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Research Article

Variability, Mean Performance Evaluation, Trait Relationship and Principal Component Analysis of Sunflower Genotypes

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Abstract

Forty nine sunflower genotypes evaluated for mean performance and Variability parameters of yield contributing traits at Kulumsa in simple lattice design. The aim is to identify desired characters of the crop, information of nature and genetic variability for seed yield improvement. The traits revealed presence of highly significant genotypic differences at P≤0.01 for yield contrbuting traits: head diameter, number of seed head^{-1}, thousand seed weight and seed yield ton ha^{-1}. Among the studied genotypes mean performance evaluation indicates that the highest seed yield ton ha^{-1} recorded for genotypes SHRS-2020#18 (3.06ton ha^{-1}), followed by SHRS-2020#4 (2.95tonha^{-1}) and SHRS-2020#16 (2.84t ha^{-1}) and the lowest average seed yield ton ha^{-1} recorded for genotype SHRS-2020#13 (1.15tonha^{-1}). Genotypes SHRS-2020#46 (83.5) and SHRS-2020#38 (84.5) the early flowered whereas, the late flowered recorded for the genotype SHRS-2020#43 (107.5) after the date of sowing. Seed yield ton ha^{-1} (YTPH), is the most economic trait, was positively and significantly associated with number seed head^{-1} and plant height. The characters indicating significantly positively correlation among seed yield and important traits would be highly effective and efficient improving respective traits. Higher estimates of heritability coupled with higher genetic advance were observed for seed yieldtonha^{-1} (46.49) and number of seed head^{-1} (42.46). This indicated that heritability of the trait is mainly due to additive gene effect and selection is effective for such traits. Principle component analysis (PCA) is usually used to identify the most significant variables in the data. In this study the principle component analysis result showed that accumulative variability original data accounted about 100% for the traits. The first Principal component which accounted for 38.5% total variation were observed through agronomic traits such as: SD, DFF, HD, days to maturity, number of seed head^{-1}. Similarily the second principal components which accounted for 17.4% of the total variations among the genoypes were attributed to differently from traits such as: yield ton ha^{-1}, number of seed head^{-1} and head diameter were the most important of seed yield positive contributors in the second Principal component. Whereas the third and fourth PCA accounted 14.4% and 14% of variations for agronomic traits such as: TSW, HD and SD in PCA 3 and for PCA 4 TSW, seed yield ton ha^{-1}, PH and DNM were the most important positive contributors traits for seed yield. Thus, these variation of traits observed in this experiment can help further as a selection index in genetic improvement of sunflower seed yield and its components.

Keywords

Sunflower Genotypes, Evaluation, Correlation, Phonetypic Variance, Genotypic Variance, Genetic Advance, Heritability, Principal Component Analysis

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1. Introduction

Sunflower (Helianthus annuus L.) belongs to the family Asteraceae. The Helianthus genus contains 65 different species of which 14 are annual plants. The sunflower plant expected to be originated in eastern North America. It is thought to have been domesticated around 3000 B.C. by Native Americans [1].

Sunflower is the world's fourth largest oil-seed crop and seeds are used for food and stalk as fuel [2]. Nutritionally, sunflower oil is superior to other vegetable oils due to the greater proportion of the unsaturated fatty acids (oleic, linoleic, and linolenic) and lower saturated fatty acids (palmitic and stearic), especially in the recently developed mid-oleic content NuSun™ hybrids. Sunflower oil contains zero trans-fats, which have been implicated in elevated cholesterol levels and increased risk of coronary heart disease [3]. The average fatty acid composition of oil from temperate sunflower crops is 55-75% linoleic acid, 15-25% oleic acid, 15-20% protein content [4]. Sunflower is well known as an important oilseed crop for the consumers, and consumed as roasted, confectionary and bird feed seed [5]. The confectionary and bird food sunflower are large seeded and stripped with 100-seed weight greater than 10g. Oil contents types are small seeded and black color [6]. Sunflower used as a supplement in the chemical industry as well as in the pharmaceutical industry and also helps in washing out cholesterol deposition in the coronary arteries of the heart and good for heart disease [23]. Sunflower species are allelopathic in nature; as well cultivated sunflower has great allelopathic potential and inhibits weed-seedling growth [7]. Numerous factors have been hypothesized as contributing to yield decline, including biotic and abiotic factors [8].

