# Assessment of Genetic Variability, Heritability and Genetic Advance in Sunflower (*Helianthus annuus* L.) Genotypes for Seed Yield and Other Agronomic Traits

**Dasari Mohan Vamsi, Meena H. P., Sandhya Sree G., Payasi S. K.**

## ABSTRACT

Genetic variability in a crop population is important for successful plant breeding. The experiment was conducted using Randomized Block Design with two replication and the traits was totally consisted sixty seven genotypes. Data on seed yield and other agronomic traits were used to estimate the genetic variability parameters, heritability and genetic advance (GA). Analysis of variance revealed highly significant and significant difference for all studied traits. Low to high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded. The highest GCV and PVC values were found particularly for seed yield per plant (38.23% and 40.35%), autogamy % (47.32% and 47.34%), 100 seed weight (14.94% and 18.02%), head diameter (14.21% and 15.08%), stem girth (12.32% and 13.92%) and plant height (10.74% and 11.41%), respectively, whereas lowest GCV and PCV (3.31% and 3.64%, respectively) manifested for days to maturity. The highest broad sense heritability value manifested for autogamy % (99.92%) followed by seed yield per plant (89.80%), head diameter (88.83%) and plant height (88.45%), while lowest heritability (62.83%) revealed only for number of leaves per plant. In present study low to moderate genetic advance were manifested and high heritability and genetic advance as percentage of mean (>30) was recorded for seed yield per plant, plant height and autogamy %, indicating predominance of additive gene action for these characters. Therefore the result of this study suggests existence of variability for seed yield and other agronomic traits in these sunflower genotypes, which should be exploited in future breeding.

Dasari Mohan Vamsi*, Payasi S. K.
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 482004, Madhya Pradesh, India

Meena H. P.
ICAR-Indian Institute of Oilseeds Research, Hyderabad 500030, Telangana State, India

Sandhya Sree G.
College of Agriculture, Baptala, ANGRAU, Andhra Pradesh, India
Email : mohhandasari@gmail.com
*Corresponding author

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## INTRODUCTION

Sunflower (*Helianthus annuus* L.) is an important oilseed crop in India popularly known as "Surajmukhi." In India, it was used mainly as ornamental crop but in recent past it became an important source of edible
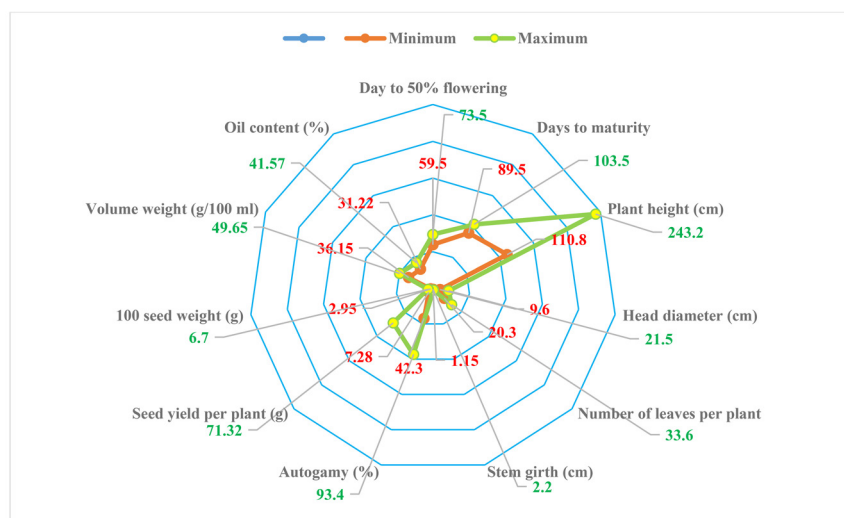
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**Fig. 1.** Graphical representation of range for different traits in sunflower.

