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RESEARCH ARTICLE

Genetic variability, correlation and cluster analysis in some safflower (*Carthamus tinctorius* L.) genotypes

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Abstract

This study aims to study genetic variability, correlation, and cluster analysis and evaluate 15 safflower (*Carthamus tinctorius* L.) genotypes during 2021 and 2022 at Shandaweel Research Station, Agricultural Research Center, Egypt. Highly significant differences were found for all studied traits. Nine lines had means of total plot yield trait higher than the two check varieties. Six lines exceeded the two check varieties and the general mean for oil % trait, and there were Line 83, 91, 97, 100, and line 103. The phenotypic coefficient of variation (PCV) values ranged from 1.91% for the total plot yield to 73.84% for seed yield/plant in the first season. Genotypic coefficient of variation (GCV) values in this season were ranged from 1.71% for the total plot yield trait to 65.20% for the oil percentage trait. PCV values ranged from 2.53% for the total plot yield trait to 67.0% for seed yield/plant trait in the second season. While second seasons GCV values ranged from 2.53% for total plot seed to 61.99% for oil percentage trait. Heritability in broad sense estimations was high for all traits and ranged from 79.54% for seed yield per plant to 99.93% for oil percentage in the first season and 85.15% for seed yield per plant 99.97% for oil percentage in the second seasons. The cluster analysis showed fifteen safflower genotypes were divided into four groups. Positive and significant phenotypic and genotypic correlation recorded between seed yield/plant trait and plant height.

Keywords: Safflower, cluster analysis, correlation coefficient, variability, oil

Introduction

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop and has been traditionally grown for its flowers as a dye source for coloring food and fibers. Subsequently, it is grown for edible oil, animal meal, bird feed, medicinal uses. It belongs to the family *Compositae* (*Asteraceae*). There are 36 species in the genus Carthamus, found in many parts of the world, namely Asia, Africa, and Mediterranean regions. Out of these, only *Carthamus tinctorius* L. (2n= 24) is cultivated. It is mainly cultivated for its seeds, which are a source of oil.

Carthamus is the Latinised version of the Arabic word "Quartum", which alludes to the color of the dye often from florets, and the modern Arabic name "Usfar" is probably a diversion of the English word "Safflower" through the various written form of Usfar, asfiore, Saffiore finally to safflower. Safflower (*Carthamus tinctorius*) is one of the most important oilseed crops with a long-term history going back to 3500 B.C., when the crop has been used for dyeing mummy wrappings and other robes. After soybean, groundnut, rapeseed, sunflower sesame, linseed, and castor safflower ranks eighth regarding the total harvested yield (Damodaram and Hegde 2002). Safflower seeds contain 13 to 46 % oil, and approximately 90 % of this oil is composed of unsaturated fatty acids called oleic and linoleic acids (Johnson *et al.*, 1999). Vegetable oils are the essential food compounds that are important for human health. The demand for vegetable oils for food application is considered the main goal for producing oilseeds (Camas *et al.*, 2007).

In Egypt, the safflower area decreased year after year in Upper Egypt because the genotypes suffered many problems: lateness (185 days to maturity), full thorns on leaf and heads, low seed yield, and low seed oil content. Therefore, the present study aimed at high seed yield with high oil content as promising lines used as new Egyptian varieties. Genetic variability, phenotypic and genotypic coefficients of variation, heritability, and genetic advances are used as tools to study the genetic variation in various crops (Bedawy and Mohamed 2018; Attia *et al.*, 2019; Hossain *et al.*, 2021). These tools could help the crop breeder carefully study his material, find all the differences in the studied material, and find the best breeding method for developing new cultivars. Also, phenotypic and genotypic correlation supports this idea by found the relationship among the studied traits, this helps in direct and indirect selection for yield, and it is components in studied plant material (Attia *et al.*, 2014; Attia and Sayed 2019). Many safflower studies studied the correlation between safflower traits (Khomari *et al.*, 2017; Ahmed et al. 2019). Furthermore, cluster analysis is a classification method used to arrange a set of cases into clusters. The aim of set clusters such cases within a cluster is more similar to each other and helps researchers summarise information on data. Cluster analysis is commonly used in social, medical, and agricultural sciences (Mohamed and Bedawy 2019; Ojagh *et al.*, 2019). This technique is closely related to multivariate variance analysis, logistic regression, as other multivariate analyses. Different procedures are being used to the fulfillment of many different functions. In addition, cluster analysis is being used to exposing of similarity and diversity (Gevrekci *et al.*, 2004). Many breeding methods are used for cultivar selection or the development of cultivars. One of them is the introduction and adaptation work. Based on this, recognizing the plant characteristics of varieties and seed yield potential must be determined. Thus, preliminary information would be available about the types and cultivars recommended for registration (Copur *et al.*, 2009). This study aimed to evaluate, screen some safflower genotypes, study seed yield and its components, and cluster 15 safflower genotypes to characterize genotype differences.