Sunflower has wide adaptability and high yielder than major oilseeds in the country. Currently some private farmers have started to grow due to high demand of raw material for oil-millers [9]. Sunflower is one of the most important oil crops in Ethiopia in terms of edible oil and holds significant promise for improvement and development improved varieties [10]. According to the previous cropping history of the crop, warmer areas with altitude of 1400-2400 m a.s.l. with well drained clay/sandy loam soil in the Hawassa, Bako and Dedessa valley, Bishoftu to Adama and Ziway to Arsi-Negele were suitable production areas [9].

The demand of sunflower oil in Ethiopia growing from time to time as population number increase and consumption preference. To alleviate this gap of improved varieties and the shortage of the edible oil seed; it's necessary to research and identify genotypes with high seed yield, high oil content, undamaged seed by birds and disease resistance. The main objective of sunflower improvement in Ethiopia developing productivity and oil rich varieties having stable performance under different agro-ecologies [11]. The success of any plant breeding program depends on the genetic variability and selection skill of plant breeder [12]. To improve any desired characters of the crop, information of nature and genetic diversity in available gene composition is very crucial.

2. Materials and Methods

Experiment Site: The study was conducted at Kulumsa during the 2020 cropping season, Kulumsa which found in Arsi Zone of Oromia Regional State, is located at 8° 01' N latitude and 39° 09' E longitude within an altitude of 2200 m. a. s, l. The soil type of the area is clay soil with soil composition of 63.123% clay, 28.125% silt and 8,75% sand soil. The pH of the is relatively acidic which 6.08. The maximum and minimum annual temperature of the area were 22.8^{o}C and 12.14^{o}C with 8737mm of annual rainfal (weather data Source: Kulumsa Agricultural research Center during the 2020 cropping season).

Plant Materials and Experimental Design: The field evaluation of 49 sunflower genotypes which have been taken from Holeta Agricultural Research Center was conducted during the main cropping season of 2020 at Kulumsa Agricultural Research Center.

Table 1. *Plant materials used in study.*

SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status
1	SHRS-2020#26	HARC	PVT	18	SHRS-2020#49	HARC	PVT	34	SHRS-2020#30	HARC	PVT
2	SHRS-2020#16	HARC	PVT	19	SHRS-2020#19	HARC	PVT	35	SHRS-2020#12	HARC	PVT
3	SHRS-2020#41	HARC	PVT	20	SHRS-2020#35	HARC	PVT	36	SHRS-2020#3	HARC	PVT
4	SHRS-2020#11	HARC	PVT	21	SHRS-2020#2	HARC	PVT	37	SHRS-2020#29	HARC	PVT
5	SHRS-2020#17	HARC	PVT	22	SHRS-2020#45	HARC	PVT	38	SHRS-2020#23	HARC	PVT
6	SHRS-2020#20	HARC	PVT	23	SHRS-2020#21	HARC	PVT	39	SHRS-2020#24	HARC	PVT

SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status
7	SHRS-2020#18	HARC	PVT	24	SHRS-2020#4	HARC	PVT	40	SHRS-2020#10	HARC	PVT
8	SHRS-2020#9	HARC	PVT	25	SHRS-2020#31	HARC	PVT	41	SHRS-2020#36	HARC	PVT
9	SHRS-2020#38	HARC	PVT	26	SHRS-2020#44	HARC	PVT	42	SHRS-2020#1	HARC	PVT
10	SHRS-2020#39	HARC	PVT	27	SHRS-2020#33	HARC	PVT	43	SHRS-2020#15	HARC	PVT
11	SHRS-2020#37	HARC	PVT	28	SHRS-2020#32	HARC	PVT	44	SHRS-2020#14	HARC	PVT
12	SHRS-2020#34	HARC	PVT	29	SHRS-2020#25	HARC	PVT	45	SHRS-2020#6	HARC	PVT
13	SHRS-2020#48	HARC	PVT	30	SHRS-2020#40	HARC	PVT	46	SHRS-2020#7	HARC	PVT
14	SHRS-2020#42	HARC	PVT	31	SHRS-2020#27	HARC	PVT	47	SHRS-2020#43	HARC	PVT

Table 1. *Continued.*

SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status	SLN	Genotypes	Source	Status
15	SHRS-2020#22	HARC	PVT	32	SHRS-2020#13	HARC	PVT	48	SHRS-2020#28	HARC	PVT
16	SHRS-2020#5	HARC	PVT	33	SHRS-2020#46	HARC	PVT	49	SHRS-2020#8	HARC	PVT
17	SHRS-2020#47	HARC	PVT								

The treatments were laid out in simple lattice design with two replications having plot size of $9m^2$ (3m*3m), Accommodating 4 rows of 3m length. The spacing between rows and plants was 75cm and 25cm. The seed rate and ferlizer rate used was 10kg/ha and 23/23kg/ha of N/P^2O^5 respectively.

