Genetic variability, Heritability and Genetic Advance Estimates in Sunflower (*Helianthus annus* L.*)* Genotypes at Holetta and Adadi, Ethiopia

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***Abstract*:** The present study was conducted with twenty five sunflower genotypes including one check at two locations, Holetta and Adadi to study genetic variability, heritability and genetic advance for seed yield and yield related components. The experiment was conducted using 5x5 simple lattice design across two locations during 2017/18 main cropping season. Data were recorded for fifteen quantitative traits and subjected to statistical analysis using a combination of statistical software by following different biometricians. The pooled analysis of varience revealed that significant differences ($P<0.05$) for all traits except for petiole length, stem diameter and ray floret number. High phenotypic coefficients of variation were observed for oil yield and seed yield per hectare. Medium genotypic coefficients of variation were recorded for oil yield and number of seed per plant whereas, Low genotypic coefficients of variation were observed for the remaining traits. Heritability in broad sense ranged from low for seed yield per plant to high for oil content. High heritability along with high genetic advance was observed for number of seed per plant.

***Key words*:** Genetic advance; Genetic variability; genotypic coefficients of variation; phenotypic coefficients of variation Heritability; Sunflower

1. INTRODUCTION

Sunflower (*Helianthus annus* L.) belongs to the compositae family. It is across pollinated crop which is domesticated about 10,000 years ago and thought to be originated from North America and disseminated to other continents Burke *et al.* (2002). It is used as oil and non-oil seed feed (forage-used as silage for animals, bird feed, snack in human diet, food for ruminant and fuel in diesel engines. Edible oil is one of the most important global commodities in the everyday life people. Sunflower oil is premium oil which has light color, mild flavor and ability to with stand high cooking temperature. Its oil has high quality when compared to others major oil crops as it comprises vitamins, minerals, proteins, fiber and photochemical (Demirer *et al*., 2004).

Although, Ethiopia has diverse agro ecological condition that enable to produce different oil seed crops the country is facing the shortage of edible oil and forced to import it from the world market. This is due to decreasing in local production of oil crops, increasing growth rate of human population and poor support and attention from government for oil crop

production. Hence, it is important to increase the production and productivity of edible oil crops to overcome the problem. Sunflower is an important oil crop with high oil quality and good adaptation ability (Hu *et al.,* 2010). In Ethiopia it is adapted to altitude below 800 to above 2400m.a.s.l and grown best in well drained and high water holding capacity soil with5.5-8 PH (Haile, 1994). At present the productivity of sunflower in the country is low compared to the world average. Since the country has the potential to grow the crop there is a great opportunity to increase the production and productivity of sunflower through breeding program by developing cultivars with traits of interest.

Any progress in breeding program depends on the magnitude of genetic variability in the genotypes and on the extent of heritability of desirable characters. Therefore Considering the magnitude of variability present in a crop species is most important as it allows effective selection. The total observable variation includes both genetic and environmental components. But, genotypic variation is the focus of plant breeders. Thus, in selection for quantitative traits more focus has to be given to those attributes with low environmental variability. Quantitative traits are highly influenced by various component traits which have polygenic inheritance.
Therefore, improvement for those traits cannot be achieved through simple phenotypic selection because of their polygenic nature and low heritability. High heritability is needed to execute effective selection scheme for the trait of interest. Heritability along with genetic advance is more reliable than heritability alone Johnson et al. (1955). Understanding of nature of inheritance of traits and extent of variability among genotypes helps breeders in formulating effective selection program.

2. MATERIALS AND METHOD

2.1 Description of the study area

The study was conducted at Holeta Agriculture Research center (HARC) and Adadi testing site of Holeta agricultural research center during the main season of 2017/18. The locations are situated at west shoa and south west shoa zones of Oromia region of Ethiopia respectively. Holeta Agricultural Research center is located at9º 00’ N, Latitude, 38º30’ E longitude with an elevation of 2400m above sea level. The area receives an average annual rain fall of 1144mm and has minimum and maximum temperature of 6°C and 22°C respectively. The soil type is Nitosoil with a PH of 6.0. Adadi is located at 08°31’ N Latitude, 38°13’ E longitude with an elevation of 2250m above sea level. The average annual rain fall of the area is 1105mm. the soil type is light brown with PH of 7.0

2.2 Experimental materials used for study

The experimental materials were obtained from the National oilseed Coordinating Center, Holetta Agricultural Research Center. Twenty four sunflower genotypes introduced and adapted to central highland of Ethiopia and one standard check were included in the study (Table 1). The genotypes were introduced from, France, Hindi and Brazil and were maintained at Holetta Agricultural Research Center. The check variety included in the study is released cultivar recommended for high and mid altitude zones of Ethiopia.

