Selection criteria for yield in safflower (*Charthamus tinctorius* L.) genotypes under rainfed conditions

H. Koç ✉

Bahri Dagdas International Agricultural Research Institute, Konya, Turkey
✉Correspondence: koc175@hotmail.com

SUMMARY: This research was conducted on 20 safflower genotypes and lasted 3 years (2014-2016) in the Central Anatolia Region of Turkey. The experiments were conducted in randomized block design with four replications. The relationships among yield 9 other traits in safflower genotypes were investigated. As the average of three years, the greatest seed yield (SY) was obtained from genotype G5 (PI 451952) with 3156.3 kg·ha^{-1}. It was followed by genotypes G4 (PI 525458) and G9 (PI 306686) with 3013.2 and 2977.1 kg·ha^{-1}, respectively. Among the standard cultivars, the greatest seed yield (2750.4 kg·ha^{-1}) was obtained from the Dinçer cultivar. The greatest oil content (OC) was obtained from the genotype G11 (PI 537665) with 36.5%. It was followed by the genotypes G9 (PI 306686) (35.4%), G6 (PI 537598) (35.4%) and G14 (PI 560169) (35.3%). Oil contents varied between 29.1-36.5%. Yield-trait relationships were assessed through both correlation analysis and GT (Genotype by Trait) biplot analysis. Based on the results of the two approaches, plant height (PH), number of branches (NB), number of heads (NH) and thousand-seed weight (TSW) were identified as the most significant selection criteria for yield from safflower. The combined use of correlation and biplot analysis in the assessment of relationships among the traits improved the chance for success.

KEY WORDS: Correlation; GT (Genotype by Trait)-biplot; Safflower; Selection; Yield

RESUMEN: *Criterios de selección para el rendimiento en genotipos de cártamo (*Charthamus tinctorius *L.) en condiciones de secano*. Esta investigación se realizó con 20 genotipos de cártamo durante 3 años (2014-2016) en la región de Anatolia central de Turquía. Los experimentos se realizaron en bloques de diseño aleatorio con cuatro repeticiones. Se investigaron las relaciones de rendimiento con los otros rasgos y las relaciones genotipo-rasgo en plantas de cártamo. Como promedio de tres años, el mayor rendimiento de semillas (SY) se obtuvo del genotipo G5 (PI 451952) con 3156,3 kg·ha^{-1}. Le siguieron los genotipos G4 (PI 525458) y G9 (PI 306686) con 3013,2 y 2977,1 kg·ha^{-1} respectivamente. Entre los cultivares estándar, el mayor rendimiento de semilla (2750,4 kg·ha^{-1}) se obtuvo del cultivar Dinçer. El mayor contenido de aceite (OC) se obtuvo del genotipo G11 (PI 537665) con 36,5%. El contenido de aceite varió entre 29,1 - 36,5%. Las relaciones rendimiento-rasgo se evaluaron mediante análisis de correlación y análisis biplot GT (Genotipo por rasgo). Con base en los resultados de dos enfoques, la altura de la planta (PH), el número de ramas (NB), el número de cabezas (NH) y el peso de miles de semillas (TSW) se identificaron como los criterios de selección más importantes para el rendimiento en el cártamo. El uso combinado de análisis de correlación y biplot en la evaluación de las relaciones entre los rasgos mejoró la posibilidad de éxito.

PALABRAS CLAVE: Cártamo; Correlación; GT (genotipo por rasgo)-biplot; Rendimiento; Selección

1. INTRODUCTION

Safflower (*Charthamus tinctorius* L.) requires less water than other oil crops such as rapeseed (*Brassica napus ssp. oleifera* L.), sunflower (*Helianthus annuus* L.) and soybean *(Glycine max* L. Merr.*)* and it is quite well adapted to dry conditions. Thus, it had become a salient crop in the midst of present climate change and global warming trends. Safflower is an important oil crop both for cooking oil and biodiesel production. High drought resistance provides significant advantages to safflower over other oil crops in cropping patterns (Kose, 2017).