Data Collected: The data for the following traits were recorded from the experimental plot and average value were considered: Days to 50% flowering, days to marurity, plant height (cm), stem diameter (cm), head diameter (cm), number of seed $head^{-1}$, thousand seed weight (gm), yield ton ha^{-1}. At physiological marurity, five plants from the central rows were randomly selected and plant height and stem diameter in centimeters were detemined. At harvest, five plants were randomly collected and yield components like head diameter, number of seed $head^{-1}$ and thousand seed weight were recorded. Grain yield was collected from two central rows of each plot ($4.5m^2$). The harvested aerial plant parts were air dried at the field condtion to determine the yield per plot.

2.1. Data Analysis

All the measured parameters were subjected to analysis of variance (ANOVA) using PROC GLM of SAS Software version 9.0 (2004) and the significance of means differences were tested by the least significant difference test $P \leq 0.05$ (LSD) as tested in [13]. Analysis of variance obtained from eight studied traits of sunflower genotypes were indicated in (Table 2).

Correlation of quantitative traits were measured to identify dependance, meaning statistical relationship between variables or observed data values. In this study the correlation was done by SAS PROC CORR method to illustrate statistical relationships among the studied traits of Sunflower genotypes.

2.2. Estimation of Variance Components

Quantifying the genetic variability present in plant populations is crucial for the success of selection plans. The partitioning of genetic variance into its components allows inferences about the inheritance of quantitative traits and prediction of the gain from selection [14]. Genetic variability is very important for selecting superior genotypes in a variety of improvement program, however environmental factors can mask real genetic variation. Phenotypic variance is the variation on the phenotypic expression of traits, and it can be determined by both genetic and environmental factors [15].

Phenotypic coefficient variance and Genetic coefficient variance:-The genotypic and phenotypic coefficients of variances are helpful in exploring the nature of variability in the breeding populations. The Genotypic variance (σ^2g), Phenotypic variance (σ^2P), Phenotypic Coefficient (PCV) and Genotypic Coefficient variance (GCV) were estimated using the formula as adopted from [16].

Environmental variance (σ^2e) =EMS, Genotypic variances (σ^2 g) = $\frac{GMS-EMS}{r}$, Phenotypic Variance (σ^2P) = σ^2 g+ σ^2e Where, GMS=Genotypic mean square, EMS=Error mean square, r=number of replication.

$$GCV=(\sqrt{\sigma^2}\ g\ /\ grand\ mean)*100$$

Where, σ^2 g = genotypic variance, GCV = Genotypic coefficient of variation.

$$PCV=(\sqrt{\sigma^2}p/\ gran\ mean)*100$$

Where, σ^2p= phenotypic standard deviation= PCV = phenotypic coefficient of variation.

Heritability in Broad Sense:-Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. It also gives an estimate of genetic advance a breeder can expect from selection applied to a population and help in deciding on a crop breeding method to choose [17]. Heritability in broad sense will be estimated for various characters as suggested by Allard [18].

$$H^2= \sigma^2\ g\ /\sigma^2p\ *100$$

where, σ^2 g=genotypic variance, σ^2p=phenotypic variance

Genetic Advance:-Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection. The methods illustrated by [19]. were used to compute expected genetic advance (GA) and GA as percent of mean assuming selection of the superior 5% of the genotypes.

$$GA= K*\sigma P*h^2$$

Where, k= selection differential (at 5% selection intensity)

σP = phenotypic standard deviation and k=constant (2.06)

h=the heritability ratio

GA as % of the mean was calculated by dividing the value with the respective grand mean of the trait being evaluated.

Principal component analysis is used to identify the most significant variables in the data set. Principal component analysis is one of the methods estimating genetic diversity and in evaluation of germplasm in sunflower [20]. The results of principal component analysis is of greater benefit to identify the parents for improving various traits and it can also be exploited in planning and execution of future breeding program [21]. In order to assess the patterns of variations, Principal Component Analysis (PCA) was done by considering eight characters for seed yield and agronomic traits in the table 6.

3. Result and Discussions

3.1. Data Analysis

According to the result, there was presence of high significant genotypic differences at P≤0.01 for head diameter, number of seed head^{-1}, thousand seed weight and yield ton ha^{-1}.

