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Variability and correlation studies in sunflower lines (*Helianthus annuus*)

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Abstract

The present study was carried out in *kharif* 2018 to study the variability in ten different traits among the sunflower genotypes. From the study it is clear that the magnitude of genotypic coefficient of variation was less than phenotypic coefficient of variation for all the trait studied. Maximum GCV recorded was 25.17 percent for oil yield and lowest of 3.11 percent for days to maturity. The maximum heritability recorded for oil yield (99.86%) and lowest for seed yield per hectare (16.25%). Similarly genetic advance observed highest for oil yield with 99.62 percent and lowest for test weight with only 0.48 percent and genetic advance over mean was more (51.81%) for oil yield. The correlation analysis depicted that two traits shown significant positive correlation with yield per hectare basis.

Keywords: Sunflower lines, *Helianthus annuus*, Asteraceae/Compositae family

Introduction

Sunflower (*Helianthus annuus* L.) is the most important oilseed crop after soybean in the world, belonging to Asteraceae/Compositae family originated from temperate North America and has high content of unsaturated fatty acids and lacks cholesterol, thus there is a high oil benefits from it with a desirable quality. It is a diploid crop with an haploid genome size of about 3000 Mb with diploid chromosome number $2n = 34$ (Darvishzadeh *et al.*, 2010) [2]. Presently, it is cultivated in an area of 20.00 million hectares globally with production of 30.00 million tonnes and productivity of 1, 500 kg ha⁻¹. Asia accounts for nearly 20-22 percent of the total sunflower area in the world, contributing 18 percent of the total production.

Effectiveness in selection of hybrids depends on the magnitude of genetic variability present in a particular trait. The present study included variability with reference to genetic parameters such as genotypic variance, phenotypic variance, heritability and genetic advance. Since the mean values and units of measurement of the characters differ, the absolute values of phenotypic and genotypic variance cannot be used for comparing the magnitude of variability for different traits. Hence, the coefficients of variation at phenotypic and genotypic levels have been used to compare the variability observed among the different characters. An assessment of heritable and non-heritable components in the total variability observed is indispensable in adopting suitable breeding procedures. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and predicted genetic advance.

Exploiting the genetic variability is most important for genetic makeup of the crop, as genetic variation is the base for effective plant improvement programme. Hence variability is a prime requisite for adoption of appropriate breeding procedure (Safavi *et al.* 2011) [10], and heritability provides vital information about transmissibility of quantitative characters of economic importance that pave way for designing effective crop breeding strategy. Besides, genetic advance provides comprehensive information of segregating generations to facilitate selection. Higher estimates of heritability and genetic advance offers much scope for selection in developing newer genotypes with desired features.

Heritability alone cannot provide clear prediction of selections made. Thus Heritability values along with the estimate of genetic advance would be more reliable. Heritability value indicates only the magnitude and type of gene actions in the expression of the quantitative characters while genetic advance is helpful in formulating the selection procedure to be adopted.

Materials and Methods

The experimental material comprised of 40 genotypes in sunflower sown in a randomized complete block design, which was replicated twice at college of Agriculture, Vijayapura during *kharif* 2018-19.

Each genotype was raised in a single row of 3m length with a spacing of 30cm between the plants and 60cm between the rows. Recommended agronomic practices were adopted to raise good crop. The observations for 10 different traits were recorded from five randomly tagged plants in each hybrid from both the replication *viz.*, days to 50 percent flowering, days to maturity, relative chlorophyll content using SPAD chlorophyll meter at 45 DAS, relative chlorophyll content using SPAD chlorophyll meter at 60 DAS, head diameter, seed yield per plant, test weight, seed yield per hectare and oil content. Genetic advance and heritability in broad sense were calculated as per Johnson *et al.*, (1955) [6] and Hanson *et al.*

(1956) [4], correlation (Johnson *et al.*, 1955) [6] and path analysis (Dewey and Lu, 1959) [3] respectively.

Results and Discussion

Genetic variability, heritability and genetic advance

The results pertaining to genetic variability component parameters *viz.*, range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2_{bs}) and genetic advance as percent of mean (GAM) for all the characters are presented in Table 1.

Table 1: Variability studies for yield and yield related parameters

Characters	Max.	Min.	AVG	V _p	V _e	V _g	h ²	σ _p	σ _g	PCV	GCV	GA	GA mean
PH (cm)	77.20	169.10	111.92	325.00	58.51	266.49	82.00	18.03	16.32	16.11	14.58	30.45	27.21
SPAD 45	30.92	44.53	38.44	8.74	3.86	4.88	55.84	2.96	2.21	7.69	5.75	3.40	8.84
SPAD 60	25.92	45.85	35.22	22.43	3.86	18.57	82.79	4.74	4.31	13.45	12.23	8.08	22.94
HD (cm)	5.72	10.19	7.67	1.66	0.16	1.49	90.13	1.29	1.22	16.82	15.91	2.39	31.16
DFF	54.00	67.00	58.18	11.71	2.25	9.46	80.79	3.42	3.08	5.88	5.29	5.70	9.80
DM	90.00	107.00	98.26	16.86	7.50	9.36	55.51	4.11	3.06	4.18	3.11	4.70	4.78
TW (g)	3.10	4.77	3.77	0.16	0.07	0.09	57.89	0.40	0.30	10.59	8.06	0.48	12.73
Yl/ha (kg)	305.77	624.00	484.32	8173.95	6845.41	1328.54	16.25	90.41	36.45	18.67	7.53	30.27	6.25
OC (%)	30.69	45.57	39.29	11.91	3.30	8.61	72.27	3.45	2.93	8.78	7.46	5.14	13.08
OY (kg ha ⁻¹)	107.54	284.70	192.26	2345.10	791.15	2341.80	99.86	48.43	48.39	25.19	25.17	99.62	51.82

DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, HD- Head diameter, TW- Test weight, Yl/ha- Seed yield per hectare, OC- Oil content, OY- Oil yield

V_p - Phenotypic variance

σ_g - Genotypic standard deviation

GCV - Genotypic coefficient of variation

V_g - Genotypic variance

σ_p - Phenotypic standard deviation

PCV - Phenotypic coefficient of variation

V_e - Environmental variance

GA- Genetic advance

h²- Heritability

GAM - Genetic advance over

From the table 1 it is clear that the magnitude of genotypic coefficient of variation was less than phenotypic coefficient of variation for all the trait studied. Maximum GCV recorded was 25.17 percent for oil yield and lowest of 3.11 percent for days to maturity.

Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment, genetic advance as percentage of mean (GAM) was calculated to predict the genetic gain. Genetic advance observed highest for oil yield with 99.62 percent and lowest for test weight with only 0.48 percent and genetic advance over mean was more (51.81%) for oil yield.

Genotypic coefficient of variation exhibited higher values than phenotypic coefficient of variation for all the traits studied. Maximum GCV recorded was 25.17 percent for oil yield and lowest for days to maturity (3.11 percent). Similar results were reported by Prabhakar (2001) [9] and Khandelwal *et al.* (2014) [7]. Similarly heritability recorded was maximum for oil yield (99.86%) and lowest for seed yield per hectare (16.25 percent) which indicates that there was much environmental variance and fluctuation for the seed yield trait. In the present study, all the characters studied showed low to high estimates of broad sense heritability. The characters *viz.*, plant height, SPAD at 60 DAS, head diameter, days to 50% flowering, oil content and oil yield exhibited very high heritability. The high heritability of these traits indicate that the characters are least influenced by the environment and selection for improvement of these traits would be rewarding.

Moderate estimates of heritability were recorded for SPAD at 45 DAS, days to maturity and test weight. Similar results were recorded by Harare and Bapat (1982) [5]. Low heritability was recorded for yield per hectare which indicated that selection based on phenotypic performance would be rewarding. In the present investigation, high heritability coupled with high genetic advance as percent of mean recorded for oil yield, head diameter, plant height and SPAD at 60 DAS. Similar results were recorded by Tiwari *et al.* (2003) [11], Arunkumar *et al.* (2004) [1], Umakanth *et al.* (2004) [12], and Patil *et al.* (2016) [8] in sorghum.

Genotypic and phenotypic correlation

Yield is a complicated trait that is influenced by the number of other characteristics that can have both positive and negative effects on it. As a result, understanding the mechanism of interaction, consequences, and cause of relationship will aid in the selection of breeding methods for increasing yield in sunflower. The magnitude of phenotypic correlation is lower than genotypic correlation, but they have a similar trend in direction, according to correlation analysis. Low phenotypic association indicates that the environment has an effect on the expression of these traits. Correlation among various traits is depicted in table 2 and table 3. Certain traits had significant positive correlation and certain had significant positive correlation. Yield per plant and plant height had significant positive correlation and rest had significant negative correlation. Similar results were obtained by Arunkumar *et al.*, 2014 [1]. This indicates that selection of traits like plant height and yield per plant can be used as major criteria for improving the yield.

Table 2: Genotypic correlation coefficient among various traits in sunflower lines

Traits	PH	SM@45	SM@60	HD	DFF	DM	TW	YL/PL	OC
SM@45	0.081								
SM@60	0.101	0.972**							
HD	0.583**	0.371**	0.334**						
DFF	-0.474**	-0.238*	-0.239*	-0.566**					
DM	-0.339**	0.060	0.059	-0.249*	0.677**				
TW	0.982**	0.028	-0.025	0.684**	-0.590**	-0.336**			
Yl/pl	0.422**	-0.005	-0.019	0.278**	-0.333**	-0.186	0.603**		
OC	0.422**	-0.005	-0.019	0.278**	-0.333**	-0.186	0.603**	1.000**	
Yl/ha	0.314*	-0.259*	-0.261*	-0.010	-0.301**	0.181	-0.002	0.563**	0.563**

*Significant at 5% level of significance and **Significant at 1% level of significance respectively

Table 3: Phenotypic correlation coefficient among various traits in sunflower lines

Traits	PH	SM@45	SM@60	HD	DFF	DM	TW	YL/PL	OC
SM@45	0.076								
SM@60	0.081	0.902**							
HD	0.573**	0.320**	0.289**						
DFF	-0.420**	-0.219*	-0.194	-0.510**					
DM	-0.210*	0.108	0.097	-0.214*	0.480**				
TW	0.492**	0.042	-0.049	0.298**	-0.208*	-0.067			
Yl/pl	0.339**	-0.033	-0.049	0.200	-0.270*	-0.057	0.276**		
OC	0.339**	-0.033	-0.049	0.200	-0.270*	-0.057	0.276**	1.000**	
Yl/ha	0.221*	-0.173	-0.170	0.006	-0.259*	0.091	0.014	0.380**	0.380**

*Significant at 5% level of significance and **Significant at 1% level of significance respectively

Conclusion

The lines which are having high heritability and greater amount genotypic coefficient of variation need to be selected and also the lines having high plant height and high seed yield per plant leads to increase in total yield per hectare basis. Thus there might be certain traits depicting negative correlation and certain positive correlation, but breeders need to concentrate on the traits which are having significant positive correlation in order to improve crop yield.

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