Low yield and decreased percentage are the basic limitation in safflower production. Therefore, plant improvement studies mostly focused on the development of new safflower lines with high seed yield and more oil content so as to meet the demands of growers and the industry (Koç *et al.,* 2010).

Success of a breeding program is directly related to the proper selection of yield components at every stage of the program, efficient interpretation and use of resultant data (Flores *et al.,* 1998; Rubio *et al.,* 2004; Baljani *et al.,* 2015).

In breeding programs for high yield cultivars, the assessment of yield and highly-heritable characteristics may improve the chance for success. Therefore, while generating breeding programs, it is useful to know the relationships among the characteristics. The ultimate target in safflower breeding is to develop new and superior cultivars with high seed yield and oil content. Breeders search for reliable selection criteria and then select the characteristics which are directly or indirectly related to yield. Especially in the early stages (F2-F5) with insufficient seed quantity for yield experiments, yield-related parameters play an important role.

Genotype selection brings a new dimension to the complexity and difficulty of plant breeding programs. Multiple breeding targets should be taken into consideration when selecting genotypes and recommending cultivars. In fact, plant breeding not only improves the yield of a plant, but also integrates high yield with the desired parameters like quality and performance (Yan *et al.*, 2019a).

Despite reasonable values for the other parameters, genotypes with a value for a certain trait below the minimum requirements are hard to register. For instance, high quality is a valuable trait only when it is related to high yield; a high-quality genotype with a low yield will not be registered as a cultivar. Therefore, it is quite significant to take entire key traits into consideration when selecting genotypes and/or agronomic methods (Yan *et al.*, 2019b).

The genotype – trait (GT) biplot procedure of GGE biplot method is used to assess the different traits of the genotypes. GT biplot allows the user to make visual assessments of genotype-trait data. Compared to conventional methods, the GT biplot approach has some advantages: 1. Graphical presentation of the data improves comprehension of data patterns; 2. It is easy to interpret, facilitate the comparison of genotypes or traits and efficiently presents the relationships among the investigated traits; 3. It is easy to see which genotype is winning or losing in which trait; 4. It can be used in multi-trait-based selections and in the comparison of selection strategies (Yan *et al.*, 2007). While correlation analysis identifies the level of relationship between the traits, the GT biplot is able to put forth both the relationships among the traits and genotype – trait relationships (Yan and Reid, 2008).

In this study, the GT (Genotype by Trait) biplot technique and correlation analysis were used together to investigate the Genotype-Trait relationships and the relations among the traits.

The aim of this study is for the findings to be useful for safflower breeders and safflower producers who are concerned with increasing seed yield with the data obtained.

2. MATERIALS AND METHODS

This research was carried out with 20 genotypes (Table 1) over 3 years (2014-2016) in the Central Anatolia Region of Turkey. The experiments were conducted in randomized block design with 4 replications. The plot size was 6 m² (1.2 x 5 m) and seeds were sown with an experimental sowing machine. Sowing was performed in the last week of March so as to have 125 seed per m². Harvest was carried out in the second week of August with a plot combine harvester.

The experimental soils were of a clay texture with a moderate organic material level (2.3%) and high lime content (29%). The soils were slightly alkaline (pH 7.8), rich in phosphorus and potassium and deficient in zinc. There were no salinity problems at the research site.

