherm 2000) and protein ratio was calculated by Kjeldahl method (AOAC, 2005).

2.1. Statistical Analysis

The combined variance analysis of the data obtained from the research was made using the JMP Pro 13 package program and the factors found to be important were evaluated according to the LSD test and grouped. In addition, Biplot analyzes of the obtained data were analyzed using Genstat version 14, using GT (Genotype × Trait) and GL (Genotype × Location) biplot method as suggested by Yan and Thinker (2005). The graphs obtained were interpreted according to the results obtained by the researchers working on different plants.

3. Results and Discussion

According to the combined variance analysis results; genotype, location and genotype × location interaction were found to be statistically significant at the level of 1 % and 5 % (Table 5). However, in terms of plant height, genotype and genotype×location interaction, and in terms of 1000 seed weight, the locations were not statistically significant (Table 5). Depending on the traits, genotypes and locations were grouped according to the LSD (0.05) test.

Table 5. Variance Analysis Table

Variation Sources	DF	Plant Height	Diameter	1000 Seed Weight	Seed yield	Oil Ratio	Protein Ratio
Model	41	50380.583	1572.8842	7462.688	1408419	1004.7634	789.1719
Genotype	18	2378.08	613.887**	4761.23**	172627**	455.256**	292.311**
Location	1	45488.1**	647.313**	347.028	1079104**	294.103**	52.6501**
Genotype*Location	18	1561.31	293.84**	2064.51**	150723**	247.607*	440.331**
Error 1	4	953.124	17.8439	289.925	5965.56	7.79675	3.88021
Error 2	72	6538.156	439.8044	2726.015	51009.9	1459429	231.269
CV (%)		**5.99**	**12.12**	**8.79**	**8.39**	**6.68**	**10.22**

**, p<0.01; *0.01<P<0.05; CV: coefficient of variation; DF: degrees of freedom

According to the variance analysis results, in terms of plant height; while locations were statistically significant at the 1% level, the interaction of genotype and genotype×location was not significant. The average plant height of the locations varied between 139.0-179.0 cm. The longest plant height was obtained from Adana location. In terms of diameter (cm); Genotype, location and genotype×location interaction were found to be statistically significant at the 1% level. The diameters of the locations were 18.0 and 22.8 cm. The largest diameter was obtained from Adana location. Genotype averages varied between 15.7-23.9 cm. The widest diameter was obtained from the H2 hybrid, and the narrowest diameter was obtained from the H19 (LG 5485) standard variety. In the genotype×location interaction, the largest diameter was obtained in Adana location and from H2 and H3 hybrids sharing the same group. The narrowest diameter was obtained from the standard variety G19 (LG 5485) from Muş location. In terms of 1000 seed weight (g) trait, genotype and genotype×location interaction was statistically significant at the level of 1%, while it was found to be insignificant in terms of locations. In terms of 1000 seed weight (g), the average of genotypes varied between 59.3-83.0 g. In genotype×location interaction, maximum 1000 seed weight was obtained from H13 hybrid in Adana location, and at least from H18 (LG 50609 SX) standard variety in Adana location. According to the variance analysis results, in terms of seed yield; Genotype, location and genotype×location interactions were found to be statistically significant at the 1% level. In terms of the average of the locations, the seed yield was 2198 and 4144 kg ha^{-1}. The highest seed yield was obtained from Adana location. According to the genotype averages, the highest seed yield was obtained from the H8 hybrid, and the lowest seed yield was obtained from the standard variety H16 (P64LE141). In the genotype×location interaction, the highest seed yield was obtained from the H8 hybrid in Adana location, and the lowest seed yield was obtained from the H2 hybrid in Muş location.