Table 2. *Analysis of Variance for eight Characters.*

Mean Sum of Square									
Source	**DF**	**DFF**	**DNM**	**PH**	**SD**	**HD**	**NSPH**	**TSW**	**YTPH**
Rep	1	3.68ns	159.54ns	71.00ns	0.743ns	9.241*	9112.5ns	236.25**	0.06ns
BLK	1	88.26ns	112.97ns	543.07ns	0.20ns	1.97ns	9640.65ns	150.83ns	0.44**
TRT	48	75.09ns	90.74ns	1154.30ns	0.36ns	7.87**	96369.68**	102.32**	0.40**

Note: **significant at p = 0.01, 0.05 significance level, respectively; ns: Non-Significant, DF: degreeof freedom, DFF: Flowering date; DNM: Marurity date; PH: Pant height; SD: Stem diameter (cm) HD: Head diametre; NSPH: Number of seed head^{-1}; TSW: Thousand seed weight; YTPH: Yield ton ha^{1}, Rep=Replication, BLK=Block, TRT=Treatment

However, there was no significant genotypic differences observed in days of flowering, days of maturity, plant height and stem diameter. The replication effect for thousand seed weight and head diameter significantly differences observed.

While all other traits in replication no significant. Blok effect Except yield ton ha^{-1}, all traits no significant difference obsrved in this study. The obtained results similar with [22].

Range and Mean Performance of genotypes:- The maximum days to flowering (107.5 days) were recorded by genotype SHRS-2020#43, while the minium value was recorded by genotype SHRS-2020#46 (83.5). Similarly the maximum days to maturity (166.5 days) were recorded by genotype SHRS-2020#37, while the minimum (129.5) was recorded for genotype SHRS-2020#11. Ninteen genoypes had days to maturity less than grand mean, which indicate that the possibility of improving the genotypes for earniness at least more than two weeks.

Table 3. Mean Performance of 49 Sunflower Genotypes Used in Study.

Sr No	Genotypes	Characters							
		DFF	DNM	PH	SD	HD	NSPH	TSW	YTPH
1	SHRS-2020#26	96.5	153.5	165	2.75	21	1009	51.02	1.7983
2	SHRS-2020#16	87	147	167	2.15	18.5	1150.5	52.72	2.8357
3	SHRS-2020#41	100	153	227.5	2.85	21	964	44.82	2.0811
4	SHRS-2020#11	93	129.5	175	2.55	19.5	1252	46.01	2.4126
5	SHRS-2020#17	94.5	146	150.5	2.1	18.5	1169.5	50.3	1.9869
6	SHRS-2020#20	90	158.5	164	2.25	19	1055.5	48.15	2.3414
7	SHRS-2020#18	105	156	219	2.85	21.5	1541.5	51.5	3.0607
8	SHRS-2020#9	90	147	151.5	2.1	17	801	56.77	2.3897
9	SHRS-2020#38	84.5	147	156.5	2.2	18.5	913.5	66.12	2.4008
10	SHRS-2020#39	92	155.5	165	2.3	19	736.5	57.63	2.421
11	SHRS-2020#37	103.5	166.5	184	3.4	21	1092.5	46.49	2.1876
12	SHRS-2020#34	100	163	183.5	3.4	22	1190.5	44	2.1562
13	SHRS-2020#48	104	162	148.5	2.85	21.5	997	51.62	1.2778
14	SHRS-2020#42	96.5	154	138	2.6	21	1341.5	61.69	2.0049
15	SHRS-2020#22	88.5	153.5	142.5	2.4	19	838.5	76.63	2.0295
16	SHRS-2020#5	90.5	157	153.5	2.2	20	1256	56.36	2.0302
17	SHRS-2020#47	105	155	199	2.75	16.5	1037.5	36.55	1.5841
18	SHRS-2020#49	103.5	161	231	2.5	17.5	978.5	54.74	1.9581
19	SHRS-2020#19	88.5	151	152	1.85	17.5	1034	51.25	2.3612
20	SHRS-2020#35	98	160.5	198.5	2.6	19.5	932	49.12	2.0263
21	SHRS-2020#2	91	156	149	2.25	19	1108	50.04	2.0603
22	SHRS-2020#45	96	158	164	2.8	21.5	929.5	53.66	2.0612
23	SHRS-2020#21	96.5	163	175	2.8	21.5	943.5	68.29	2.3084

Table 3. Continued.