Monthly average temperatures during the experimental years were close to long-term averages

TABLE 1. Name and origin of the studied safflower genotypes

Entry	Genotip	Code	Accession number	Origin
1	28-2	G1	PI 537110	Mexico
2	11-1	G2	PI 560172	United States
3	77-2-a	G3	PI 537606	United States
4	82-3	G4	PI 525458	United States
5	25-4-b	G5	PI 451952	India
6	106-2	G6	PI 537598	United States
7	Göktürk	Göktürk	BDYAS-4	Turkey
8	63-2-b	G7	PI 537702	United States
9	Dinçer	Dinçer	GKTAE	Turkey
10	64-3-b	G8	PI 537703	United States
11	91-2	G9	PI 306686	Israel
12	Linas	Linas	TTAE	Turkey
13	Balcı	Balcı	EGKTAE	Turkey
14	77-1-d	G10	PI 537607	United States
15	89-1-c	G11	PI 537665	United States
16	13-2-c	G12	PI 537607	United States
17	96-3	G13	PI 544059	China
18	56-2-c	G14	PI 560169	United States
19	52-1	G15	PI 307056	Mexico
20	83-1-a	G16	PI 537694	United States

(Table 2). On the other hand, total temperatures throughout the vegetation period (March - August) were 5.8 °C greater in 2014 and 2016 than the long-term averages (104.8 °C).

Total precipitation was measured as 366 mm in 2014 (44 mm greater than the long-term average), as 309 mm in 2015 (close to long-term average of 322 mm) and as 201 mm in 2016 (121 mm lower than long-term average) (Table 2).

Observations and measurements: Seed yield (kg·ha^{-1}), oil content (%), oil yield, plant height (cm), number of days to 50% flowering, number of branches, number of heads, head diameter (cm), thousand-seed weight (g).

Variance analyses were run on the data obtained from 20 safflower genotypes. A linear correlation analysis was applied pairwise to all the parameters studied, yield (SY) and other traits (OC, OY, PH, NDF, NB, NH, HD, and TSW). The experimental data were subjected to variance and correlation analyses with the aid of JMP 5.0 software. Significant means were compared with the aid of the LSD test. A GT biplot analysis for the visual assessment of Genotype − Trait relationships and the relationships among the traits was conducted with the use of XLSTAT software. The GT biplot analysis was employed to display the two-way relationship between genotype and trait. It was based on the following formula:

$$\frac{T_{ij} - \beta_j}{s_j} = \sum_{n=1}^{2} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{2} \xi * in\eta * jn + \varepsilon_{ij}$$

where T_{ij} is the average value for genotype i for trait j; β_j is the average value for all genotypes in trait j; S_j is the standard deviation of trait j among the genotype averages; λ_n is the singular value for principal component PC_n; ξ_{in} and η_{jn} are scores for genotype I and trait j on PC_n, respectively; and ϵ_{ij} is the residual associated with genotype i in trait j. To achieve symmetric scaling between the genotype

TABLE 2. Monthly precipitation (mm) and monthly temperature averages (C0) for years and during years (1929-2016) of the experiment

							Months							
	Years	**Jan.**	**Feb.**	**Mar**	**Apr**	**May**	**June**	**July**	**Aug.**	**Sept**	**Oct**	**Nov.**	**Dec.**	**TOT**
Prep.	**2014**	58.8	17.4	20.4	19.2	26	31.4	3	4.6	31.4	89.6	32.2	32.1	366
	2015	24.6	23.5	55.9	7.6	53.2	39.6	8.6	17.2	31.4	39.0	5.8	2.6	309
	2016	42.4	2.8	37.8	9.4	35.2	18.4	0.2	0.0	23	0.0	16.0	16.4	201
	Long years	38	29	28	32	43	24	6	5	13	30	32	42	322
Temp.	**2014**	2.4	6.4	7.2	12.3	15.5	19.7	25.1	25.0	22.6	15.8	5.8	5.5	163
	2015	0.7	4.8	5.9	8.1	15.7	18.7	24.0	24.6	21.8	14.6	7.9	-0.8	146
	2016	0.1	6.8	7.7	14.5	15.9	22.2	24.9	19.6	17.9	12.8	7	2	151
	Long years	-0.3	1	5.7	11	15.8	20.4	23.6	23.2	18.7	12.6	5.9	1.5	139