Table 6. The averages of the examined traits and the resulting groups

Genotypes	Plant Height			Diameter			1000 seed weight		
	Adana	**Muş**	**Average**	**Adana**	**Muş**	**Average**	**Adana**	**Muş**	**Average**
H1	169.7	135.1	152.4	22.3 c-h	17.5 ı-m	19.9 E-J	60.0 l-o	63.3 j-n	61.7 GH
H2	178.7	139.3	159.0	29.7 a	18.1 ı-l	23.9 A	76.3 b-g	58.9 m-o	67.6 D-G
H3	178.2	142.9	160.5	28.7 a	18.1 ı-m	23.4 A-C	70.7 e-k	64.3 ı-n	67.5 D-G
H4	182.8	141.3	162.1	23.5 c-e	17.4 ı-m	20.4 D-H	86.3 ab	79.7 a-e	83.0 A
H5	178.3	142.7	160.5	22.5 c-h	18.1 ı-m	20.7 E-I	75.3 c-h	69.2 f-l	72.3 B-D
H6	183.7	130.6	157.1	23.3 c-f	18.7 g-l	21.0 B-G	75.2 c-h	72.6 c-j	73.9 B-E
H7	176.3	142.1	159.2	22.7 c-g	19.7 e-k	21.2 A-F	72.3 c-k	69.3 f-l	70.8 C-E
H8	181.0	141.5	161.2	24.6 b-d	19.1 g-l	21.9 A-E	81.8 a-c	76.1 c-h	79.0 AB
H9	176.3	136.7	156.5	22.5 c-h	17.3 ı-m	19.9 E-J	66.7 g-n	74.2 c-ı	70.4 C-F
H10	166.5	135.3	150.9	21.2 d-ı	20.4 e-j	20.8 C-G	62.5 k-n	64.3 ı-n	63.4 F-H
H11	186.8	132.5	159.7	26.2 a-c	21.2 d-ı	23.7 AB	78.7 a-f	72.3 c-k	75.5 A-C
H12	188.5	138.3	163.4	27.7 a-c	18.6 h-l	23.1 A-D	72.8 c-j	68.0 g-m	70.4 C-F
H13	177.5	147.7	162.6	25.8 d-ı	19.3 f-l	22.5 A-E	86.5 a	66.5 g-n	76.5 A-C
H14	170.2	135.6	152.9	21.1 d-ı	15.3 lm	18.2 G-K	66.3 g-n	59.0 m-o	62.7 GH
H15	176.3	131.4	153.9	18.3 ı-l	19.0 g-l	18.6 F-J	71.7 d-k	73.2 c-j	72.4 B-D
H16	196.2	144.3	170.2	17.0 j-m	17.8 ı-m	17.4 JK	57.2 no	66.3 h-n	61.7 GH
H17	180.0	143.4	161.7	19.1 g-l	16.5 j-m	17.8 H-K	70.5 e-k	58.7 m-o	64.6 E-H
H18	170.8	138.8	154.8	19.2 g-l	15.9 k-m	17.6 I-K	51.2 o	67.4 g-m	59.3 H
H19	182.7	142.1	162.4	17.2 ı-m	14.1 m	15.7 K	81.0 a-d	73.5 c-ı	77.3A-C
Mean	**179.0 A**	**139.0 B**		**22.8 A**	**18.0 B**		**71.7**	**68.2**	
LSD 0.05 Location		8.02			1.09				
LSD 0.05 Genotype					2.84			7.08	
LSD 0.05 Genotype*Location					4.02			10.01	

LSD: Low singificant difference

In terms of oil ratio (%), genotype and locations were found to be statistically significant at the level of 1%, and the interaction of genotype×location was statistically significant at the level of 5%. In terms of the average of locations, the oil ratio was 38.1 and 41.3 (%). According to the location averages, the highest percentage of oil ratio (%) was obtained in Adana location. According to genotype averages, the highest oil ratio was obtained from H16 (P64LP140) and H11 and H14 hybrids sharing the same group. In the genotype×location interaction, the highest oil ratio was obtained from Adana location and H16 (P64LP140) standard variety, and the lowest oil ratio was obtained from H5 and H6 hybrids sharing the same group in Muş location. In terms of protein ratio (%); Genotype, location and genotype×location interaction were found to be statistically significant at the 1% level. In terms of the averages of their locations, the protein ratio was 16.8 and 18.2 (%). The highest protein ratio was obtained from Muş location. In terms of the averages of genotypes, it varied between 14.3-19.7 (%). The highest protein ratio was obtained from H13 and H4, H9 and H14 hybrids sharing the same group, and the lowest protein ratio was obtained from the H16 (P64LP140) standard variety. In the genotype×location interaction, the highest protein ratio was obtained from the H9 hybrid in Muş location, and the lowest protein ratio was obtained from the H16 (P64LP140) standard variety in Adana location.