Sr No	Genotypes	Characters							
		DFF	DNM	PH	SD	HD	NSPH	TSW	YTPH
24	SHRS-2020#4	88.5	161	166	2.95	22	1180.5	47.84	2.9489
25	SHRS-2020#31	102.5	164	163	3.35	19.5	895.5	55.3	1.1735
26	SHRS-2020#44	91.5	156	147.5	2.35	16.5	653	57.36	1.4743
27	SHRS-2020#33	94	155.5	151	2.95	20.5	959.5	53.62	2.2516
28	SHRS-2020#32	93	156	159	2.6	20	998	50.07	1.9836
29	SHRS-2020#25	102	161	159	2.95	19	688	50.96	1.418

Sr No	Genotypes	Characters							
		DFF	DNM	PH	SD	HD	NSPH	TSW	YTPH
30	SHRS-2020#40	87.5	143.5	131.5	2.25	17	827	53.15	1.6731
31	SHRS-2020#27	94	148	146	3	21	1190	61.44	1.9184
32	SHRS-2020#13	102.5	153.5	166.5	3.25	22	1524	46.52	1.9141
33	SHRS-2020#46	83.5	153	130	2.05	16.5	761.5	52.36	1.1464
34	SHRS-2020#30	92.5	157	165	2.2	19.5	807	54	1.2901
35	SHRS-2020#12	100	154.5	182.5	2.4	17.5	985	48.41	1.8565
36	SHRS-2020#3	104.5	160	161	2.8	21	1207.5	45.14	1.516
37	SHRS-2020#29	102.5	163	173	3.3	19	764	52.01	1.4394
38	SHRS-2020#23	95	154.5	187	2.6	20	672.5	56.68	1.5044
39	SHRS-2020#24	94	151	167.5	2.4	16	619	58.81	2.159
40	SHRS-2020#10	91	151	142.5	2.65	20	828	53.66	2.409
41	SHRS-2020#36	102.5	152.5	175	2.9	22	1203	42.43	1.9063
42	SHRS-2020#1	88.5	146	136.5	2.1	18.5	913	53.41	1.7121
43	SHRS-2020#15	96.5	159	211	2.55	17.5	803	61.1	1.9456
44	SHRS-2020#14	97.5	153.5	143.5	3.2	21.5	1077.5	60.7	1.9833
45	SHRS-2020#6	90.5	150.5	158	2.5	21.5	1076	45.25	1.8778
46	SHRS-2020#7	93	154.5	131.5	3	25	1369	50.37	1.7744
47	SHRS-2020#43	107.5	161.5	185	3.55	22.5	1379	39.92	1.3035
48	SHRS-2020#28	102.5	153.5	151	3.1	20	887.5	47.34	1.1802
49	SHRS-2020#8	87.5	143	137.5	2.1	16	801.5	49.01	1.78
Range		83.5-107.5	129.5-166.5	130-231	1.85-3.55	16-25	1009-1541.5	36.55-76.63	1.1464-3.0607
Mean		95.48	154.49	165.03	2.64	19.64	1006.97	52.45	1.95
CV		9.04	6.1	17.33	23	10.35	20.76	14.05	17.04
LSD		17.36	18.96	57.539	1.22	4.09	420.45	14.84	0.67

In this experiment The highest plant height was recorded by genotype SHRS-2020#15, followed by SHRS-2020#18, SHRS-2020#41 and SHRS-2020#49 exhibited the longest plant stature of all the genotypes with the values of 211cm, 219cm, 227.5cm and 231cm respectively in (Table 3). Whereas, the shortest plant height was recorded by genotype SHRS-2020#7 and SHRS-2020#40 followed by SHRS-2020#46, with above ground heights of 131.5cm, 131.5cm and 130cm respectively. The highest of stem diameter was recorded by genotype SHRS-2020#43 (3.55cm) in table 3. Whereas, the lowest value of stem diameter was recorded by genotype SSHRS-2020#19 (1.85cm). The maximum value of head diameter was recorded by genotype SHRS-2020#7 (25cm). On the contrary, the lowest value of head diameter was recorded by genotype SHRS-2020#8 (16cm).