TOT: Total, Prep: Precipitation, Temp: Temperature

scores and the trait scores the singular value λ_n had to be absorbed by the singular vector for genotypes ξ_{in} and that for traits η_{jn}. That is, $\xi^{in} = \lambda^{n.5} \xi_{in}$ and $\eta^{jn} = \lambda^{n.5} \eta_{jn}$. Only PC1 and PC2 were retained in the model because such a model tends to be the best for extracting pattern and rejecting noise from the data. The GT biplot was generated by plotting ξ^{i1} and ξ^{i2} against η^{j1} and η^{j2}, respectively, so that each genotype or trait was represented by a marker in the biplot. In the GT biplot, a vector was drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships between and among the traits (Yan and Rajcan, 2002; Akçura, 2011).

3. RESULTS AND DISCUSSION

The variance analysis revealed that there were significant differences among all the traits of the genotypes (P < 0.01). Year x genotype interaction

was also found to be significant for all traits, except for head diameter (HD) (Table 3).

For the average of the three years, genotype G5 had the greatest seed yield (SY) with 3156.3 kg·ha⁻¹. It was followed by genotypes G4 and G9 (with 3013.2 and 2977.1 kg·ha⁻¹) (Table 4). Among the standard cultivars, the greatest seed yield (2750.4 kg·ha⁻¹) was obtained from the Dinçer cultivar. The greatest oil content (36.5%) was observed in genotype G11 and it was followed by genotypes G9 (35.4%), G6 (35.4%) and G14 (35.3%). The oil contents in the genotypes varied from 29.1 - 36.5%. The oil yield (OY) values, calculated by multiplying seed yield by oil content, varied from 717.9 - 1058.6 kg·ha⁻¹.

Plant height (PH) values varied from 67.8 - 81.5 cm. Ideal safflower plant heights for machine harvest should be between 60 - 80 cm (Weiss, 2000). All the present genotypes yielded plant heights within this range. The number of days to flowering (NDF) values varied from 68 - 76 days; the number of branches
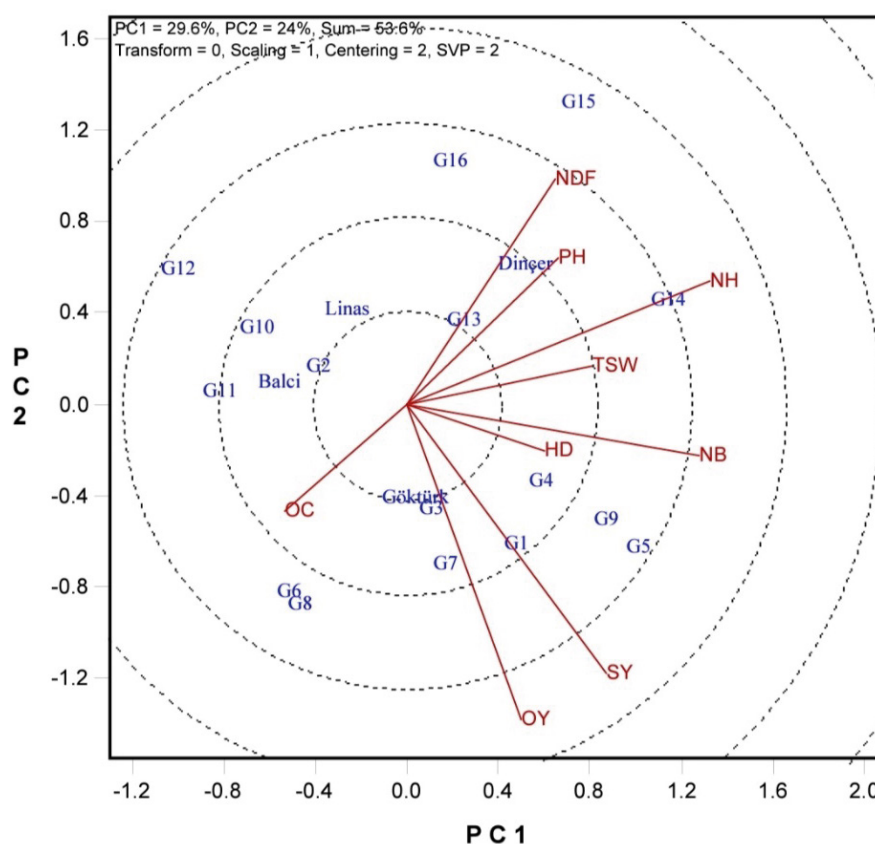

