

## CHARACTERIZATION AND ASSOCIATION AMONG YIELD AND YIELD RELATED TRAITS IN SUNFLOWER (*HELIANTHUS ANNUUS*L) GENOTYPES

Zenebe Mekonnen Adare<sup>1</sup>

<sup>1</sup>College of Agricultural Science, Arbaminch University, Arbaminch, Ethiopia

### ABSTRACT

Development of genetically improved high yielding genotypes urges the knowledge on nature and magnitude of variability present in the available germplasm. Characterization and association among yield components and their direct and indirect effects on the seed yield of 100 sunflower germplasm introduced from U.S. National Plant Germplasm System (NPGS) were investigated using a simple lattice design during 2011/12 cropping season. The ANOVA results showed significant differences ( $P < 0.05$ ) in all the traits studied among the sunflower germplasm. Out of 100 genotype, 38 were found to be distinctive on the basis of studied traits, two genotypes (PI265499, PI650655) were classed individually while the remaining genotypes were distributed into five clusters. The phenotypic and genotypic variances, correlation, heritability and genetic advances were estimated for grain yield and yield related traits. The highest genotypic and phenotypic variances were observed for plant height (PH), seed yield (YLD), and days to flower (DF) while the lowest were observed for hundred seed weight (HSW), head diameter (HD) and oil content % (OC %). The highest genotypic coefficient of variance was recorded for YLD (31.03) followed by PH (26.20) and OC % (23.74). Broad sense heritability ranged from 63.71 (HSW) to 90.98 (PH). High genetic advance were observed for PH (10013.01), YLD (2227.01), DF (1853.00), and days to mature (DM) (1560.47) indicating the prevalence of additive gene action for inheritance of these traits. Spearman's coefficient of rank correlation analysis revealed that HD (0.57121\*\*), HSW (0.49039\*\*), DM (0.53312\*\*), DF (0.24103\*) and PH (0.5491\*\*) had maximum direct effect resulted positively and significantly ( $P \leq 0.01$ ) correlated with YLD. These traits can be used to improve the grain yield of sunflower.

**Keywords:** Correlation coefficients, Genetic variance, Heritability, Phenotypic variance.

### Contribution/ Originality

This study is one of very few studies carried in Ethiopia which have investigated the genetic, phenotypic and environmental variances of sunflower germplasm collection from various sources of origin. The outputs of this study help breeders for easy selection and promotion of germplasms for further study and extrapolation of genes of superior characters in yield improvement.

### 1. INTRODUCTION

Sunflower (*Helianthus annuus*) is the third most important oil seed crop following soybean and groundnut in the world. It is a good feed for livestock, poultry and cage birds. The refined oil is

† Corresponding author

used as salad & cooking oil, and for manufacture of margarine, paints, varnishes, compound cooking fats and shortenings. The oil is a rich source of linoleic acid, which helps in washing out cholesterol deposition in the coronary arteries of the heart and good for heart patients [1]. Cultivation of sunflower were take place in pockets of land in many parts of Ethiopia and are included in cropping systems in Southern region around Konso and South Ommo in particular [2]. Production and productivity of sunflower seed in the world during 2012 was 37,449,403 ton and 15,074 Hg/ha, while this figure in Africa was 2,223,502 ton and 12,419 Hg/ha [3]. The production of sunflower is limited due to lack of improved varieties, production technologies, and priority given for production of food securing crops. Besides, its production is greatly reduced due to bird damage which demands effective guarding for checking bird damage during seed setting as practiced in sorghum production by local farmers. On contrary, the demand for oil consumption is continuously increasing at high rate. The oil mills were also running below their maximum production capacity. Ethiopia, regardless of being major producer and exporter of oil seeds, imports about three quarters of its domestic edible oil consumption and this import have grown five fold over the past five years [Ethiopia Revenue and Customs Authority \(ERCA\)](#) [4]. Hence, a country has to be meet edible oil demand either with increasing production of oil seeds crop or importing large amount of edible oil from other countries.

To overcome such situation, to increase oil seed production and to enhance the income of the rural community, the development of genetically improved varieties having high yield potential is of paramount significance. For genetic improvement of any crop plant, it is prerequisite to know the nature and magnitude of variability present in the available germplasm of the crop. Similarly, information on the extent and nature of interrelationships among traits helps in formulating efficient scheme of multiple trait selection as it provides means of direct and indirect selection of component traits. Therefore, in the present study, characterization, association among yield and yield related traits, the magnitude of heritability, coefficient of variation, and correlation of different agronomic traits were studied on sunflower germplasm.

