



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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www.agronomyjournals.com
2019; 2(2): 45-50
Received: 25-07-2019
Accepted: 28-09-2019

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Genetic variability, evaluation and multivariate analysis for yield and yield components in sunflower (*Helianthus annuus L.*)

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Abstract

The current experiments were carried out to evaluate some sunflower (*Helianthus annuus L.*) genotypes through study genetic variability, heritability, genetic advance, and genetic advance as percent of mean, correlation coefficient and cluster analysis. In this context, a total of 11 sunflower genotypes were grown in a randomized complete block design with four replications at experimental field of Oilseeds Section during the growing two season, 2018 and 2019 at Sakha Agric. Res. Station, Kafr El-Sheikh, Governorate, the mean squares were significantly differed ($P < 0.01$) for all the studied traits among the tested genotypes, these genotypes might be useful in sunflower breeding programme. The genotype G4 gave higher seed yield plant⁻¹ and seed yield fed⁻¹. The correlation values depicted that traits, such as, days to 50% flowering, stem diameter, head diameter, plant height, established positive and significant correlations with seed yield plant⁻¹, head diameter also established positive and significant correlations with plant height and yield fed⁻¹. The values of Phenotypic coefficient of variation (PCV) were marginally higher than Genotypic coefficient of variation (GCV). This indicates that the large amount of variation was contributed by genetic component and least by environment. Demonstrating that genotypes having higher extent of these traits may be preferred in selection for evolving high yielding sunflower genotypes. High heritability broad sense estimates were obtained for all the characters studied. High heritability (>60%) and high genetic advance (>10) were shown by Seed yield fed⁻¹ and seed yield plant⁻¹, High heritability and moderate genetic advance were exhibited by oil %, Head diameter showed high heritability but low genetic advance. The highly heritable character with high or moderate genetic advance could be further improved with individual plant selection. Characters with high heritability and low genetic advance indicated little scope for further improvement through individual plant selection. Cluster analysis proved to be better tools for assessing genetic diversity and precise associations among genotypes. The selection of genotypes from different clusters and components having more than one positive trait may lead to improvement in seed yield and oil contents in sunflower. Cluster analysis classified the sunflower varieties into three groups based on agronomic traits and seed yield. The largest number of genotypes were included in cluster I (6 genotypes) and II (4 genotypes) followed by cluster III, the genotype 4, which has the highest value for seed yield, was separate.

Keywords: sunflower, seed yield, genetic variability, genetic advance, heritability, correlation, cluster analysis

Introduction

Sunflower (*Helianthus Annuus L.*) is being considered as an important oilseed crop of the world beside rape seed oil, soybean, cotton, and palm oil (Yadava *et al.* 2012) [38]. At present, it is also catching the interest of agriculturists, farmers and companies' day by day since it is possible of using its oil as raw material for manufacturing biodiesel (Backes *et al.* 2008) [5]. In order to improve the crop production of sunflower, different aspects of research through plant breeding are being carried out for obtaining desirable genotypes (Messetti and Padovani 2004) [22]. The main objectives of any plant breeder include the highest seed yield and oil content. The success of breeding programs primarily depends on the variation present for yield and yield components as well as nature of initial genetic materials. In sunflower, the plants obviously differ in head diameter, plant height, number of leaves, seeds per head and 1000-seed weight. In quantitative traits, these variations are partly attributable to the environmental factors and to a certain extent contributed by the genetic influence (Nehru and Manjunath 2003) [26].

Seed yield in sunflower is a complex character because it is expressed with the function of many component traits and their interactions with the environment. It is obvious that the important aspiration of plant breeders is to know the extent of relationship between phenological, seed yield and oil traits, which will ultimately enhance their selection efficiency for above traits. Thus, it is very essential to size the mutual associations between various plant characters so as to define the component traits which may be capitalized as reliable selection criteria for genetic improvements of yield and other important traits (Memon *et al.* 2014) [23]. Correlation studies also help to improve different characters simultaneously (Sujatha and Nadaf 2013) [34]. Correlation studies determine as how far two variables are associated with each other. The correlation actually reduces the chance of uncertainty to happen, thus the predictions based on correlation analysis are likely to be very closer to reality. Several researchers observed different types of correlations among seed yield, oil content and yield components. Seed yield was significantly and positively correlated with head diameter and 100-seed weight as reported by (Lakshminarayana *et al.* 2004) [18] and (Sujatha and Nadaf 2013) [34]. With this background, the present investigation was aimed to assess interrelationship, genetic variability, heritability (broad sense) and genetic advance over mean for seed yield and its components traits in sunflower.