Table 1: Experimental materials used for the study

Entry no.	Genotype	Origin	Source	Status
1	Adadi-3-SPS-2/4	India	HARC	PVT
2	Adadi-3-SPS-5/4	India	HARC	PVT
3	Adadi-3-SPS-9/4	India	HARC	PVT
4	NK-FERTI-SPS-1/4	France	HARC	PVT
5	NK-FERTI-SPS-4/4	France	HARC	PVT
6	NK-KONDI-SPS-2/4	France	HARC	PVT
7	NK-KONDI-SPS-7/4	France	HARC	PVT
8	NK-NEOMA-SPS-2/4	France	HARC	PVT
9	Brazil Long seed PL2-SPS-3/4	Brazil	HARC	PVT
10	Brazil Long seed PL4-SPS-4/4	Brazil	HARC	PVT
11	NK-FERTI-SPS-8/1	France	HARC	PVT
12	Brazil Long Seed PL6-SPS-7/4	Brazil	HARC	PVT
13	Brazil Long Seed PL9-SPS-4/4	Brazil	HARC	PVT
14	H-45-SPS-5/4	India	HARC	PVT
15	NK-FERTI-SPS-7/4	France	HARC	PVT
16	NK-KONDI-SPS-7/4	France	HARC	PVT
17	NK-NEOMA-SPS-7/4	France	HARC	PVT
18	VSFH-180-SPS-5/4	India	HARC	PVT
19	VSFH-1044-SPS-1/4	India	HARC	PVT
20	VSFH-1044-SPS-2/4	India	HARC	PVT
21	VSFH-1044-SPS-3/4	India	HARC	PVT
22	VSFH-1044-SPS-9/4	India	HARC	PVT
23	VSFH-1044-SPS-10/4	India	HARC	PVT
24	VSFH-2006-SPS-2/4	India	HARC	PVT
25	Oissa	Released	HARC	Breeder seed

2.3 Experimental design and trial management

The experiment was replicated twice using simple lattice Design (5x5). Each plot had a length of 4m and 4 rows with row to row spacing of 75cm and plant-to-plant 25cm respectively. The seed sown at two locations (Holeta and Adadi) and all seeds emerged. Two seeds were dibbled in each hill for better emergency and thinning was carried after emergency to retain one plant per hill. Sowing date was done on June, 29/2017. Planting was performed manually and hand weeding was carried out twice. All other agronomic practices recommended for the area were followed during the crop growth period.

2.4 Quantitative data collected

1. Number of Leaves per plant: Leaves of 5 randomly selected plants were counted after attaining of maximum number of leaves.

2 .Height of plant (cm): At full development of crop 5 plants were sampled randomly and heights of plants were recorded from ground level to the point of attachment of disk with the stem.

3. Head diameter (cm): Lengths of disks of 5 randomly taken plants were measured from one edge of the disc to the other and their averages were taken.
4. Petiole length (cm): The lengths of petioles were recorded for five randomly taken plants per plot and average was computed.
5. Number of leaves on main stem: Numbers of leaves for five plants per plot were counted at flowering stage and average was computed.
6. Ray floret number: Ray florets of 5 randomly taken plants were counted at flowering stage and average was computed.
7. Days to 50% flowering: Numbers of days from the date of sowing to the day on which 50 per cent of plants per plot flowers were recorded.
8. Days to maturity: Number of days from the date of sowing to the day on which back of capitulum in 50 per cent of plants in a line turned to lemon yellow color was recorded.
9. Stem diameter (cm): was measured for 5 plants randomly taken from a plot at one third height of the plant from ground level with the help of digital vernier calipers in millimeter and converted to centimeters.
10. Seed filling Percentage (%): the seed filling percentage was computed using the following formula.

$$\text{Seed filling percent} = \frac{\text{number of filledd seeds}}{\text{total number of filled and unfilled seeds}} \times 100$$

11. Hundred Seed weight (g): One hundred filled seeds were sampled randomly, weighed and the weight was recorded in grams.
12. Seed yield per plant (g): The total weight of seeds per plant was recorded in grams for five plants and averages were computed.
13. Oil content (%): The seed oil content was determined through non-destructive method by utilizing nuclear magnetic resonance (NMR) technique in the laboratory of Oil Seeds Research at HARC. Oil percentage (%) was determined by using nuclear magnetic resonance spectrometry (NMRS). Sample of 10g of seeds were dried in an oven for 3hr at 78℃ and cooled for 3hours.Then oil contents of seeds were measured using nuclear magnetic resonance machine.
14. Seed yield per hectare (kg): Seed Yield recorded per plot was converted to hectare for all plots.
15. Oil yield (kg/ha): Oil yield in kg/ha was calculated by using the following formula.

$$\text{Oil yield } \left(\frac{\text{kg}}{\text{ha}}\right) = \frac{\text{seed yield } \left(\frac{\text{kg}}{\text{ha}}\right) \text{ x oil content (\%)}}{100}$$

2.5 Statistical data analysis
The data collected from the two locations for all parameters were subjected to statistical analysis by using SAS 9.3(2012) computer software.