## 2. MATERIALS AND METHODS

One hundred sunflower germplasm kindly provided by the U.S.D.A, Western Regional Plant Introduction & Research Station were investigated using a simple lattice design during 2011/12 cropping season in the research field of Arbaminch University. The research field was located at altitude of 1219 m.a.s.l., 6°08' N latitude and 37°66' E longitude. Each germplasm was sown in 4 rows of 2.5m length, with 0.75m and 0.25 m inter- and intra row spacing. Data were collected for the following seven different traits: Plant height (PH) (cm), days to flowering (DF), days to maturity (DM), hundred seed weight (HSW) (gm), head diameter (HD) (cm), oil content (OC) %, and seed yield (YLD) in plot bases. Genetic parameters of variability viz., phenotypic variance ( $\sigma^2_p$ ), genotypic variance ( $\sigma^2_g$ ), environmental variance ( $\sigma^2_e$ ), genotypic and phenotypic coefficient of variance (GCV, PCV), genetic advance (GA) were estimated from the results of variance analysis according to the methods suggested by [Singh and Chaudhary](#) [5], [Burton and Devane](#) [6] and; [Johnson, et al.](#) [7]. Heritability is described according to [Allard](#) [8]. Clustering

of genotypes was done using average linkage cluster analysis method as described by Singh and Chaudhary [9]. [10]. All the data were analyzed using SAS version 9.2 [11]. Spearman's coefficient of rank correlation [10] was used to determine the possible pair wise relation among the agronomic traits.

### 3. RESULTS AND DISCUSSIONS

The ANOVA results obtained for plant height (PH), days to flowering (DF), days to maturity (DM), head diameter (HD), oil content percent (OC) %, seed yield (YLD) and 100 seed weight (HSW) of the test germplasm of different sources of origin introduced from U.S. National Plant Germplasm System (NPGS) tested at Arbaminch during the 2011/12 cropping season were presented in Table 1. Significant differences ( $P < 0.05$ ) were observed in all the traits among the sunflower germplasms. It indicates that the 100 genotypes were genetically divergent. Thus, there is a huge scope for selection of promising genotypes with different agronomic traits from the present collection pool. The presence of a wide range of variability might be due to diverse sources of the materials, as well as environmental influence affecting the phenotypes.

The extents of genetic diversity among the genotypes were indicated with clustering. The genotypes were classified into eight main groups using cluster analysis (Fig. 1). The first group consists of 38 genotypes, 22 in the second group, 6 in the third group, 23 in the fourth cluster, four in cluster 5, 5 genotypes grouped in the sixth cluster, and two germplasms (PI265499, PI650655) were grouped individually in 7<sup>th</sup> and 8<sup>th</sup> cluster, respectively.

The estimation of genotypic ( $\sigma^2_g$ ) and phenotypic ( $\sigma^2_p$ ) variance, genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense heritability ( $h^2$ ), genetic advance in % of mean and genetic advance (GA) of the sunflower genotypes were given in Table 2. A wide range of variation was observed with regard to different traits. The differences among maximum and minimum values of all characters were high in PH (292.5), days to flower (88.5) and seed yield (83.4). The other characters showed non-significant differences.

Genetic parameters of yield and their components computed using the variance components based on the analyses of variance was shown in Table 2. The highest genotypic variances were found for PH (2596.81cm), YLD (176.78 kg/ha), and DF (122.55 days) while the lowest genotypic variances were found for HSW (1.81 g), HD (10.87 cm) and OC% (21.03 %). The results for phenotypic variances were also the same as that found for genotypic variation. The highest environmental variances were found for PH, YLD and DF. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the observed traits, indicating that genotypic expression was superimposed by the environmental influence. Similar results were reported by Khan, et al. [12]. Across the traits studied, the PCV ranged from 9.94% for DM to 38.18% for seed yield. The GCV values were the lowest (8.79%) for DM and highest (31.03%) for seed yield. DF, HSW and HD were also showed relatively low GCV values (13.86 – 18.60%). The  $h^2$  estimates were comparatively high (90.98% and 86.26%) for PH and OC % respectively while broad sense heritability significantly decreased for HSW and DF. High heritability coupled with high genetic advance was observed for PH and DM. Selection on the basis of these characters

would be more effective for the improvement of sunflower. The higher value of heritability for PH and OC% indicates that these characters can be used as the genetic parameters for the improvement and selection of high yielding genotypes. High heritability suggests high component of heritable portion of variation that can be exploited by breeders in the selection of superior genotypes on the basis of phenotypic performance. Very low heritability indicates greater role of environment on the expression of the trait, therefore, direct selection for such traits is ineffective. High heritability coupled with high genetic advance was observed for PH, YLD and OC%. The high heritability combined with high genetic advance could be regarded as an indication of additive gene action and the consequent high expected genetic action from selection for these characters.