Materials and Methods

The present investigation was carried out at Sakha Agric. Res. Station, Kafr El-Sheikh, Governorate, Egypt, during the two successive seasons of 2018 and 2019 to evaluate eleven sunflower genotypes as shown in Table (1). The genotypes were planted in randomized complete block design, with four replications. The proceeding crop was the Egyptian clover in both seasons. Seeds of each sunflower genotype were sown on May 17th and 19th in 2018 and 2019 seasons, respectively. Plot size was 12m² (3 x 4 m) in 6ridges each 4 meters long and 60 cm apart; 3-4 seeds per hill were placed with 20 cm between hills. One plant per hill was maintained by thinning of 21days after sowing. The conventional cultural practices of growing sunflower were conducted as recommended. Number of days from planting to 50% flowering in each plot were recorded. Two outside ridges were left to avoid border effects and the four inner ridges were used for the determination of seed yield and its components. The heads of four inner ridges in each plot were bagged at the end of pollination and fertilization to avoid damage that could be caused by birds until maturity.

Table 1: Pedigree of the different genotypes used in this study

No.	Genotype	Pedigree
1	S5	Bulgarian
2	S6	Bulgarian
3	S7	Bulgarian
4	S8	Bulgarian
5	S15	Bulgarian
6	S19	Bulgarian
7	S26	Bulgarian
8	S65	Local
9	S105	Local
10	Giza102	Local variety
11	Sakha53	Local variety

For measuring studied plant traits, ten guarded plants were randomly taken from the four inner ridges of each experimental

unit at harvest and the following data were recorded: plant height (cm), head diameter (cm), stem diameter (cm) seed yield per plant (g). The heads of four inner ridges of each plot were harvested to determine seed yield per feddan. Seed oil percent (O %) was determined according to methods described by (AOAC. 2005) [4].

Statistical analysis

The collected data were analyzed according to the standard statistical procedure described by (Gomez and Gomez 1984) [8]. The data recorded over two years were averaged and used to compute mean values were compared using least significant difference (LSD) test at 0.05 probability level.

Pearson's correlation coefficients were worked out between the traits following (Snedecor 1956) [33] with the help of SPSS 24. Multivariate techniques including Cluster analysis (CA) divides the genotypes into similar groups based on their agronomic traits. Clustering of genotypes into similar groups was analyzed using a hierarchical algorithm based on squared Euclidean distance. Then dendrogram was constructed utilizing Ward's method based on squared Euclidean distance (Kumar *et al.* 2009) [17].

Phenotypic and genotypic variability

The variability present in the genotypes was estimated by simple measure, namely range, mean, standard error, phenotypic and genotypic variance, and coefficient of variation. The phenotypic and genotypic variance and coefficient of variation were estimated according to the methods suggested by (Burton and Devane, 1953) [7] as follows:

$\sigma^2 g = (Mg - Me) / r$ Where:

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental (error) variance (Error mean square)

Mg = mean square of genotypes

Me = mean square of error,

r = Number of replications

Phenotypic coefficient of variation, PCV = $(\sqrt{\sigma^2 g / \bar{x}}) \times 100$

Genotypic coefficient of variation, GCV = $(\sqrt{\sigma^2 p / \bar{x}}) \times 100$

Where \bar{x} = Grand mean

Estimate of heritability

Heritability (H²) in broad sense for all characters was computed using the formula adopted by (Allard, 1960) as:

$$H^2 = (\sigma^2 g / \sigma^2 p) \times 100$$

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where: $\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\sigma^2 e$ = error variance

Estimation of expected genetic advance Genetic advance (GA) for each character was computed using the formula adopted from (Johnson *et al.* 1955) [13] and (Allard, 1960) [2].

$$GA = (k) (\sigma p) (H^2), \text{ and } GA \text{ (as \% of the mean)} = (GA / \bar{x}) \times 100$$

Where,

k= selection differential (k = 2.06 at 5% selection intensity)

σp = phenotypic standard deviation, H² = heritability (Broad sense)

\bar{x} = Grand mean

Results and Discussion

The obtained results Table (2) revealed that genotypes significantly differed ($P \leq 0.01$) for days to 50% flowering, stem diameter, head diameter, plant height, head diameter, 100-seed weight, yield per plant, seed oil percent and seed yield

perfeddan, signifying the existence of significant genetic divergence among the genotypes for studied traits. Similar results were also obtained by (Khan *et al.* 2013)^[15], (Memon *et al.* 2014)^[23] and (Munaiza *et al.* 2016)^[25]