FIGURE 1. Vector view of genotype by trait biplot, showing the interrelationship among all measured traits for 20 different safflower genotypes. Traits: SY: Seed Yield, OC: Oil Content, OY: Oil Yield, PH: Plant Height, NDF: Number of Days to %50 Flowering, NB: Number of Branches, NH: Number of Heads, HD: Head Diameter, TSW: Thousand-Seed Weight

TABLE 3. Analysis of the combined variance of the properties studied

SV	DF	SY	OC	OY	PH	NDF	NB	NH	HD	TSW
		MS	MS	MS	MS	MS	MS	MS	MS	MS
Replication	3	3541**	0.9	383**	98	4.6*	0.7	3*	0.06	0.3
Year	2	278845**	43**	30859**	10194**	3222**	18**	89**	0.01	81**
Genotyp	19	7674**	42**	1021**	138**	48**	7.4**	13**	0.06*	58**
Year x Genotyp	38	6179**	9**	870**	97**	34**	1.2*	5.8**	0.04	30**
Error	177	575	0.4	65	38	1.6	0.7	1.0	0.04	0.8
Total	239	4396**	5.5**	530**	141**	37**	1.5**	3.4**	0.04	11**

SV: Source of Variance, **DF:** Degrees of Freedom, **MS:** Mean Square, ****P<0.01** significant, ***P<0.05** significant
SY: Seed Yield, **OC:** Oil Content, **OY:** Oil Yield, **PH:** Plant Height, **NDF:** Number of Days to %50 Flowering, **NB:** Number of Branches,
NH: Number of Heads, **HD:** Head Diameter, **TSW:** Thousand Seed Weight**(g)**

TABLE 4. Mean yield and yield components (4 replications) of 20 safflower genotypes tested over 3 (2014-2016) years