Table 7. The averages of the examined traits and the resulting groups

Genotypes	Seed yield)			Oil ratio			Protein ratio		
	Adana	**Muş**	**Average**	**Adana**	**Muş**	**Average**	**Adana**	**Muş**	**Average**
H1	4023 ef	2561 ıj	3292 C-E	45.8 ab	36.8 ı-l	41.3 A-C	14.8 j-m	20.4 a-d	17.6 A-E
H2	4629 bc	1737 o	3183 D-F	38.1 g-l	39.0 e-k	38.6 C-E	19.9 a-e	15.8 g-l	17.9 A-D
H3	3984 ef	1979 l-o	2982 FG	37.2 h-l	37.1 ı-l	37.1 DE	18.7 c-g	17.2 e-k	18.0 A-D
H4	4535 b-d	1938 m-o	3236 C-F	41.0 c-ı	37.7 g-l	39.4 B-E	19.1 b-f	19.9 a-e	19.5 A
H5	4863 ab	2385 ı-l	3624 AB	39.8 d-k	34.5 l	37.1 DE	15.8 g-l	18.2 d-g	17.0 B-F
H6	4952 ab	2298 ı-n	3625 AB	38.5 f-l	34.4 l	36.4 E	18.1 d-h	18.0 d-h	18.1 A-D
H7	4163 de	2057 k-o	3110 EF	42.7 a-f	36.6 j-l	39.7 B-D	17.7 d-j	19.8 a-e	18.7 AB
H8	5260 a	2286 ı-n	3773 A	40.5 d-j	37.9 g-l	39.2 B-E	22.0 ab	15.1 ı-l	18.5 AB
H9	4827 ab	2225 ı-n	3526 A-C	41.9 b-g	37.4 h-l	39.7 B-D	16.6 f-l	22.4 a	19.5 A
H10	4275 c-e	2230 ı-n	3253 C-F	43.4 a-d	40.8 c-j	42.1 AB	14.4 k-m	18.5 c-g	16.5 C-G
H11	4656 bc	2600 ı	3628 AB	44.9 a-c	41.0 c-ı	43.0 A	16.4 f-l	18.9 c-f	17.6 A-E
H12	4327 c-e	2332 ı-m	3330 B-E	40.6 c-j	38.1 g-l	39.3 B-E	20.2 a-d	16.5 f-l	18.4A-C
H13	4676 bc	2268 ı-n	3472 A-D	35.9 kl	41.0 c-ı	38.5 C-E	21.2 a-c	18.1 d-g	19.7 A
H14	3992 ef	2248 ı-n	3120 EF	43.3 a-e	42.8 a-f	43.0 A	20.4 a-d	18.8 c-f	19.6 A
H15	3097 h	2131 j-o	2614 HI	43.7 a-d	38.8 f-k	41.2 A-C	14.2 lm	17.9 d-ı	16.0 D-H
H16	2484 ı-k	2372 ı-l	2428 I	46.2 a	40.3 d-j	43.2 A	11.0 n	17.5 d-j	14.3 H
H17	3612 fg	1882 n-o	2747 GH	39.6 d-k	36.5 j-l	38.1 DE	15.2 h-l	15.8 g-l	15.5 F-H
H18	3145 h	2177 ı-n	2661 HI	41.5 b-h	37.0 ı-l	39.2 B-E	12.2 mn	17.8 d-ı	145.0 GH
H19	3229 gh	2049 l-o	2639 HI	41.0 c-ı	36.7 ı-l	38.9 C-E	12.1 mn	19.2 b-f	15.6 E-H
Mean	4144 A	2198 B		41.3 A	38.1 B		16.8 B	18.2 A	
LSD 0.05 Location		20.08			0.72			0.51	
LSD 0.05 Genotype		30.63			3.05			2.06	
LSD 0.05 Genotype*Location		43.32			4.32			2.91	