Table 2: Mean squares from analysis of variance for various traits in sunflower Genotypes

Source of variation	D.F	Days to 50% flowering	Stem diameter (cm)	Head diameter (cm)	Plant height (cm)	100-seed weight (g)	Yield per plant (g)	Oil %	Seed yield k.g /feddan
Replication	3	2.915	0.09976	6.8773	431.77	0.3081	266.14	2.769	6238
Genotype s	10	12.231**	0.04540**	2.0458**	211.48**	0.3586**	42.51**	7.489**	35711.**
Error	30	2.473	0.01641	0.6502	75.79	0.1132	10.65	1.305	3399.

** = indicates significant at 0.01 of probability level

The data regarding mean performance of genotypes is given in Table (3). The data revealed that genotype 11 took long time for days to 50% flowering (56.88days), while G6 took short time for days to 50% flowering (50.50 days) as compared to the rest of the genotypes. In case of Stem diameter, the genotype G4revealed maximum value (2.37); however, the minimum value (2.01) was recorded in G8genotype.

For the trait of head diameter, G2 produced big heads of 21.61 cm, while smaller heads of 19.11 cm were observed in the genotype G9with regard to plant height, the genotype G10 produced taller plants of 171.4 cm, while short stature plants of 149.8 cm were obtained in the genotype G1. With respect to 100-seed weight, genotype G4 produced heaviest100-seed weight (6.65g), whereas the genotype G8 set low 100-seed weight (5.89g) as compared to other genotypes. The genotype G4 gave higher seed yield plant⁻¹ (47.91 g); however, the genotype G2 gave the lower seed yield plant⁻¹(35.68g). The genotype G3 produced maximum oil% (38.96), whereas the

genotype G4 gave minimum seed oil% (34.73). The mean performance revealed that the G4 produced maximum seed yield fed⁻¹ (1356 Kg.) than rest of the genotypes. It is recommended that the G4 proved superior accession which can be released as new variety, after testing its stability in different environments. Second, this superior accession may be used as one of the parents in hybridization programs in order to introduce additional desirable characters in sunflower cultivars. To work out correlation between grain yield and its major components serves as the base line for bringing genotypic improvement, the same has been the major focus of plenty of researchers working in the area of plant breeding. seed yield is the resultant product after interactions of many factors identified as contributing components; hence being polygenic it is a complex trait (Zia *et al.* 2013)^[39] The awareness of such interactions between characters of utmost importance and environment has been of prime significance in the breeding programs

Table 3: Mean values for different traits studied in sunflower

Characters	Days to 50% flowering	Stem diameter (cm)	Head diameter (cm)	Plant height (cm)	100-seed weight (g)	Yield per plant (g)	Oil %	Seed yield k.g /feddan
G1	54.38	2.360	19.96	149.8	6.047	37.90	37.27	1168
G2	55.25	2.297	21.61	158.3	6.490	35.68	36.23	1039
G3	54.38	2.295	19.70	157.3	6.219	39.13	38.96	1156
G4	53.75	2.375	20.68	169.7	6.654	47.91	34.73	1356
G5	54.62	2.265	20.45	155.9	6.650	39.64	38.47	1201
G6	50.50	2.217	19.29	152.4	6.636	38.44	37.32	1196
G7	54.75	2.187	19.84	156.0	6.581	39.68	38.51	1211
G8	53.00	2.010	20.48	158.6	5.890	37.75	35.23	1087
G9	54.75	2.221	19.11	162.7	6.242	38.14	37.79	1181
G10	51.62	2.112	19.88	171.4	6.001	35.77	37.81	1057
G11	56.88	2.194	19.53	169.5	5.999	39.85	38.09	1039
LSD.05%	2.271	0.1850	1.164	12.57	0.4859	4.713	1.650	84.20