Materials and methods

In this study, a collection of 15 safflower genotypes; 13 safflowers promised lines (Assad 1, Line 13, Line 83, Line 85, Line 91, Line 97, Line 100, Line 101, Line 103, Line 104, Line 114, Line 120 and Line 129) and two safflower chick verities (Giza 1 and Kharega 1). These genotypes were collected from Egypt's natural vegetation and considered local landraces provided by Oil Crops Research Department – Field Crops Research Institute (FCRI) –Agricultural Research Center (A.R.C.), Egypt.

This research was conducted in the "Randomized Complete Block Design" with three replications in the research field of Agricultural Research Center, Shandawell Research Station, Sohag, Egypt, to study the phenotypic, genotypic variability, phenotypic and genotypic correlation, and cluster analysis in two winter seasons 2021 and 2022. The soil in both seasons was sandy loam, with pH 7.60, and contained phosphorous, potassium, zinc, organic matter, and CaCO3 contents of 6.30 ppm, 0.26 meg/100 g soil, 18.10 ppm, 1.89%, and 2.86 meg/100 g soil, respectively. The experiment was planted in two winter seasons; first on 17th November 2015 and the second one on 20th November 2016. Each genotype was sown in plots with two rows, 4 m of longitude spacing 50 cm between rows. Planting was done in hills spaced 20 cm apart, and each hill had one plant. The cultural practices followed the recommendations for oilseed sunflower production. The following agronomic traits were measured on a random sample of five guarded plants from each plot. Samples of each plot were obtained to the determination of plant height (cm), the number of branches/plant, 100-seed weight (g), seed yield/plant (g), seed yield/plot (g), and oil content (%). The oil content was determined by the soxalet apparatus using petroleum ether (Bp40 - 60 ºC) as solvent according to the official method (A.O.A.C., 1980).

Statistical analysis

The data were analyzed using SAS statistical software ver. 9.2 (SAS Institute, 2008). The LSD was calculated at 5% and 1% significant levels, according to Petersen (1985), for comparing the mean values of the studied genotypes of all studied traits. Also, the parameters for the heritability, phenotypic variability, and genotypic variability were calculated according to Burton (1952) and Al-Jibouri *et al.,* (1958).

Results and discussion

Phenotypic parameters

The safflower genotypes significantly differed at a 1% level for all studied traits in the two seasons (Table 1). These results were showed that genetic variability is present within studied safflower genotypes in investigated traits. Wherefore, this variation could be useful for improving these traits under the selection process. These results match those obtained by Attia *et al.,* (2014), Attia and Sayed (2019), Bedawy and Mohamed (2018), and Tahernezhad *et al.,* (2018).

In the first season, the phenotypic values (Table 2 and Figure 1 and 2) were ranged widely around the general mean values and represented 53.84, 61.53, 46.15, 69.23, 46.15, and 46.15% of the genotypes higher than the general mean for plant height, the number of branches per plant, seed yield per plant, total plot yield, hundred seed weight, and oil percentages traits, respectively. All studied lines were taller than the check variety "Kharga 1" except line114, "Assed 1" and "Line 120" were taller than the check variety "Giza 1" with means of 185.33 and 176.67 cm, respectively. The performance of "Giza 1" for the number of branches/plant was so low with a mean of 10.20. This performance certainly was the lowest mean for this trait. Otherwise, ten lines also had higher branch number/plant traits than the other check variety, "Kharga 1".

