



## GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR SEED YIELD IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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### ABSTRACT

A field experiment was conducted to study genetic variability, heritability and genetic advance for seed yield and associated characters under irrigated conditions using 80 diverse sunflower genotypes during *Kharif*-2023 at MARS, Raichur. The analysis of variance revealed the significant differences among the genotypes for all the traits except stem diameter indicating presence of sufficient variability among the genotypes for various traits. High estimate of genotypic and phenotypic coefficient of variation were observed for head diameter and seed yield per plant. While, high heritability coupled with high genetic advance observed for plant height, head diameter, test weight, yield per plant, leaf trichome length and leaf trichome density indicated that selection may be effective for improving these characters.

**Key words :** Sunflower, Variability, Heritability, Genetic advance.

### Introduction

In Indian agricultural economy, oilseeds are important next to food grains. Sunflower is one of the important oilseed crops among all the oil seed crops. It has about 46-52% oil content of good quality with higher proportion of polyunsaturated fatty acids (55-60 percent linoleic acid, 20-30 percent oleic acid), which helps to reduce the risk of coronary diseases (Das *et al.*, 2020). It is an important crop for production of healthy edible oil for cardiac problems due to which sunflower oil has great demand in commerce. Breeding programmes aim at development of cultivars with high yield and yield components. The seed yield of sunflower (*Helianthus annuus* L.) is a complex character, which is highly influenced by environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non-genetic factors is an important prerequisite for systematic breeding programme.

In India, sunflower is cultivated in an area of 364.44 (000'ha) with an annual production of about 363.14 (000't). Karnataka is the leading state in the country with an area of 246 (000'ha) and production of 234.87 (000't) contributing 67.5 and 64.4 per cent to total area and

production, respectively. However, productivity (955 kg ha<sup>-1</sup>) is lesser than the national average of 996 kg ha<sup>-1</sup> (Anonymous, 2023).

The development of an effective plant breeding program is dependent upon the existence of genetic variability. Hence, an insight into the magnitude of variability present in a cross combination is an indirect indication of genetic variability present in crop species.

The heritability estimates aid in determining the relative amount of heritable portion in variation and thus help plant breeder in selecting the elite inbred from a diverse population based on magnitude of heritability of a trait in particular population. Heritability estimates along with genetic advance are normally more helpful in predicting the incremental gain under selection than heritability estimates alone. Therefore, the present study was undertaken to study the genetic variability, heritability and genetic advance in 80 genotypes of sunflower.

### Materials and Methods

The experiment was conducted with 80 diverse genotypes under rainfed condition during *Kharif* 2023 at AICRP on Sunflower, MARS, Raichur. The material was

laid in a Augmented Block Design (ABD) of two rows each with 4.2m row length. The seeds were sown by hand dibbling two seeds per hill at 60 cm between rows and 30 cm between plants within the row. The experimental material included in the present study consisting of 75 sunflower lines with 5 checks (CMS-104B, CMS-38B, R-630, R-127-1 and LTRR-341) developed at AICRP on Sunflower, MARS, University of Agricultural Sciences, Raichur. All recommended cultural practices and plant protection measures were followed to raise good crop. Five plants from each genotype were selected at random for recording observations on 12 characters *viz.*, days to 50% flowering, plant height (cm), head diameter (cm), days to maturity, stem girth (cm), number of leaves per plant, 100 seed weight (g), volume weight, oil content (%), seed yield per plant (g), leaf trichome length and leaf trichome density.

The length and density of trichomes were assessed using new tool called foldscope. The genotypes with more trichome density and length on the leaves are not preferred by the insect pests giving good scope for selection.

The data were subjected to statistical analysis using WINDOSTAT ver.8.5 software and calculated analysis of variance. The estimate of Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were computed for each character as per the method suggested by Burton and Devane (1953). Heritability (broad sense) and genetic advance as percent of mean (GAM) were estimated and categorized as suggested by Hanson (1956) and Johnson *et al.* (1955), respectively.

## Results and Discussion

Analysis of variance revealed significant differences among the genotypes for all the characters except stem diameter (Table 1). A wide range of variation exhibited by most of the traits would offer scope for selection of desirable types. The components of variance revealed that the PCV was found higher than GCV for all the traits (Table 2) indicating the predominance role of environment in the expression of all the traits which confirmed the finding of Khan and Muhammad (2007); Tyagi and Tyagi (2010). However, difference between GCV and PCV was low for all the traits studied which indicates less influence of environment. Hence, the observed variability is under genetic control.