Code	SY	OC	OY	PH	NDF	NB	NH	HD	TSW
G5	3156.3 a	32.34 g	1024.2 ab	76.9 abc	71.3 fg	6.2 ab	6.7 bc	2.30a-d	41.5def
G4	3013.2 ab	32.89 ef	978.7 bcd	76.4 bcd	73.0cde	5.5 bcd	6.0 cde	2.35 ab	39.1 k
G9	2977.1 abc	35.46 b	1058.6 a	77.2 abc	72.5cde	6.4 a	6.6 bc	2.25a-d	41.2 fg
G7	2975.4 abc	32.05 g	947.0 cde	69.9 fg	70.7 g	5.2 cde	5.6 def	2.37 a	40.2 hı
G3	2955.2 bc	32.91 ef	968.9 bcd	71.5 d-g	71.4 fg	5.0 def	5.9 cd	2.17 d	42.1cde
G1	2892.9 bcd	33.24 de	967.3 bcd	73.8 b-f	69.5 h	5.5 bcd	6.0 cde	2.33abc	43.7 b
G8	2854.1 bcd	33.68 cd	967.6 bcd	67.8 g	69.2 h	4.7 efg	4.9 fg	2.26a-d	40.0hıj
G6	2819.5 cde	35.45 b	1009 abc	70.2 efg	69.2 h	4.3 fgh	5.0 fg	2.18 cd	42.3 cd
Dinçer	2750.4 def	29.11 h	803.6 ıj	78.4 ab	71.4 fg	5.8 abc	6.3 bcd	2.16 d	41.3 fg
G2	2640.9 efg	32.08 g	849.5 ghi	71.7 d-g	73.2bcd	4.4 fgh	4.9 fg	2.35 ab	37.5 m
Göktürk	2635.7 e-h	34.19 c	897.1 efg	71.6 d-g	68 hı	6.4 a	6.1 cde	2.18 cd	39.8ıjk
G14	2634.7 e-h	35.33 b	935.2 def	78.4 ab	74.0 b	5.7 a-d	8.5 a	2.37 a	42.7 c
G13	2582.7 f-ı	33.23 de	858.1 ghı	75.4 bcd	72.0 ef	4.6 efg	5.8 cde	2.32a-d	45.5 a
Linas	2557.6 f-ı	35.02 b	895.5 efg	81.5 a	72.5 de	4.1 gh	5.3 efg	2.19bcd	40.6 gh
Balcı	2497.4 g-j	35.00 b	873.2 fgh	72.5 e-g	71.3 fg	4.7 efg	5.3 efg	2.16 d	39.9hıj
G10	2442.7 h-k	33.39 de	816.5 hıj	74.3 b-f	70.5 g	4.2 gh	4.8 fg	2.20bcd	41.7def
G15	2421.6 ı-k	29.51 h	717.9 k	73.0 c-f	73.5 bc	6.0 ab	7.9 a	2.18 cd	45.2 a
G16	2401.1 ı-k	32.48 fg	779.1 jk	73.8 b-f	76.2 a	5.0 def	6.9 b	2.31a-d	39.3 jk
G11	2336.0 jk	36.46 a	853.4 ghı	71.8 d-g	68.9 hı	4.7 efg	5.5 def	2.23a-d	37.7 lm
G12	2297.6 k	33.67 c	779.3 jk	75.2 b-e	71.1 fg	3.8 h	4.5 g	2.24a-d	38.2 l
LSD (%5)	187.2	0.51	64.9	4.9	1.0	0.3	0.8	0.15	0.7
CV (%)	8.5	1.8	8.7	8.0	1.8	15	16	8	2.2

SY: Seed Yield (kg·ha⁻¹), OC: Oil Content (%), OY: Oil Yield (kg·ha⁻¹), PH: Plant Height (cm), NDF: Number of Days to %50 Flowering, NB: Number of Branches, NH: Number of Heads, HD: Head Diameter (cm), TSW: Thousand-Seed Weight (g)

TABLE 5. Correlation coefficients among characteristics of safflower genotypes

	SY	OC	OY	PH	NDF	NB	NH	HD	TSW
SY	1.00								
OC	0.03NS	1.00							
OY	0.96**	0.30**	1.00						
PH	0.56**	-0.07 NS	0.51**	1.00					
NDF	0.15*	0.13*	0.17**	0.009 NS	1.00				
NB	0.16*	-0.20**	0.09 NS	0.24**	-0.16*	1.00			
NH	0.44**	-0.05 NS	0.40**	0.47**	0.34**	0.48**	1.00		
HD	0.06 NS	0.002 NS	0.06 NS	0.14*	0.02 NS	0.13*	0.20**	1.00	
TSW	0.18**	-0.08 NS	0.15 *	0.04 NS	0.19**	0.07 NS	0.26**	0.09 NS	1.00

**Significant at $P < 0.01$, * Significant at $P < 0.05$ and NS: not significant.
SY: Seed Yield, **OC**: Oil Content, **OY**: Oil Yield, **PH**: Plant Height, **NDF**: Number of Days to 50% Flowering, **NB**: Number of Branches, **NH**: Number of Heads, **HD**: Head Diameter, **TSW**: Thousand-Seed Weight.

(NB) varied from 3.8 - 6.4; the number of heads per plant (NH) varied from 4.5 - 8.5; head diameters (HD) varied from 2.16 - 2.37 cm; and thousand-seed weights (TSW) varied from 37.5 - 45.5 g.