Table 1: Mean squares, heritability (H), means, phenotypic (PCV), genotypic (GCV) coefficient of variation and genetic advance (GA) for six studied traits in two seasons

Item		Plant height (cm)	No. of branches	Seed yield/plant (g)	Total plot yield (kg)	Seed index (g)	Oil percentage
Source	**DF**	**First season mean squares**					
Replication	**2**	162.16**	2.45	192.80*	0.029*	0.47**	1.93**
Genotypes	**14**	738.23**	29.84**	178.86**	0.22**	1.20**	127.20**
Error	**28**	28.73	1.14	42.37	0.0076	0.04	0.09
H		96.21	96.26	79.54	96.61	97.12	99.93
Mean		160.04	16.73	39.67	0.139	5.05	21.66
PCV		55.24	21.34	73.84	1.90	2.80	65.34
GCV		49.26	19.06	38.23	1.71	2.57	65.20
GA 5%		525.87	21.24	138.32	0.16	0.848	87.53
Source	**DF**	**Second season mean squares**					
Genotypes	**14**	319.90**	9.35**	177.50**	0.30**	2.50**	126.43**
Error	**28**	26.92	0.93	29.26	0.0047	0.05	0.04
H		92.03	90.69	85.15	98.42	98.14	99.97
Mean		146.87	16.78	39.02	0.138	4.52	22.65
PCV		28.27	7.42	67.20	2.53	6.38	62.05
GCV		22.16	5.57	42.21	2.41	6.03	61.99
GA 5%		235.37	6.94	135.54	0.21	1.75	86.97

*,** Significant and highly significant, respectively

Fig. 1: Genotypes means for three studied traits; Number of branches/ plant, seed yield/ plant and oil percentage in the first year

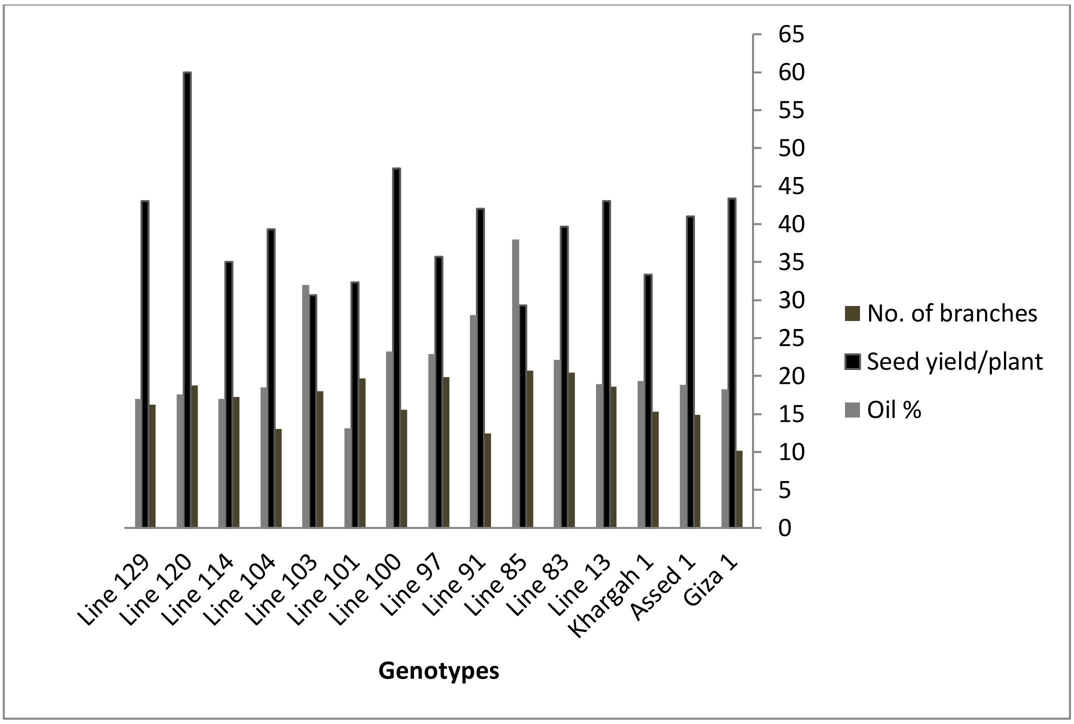

Fig. 2: Genotypes means for three studied traits; Number of branches/ plant, seed yield/ plant and oil percentage in the second year