The highest GCV and PCV were observed for seed yield per plant (27.97% and 31.50%) followed by head diameter (20.02% and 21.79%), indicating the scope of improvement through simple selection procedure for

**Table 1 :** Analysis of variance for yield and yield attributing traits of sunflower genotypes.

Source of variation	Df	Mean Sum of Squares											
		DF	PH	HD	DM	SD	NL	TW	VW	OC	SY/PL	Tr:lgt	Tr:den
Checks	4	7.650	45.503	0.364	10.63*	2.622	5.132	1.892**	68.871*	4.47	29.175**	0.02**	18.45**
Block	4	22.000*	29.986	4.465*	1.66	1.223	2.524	0.402	10.04*	27.62	10.964	0.001	0.005
Entries	79	13.929*	299.841**	11.255**	13.95**	0.865	14.176*	0.831**	26.72**	24.19*	32.283**	0.002**	6.118**
Genotypes	74	14.381*	309.820**	11.521**	10.89**	0.779	14.652*	0.785**	18.81**	23.33**	32.698**	0.002**	5.480**
Check vs Genotypes	1	5.603	578.685**	35.130**	253.53**	0.212	15.187	0.000	696.37**	166.15**	13.988	0.001	4.014
Error	16	6.088	20.844	1.445	2.56	1.799	5.551	0.227	3.10	11.05	5.647	0.000	0.048

\* - Significant at 5 per cent; \*\* - Significant at 1 per cent.

DF : Days to 50% flowering

HD : Head diameter (cm)

DM : Days to maturity

SD : Stem Diameter (cm)

PH : Plant height (cm)

NL : Number Of Leaves

VW : Volume Weight(g)

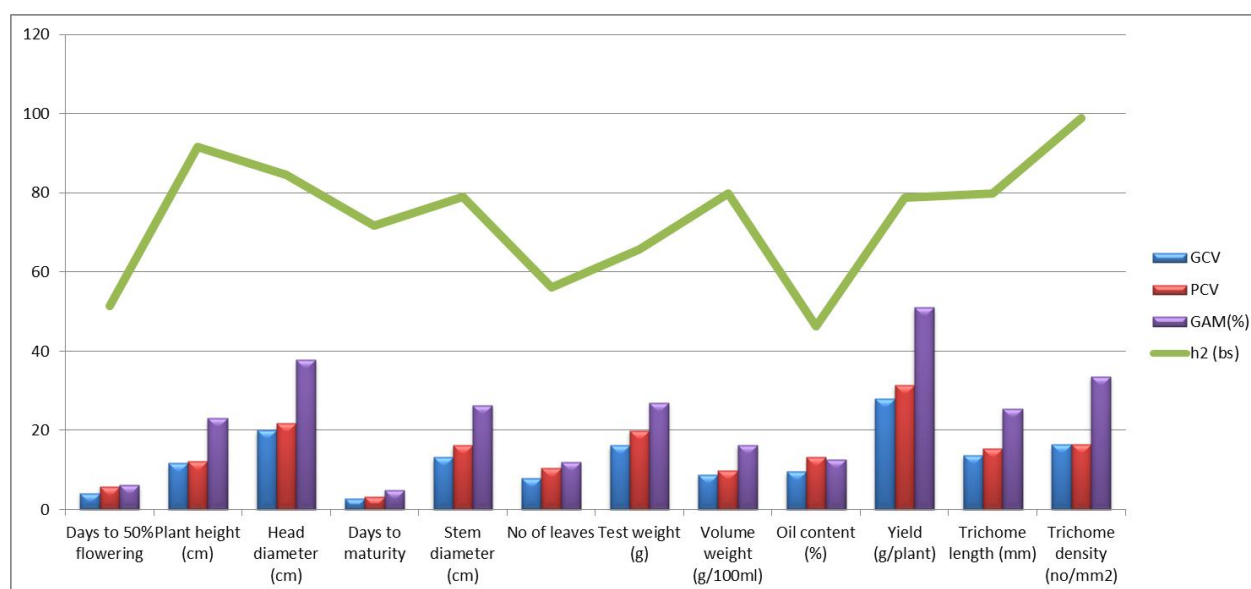
TW : 100 seed weight (g)

SY/PL : Seed yield per plant (g)

OC : Oil Content(%)

Tr.lgt : Trichome length(mm)

Tr.den : Trichome density(mm<sup>2</sup>)



**Fig. 1 :** Genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean for twelve traits in sunflower.

obtaining high yield. This is in line with the results of Rani *et al.* (2017), Baraiya *et al.* (2018) and Singh *et al.* (2019).

The GCV was moderate for leaf trichome density (16.38%) followed by test weight (16.17%), leaf trichome length (13.76), stem diameter (13.18%) and plant height (11.72%). Whereas, PCV was moderate for test weight (19.96%), leaf trichome density (16.47%), stem diameter (16.18%), leaf trichome length (13.21%), oil content (9.67%), plant height (12.25%) and number of leaves (10.42%) indicating moderate variation.