Spearman's coefficient of rank correlation [10] was determined for each of the possible pair wise comparison of the different yield and yield related traits of sunflower (Table 3). DS, HSW, DM, DF and PH were positively and significantly ( $P \leq 0.05$ ) correlated with YLD. Similar results were also reported with Khan, et al. [12] and Sowmya, et al. [13]. Oil content was significantly and negatively correlated with DF, HSW, but non significantly and negatively correlated with PH and YLD. This result is contrary to Sowmya, et al. [13] when a positive and significant correlation reported. Positive and non significant correlation was noted between OC, DM and DS.

#### 4. CONCLUSIONS

Hundred germplasm of sunflower were studied for their characteristics and associations among yield and yield related traits. Significant difference was observed for all the traits studied in sunflower germplasm. It indicates that they were genetically divergent and the presence of a huge scope for selection of promising genotypes with different agronomic traits from the present collection pool. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the observed traits for sunflower, indicating that genotypic expression was superimposed by the environmental influence. In the studied traits, phenotypic variances of all traits were greater than genotypic variances in sunflower germplasms, and this indicated that the traits were more influenced by environmental effects. The  $h^2$  estimates were comparatively high for PH and OC (%) while broad sense heritability significantly decreased for HSW and DF. High heritability coupled with high genetic advance was observed for PH, YLD and OC%. According to the results of the correlation analysis, YLD was significantly and positively correlated with DS, HSW, DM, DF and PH. Improving these traits may increase seed yield.

#### 5. ACKNOWLEDGEMENT

Financial assistance from ArbaMinch University for conducting the experiment is highly acknowledged. I am also grateful to the U.S.D.A, Western Regional Plant Introduction & Research Station for kindly providing collections of sunflower germplasm.

## REFERENCES

- [1] I. C. Onwueme and T. D. Sinha, *Field crops production in tropical Africa*. The Netherlands: CTA, Ede, 1991.
- [2] CSA, "Central statistical authority report," A.A., Ethiopia, 2000.
- [3] Food and Agricultural Organization (FAO), Available: <http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#ancor>, 2014.
- [4] Ethiopia Revenue and Customs Authority (ERCA), In: *Sertse, Y, M. De Ruyter de Wildt, Y. Dijkstra, M. Danse (2011) Small-scale edible oil milling operations: Alternative business model for Ethiopia*. LIE, Wageningen: The Hague, 2010.
- [5] R. K. Singh and B. D. Chaudhary, *Biometrical methods in quantitative genetics analysis*. New Delhi: Kalyani Publishers, 1979.
- [6] G. W. Burton and E. H. Devane, "Estimating heritability in tall fescue (*Festuca Arundinacea*) from replicated colonial material," *Agronomy Journal*, vol. 45, pp. 481-487, 1953.
- [7] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of genetic and environmental variability in soybeans," *Agronomy Journal*, vol. 47, pp. 314-318, 1955.
- [8] R. W. Allard, *Principle of plant breeding*. New York: John Willey & Sons. Inc, 1960.
- [9] R. K. Singh and B. D. Chaudhary, *Quantitative genetics analysis*. New Delhi, India: Timberland Publishers, 1999.
- [10] R. G. D. Steel and J. H. Torrie, *Principles and procedures of statistics*. New York, USA: McGraw Hill Book Co. Inc., 1984.
- [11] SAS Institute Inc, *SAS/STAT® 9.2 user's guide*. Cary, NC: SAS Institute Inc, 2008.
- [12] H. Khan, S. Muhammad, R. Shah, and N. Iqbal, "Genetic analysis of yield and some yield components in sunflower," *Sarhad J. Agric.*, vol. 23, p. 4, 2007.
- [13] H. C. Sowmya, Y. G. Shadakshari, K. J. Pranesh, A. Srivastava, and B. Nandini, "Character association and path analysis in sunflower (*Helianthus annuus* L.)," *Electronic Journal of Plant Breeding*, vol. 1, pp. 828-831, 2010.