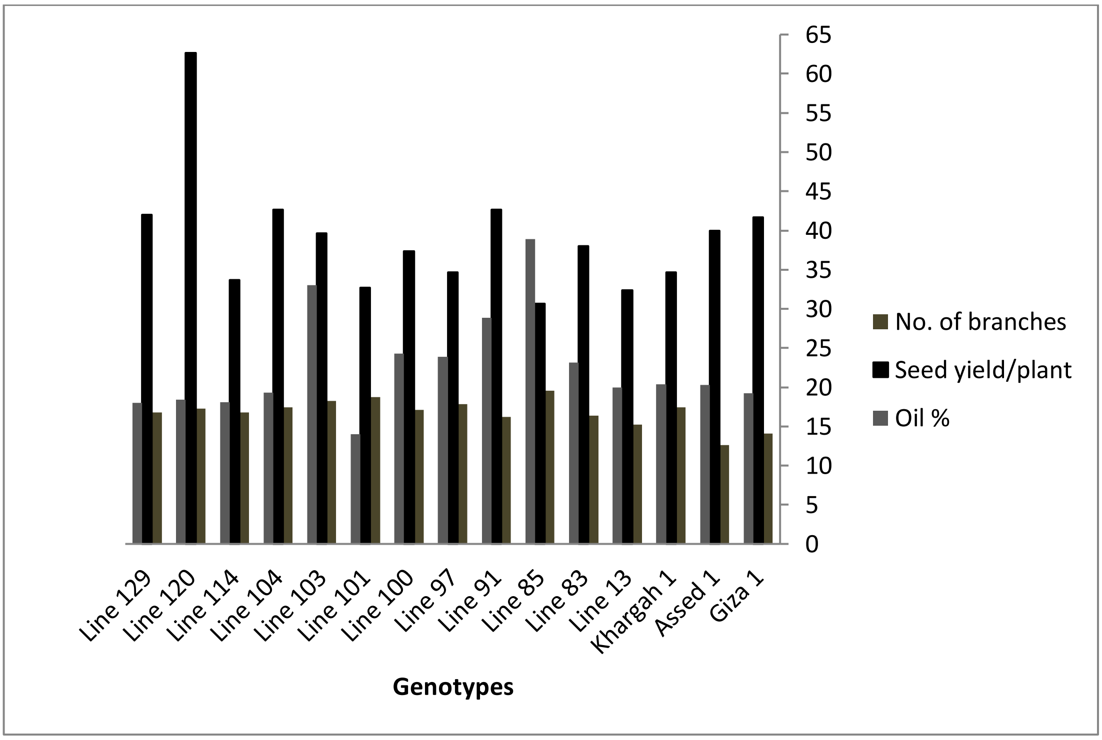

Table 2: Means of six examined traits for the 15 safflower genotypes in two seasons