The characters *viz.*, volume weight (8.86% and 9.92%), days to 50% flowering (4.14% and 5.78%), days to maturity (2.76% and 3.26%) expressed low degree of genotypic and phenotypic coefficients of variation respectively, indicating a narrow range of variability in the population. The results obtained are on par as reported by Supriya *et al.* (2016), Supriya *et al.* (2017) and Singh *et al.* (2019).

High heritability was recorded for leaf trichome density (98.88%), plant height (91.52%), head diameter (84.45%), trichome length (79.89%), volume weight (79.75%), stem diameter (79.09%), yield per plant (78.87%), days to maturity (71.33%) and test weight (65.66%). The moderate value of heritability was noticed for number of leaves (56.08%), days to 50% flowering (51.48%) and oil content (46.38%). High heritability reflects the predominance of genetic component with less influence of environmental effects on these traits. These results are in confirmatory with the findings of Dudhe *et al.* (2017), Rani *et al.* (2017), Baraiya *et al.* (2018) and Singh *et al.* (2019).

The high estimate of GAM was observed for the seed yield per plant (51.17%) followed by head diameter (37.91%), leaf trichome density (33.56%), test weight (27.00%), stem diameter (26.36%), leaf trichome length (25.33%), plant height (23.09%). Whereas, it was moderate for volume weight (16.3%), oil content (12.63%) and number of leaves (12.04%). It was low for days to 50 percent flowering (6.13%) and days to maturity (4.82%).

High heritability coupled with high GAM was observed for plant height, head diameter, stem diameter, 100 seed weight, seed yield per plant, trichome length and trichome density. High heritability coupled with high genetic advance as per cent of mean indicating additive gene effects (Panse, 1957) and least influenced by environmental effects. Selection based on such characters would be rewarding and effective. Therefore, these traits should be given top priority during selection of genotype by phenotype. Similar results were reported earlier by Supriya *et al.* (2016), Baraiya *et al.* (2018) and Singh *et al.* (2019).

While high heritability coupled with moderate GAM was observed for volume weight (Fig. 1). These results are in agreement with Kulkarni *et al.* (2015), Dudhe *et al.* (2017), Singh *et al.* (2019). Moderate heritability along with moderate GAM was expressed by number of leaves per plant and oil content, while high heritability coupled with low GAM was observed for days to maturity and moderate heritability accompanied with low GAM was recorded for days to 50% flowering indicating this trait is influenced by environmental effect and governed by non-additive gene action. Therefore, direct selections for non-

**Table 2 :** Genetic variability parameters for 80 sunflower genotypes.

S. no.	Characters	Mean	Range		Coefficient of variation		h <sup>2</sup> (bs)	GA (%)	GAM (%)
			Min	Max	GCV	PCV			
1	Days to 50% flowering	61.25	53.50	69.00	4.14	5.78	51.48	3.75	6.13
2	Plant height (cm)	128.04	85.50	180.00	11.72	12.25	91.52	29.56	23.09
3	Head diameter (cm)	13.98	7.80	24.80	20.02	21.79	84.45	5.30	37.91
4	Days to maturity	91.70	86.50	101.00	2.76	3.26	71.66	4.44	4.82
5	Stem diameter (cm)	6.19	4.20	7.99	13.18	16.18	79.08	1.63	26.36
6	No of leaves	34.10	27.00	49.55	7.80	10.42	56.08	4.10	12.04
7	Test weight (g)	4.07	2.50	6.20	16.17	19.96	65.66	1.10	27.00
8	Volume weight (g/100ml)	39.48	31.85	48.70	8.86	9.92	79.75	6.43	16.3
9	Oil content (%)	34.35	21.15	43.77	9.67	13.21	46.38	4.33	12.63
10	Yield (g/plant)	16.40	3.96	35.50	27.97	31.50	78.87	8.39	51.17
11	Trichome length (mm)	0.23	0.17	0.32	13.76	15.39	79.89	0.05	25.33
12	Trichome density (no/mm <sup>2</sup> )	12.59	7.33	18.00	16.38	16.47	98.88	4.27	33.56

additive genetic traits *viz.*, days to 50% flowering, days to maturity, volume weight, number of leaves and oil content may not result in improvements of traits using study population. However, these traits can be targeted with diverse population involving different parental combinations.

### Conclusion

The most important yield attributing traits *viz.*, plant height, head diameter, stem diameter, 100 seed weight, seed yield per plant, trichome length and trichome density are under the influence of additive gene action and can be improved by simple selection method, while remaining characters are under the influence of non-additive gene action and can be improved through heterosis breeding.

### Conflict of interest

The authors declare no conflicts of interest.

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