and nutritious oil. Sunflower crop has acquired the status of an important commercial oilseed crop in India within a span of three and half decades of its introduction due to its short duration nature, excellent quality of oil, photo-insensitivity, wider adaptability it has great potential for diversification of major cropping systems in the country. According to FAO statistics, it has been observed that sunflower was grown in about 26.53 million hectares of land with production of 47.86 million tonnes and productivity of 1804 kg/ha during 2018 in the world. Russian Federation is the largest sunflower growing country followed by Ukraine and Argentina (FAOSTAT 2018). In India, sunflower crop is grown in 2.83 lakh ha and a production of 2.22 lakh tonnes with a productivity of 784 kg/hectare compared to the world's average productivity of 1804 kg/hectare (FAOSTAT 2018). Karnataka, Maharashtra, Andhra Pradesh, Telangana and Tamil Nadu are the major sunflower growing states. Now it is spread in non-traditional areas like Punjab, Haryana, Bihar, Uttar Pradesh and Odisha. Presently, the area of sunflower crop is reduced it may be due to the fact that unavailability of the superior genotypes can yield more than 3.0 tons/ha, price fluctuations, shift in cropping pattern, profitability of other crops compared to sunflower, withdrawal of private players from sunflower research, bird damage and menace of diseases such as alternaria, powdery mildew, sunflower necrosis and sunflower leaf curl

virus disease (Dudhe *et al*. 2019).

The success of any plant breeding program depends on the genetic variability and selection skill of plant breeder (Adhikari *et al.* 2018). The knowledge of the magnitude of genetic variability present in a crop species for the traits is insignificant for the success of any plant breeding program. The genotypic and phenotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations, whereas estimates of heritability provides index of transmissibility of characters. 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. Hence, the present study was conducted to estimate the amount of genetic variability, heritability and genetic advance over mean for yield and its components and to characterize the different genotypes based on quantitative characters.

**MATERIALS AND METHODS**

The present investigation was carried out during *rabi*, 2019-20 at ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad. The breeding material consisted of 67 genotypes which included
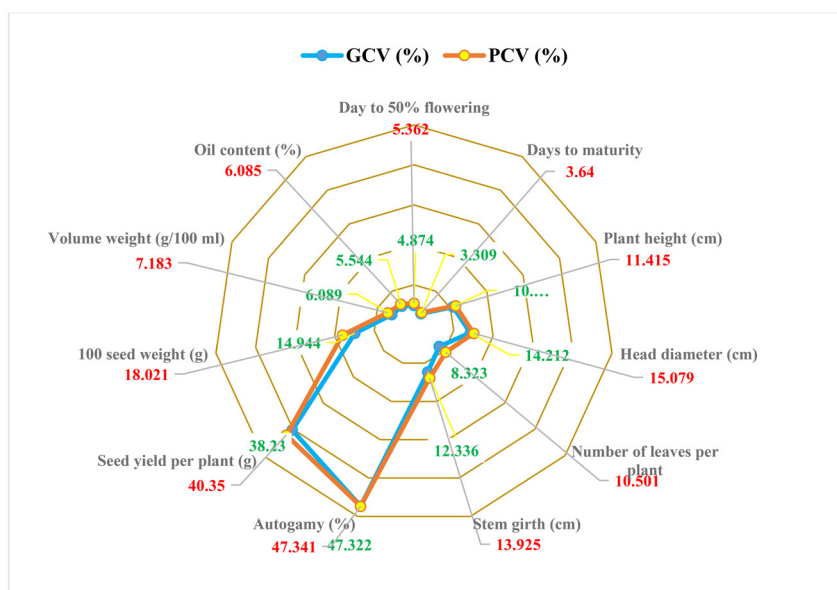
**Fig. 2.** Graphical representation of coefficient of variation for different traits in sunflower.