Season	Genotype	Plant height (cm)	No. of branches	Seed yield/plant (g)	total plot yield (kg)	Seed index (g)	Oil (%)
Means of first Season	Assed 1	185.33	14.87	41.00	1.54	5.67	18.86
	Line13	151.00	18.60	43.00	1.29	4.59	18.94
	Line83	141.33	20.43	39.67	1.39	5.88	22.14
	Line85	133.33	20.73	29.33	1.626	4.67	38.00
	Line91	162.00	12.47	42.00	1.490	4.89	28.00
	Line97	153.33	19.83	35.67	1.433	3.43	22.91
	Line100	164.00	15.53	47.33	1.18	4.83	23.26
	Line101	161.00	19.67	32.33	1.255	5.56	13.11
	Line103	166.33	18.00	30.67	1.23	4.88	32.00
	Line104	176.67	13.07	39.33	1.46	4.85	18.53
	Line114	131.67	17.27	35.00	1.423	5.55	16.98
	Line120	174.67	18.80	60.00	1.93	5.27	17.58
	Line129	164.00	16.20	43.00	1.43	5.21	17.01
	Giza1	175.67	10.20	43.33	0.956	4.58	18.23
	Khargah1	160.33	15.27	33.33	1.303	5.82	19.37
	General mean	160.04	16.73	39.67	1.397	5.05	21.66
	LSD $_{0.05}$	8.96	1.78	10.88	0.15	0.31	0.50
	LSD $_{0.01}$	12.09	2.41	14.68	0.20	0.42	0.67
Means of second season	Assed 1	152.33	12.60	40.00	1.744	5.61	20.25
	Line13	147.33	15.20	32.33	1.11	4.43	19.94
	Line83	154.67	16.40	38.00	1.367	5.89	23.16
	Line85	125.00	19.53	30.67	1.72	4.53	38.89
	Line91	143.33	16.20	42.67	1.308	4.33	28.89
	Line97	147.67	17.87	34.67	1.663	2.89	23.91
	Line100	148.33	17.07	37.33	1.21	2.97	24.26
	Line101	147.00	18.70	32.67	1.11	5.20	14.04
	Line103	151.00	18.27	39.67	1.34	5.13	33.01
	Line104	144.00	17.40	42.67	1.220	3.29	19.29
	Line114	141.00	16.80	33.67	1.556	3.94	18.11
	Line120	159.33	17.27	62.67	1.823	4.78	18.43
	Line129	127.67	16.80	42.00	1.428	5.01	18.01
	Giza1	164.67	14.07	41.67	0.996	4.51	19.23
	Khargah1	149.67	17.47	34.67	1.211	5.27	20.36
	General mean	146.87	16.78	39.02	1.389	4.52	22.65
	LSD $_{0.05}$	8.67	1.61	9.04	0.12	0.36	0.33
	LSD $_{0.01}$	11.79	2.17	12.20	0.16	0.48	0.45
Combined means	Assed 1	168.83	13.74	40.50	1.644	5.64	19.56
	Line13	149.17	16.90	37.67	1.204	4.51	19.44
	Line83	148.00	18.42	38.84	1.378	5.89	22.65
	Line85	129.17	20.13	30.00	1.677	4.60	38.45
	Line91	152.67	14.34	42.34	1.399	4.61	28.45
	Line97	150.50	18.85	35.17	1.548	3.16	23.41
	Line100	156.17	16.30	42.33	1.199	3.90	23.76
	Line101	154.00	19.19	32.50	1.186	5.38	13.58
	Line103	158.67	18.14	35.17	1.29	5.01	32.51
	Line104	160.34	15.24	41.00	1.344	4.07	18.91
	Line114	136.34	17.04	34.34	1.49	4.75	17.55
	Line120	167.00	18.04	61.34	1.875	5.03	18.01
	Line129	145.84	16.50	42.50	1.42	5.11	17.51
	Giza1	170.17	12.14	42.50	0.976	4.55	18.73
	Khargah1	155.00	16.37	34.00	1.25	5.55	19.87

Table 3: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among six studied traits across two seasons

Trait	Plant height	No. of branches	Seed yield/plant	Total plot yield	Seed index	Oil %
Plant height	1.000	-0.497**	0.413*	-0.157	0.110	-0.319
No. of branches	-0.640**	1.000	-0.163	0.309	-0.086	0.244
Seed yield/plant	0.722**	-0.395*	1.000	0.209	0.072	-0.240
total plot yield	-0.346	0.583**	0.251	1.000	0.096	0.197
Seed index	0.103	0.042	-0.007	0.066	1.000	-0.173
Oil %	-0.450*	0.323	-0.353	0.222	-0.192	1.000

*,** Significant and highly significant, respectively

Fig 3: Cluster analysis of 15 safflower genotypes based on six studied traits

Lines 100 and 120 surpassed "Giza 1" the check variety with 47.33 and 60 g, respectively, for seed yield/plant trait. Moreover, nine lines had means of total plot yield trait higher than the two check varieties. Six lines exceeded the two check varieties and the general mean for oil % trait, and there were Line 83, 91, 97, 100, and line 103. The second season showed higher phenotypic values of the genotypes than the overall mean 61.53, 69.23, 46.15, 46.15, 53.84, and 46.15% for plant height, the number of branches per plant, seed yield per plant, total plot yield, hundred seed weight, and oil percentage traits, respectively. The maximum values of examined traits were recorded in genotypes "Assed 1" (185.33 cm), "Line 85" (20.73), "Line 120" (60 g), "Line 120" (1928.33 g), "Line 83" (5.88 g) and "Line 85" (38%) for plant height, number of branches per plant, seed yield per plant, total plot yield, hundred seed weight and oil percentages in the first season, respectively. All examined lines were shorter than "Giza 1", and four were taller than the other check "Kharga 1". Only four lines had higher means of the number of branches/plant mean than "Kharga 1", the check variety. Superior four lines 91, 104, 120, and 129 exceeded the "Kharga 1" mean for the seed yield/plant trait. All studied lines had a total plot yield means higher than "Kharga 1" except line13. Six lines provided oil % trait means over "Kharga1". Furthermore, the genotype "Line 120" showed values above the general mean of all studied traits except the oil percentage trait (Table 2). The opposite was genotype "Line 85", which had the best mean of oil percentage and lower means for the other traits. While the higher mean values of examined traits were observed in genotypes "Line 120" (159.33 cm), " Line 85" (19.53), " Line 120" (62.67 g), "Line 120" (1823.33 g), "Assed 1" (5.61 g) and "Line 85" (38.89%) for plant height, number of branches per plant, seed yield per plant, total plot yield, hundred seed weight, and oil percentage, respectively in the second season.