Correlation studies are informative in a sense that the nature and extent of association between metric traits can be figured out successfully. Among the component characters Table(4), days to flowering had positive significant correlations with stem diameter ($r = 0.244^*$), head diameter, plant height ($r = 0.222^*$) and seed yield plant⁻¹ ($r = 0.307^{**}$) while stem diameter developed positive and significant associations with plant height ($r = 0.381^{**}$), seed yield plant⁻¹ ($r = 0.559^{**}$). It could be attributed from above results that earlier genotypes may improve yield related traits and in turn yielded high seed yield plant⁻¹. Similarly, plant height also had positive and significant correlations with seed yield plant⁻¹ ($r = 0.293^{**}$), while head diameter also established positive and significant correlations with plant height ($r = 0.344^{**}$) and yield per feddan ($r = 0.230^*$). Plant height displayed positive significant and associations with

most of the traits under investigations. When the plant height is more, obviously the number of leaves will be more, giving superior fixation of carbon that leads to additional accumulation of dry matter. This may lead to increase in stem diameter, head diameter and 1000-seed weight, resulting in higher seed yields (Vanishree *et al.* 1988 and Zia *et al.* 2013)^[39]. The inter correlations among these important component traits is also important in order to decide which trait is to be given due weight age in exercising selection. The inter correlations among the above traits, indicating the possibility of simultaneous improvement of these traits. These results were also confirmed by (Ilahi *et al.* 2009)^[10], (Razzaq *et al.* 2014)^[28], (Safavi *et al.* 2015)^[31] and (Mangesh *et al.* 2019)^[21]. The results revealed that seed yield plant⁻¹ established positive significantly correlation with plant height ($r = 0.293^{**}$), stem diameter ($r = 0.559^{**}$), 100

seed weight ($r= 0.260^*$) and days to 50% flowering ($r= 0.307^{**}$). So, selection of these characters for seed yield would be useful in future breeding of sunflower genotypes. Several

other scientists have also been stated significantly positive correlations of seed yield plant⁻¹ with plant height (Iqbal *et al.* 2013)^[11].

Table 4: Correlation coefficients between various quantitative traits of sunflower genotypes

	Days to 50% flowering	Stem diameter (cm)	Head diameter (cm)	Plant height (cm)	100-seed weight (g)	Yield per plant (g)	Oil %	Seed yield k.g /feddan
F	1							
SD	.244*	1						
HD	.222*	.021	1					
PH	.234*	.381**	.344**	1				
100 W	.201	.074	.162	.076	1			
YP	.307**	.559**	.103	.293**	.260*	1		
O%	.050	-.173	-.059	-.230*	.447**	-.100	1	
YF	.084	.148	.230*	.123	.304**	.619**	-.121	1

** = indicates significant at 0.01 of probability level * = indicates significant at 0.05 of probability level

Genetic parameters

The values of PCV were marginally higher than GCV. This indicates that the large amount of variation was contributed by genetic component and least by environment. Duration of Seed yield feddan⁻¹ was most affected by environment as compared with the other characters. (Table 5 and figure 1) Very high values of PCV and GCV were obtained for seed yield plant⁻¹ (8.79 and 8.34%), 100-seed weight (4.87 and 4.53%) and stem diameter (4.81 and 4.41%), which indicates significant role of these characters in the improvement of breeding programmes. Similar results were obtained by (Reddy and Reddy 2006)^[29], (Kalukhe *et al.* 2010)^[14] and (Vivek *et al.* 2019)^[37]. Moderate levels of PCV and GCV were obtained for the plant height and oil% in the decreasing order of magnitude. These results are in

agreement with the results obtained (by Patil *et al.* 1996). However, low values were obtained for days to 50% flowering (3.48 and 3.34%) and Head diameter (3.66 and 3.4) (Satisa 1995)^[32]. high heritability (>60%) and high genetic advance (>10) were shown by Seed yield fed⁻¹ and seed yield plant⁻¹ (Table 5 and figure 2). high heritability and moderate genetic advance were exhibited by oil %. (Mangesh. *et al.* 2019)^[21] also found high heritability and high genetic advance for seed yield per feddan., head diameter showed high heritability but low genetic advance. The highly heritable character with high or moderate genetic advance could be further improved with individual plant selection. Characters with high heritability and low genetic advance indicated little scope for further improvement through individual plant selection.

Table 5: Coefficients of variation, heritability and genetic advance for 8 traits sunflower.