**Table-1.** Analysis of variance for yield and yield related traits for 100 sunflower germplasm

Sources of variation	DF	PH	DM	Head diameter (cm)	OC%	YLD (kg/ha)	HSW
Block	115.93 <sup>NS</sup>	775.40 <sup>NS</sup>	49.07 <sup>NS</sup>	16.27*	53.48**	282.58 <sup>NS</sup>	1.68 <sup>NS</sup>
Genotypes	371.21**	5708.43**	188.19**	29.99**	48.75**	535.42**	5.67**
Error	126.11	514.8063	41.23	8.25	6.70	181.65	2.06
CV	11.67	18.87	6.58	15.37	12.07	13.40	31.45

Figure-1. Cluster analysis of 100 sunflower germplasm

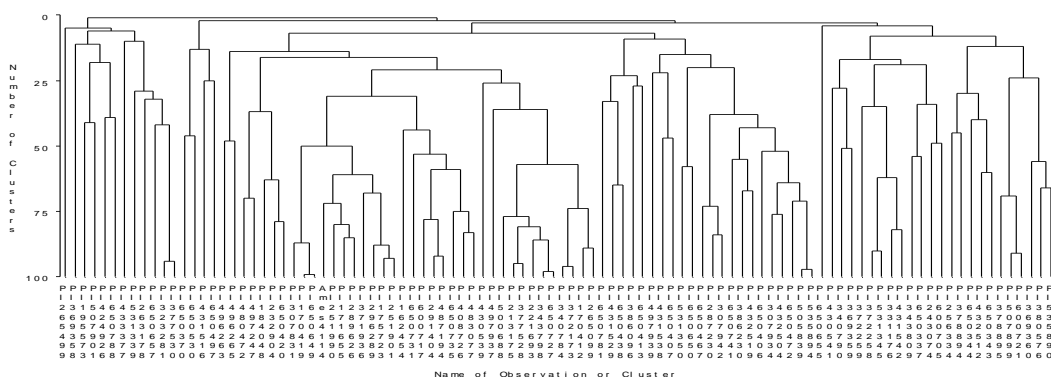


Table-2. Estimates of coefficient of variations, heritability and genetic advance in percentage of mean for plant traits of sunflower germplasms at Arbaminch

Characters	Mean	C.V.	Range		Components of variance			GCV	PCV	ECV	H	GA	GA in % of mean
			Min.	Max.	$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_e$						
PH	194.50	11.67	57.50	350.00	2596.81	2854.22	514.81	26.20	27.47	11.67	90.98	10013.01	5148.00
DF	59.52	18.87	43.00	131.50	122.55	185.60	126.11	18.60	22.89	18.87	66.03	1853.00	3113.23
DM	97.57	6.58	67.50	113.00	73.48	94.09	41.23	8.79	9.94	6.58	78.09	1560.47	1599.34
HSW (gm)	9.34	15.37	5.00	17.00	1.81	2.84	2.06	14.40	18.04	15.37	63.71	221.01	2367.57
Head diameter (cm)	23.80	12.07	13.35	35.15	10.87	14.99	8.25	13.86	16.27	12.07	72.50	578.35	2430.55
OC%	19.31	13.40	6.50	35.65	21.03	24.37	6.70	23.74	25.56	13.40	86.26	877.34	4542.77
YLD (QT/ha)	42.86	31.45	9.45	92.85	176.88	267.71	181.65	31.03	38.18	31.45	66.07	2227.01	5196.57

Table-3. Correlation coefficients among different pairs of characters in sunflower germplasm at Arbaminch

	PH	DF	DM	HSW	DS	OC	YLD
PH	1	0.5856**	0.75998**	0.43751**	0.66807**	-0.07794 <sup>NS</sup>	0.5491**
DF		1	0.48849**	0.22452*	0.30164*	-0.27693*	0.24103*
DM			1	0.38075**	0.66007**	0.01942 <sup>NS</sup>	0.53312**
HSW				1	0.46401**	-0.32335**	0.49039**
DS					1	0.15809 <sup>NS</sup>	0.57121**
OC						1	-0.15934 <sup>NS</sup>
YLD							1

Views and opinions expressed in this article are the views and opinions of the author(s), Current Research in Agricultural Sciences shall not be responsible or answerable for any loss, damage or liability etc. caused in relation to/ arising out of the use of the content.