Genotypic parameters

The selection process is depending on the phenotypic and genotypic variation in safflower breeding programs (Pushpavalli and Kumar 2017). The calculated genotypic data in Table 1 showed that the PCV and GCV are close together for most studied traits in both seasons that indicate the minimum environmental effects on the genetic expression for studied traits; herein, the selection is based on phenotypic values will be sufficient. The PCV calculated values in the first season were ranged from 1.91% for the total plot yield trait to 73.84% for seed yield/ plant trait. Moreover, this season's GCV values ranged from 1.71% for the total plot yield trait to 65.20% for the oil percentage trait. The higher value of genetic advance (525.87%) was recorded for plant height traits. On the other hand, in the second season, the lowest PCV value was also recorded for the same trait total plot yield with 2.53%, and the heights PCV value was recorded for seed yield/plant with a value of 67.20%. In comparison, GCV values were ranged from 2.53% for full plot seed to 61.99% for oil percentage trait. The second year's genetic advance values ranged from 0.21 to 235.37% for total plot yield and plant height traits, respectively. Similar results were approved by Omidi *et al.*, (2009), who found that PCV ranged from 3.3% for days to maturity trait to 42% for ineffective capitula trait, and GCV values ranged from 3.65% for days to bud formation trait to 35.7% for oil yield trait. Patil and Lokesha (2018) reported that the PCV was higher than the GCV for the yield and its attributes with low difference interpreted environmental effect, which was low and the genetic factors controlling variability in these traits. Heritability in broad sense estimations (Table 1) in this work was high for all traits and ranged from 79.54 % for seed yield per plant to 99.93% for oil percentage in the first season and from 85.15% for seed yield per plant to 99.97% for oil percentage in the second seasons.

This result refers to the small effect of the environment in the phenotype expression. These results matched those obtained by Hika *et al.*, (2015) and Attia and Sayed (2019). They found that broad sense heritability values were more than 80% for almost all traits. Also, Bedawy and Mohamed (2019) had closed GCV and PCV values coupled with high broad-sense heritability for all the characters in their study.

Cluster analysis

Cluster analysis for 15 studied safflower genotypes was done using six studied traits over two years (Table 3). The cluster analysis figure (Fig. 3) showed that the fifteen safflower genotypes were divided into four groups. The first group included Assed 1, Line 85, and Line 120 genotypes. The second group had five genotypes; the check variety (Khargha1 and Line103), Line 100, Line 13, and line 101. The third group included six lines; Line 129, Line 91, Line 83, Line 104, Line 114, and Line 97. The last group had the check variety Giza 1. Khalili *et al.,* (2014) divided 15 safflower genotypes into four groups based on grain yield and drought tolerance indices. While Ada (2013) had two main groups for 16 safflower genotypes in his work, this cluster analysis was done by using eight agronomic traits.

Phenotypic and genotypic correlation

The phenotypic and genotypic correlation was calculated between six studied traits over two years (Table 3). Correlation values showed positive and significant phenotypic and genotypic correlation recorded between seed yield/ plant trait and plant height with the value of (r= 0.413 and r= 0.722, respectively). A positive and significant genotypic correlation (r= 0.583) was also found between the number of branches/plant and total plot yield traits. While the highly significant negative phenotypic correlation was recorded between the number of branches/ plant and plant height traits estimated by (r = -0.497). Moreover, a negative significant genotypic correlation was found between plant height trait and oil percentage trait. Ahmed et al. (2019) approved the same correlation result, who reported a significant positive correlation between plant height and seed weight per plant. A highly significant positive phenotypic and genotypic correlation between grain yield per plot and the number of secondary branch traits with r values of 0.578 and 0.664 in the evaluation study 100 safflower genotypes was earlier reported (Omidi *et al.*, 2009).

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