LSD: Low singificant difference

When the correlation values of the bilateral relations between the examined traits are examined; It was determined that there was a statistically significant and positive relationship at the level of 1% between seed yield (kg ha^{-1}), plant height, diameter, oil ratio and 1000 seed weight. There was no significant relationship between seed yield and protein ratio.

Table 8. Correlation values of the bilateral relations between the examined traits

Examined traits	Plant height	Diameter	Seed yield	Oil ratio	Protein ratio
Diameter	0.5348**				
Seed yield	0.7613**	0.7186**			
Oil ratio	0.4028**	0.126	0.2704**		
Protein ratio	-0.2195*	0.2655**	0.1122	-0.3821**	
1000 seed weight	0.1999*	0.295**	0.364**	-0.1853*	0.3921**

**:%1; *: %5 statistically significant at the level

According to the analysis of variance results, genotype, location and genotype×location interaction contributed to the total variation by 12.30%, 76.94 and 10.74%, respectively, in terms of seed yield (Table 5). When a general evaluation is made in terms of the examined traits, the large difference between locations in terms of seed yield indicates that this trait is largely under the effect of the environment. It has been shown that the environment has a significant effect on plant height. The diameter differed significantly according to the locations. Since there is a parallel relationship between the diameter and the number of seeds in the diameter, this situation directly affected the seed yield. Since the heritability of 1000 seed weights is quite high, it did not show significant differences according to the locations. However, 1000 seed weights of the same genotypes according to locations showed higher values in Adana location. The data obtained in the study are in harmony with many researchers (Kaya et al., 2009; Sefaoğlu and Kaya, 2018; Çetin and Öztürk, 2018; Jockovic et al., 2019; Ghaffari et al., 2021).

When the climatic data of the locations are examined in general terms, the precipitation in Muş location in April and May caused the sowing date to delay. However, although the average of May is a suitable planting date according to the long-term averages of the temperatures suitable for planting in Muş location, it does not allow sowing in these months when the average precipitation for long years is taken into account. (Table 3). However, due to the effects of global warming, they reported that there were significant changes in the average temperature variable in Muş location, and this change was in an increasing trend (Atabey and Toprak, 2018). Accordingly, it suggests the possibility that temperature changes may change the precipitation regime. This situation reveals the possibility that the sowing dates may be brought forward in the following years in the region. It is thought that planting in Muş location in June causes yield decreases due to the high temperature and low relative humidity, especially during the seed development stage. In terms of the examined traits, it is thought that the differences in the locations are caused by the climate.

3.1. GGE biplot analysis

In GT biplot technique, both the relationship between traits and the relationship between genotype traits can be explained. As the angle value (>0--<90°) decreases between the vectors of the two traits, it shows a positive relationship, and as the angle value (90°>-<180°) increases, there is a negative relationship (Kendal and Sayar, 2016; Kendal, 2022). In addition, the positioning of genotypes according to traits also shows which genotype has high values in terms of which traits (Figure 1).

Especially, the H2 and H7 hybrids are located in the region of seed yield, diameter and protein ratio, showing that they are satisfactory in terms of these parameters. In addition, H11, H9, H1, H10 and H14 hybrids are located at the intersection of protein and oil ratio, showing that they have both good protein and high oil ratio. On the other hand, the angle between the vectors of seed yield and protein ratio and diameter is quite narrow, indicating a high positive correlation between these traits, and a wide angle between seed yield and oil ratio and plant height, indicating a negative correlation between the two (Figure 1 and Table 8).