The maximum value of grain yield performance was recorded by genotype SHRS-2020#18 (3.06t ha^{-1}) and followed by SHRS-2020#4 (2.95ton ha^{-1}) and SHRS-2020#16 (2.84t ha^{-1}). On the contrary, the lowest value of grain yield was recorded by genotype SHRS-2020#46 (1.1464 ton ha^{-1}). The maximum value number of seed $head^{-1}$ was recorded by genotype SHRS-2020#18, and followed by SHRS-2020#13, SHRS-2020#7 and SHRS-2020#42 respectively. Wheras, genotypes SHRS-2020#24, SHRS-2020#44, SHRS-2020#23, SHRS-2020#25, SHRS-2020#39, SHRS-2020#46 and SHRS-2020#29 bearing lower value for number of seed $head^{-1}$ in (Table 3). Better thousand seed weight was noted by SHRS-2020#22 genotype, followed by SHRS-2020#21, SHRS-2020#38, SHRS-2020#42 and SHRS-2020#27. However, the lower value of thousand seed weight were recorded

by genotypes SHRS-2020#47, SHRS-2020#43 and SHRS-2020#36, with the value of 36.55gm, 39.93gm and 42.43 gm, respectively in (Table 3).

The obtained results of range and mean performance of the Sunflower genotypic traits in table 3 indicates that a wide range of variation for each studied traits such as: days to lowering, days to marurity, plant height (cm), stem diameter (cm), head diameter (cm), number seed ha^{-1}, thousand seed weight (gm) and yield ton ha^{-1} as indicated in table 3 below.

From the result obtained, most of the measured quantitative traits were significatly correlated among each other. Crop phenological traits, days flowering had postively and significantly (P≤0.01) assocaited with days of maturity (r=0.54), plant height (r=0.5), stem diameter (r=0.64), head diameter (r=0.32), number of seed head^{-1} (r=0.34). Indicating independence of the traits to each other. Both days flowering and days of maturity had positively and significantly (P≤0.01) to plant height, stem diameter and head diameter (r=0.5, 0.64 and 0.32) respectively. Stem diameter and head diameter had positively and siginificantly (P≤0.01) to number seed head $^{-1}$ (r=0.42, 0.61) respectively. Whereas, number seed head $^{-1}$ had positively and significantly (P≤0.01) associated to seed yield ton ha^{-1} (r=0.24) in (Table 4).

In General, yield ton ha^{-1} had significantly at (P≤0.01) and (P≤0.05) and positively associated to the number of seed head^{-1} and plant height (r=0.24, 0.20) respectively. Indicating the traits contributed positively for grain yieid. However, it had relativel small negaively assocated to the days of flowering (0.26), days maturity (-0.13) and stem diameter (-0.18). This indicating that traits of crops resulted in exhibiting of negative impact on seed yield of sunflower in this study (Table 4).

Table 4. *Correlation coeffients of Eight Traits Sunflower Genotypes in Study.*

Traits	DFF	DNM	PH	SD	HD	NSPH	TSW	YTPH
DFF	1							
DNM	0.54**	1						
PH	0.5**	0.38**	1					
SD	0.64**	0.55**	0.29**	1				
HD	0.32**	0.35**	0.09	0.63**	1			
NSPH	0.34**	0.1	0.14	0.42**	0.61**	1		
TSW	-0.27	0.05	-0.16	-0.08	-0.03	-0.30**	1	
YTPH	-0.26	-0.13	0.20*	-0.18	0.05	0.24**	0.08	1

The values of PCV were marginally higher than GCV in (Table 5). This indicates that the amount of variation was contributed by genetic component and least by enviroment; the result was correspondent with the report of [23]. High PCV value was observed for number of seed head^{-1}, yield ton ha^{-1}, stem diameter, plant height, thousand seed weight and head diameter. Whereas the lower observed for days of flowering and days to maturity. These indicate the exixtence of wide phenotypic variation among genotypic considered in the present study and possibilty of genetic improvement of those traits through selection. This findings were correspondent with [24]. In this study low PCV was observed for days of flowering and days of maturity. The improvement of these traits could be possible through hybridization followed by selection; The findings were similarily with [25]. Medium GCV was observed for number of seed head^{-1} and yield ton ha^{-1}. Low GCV estimates was observed for days of flowering, days of maturiy, plant height, head diameter and thousand seed weight. The results were similar with the findings of [26].