Correlation coefficients among the investigated traits are provided in Table 5 and the genotype – trait (GT) biplot graph is presented in Figure 1.

Seed yield (SY) showed significant positive correlations with oil yield (OY), plant height (PH), number of days to flowering (NDF), number of branches (NB), number of heads (NH) and thousand-seed weight (TSW). Seed yield (SY) had insignificant correlations with oil content (OC) and head diameter (HD).

Safflower breeding programs are implemented to obtain seed yield components, to determine the relationships among these components and to identify proper selection criteria. Similar to the present study, Mozaffari and Asadi (2006), Camas et al. (2007), Hussein et al. (2018) and Ali et al. (2020) reported the number of heads per plant as the most significant yield component and indicated significant correlations between seed yield and number of heads per plant.

Koç et al. (2010) conducted studies on safflower genotypes and reported significant positive correlations between number of days to flowering and seed yield. In the present study, a significant positive correlation (r = 0.15*) was observed between seed yield and number of days to flowering at the 5% level (Table 5). The lower level of significance in the present study compared to previous studies was mainly attributed to the effects of environmental factors on

the number of days to flowering. Especially under water stress conditions, plants pass into the generative stage faster. The levels of relationships between seed yield and number of days to flowering is higher and positive under normal climate conditions, but weaker under stress conditions. Plant height is also used as a selection criterion for safflower. Alizadeh (2005), Arslan (2007), Coşge and Kaya (2008), Nabloussi et al. (2008), Eslam et al. (2010) and Koç et al. (2010) conducted research on safflower genotypes and reported significant positive correlations between seed yield and plant height. Similar to those studies, a significant positive correlation (r = 0.56**) was observed between seed yield and plant height in this study (Table 5).

Branching is an important parameter for the number of heads per plant. Thus, the number of branches increases seed yield. Similar to the present study, Camas et al. (2007), Golkar et al. (2012), Ali et al. (2020) also reported significant positive correlations between seed yield and number of branches.

Head diameter is an important morphological trait of safflower. However, the correlations between seed yield and head diameter were not found to be significant (r = 0.06) (Table 5). Akbar and Kamran (2006), Baljani et al. (2015), Hussein et al. (2018) and Ali et al. (2020) reported significant positive correlations between seed yield and head diameter. There were significant positive correlations between thousand-seed weight and seed yield in the present study. Head diameter alone does not influence seed yield, but becomes significant with the number of

heads. High seed yields are achieved with both greater number of heads and greater head diameters and head diameter alone is not significant for seed yield.

Oil content (OC) showed significant positive correlations with oil yield (OY), number of days to flowering (NDF) and number of branches (NB). While seed yields are mainly influenced by environmental conditions, plant genetics play a key role in oil content (Kaya *et al*., 2009). Therefore, it is not efficient to select genotypes for oil content based on morphological traits.

Oil yield (OY) had insignificant correlations with number of days to flowering (NDF) and head diameter (HD), but had significant positive correlations with the other traits (Table 5).

The crude oil yield of safflower is calculated from the crude oil ratio and seed yield values. Therefore, the factors influencing oil content and seed yield also influence oil yield. Therefore, it is possible to state that all factors influencing seed yield also influence crude oil yield (Oztürk *et al*., 2009).

The GT biplot graph showed two principle components (PC1 and PC2) and explained 53.6% of total variation (PCI 29.6% and PC2 24%) (Figure 1). High explanation ratios are desired in GT biplot graphs since such graphs allow researchers to better and more reliably assess experimental data (Yan *et al*., 2007).

Provided that the biplot graph sufficiently explains total variation ($\geq$ 50%), the correlation coefficient is almost equal to the *cosine* of the angle between the vectors of two traits (Kroonenberg, 1995).