In addition, the most suitable genotypes for each sector and trait group were determined by the sector analysis (Figure 2). When the traits examined in the research were examined in the sector analysis, the traits were gathered in four different sectors and four groups. The 1st group consisted of 1000 seed weight, the 2nd group consisted of seed yield, protein ratio and diameter, the 3rd group oil ratio and the 4th group the plant height. Particularly, seed yield, protein ratio and diameter formed the same group in the same sector. All standard varieties (H15, H16, H17, H18 and H19) used in the trial show that they are not correlated with any traits by taking place in the sector where no traits are present. It is possible to say that the genotypes in the sectors where the traits are not included are weak in terms of traits.

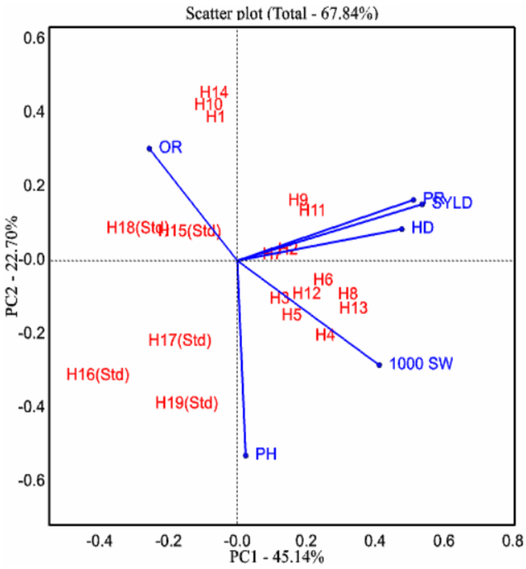

Figure 1. The relationship between genotypes and traits.

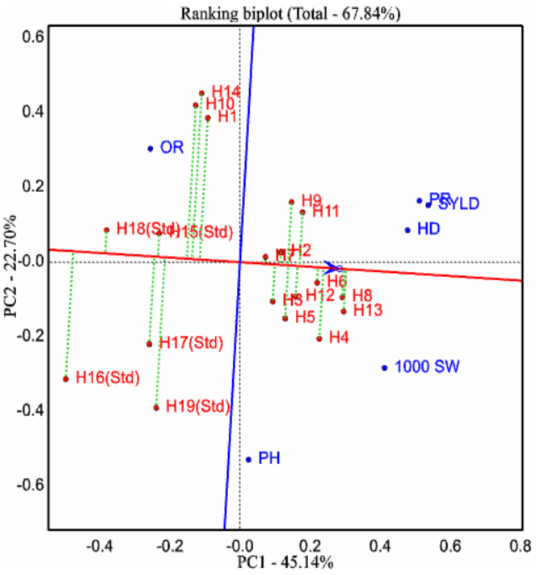

Figure 2. Grouping of genotypes in terms of traits.

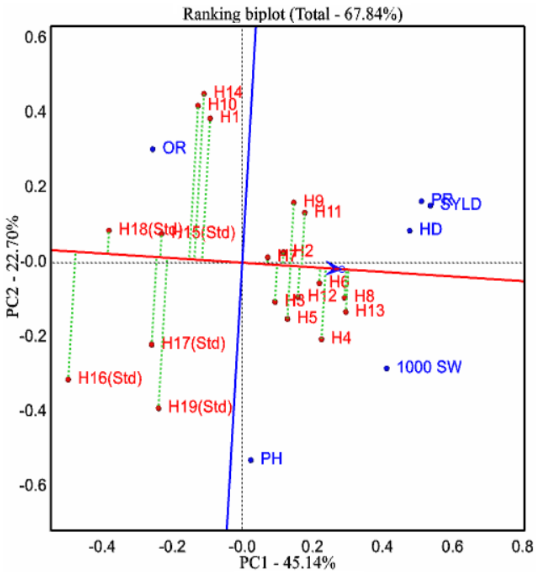

Figure 3. Ranking of genotypes in terms of traits.