2.6 Analysis of variance (ANOVA): since the relative efficiency of simple lattice design obtained was better than randomized complete block design at both locations the analysis of

variance was done based on simple lattice design. Test for homogeneity of error variance was done following Hartley (1950). All traits showed homogeneity for error variance. Therefore separate and combined analysis of variance was performed for all traits. Proc GLM and Proc lattice procedures were used based on simple lattice design.

2.7 Estimation of variance components

Estimation of the phenotypic and genotypic variance for the pooled data analysis across the two locations was done following the formula suggested by Hallauer and Miranda (1988) as shown below.

$$\sigma^2_{ph} = \sigma^2_{g} + \sigma^2_{ge/e} + \sigma^2_{e/re} = msg/re$$

Genotype variance (σ^2g) = [(σ^2e+ Rσ^2gl+ RLσ^2g) - (σ^2e + Rσ^2gl)]/RL = (MSG-MSGXL)/ RL

Genotype x location interaction variance (σ^2gl) = [(σ^2e+ Rσ^2gl) – (σe2)]/R = (MS5-MSE)/R

Environmental variance (σ^2e) =MSE

The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were also computed following the formula suggested by Burton and Devane (1953).

$$\text{Phenotypic cofficient of variation(PCV)} = \frac{\sigma^2 \text{P}}{\bar{\times}} \times 100$$

$$\text{Genotypic coefficient of variatio(GCV)} = \frac{\sigma^2 \text{g}}{\bar{\text{X}}} \times 100$$

2.8 Heritability and Genetic advance

Heritability in the broad sense (H^2) was estimated by following the formula suggested by Falconer and MacKay (1996). Classified as low (below 30%), medium (30-60%) and high (above 60%) following Johnson *et al*. (1955).

$$\text{H}^2 = \left[\sigma^2\text{g} \Big/ \sigma^2\text{p} \right] \times 100$$

Where, H^2 =heritability in broad sense

σ2g = Genotypic variance and

σ2p= Phenotypic variance

GA and GAM% were calculated as per the procedure recommended by Singh and Chaudhury (1985). $GA = K * H^2 \sqrt{\sigma^2 ph}$

Where, H^2 = Heritability in broad sense, σph= Phenotypic standard deviation, GA= Expected genetic advance k = the standardized selection differential at 5% selection intensity (2.06).

The genetic advance as percentage population mean (GAM) was estimated following the methods described by Johnson *et al*. (1955) and classified as low (<10%), moderate (10-20%) and high (>20%). $GAM = \frac{GA}{\bar{X}} \times 100$ Where as, GA=Genetic advance under selection and x̄=Grand Mean of the trait.

3. RESULTS

3.1 Analysis of variance (ANOVA): Mean squares from the analysis of variance (ANOVA) of twenty five sunflower genotypes for fifteen quantitative traits studied are presented in Table 2. The pooled analysis of variances showed that there was significant (P<0.01or 0.05) differences among genotypes for all traits (Table 2). The mean square due to genotype x location (GxL) interaction were significant (P<0.01 or P<0.05) for yield per plant, days to flowering, plant height, yield per hectare, oil yield, days to maturity, oil content, head diameter and leaf number. Non-significant (GxL) interactions were observed for ray floret number, petiole length, hundred seed weight and stem diameter (Table 2).

3.2 Phenotypic and genotypic variability

Estimation of genotypic varience, phenotypic varience, phenotypic coefficients of variance (PCV) and genotypic coefficients of variance (GCV) were presented in Table 3. Phenotypic coefficients of variance (PCV) were ranged from 1.4 % for days to maturity to 31.21 % for oil yield (kg) per hectare where as the genotypic coefficients of variance (GCV) were ranged from 0.762% for days to maturity to 12.04 % for oil yield (Table 3).