A correlation coefficient (r) is positive when the angle between the vectors of two traits is < 90°, negative when the angle is > 90° and independent (0) when the angle is 90°. The traits with longer vector lengths are more susceptible to genotype combinations; the traits with shorter vector lengths are less susceptible to genotype combinations (Rad *et al*., 2013). According to the present biplot graph, the angle of seed yield (SY) vector with oil yield (OY), head diameter (HD), number of branches (NB), thousand-seed weight (TSW), number of heads (NH) and plant height (PH) vectors was < 90o (Figure 1). Seed yield had significant positive correlations with these traits. The angle of seed yield (SY) vector with number of days to flowering (NDF) and oil content (OC) was about 90o (Figure 1). Therefore, seed yield had insignificant correlations

with these traits (r = cos 90 = 0). The angle between the oil content (OC) and oil yield (OY) vectors was < 90o and there was a positive correlation between these traits (r = cos 0 = +1 and r = cos 60 = 0.5). The angle of oil content (OC) vector with seed yield (SY) and head diameter (HD) vectors was about 90º, thus the correlation coefficient was almost zero (0), indicating insignificant correlations (r = cos 90= 0). The angle of oil content (OC) vector with number of days to flowering (NDF), number of heads (NH), thousand-seed weight (TSW) and number of branches (NB) vectors was >90, thus oil content had negative correlations with these traits (r = cos 120 = -0.5 and r = cos 180= -1). Since oil yield was calculated from seed yield and oil content values, it yielded similar outcomes with these traits. Although the biplot analysis was developed for the analysis of genotype x environment interactions on seed yield, such as quantitative traits, it is also used to assess the relationships between the agronomic traits of the genotype (Yan and Kang, 2003).

With regard to genotype-trait relationships, it was observed that the genotypes G5, G4, G9 and G1 were prominent for seed yield (SY); G6, G11, Linas, Balcı and Göktürk genotypes were prominent for oil content (OC); G7, G3, G1, Göktürk, G4, G5, G9 genotypes were prominent for oil yield (OY). The genotypes Dinçer, G14 and G13 generated a difference for plant height (PH) and the genotypes G16, G13 and G15 generated a difference for number of days to flowering (NDF). The genotypes G5, G9, G4 and G1 were superior for head diameter (HD) and the genotypes G13, G15 and G14 were superior for thousand-seed weight (TSW) over the other genotypes.

The outcomes from the biplot graph (Fig.1) and correlation table (Table 5) mostly supported each other. Slight differences were attributed to normalized values for the biplot analysis and 53.6% rate of explanation of total variance by the biplot graph (PC1 and PC 2: 53.6%).

Since the GGE Biplot analysis allowed visual assessment of several traits simultaneously and thus influenced the success of selection, it was considered as an innovative approach to be used in plant breeding programs (Yau, 1995; Yan *et al*., 2007).

4. CONCLUSIONS

This study is significant in that it presented the relationships between traits through both correlation

analysis and biplot analysis. Based on the results of the two approaches, plant height (PH), number of branches (NB), number of heads (NH) and thousand-seed weight (TSW) were identified as the most significant selection criteria for yield in safflower. On the other hand, while there were significant positive correlations between seed yield (SY) and head diameter (HD) in the biplot graph, the relationships between these traits were not found to be significant in the correlation analysis.

Seed yield had insignificant correlations with number of days to flowering (NDF) in the biplot analysis, but significant correlations at 5% level in the correlation analysis. Combined use of different approaches in the assessment of relationships between the traits will improve the chance for success.

The data obtained from this study could be useful for safflower breeders and safflower producers concerned with increasing seed yield. The main traits determined in this study which affected seed yield in safflower were plant height (PH), number of branches (NB), number of heads (NH) and thousand-seed weight (TSW) and this can be used as selection criteria during safflower breeding programs.

The GT biplot graph put forth the relationships among the investigated traits of the genotypes and provided significant advantages for the selection of genotypes and cultivars to be used as parent materials in breeding programs. The method also offered practical and efficient assessment of the strong and weak points of the genotypes.

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