Table 5. *Variability parameters for some quantitative Traits of 49 sunflow er genotypes.*

Sr.No	Traits	σ2g	σ2e	(σ2p)	GA	GAM	gcv	pcv	hb2
1	DFF	0.33	74.43	74.76	4.6	4.82	0.6	9.06	6.66
2	DNM	0.94	88.85	89.8	6.26	4.05	0.63	6.13	10.26
3	PH	168.12	818.05	986.18	41.63	25.22	7.86	19.03	41.29

Sr.No	Traits	σ2g	σ2e	(σ2p)	GA	GAM	gcv	pcv	hb2
4	SD	0.01	0.37	0.38	0.44	16.83	2.87	23.18	12.38
5	HD	1.87	4.14	6	3.78	19.22	6.96	12.47	55.78
6	NSPH	26344.48	43680.71	70025.19	427.55	42.46	16.12	26.28	61.34
7	TSW	23.97	54.38	78.35	13.58	25.87	9.33	16.86	55.31
8	YTPH	0.14	0.11	0.25	0.9	46.49	19.57	25.95	75.43

Note: Genotypic variance: σ^2g; σ^2e = Error variance, σ^2p: Phenotypic variance, GCV: Genotypic coefficient of variance, PCV: phenotypic coefficient variance, H^2: heritability in broad sense, GA: genetic advance, GAM: Genetic advance mean percent

The genotypes under the study showed high heritability values for yield ton ha^{-1} and number of seed $head^{-1}$ and whereas medium heritability values were recorded for thousand seed weight, head diameter and plant height traits. The estimates of heritability in broad sense showed considerable variation for different characters in (Table 5). The high value of heritabilty was recorded for yield ton ha^{-1} (75.43%), followed by number of seed $head^{-1}$ (61.34%). The heritability gives an idea of transmission of a character from parents to offspring. The obtained result under present experiment is in similar with the earlier reports of [27].

The higher estimates of heritability coupled with higher GAM for yield ton ha^{-1} (75.43, 46.49), number of seed $head^{-1}$ (61.34% and 42.46%), head diameter (55.78% and 19.22%), thousand seed weight (55.31%, and 25.87%) and plant height (41.29% and 25.22%) indicated that heritability of the trait is mainly due to additive effect and selection is effective for such traits. It also predicts the gain under selection than heritabilty estimate alone. This indicates that improvement in these traits could be made by simple selection. The results were correspondent with [28].

3.2. Principal Component Analysis

In this experiment four principal components which account for most of variability have been extracted, since four components had eigen value greater than one. These eigen value are 3.07756, 1.39437, 1.15234 and 1.12029 from fist to fourth PCA respectively. The first principal component is the largest contributor to the total variation in the population followed by subsequent components according to the creteria used by [29] and corroborated by [30], suggested that the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these are more useful in differentiating the accessions this information cited by [31]. Thus it is useful for genetic improvement of important traits having larger contributions to the variability rather than going for all the characters under study. The original data had accounted about 100% of accumulative variability in (Table 6). According former secientist that [32] on interpretion of the principal components result are depends on findings of variables are most strongly correlated with each component, i.e, which of these values are larger maginitude and farthest from zero in either direction influence the clustering more than those lower value closer to zero. The values in the PCA of 0.30 or higher can be consedered as important according to [33] reported.

The first Principal component which accounted for 38.5% total variation were observed through agronomic traits such as: stem diameter, days to flowering, head diameter, days to maturity, number of seed $head^{-1}$. Similarily the second principal components which accounted for 17.4% of the total variations among the genoypes were attributed to differently from traits such as: yield ton ha^{-1}, number of seed $head^{-1}$, head diameter were the most important of seed yield positive contributors in the second Principal component.

Table 6. *Principal component Scores of Some quantitative parameters in the study.*

Principal component Scores								
Traits	**Prin1**	**Prin2**	**Prin3**	**Prin4**	**Prin5**	**Prin6**	**Prin7**	**Prin8**
Days to Flowering	0.46633	-0.25124	-0.21314	-0.06883	0.31278	0.43646	0.16786	0.59392
Days to Marurity	0.3874	-0.32942	0.08802	0.32506	-0.7218	0.25024	-0.16456	-0.13153
Pant height	0.29869	-0.04794	-0.56261	0.45321	0.3016	-0.37387	-0.34569	-0.19056
Stem diameter	0.48828	-0.08756	0.23413	-0.03007	0.15756	-0.25117	0.65628	-0.42378

Principal component Scores								
Traits	**Prin1**	**Prin2**	**Prin3**	**Prin4**	**Prin5**	**Prin6**	**Prin7**	**Prin8**
Head diameter	0.39909	0.3001	0.44575	-0.06106	-0.08459	-0.4958	-0.29238	0.45803
Number seed head-1	0.347	0.55008	0.06006	-0.21357	0.16205	0.48946	-0.32362	-0.39652
Thousand seed weight	-0.15064	-0.15064	0.586	0.59682	0.43674	0.2196	-0.12481	-0.02208
Yield ton ha-1	-0.04959	0.63486	-0.17257	0.52703	-0.20304	0.10208	0.43445	0.21577
Eigen value	3.07756	1.39437	1.15234	1.12029	0.43688	0.32944	0.28644	0.20268
Variance	74.1697	88.4793	97.9	0.3689	6.0876	69.046	80.9692	0.2562
Proportion	38.5	17.4	14.4	14	5.5	4.1	3.6	2.5
Comulative	38.47	55.9	70.3	84.31	89.77	93.89	97.47	100