3.3 Heritability and genetic advance

Heritability in broad sense, genetic advance and genetic advance as the percentage of the mean (GAM) at 5% selection intensity are shown in Table 3. Heritability in broad sense ranged from 3.56 % for yield per plant to 65.32% for oil content whereas the expected genetic advance as percent of the mean ranged from 0.56 for number of leaves per plant to 17.89 for number of seed per plant (Table 3)

Table 2: Mean square from analysis of variance for different sources of variation and the corresponding CV for quantitative traits of sunflower genotypes tested at Adadi and Holetta

	Mean squares								
TRAIT	LOC(1)	Rep(L) (2)	Block (Rep) (8)	Geno (24)	Loc*Geno (24)	Error (40)	CV (%)	Lsd (0.05)	R-Square
Ray floret number (no.)	542.9**	28.1	23.9	40.81*	11.973 ns	15.3	8.1	5.6	0.76
Leaf number(no.)	324**	9	2.22	4.94*	4.542*	1.8815	5.7	1.96	0.895
Petiole length (cm)	66.75**	0.012	1.49	3.242*	1.071 ns	0.953	7.08	1.395	0.832
Head diameter(cm)	5.36 ns	5.34	5.87	4.83*	3.98*	1.39	5.74	1.69	0.84
Stem diameter (cm)	0.12*	0.002	0.12	0.058*	0.0284 ns	0.0287	6.46	0.24	0.73
Plant height(cm)	11815.7**	110.25	121.5	791.05**	289.65**	71.33	4.6	12.07	0.932
Days to flowering(days)	2470.1**	47.61	6.21	84.83**	22.9**	5.77	2.34	3.43	0.958
Days to Maturity(days)	3540.2**	68.9	2.665	11.79*	6.42*	3.28	1.2	2.59	0.97
Number of seed per plant	3018211.29	79.21	8830.4	69169.3**	22915.3*	11207.3	10.46	151.9	0.925
Seed filling percentage (%)	11.614*	2.585	1.11	7.71*	3.99*	2.17	1.54	2.11	0.804
Hundred seed weight(g)	14.22	0.81	1.06	2.07**	0.653ns	0.53	12.01	1.04	0.82
Seed yield per plant (g)	14400**	4.75	23.44	120.77**	112.47**	28.76	10.2	7.66	0.948
seed yield per hectare(kg)	954646.24*	135085.65	42855.9	641897.4**	511191.6**	30331.6	8.95	248.9	0.965
Oil content (%)	292.1**	0.073	1.88	46.57**	9.71*	3.085	5.2	2.51	0.941
Oil yield per hectare(kg)	4018.04**	170.8	25.4	797.9**	591.14**	46.7	10.3	9.8	0.96

Whereas, **, highly significant at 0.001, * significant at 0.05, ns, non-significant at 0.05, CV, coefficient of variation, df, degree of freedom,

Table 3: Heritability, genetic advance and coefficients of variations in 25 sunflower genotypes studied at Holetta and Adadi

TRAIT	$\sigma^2 g$	$\sigma^2 p$	$\sigma^2 i$	$\sigma^2 e$	PCV %	GCV %	H^2 %	GA	GAM %
Leaf number(no.)	0.1	2.37	1.33	0.94	6.41	1.32	4.22	0.134	0.56
Head diameter(cm)	0.213	2.21	1.295	0.7	7.25	2.25	9.64	0.295	1.44
Plant height(cm)	125.35	270.21	109.16	35.7	8.93	6.1	46.39	15.71	8.54
Days to flowering(days)	15.5	26.96	8.56	2.9	5.46	4.14	57.49	6.15	6.47
Days to maturity(days)	1.34	4.55	1.57	1.64	1.4	0.762	30.01	1.32	0.87
Number of seed/plant(no.)	14434	26453.3	6415.65	5603.65	15.91	11.76	54.56	182.8	17.89
Seed filling percentage (%)	0.93	2.94	0.91	1.1	1.8	1.01	31.63	1.12	1.17
Seed yield per plant(g)	2.075	58.3	41.85	14.38	14.47	3.93	3.56	0.56	1.06
Oil content (%)	9.21	14.1	3.31	1.54	11.04	8.93	65.32	5.05	14.86
Oil yield per hectare(kg)	51.69	347.26	272.22	23.35	31.21	12.04	14.89	5.98	10.02
Seed yield per hectare(kg)	32676.45	288272	240430	15165.8	26.85	9.04	11.34	125.42	6.27
Ray floret number(no.)	7.21	67.1	52.2	7.65	17.06	5.6	10.75	1.82	3.78
Petiole length(cm)	0.543	1.1	0.06	0.48	7.49	5.26	49.36	1.07	7.62
Stem diameter(cm)	0.01	0.024	0.0002	0.014	5.89	3.8	41.67	0.133	5.06
Hundred seed weight(g)	0.354	0.724	0.1	0.27	13.95	9.75	48.9	0.86	14.1