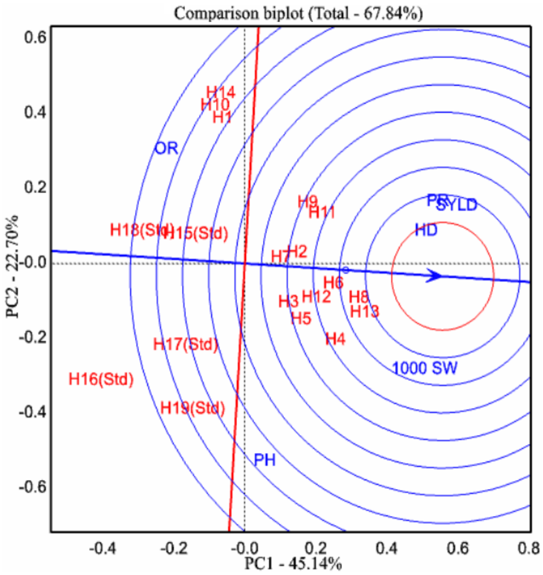

Figure 4. Ranking of genotypes according to ideal center.

The stability curve formed over the average data of all the traits examined in the study and the ranking biplot method that ranks the genotypes according to this stability curve are shown in Figure 3. It is a model that ranks genotypes according to stability (horizontal) and mean (vertical) baseline curves for all traits in multi-trait studies. In line with these explanations, in Figure 3, it was determined that H6 was the most stable in terms of all traits, H13 and H8 hybrids had the highest values in terms of all traits, and H14 was the genotype with the weakest stability. In addition, H19, H16 and H17 standard varieties did not perform well because they were below the curve (vertical curve), and stable genotypes H9 and H11 hybrids above the vertical curve and close to the horizontal curve could be selected for selection because they were good performing genotypes.

In addition, genotypes can be ranked according to the ideal center created according to the average of the traits in the Comparison biplot model (Figure 4). Accordingly, H13 and H8 hybrids were found to be the most ideal genotype since they are located in the region closest to the ideal center. The GT biplot technique seems to be a useful technique that can be used easily in selection, as it provides us with a lot of convenience in visually interpreting the relationships. Many researchers have reported that this technique is beneficial in the results of their research on this subject (Gauch, 2006; Balalic et al., 2013; Xu et al., 2014; Movahedi et al., 2020; Khan et al., 2021).

Figures 5, 6, 7 and 8 show the GGE biplot based on a two-way yield table over genotype × environment interaction in the study conducted at Adana and Muş locations.

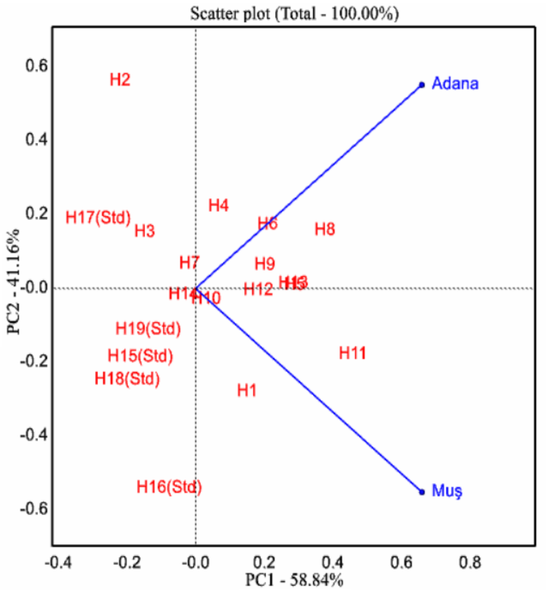

Figure 5. Locations and Genotype×Location relationship.