Characters	Coefficient of variation		Genetic advance	Genetic advance as percent	Broad sense heritability (%)
	Phenotypic	Genotypic			
Days to 50% flowering	3.48	3.34	3.31	6.13	0.86
Stem diameter	4.81	4.41	0.16	7.19	0.73
Head diameter	3.66	3.4	1.15	5.75	0.76
Plant height	4.58	4.2	10.99	6.87	0.73
100-seed weight	4.87	4.53	0.48	7.67	0.76
Yield per plant	8.79	8.34	5.79	14.81	0.82
Oil %	3.98	3.85	2.68	7.19	0.88
Seed yield k.g /feddan	9.15	8.99	203.25	17.62	0.93

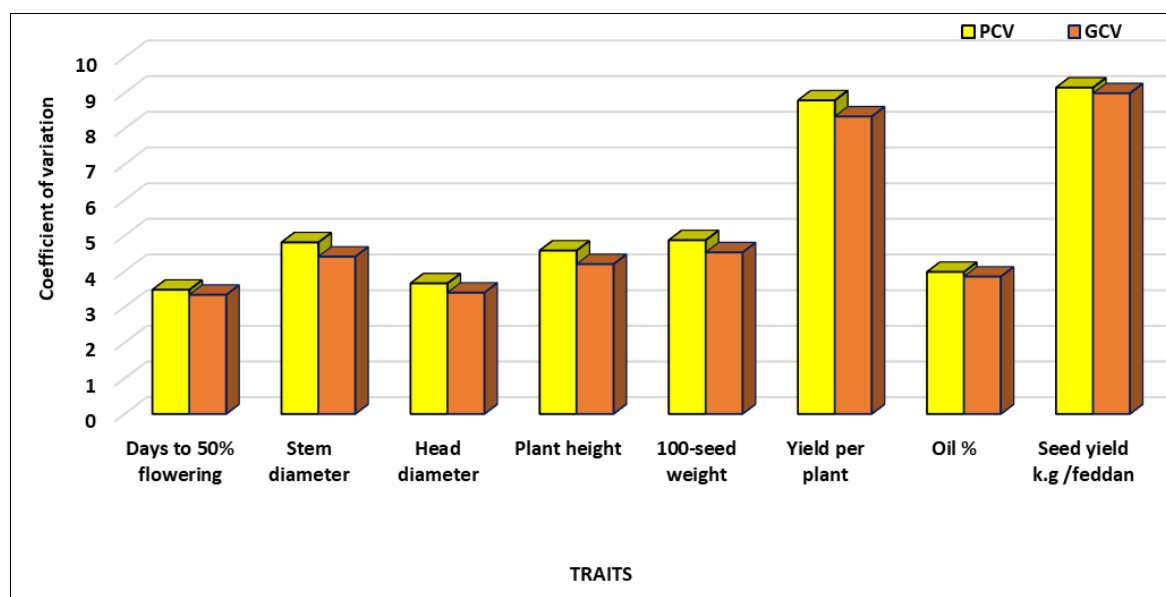


Fig 1: PCV and GCV for 8 traits sunflower

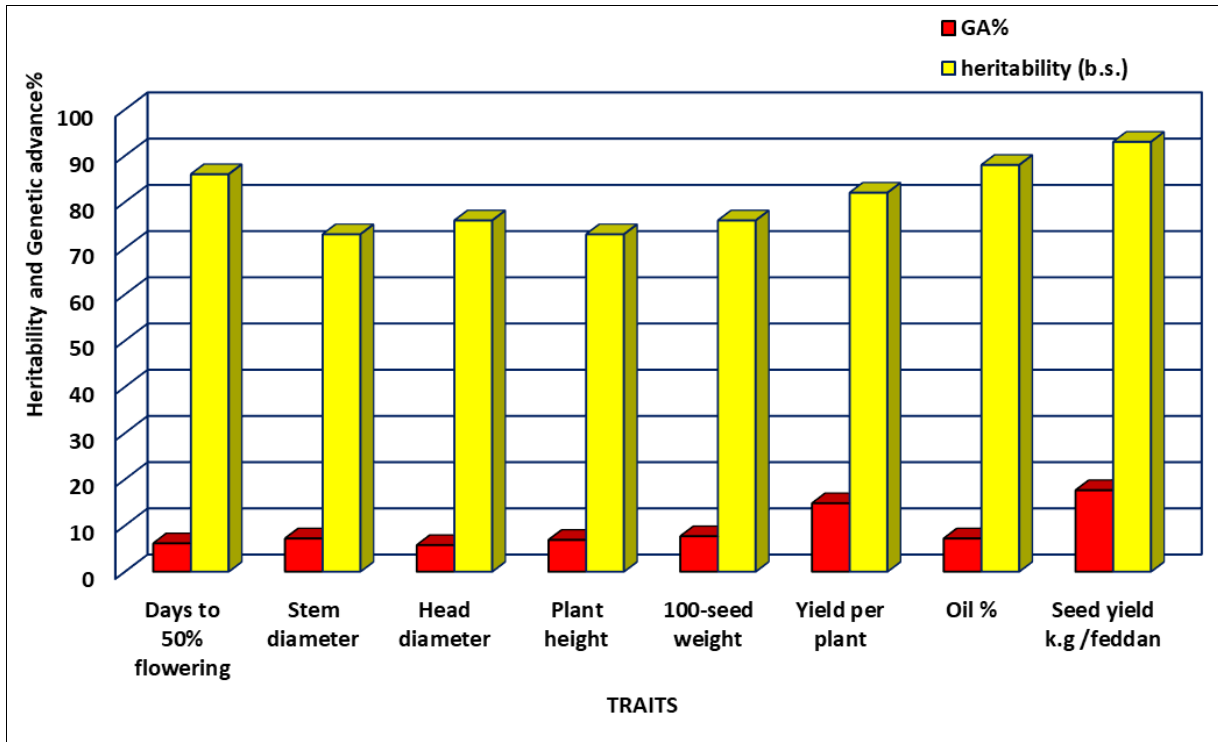


Fig 2: Heritability and genetic advance for 8 traits in sunflower

Multivariate statistical techniques are widely used tools in analysis of genetic diversity. Most commonly useful are cluster analysis (CA), (Mohammadi and Prasanna, 2003) [24]. Multivariate analysis has been used for evaluation of genetic diversity in many crops such as wheat (Hailu *et al.*, 2006) [9], sorghum (Ayana and Becele, 1999) [3] and sunflower (Kholghi *et al.*, 2011) [16]. Based on agronomic traits and seed yield, all sunflower genotypes by cluster analysis were divided into three groups (Figure 3). The largest number of genotypes were included in cluster I (6 genotypes) and II (4 genotypes) followed by cluster III. The genotype 4, which has the highest value for seed yield, was separate. Similar results were reported by (Teklewold *et al.* 2000, Kholghi *et al.* 2011, Vivek *et al.* 2019 [37] and Mangesh *et al.