4. DISCUSSION

According to Siva Subramanian and Menon (1973) phenotypic coefficients of variance (PCV) and genotypic coefficients of variance (GCV) Values more than 20%, less than 10% and between 10 % and 20 % are regarded as high, low and medium respectively. Based on this, phenotypic coefficient of variance (PCV) was high for oil yield (31.21 %) and seed yield (kg) per hectare (26.85 %). Moderate PCV and GCV were recorded for number of seed per plant. High to moderate values of PCV and GCV observed for the above traits in the present study indicated the existence of variability for characters and selection may be effective based on these characters. Low PCV and GCV were recorded for leaf number, days to maturity, head diameter, plant height, days to flowering, days to maturity and seed filling percentage implies that selection for these characters may not be effective. The value of GCV was close to the value of PCV for all traits except seed yield per hectare and oil yield per

hectare. The result of this study indicates the contribution of genotypic effect for phenotypic expression of those characters is high. This implies the expressions of those characters under study were less influenced by environmental factors except seed yield per hectare and oil yield per hectare wich are highly influenced by environment. Similar result was founded by Gangappa (1991) who reported low variability for seed yield and oil content. The result is not line with the findings of Reddy and Reddy (2006) who reported high PCV and GCV for these traits. These differences may happen due to differences in the studied genotypes and locations.

Since, genotypic coefficient of variance provides information on the genetic variability present in quantitative characters in base population; it is not possible to determine the amount of the variation that was heritable only from the genotypic coefficients of variance. The best picture of the amount of advance to be expected from selection would be obtained from genetic coefficient of variance together with heritability estimates (Burton and Devane, (1953). Therefore, estimation of the heritable portion of the variation could be more useful. According to Johnson *et al*. (1955) heritability values more than 60%, less than 30% and between30% and 60 % are regarded as high, low and moderate respectively. Based on this high heritability was observed for oil content (65.32%) indicating high genotypic influence and low environmental influence. This shows Selection based on phenotypic performance of this trait may help to improve this trait. Medium heritability was noticed for days to maturity (30.01), plant height (46.39), days to flowering (57.49), number of seed per plant (54.56), petiole length, (49.36), stem diameter (41.67), hundred seed weight (48.9) and seed filling percentage (31.63). Low heritability was observed for number of leaves per plant (4.22), head diameter (9.64), yield per plant (3.56), oil yield per hectare14.89), number of ray floret (10.75) and seed yield per hectare (11.84). Since those traits are highly influenced by environment, direct selection based on their phenotypic performance may not be effective to improve those traits.

According to Johnson *et al.* (1955) genetic advance was classified as low (>10), medium (10-20) and high (>20). Based on this, moderate genetic advance as percent of mean was observed for number of seed per plant (17.89), oil content (14.86), hundred seed weight (14.1) and oil yield per hectare (10.02). leaf number (0.56), head diameter (1.44), days to flowering (6.47), days to maturity (0.87), seed filling percentage (1.17), seed yield per plant(1.06), number of ray floret (3.78), petiole length (7.62), stem diameter (5.06) and seed yield (kg) per hectare (6.27) showed low genetic advance.

Heritability accompanied with genetic advance is useful than heritability alone in the estimation of the selection effects. If a character is governed by non-additive gene action it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action heritability and genetic advance would be high. In this study High heritability (65.32) along with moderate genetic advance as percent of mean (14.86) was recorded for oil content indictes the involvement of both additive and non-additive gene actions in the inheritance of this trait. Therefore this trait can be improved through any modified selection procedures aiming to exploit the additive gene effects. This result is in line with the finding

of Hassan *et al*. (2012) who reported high heritability with moderate genetic advance as percent of mean for oil content.

5. CONCLUSION

Significant to highly significant mean square due to genotypes observed from the analysis of varience indicates the substantial variability among genotypes. The value of PCV observed in this study was higher than GCV for all traits suggesting that the influence of environmental factors on the studied traits. High heritability observed for traits indicates the possibility of selection at phenotypic level. High heritability coupled with moderate genetic advance indicates the involvement of both additive and non-additive gene action in the inheritance of traits. Moderate heritability along with moderate genetic advance implies those traits are governed by non-additive gene action thus, direct selection is not beneficial. Moderate heritability with low genetic advance indicates less genetic gain is expected through selection from these traits. Low heritability with low genetic advance observed for some traits in this study indicates that those traits are governed by non-additive gene action and highly influenced by the environment. Totally the results obtained from GCV, PCV, broad sense heritability and genetic advance as percent of mean indicates the considerable possibility of further improvement in genotypes used in the present study by using appropriate breeding scheme for those traits.

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