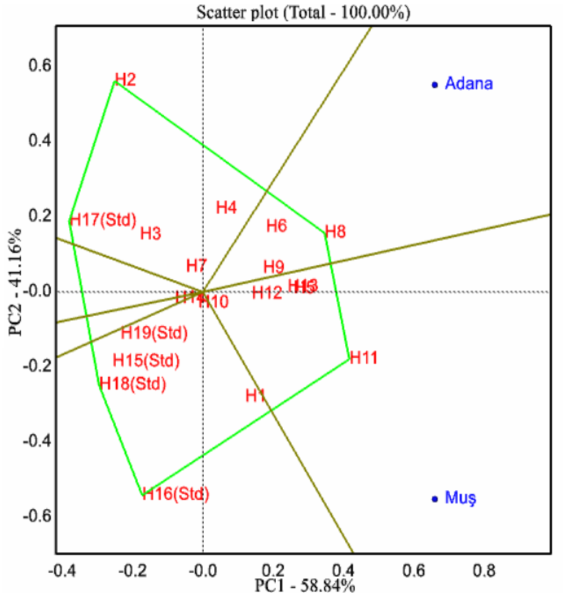

Figure 6. Grouping of locations by sector analysis and position of genotypes relative to location.

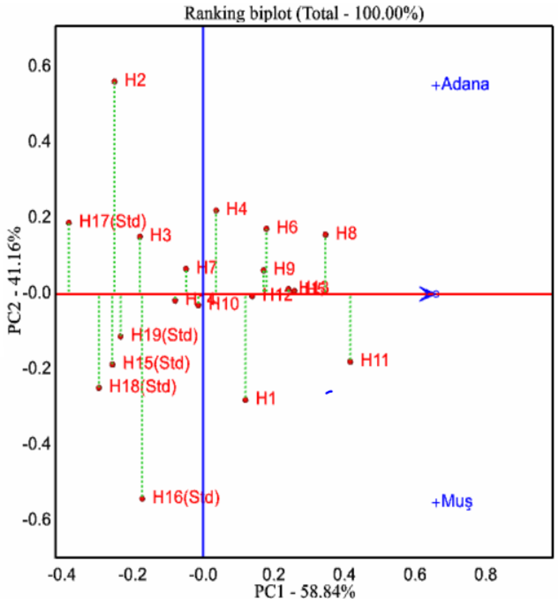

Figure 7. Stability of genotypes according to locations.

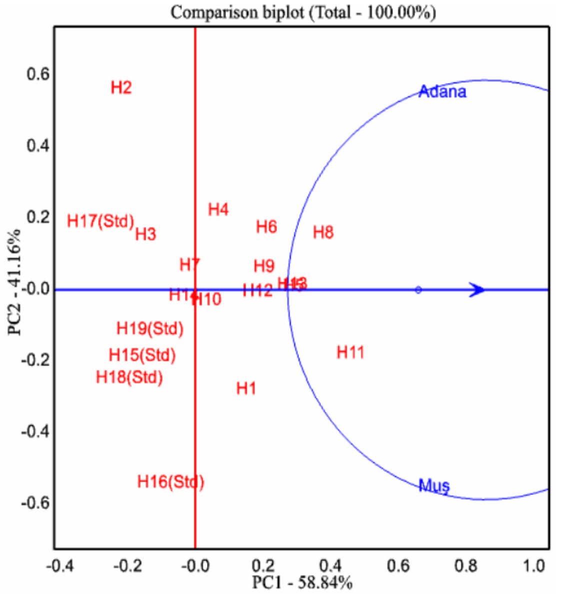

Figure 8. Ranking the genotypes according to the ideal center according to the locations.