The third and fourth PCA accounted 14.4% and 14% of variations for agronomic traits such as: thousand seed weight, head diameter and stem diameter in PCA 3 and where as thousand seed weight, seed yield ton ha^{-1}, plant height and days maturity in PCA 4; these traits are the most important positive contributors for seed yield. Similar results were reported by [34] in the principal component analysis the first three components explained 91.60% of total variations, that the first, second and third components accounted 46.50%, 32.90% and 12.20% of the variation for the first principal component, seed yield plant-1 (0.48), plant height (0.45) and head diameter (0.44) were the most important contributing characters. whereas days to heading (0.51), days to maturity (0.50) and seed index (0.49) were the important traits that chiefly contributes to the second principal components. [31] also revaeled that the first five principal components extracted showed 84.72% of total variation; for the first principal component attributes 31.9% of total variation whereas, the second, the third, the fourth and the fifth principal components contributes, 22.72%, 12.25%, 10.11%, and 7.75% respectively in his experimental studied traits.

In general, it assumed that traits with larger absolute values closer to unity within the first, second, third, and fourth principal components, respectively influence the clustering more than those with lower absolute values closer to zero (0). In this experiment, most of the traits individually contributed small effects ranged (±0.060--7.28) to the total variations and, therefore, defferential grouping of genotypes was mainly attributed by the cumulative effect of the individual traits. However, traits which had relatively greater weight in the first, second, third, and fourth principal components largely contributed to the total variation and there were accountable for differential grouping of genotypes.

4. Conclusion

The ANOVA showed highly significant differences ($p \leq 0.01$) among sunflower genotypes for head diameter, number of seed $head^{-1}$, thousand seed weight and yield ton ha^{-1}. Among the studied genotypes mean performance evaluation indicates that the highest seed yield ton ha^{-1} recorded for genotype SHRS-2020#18 (3.06t ha^{-1}), followed by SHRS-2020#4 (2.95t ha^{-1}) and SHRS-2020#16 (2.84t ha^{-1}) and the lowest average seed yield ton ha^{-1} recorded for genotype SHRS-2020#13 (1.15t ha^{-1}). Seed yield ton ha^{-1} (YTPH), is the most economic trait, was positively and significantly associated with number of seed $head^{-1}$ and plant height. The characters Indicating significantly positively correlation among seed yield and important traits would be highly effective and efficient improving respective traits. High PCV value was observed for stem diameter, number seed $head^{-1}$ and yield ton ha^{-1}. These indicate the existence of wide phenotypic variation among genotypic considered in the present study and possibilty of genetic improvement of those traits through selection. The higher estimates of heritability coupled with higher genetic advance were observed for seed yield ton ha^{-1} (46.49) and number of seed per head (42.46). This indicated that heritability of the trait is mainly due to additive gene effect and selection is effective for such traits. The characters identified above as important direct and indirect yield components merit due to consideration in formulating effective selection strategy for developing high yielding Sunflower genotypes. Therefore, the best performing genotypes with desirable characters identified above are more important indication of parents which serve for further breeding effort. The first Principal component which accounted for 38.5% total variation were observed through agronomic traits such as: stem diameter, days to flowering, head diameter, days to maturity, number of seed $head^{-1}$. Similarily the second principal components which accounted for 17.4% of the total variations among the genoypes were attributed to differently from traits such as: yield ton ha^{-1}, number of seed $head^{-1}$ and head diameter were the most important of seed yield positive contributors in the second Prin-

cipal component. Whereas the third and fourth PCA accounted 14.4% and 14% of variations for agronomic traits such as: thousand seed weight, head diameter and stem diameter in PCA 3 and for PCA 4 thousand seed weight, seed yield ton ha^{-1}, plant height and days maturity were the most important positive contributors traits for seed yield. Thus, these variation of traits observed in this experiment can help further as selection index in genetic improvement of sunflower seed yield and its components.

Abbreviations

CV	Coefficient Variance
LSD	Least Significant Difference
HARC	Holeta Agricultural Research Center
PVT	Preliminary Variety Trial

Conflicts of Interest

The authors declare no conflicts of interest.

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