* 2019) [35, 16, 21]. According to (Murthy and Arunachalam 1996) selection of genotypes for parent must be based not only on geographical diversity actually more on genetic drift. The genotypes from cluster II (G2, G11, G10 and G8) were actually the genotypes with lowest seed yield.

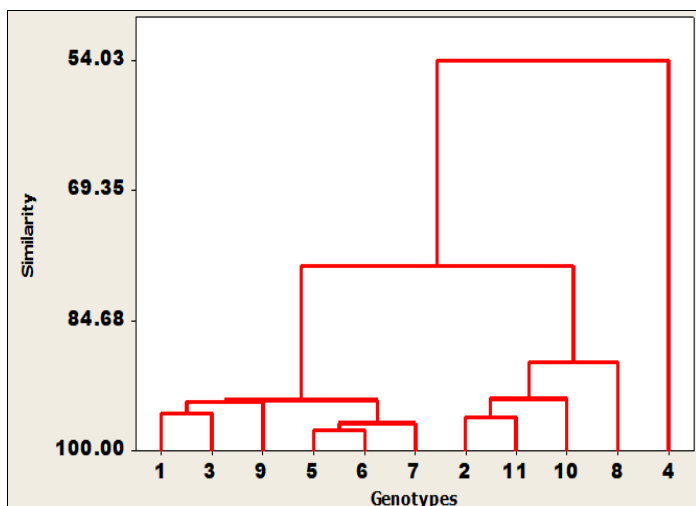


Fig 3: Cluster analysis for the examined sunflower genotypes based on agronomic traits and seed yield

Conclusions

It can be concluded from the results

1. The genotype G4 gave higher seed yield plant⁻¹ and seed yield fed⁻¹.
2. Days to 50% flowering, stem diameter, head diameter, plant height, significantly positive correlations with seed yield plant⁻¹, head diameter also positive and significant correlations with plant height and yield fed⁻¹
3. The values of Phenotypic coefficient of variation (PCV) were marginally higher than Genotypic coefficient of variation (GCV). This indicates that the large amount of variation was contributed by genetic component and least by environment. Demonstrating that genotypes having higher extent of these traits may be preferred in selection for evolving high yielding sunflower genotypes.
4. High heritability and high genetic advance were shown by Seed yield fed⁻¹ and seed yield plant⁻¹ could be further improved with individual plant selection
5. Cluster analysis classified the sunflower varieties into three groups based on agronomic traits and seed yield cluster III, the genotype 4, which has the highest value for seed yield, was separate

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