All environments are assumed to be equally important in genotype assessment as environment standardized data are used. It allows for appropriate visualization of relationships between environments for environment-focused singular value segmentation. This biplot explained all (100 %) of the GGE and showed that the GGE is fairly straightforward for the genotypes in this dataset. The effect of PC1 on the total variation was explained as 58.84 % versus the value of PC2 as 41.16 %, demonstrating that it could adequately explain the GGE patterns dependent on the GGE biplot. Figure 5 gives information about the relationship between Adana and Muş location and the relationship between genotype location. Visually, it shows that both locations are not very closely related and differ from each other and can be considered as separate environments in the selection of genotypes. When we evaluate the genotypes according to both locations in terms of the average of all characteristics; H1 hybrid especially for Muş location, H4 hybrid has better results for Adana location and can be recommended in years and locations with similar ecological conditions and can be selected in selection, while H15, H16, H17, H18 and H19 standard varieties do not have suitable results for locations, but more It is thought that the experiment should be repeated in the following years in order to make decisive decisions (Figure 5). The determination of mega-environments according to the averages of genotypes reveals that similar environments should be excluded in future studies, and environments that increase operating costs and do not create differences should not be used unnecessarily (Figure 6). In the sector analysis made in this sense, 6 sectors were formed and the circles defining each location were included in different sectors and mega-groups, revealing the differences of the circles. H8, H6 and H9 hybrids of the genotypes in the same sector with the environments have good results in Adana location, and the H11, H13, H5 and H12 hibrids in Muş location, while the H2, H17, H18 and H19 hybrids of the genotypes in different sectors from the environments have good results in Adana and Muş locations. The ranking biplot method, which creates the stability curve over the average data of all the traits examined in the study and ranks the genotypes according to this stability curve, is shown in Figure 7. According to this model, which ranks genotypes according to stability (horizontal) and mean (vertical) baselines in terms of all traits in multi-feature studies, it shows that H8 and H11 hybrids have both stable and good results in terms of all traits in Adana and Muş locations. These genotypes were followed by the H13, H5, H0 and H12 hybrids. However, H2 hybrid and H16 standard variety, which are above average but unstable H1 and H4 hybrids and which are unstable but below average, can be eliminated for Adana and Muş locations. Genotypes can be ranked according to the ideal center formed according to the average of the traits (Figure 9). Accordingly, it has been determined that H8 and H11 hybrids are quite ideal genotypes by being located in the ideal center, and H13, H5, H12 and H9 hybrids can be preferred after these genotypes because they are located in the region close to the ideal center. In addition, it has been determined that it is very convenient for us to determine the genotypes to be selected and eliminated by easily observing the genotypes above and below the average vertical curve. These results are confirmed by the results of many researchers (Mousavi et al., 2016; Jockovic et al., 2019; Saremi-Rad et al., 2020; Ghaffari et al., 2021; Gholizadeh et al., 2022).

4. Conclusion

In this study, which was carried out in Adana and Muş locations in 2022 and tested 14 hybrids sunflower and 5 standard sunflower varieties; According to the results of the research, it was concluded that the hybrids used in the research were superior in terms of both yield ve yield components and quality traits when compared with the standards. According to the research results; H6, H18 and H3 showed high performance in terms of yield and yield components, H1, H10 and H14 hybrids showed high performance in terms of oil ratio, while H9 and H11 showed high performance in terms of both yield and yield components and oil ratio. In addition, according to the biplot results, it was determined that H6 was the most stable genotype in terms of all traits, while H8 and H13 were the genotypes with high values. In the genotype location evaluation made with biplot analysis technique, it was shown that the locations were in different groups and H8 and H11 had good results. As a result, it was concluded that Biplot analysis technique visually facilitated the work of breeders in selection, and H1, H10 and H14 hybrids in terms of oil ratio, H6, H18 and H3 genotypes in terms of seed yield, and H9 and H11 hybrids for both criteria and H8 and H13 in all parameters hybrids are recommended. It has been concluded that different genotypes can be candidates for registration in terms of oil production, yield and quality traits, or all parameters.

Declaration of Author Contributions

The authors declare that they have contributed equally to the article. All authors declare that they have seen/read and approved the final version of the article ready for publication.

Declaration of Conflicts of Interest

All authors declare that there is no conflict of interest related to this article.

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