5 CMS lines, 10 newly developed restorer lines and their 50 $F_1$ hybrids along with two checks. Each genotype was sown in 2 rows of 3.0 m length following a spacing of 60 × 30 cm maintaining row to row and plant to plant distance in Randomized Block Design with two replications. Standard agronomic practices were performed uniformly for all the experimental units. At maturity five plants from each accession were selected randomly for recording of data on yield and its related characters viz., days to 50 % flowering, days to maturity, plant height (cm), number of leaves per plant, stem girth (cm), head diameter (cm), autogamy (%), 100 seed weight (g), volume weight (g/100 ml), seed yield per plant (g) and oil content (%). The observations on days to 50% flowering were recorded on plot basis. The mean over replication of each character was subjected to statistical analysis. The estimate of genotypic and phenotypic coefficient of variation was estimated by using the formula given by Burton (1952) and categorized according to Sivasubramanian and Menon (1973). The genotypic coefficients of variation (GCV) and phenotypic coeffi-

**Table 1.** Analysis of variance (mean sum of square) for different characters in sunflower. df – Degrees of freedom, DF – Days to 50 % flowering (days), DM – days to maturity (days), PH – Pant height (cm), HD – Head diameter (cm), NL – Number of leaves per plant, SG – Stem girth (cm), SW – 100 seed weight (g), VW – Volume weight (g/100 ml), A – Autogamy (%), SY – Seed yield per plant (g), OC – Oil content (%).

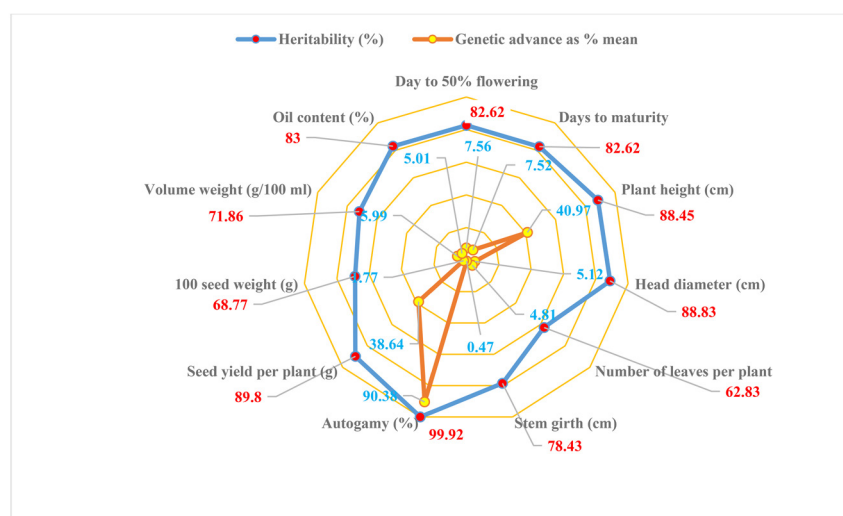| Source of variation | df | DF | DM | PH | HD | NL | SG | SW | VW | A | SY | OC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Mean sum of squares | | | | | | | | |
| Replications | 1 | 2.41 | 2.98 | 2.417 | 1.18 | 10.21 | 0.02 | 0.29 | 1.05 | 1.47 | 22.72 | 8.12 |
| Genotypes | 66 | 21.91** | 21.68** | 21.91** | 8.99** | 13.68** | 0.09** | 1.59** | 17.17** | 2346.90** | 587.22** | 9.57** |
| Error | 66 | 2.08 | 2.06 | 2.08 | 0.53 | 3.12 | 0.01 | 0.29 | 2.81 | 0.93 | 27.38 | 0.88 |
| Total | 133 | 26.40 | 26.72 | 26.407 | 10.70 | 27.01 | 0.12 | 2.17 | 21.03 | 2349.3 | 637.32 | 18.57 |

**Fig. 3.** Graphical representation of heritability and genetic advance as per cent of mean for different traits in sunflower.

cients of variation (PCV) were computed according to the methods suggested by Burton and Devane (1953), estimation of heritability in broad sense ($h^2$) expressed as the percentage of the ratio of the genotypic variance (g) to the phenotypic variance (p) and was estimated on genotype mean basis as described by Allard (1960) and genetic advance (GA) and the percentage of the mean (GAM) assuming selection of the superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955).

**RESULTS AND DISCUSSION**
**Genetic variability**

The analysis of variance exhibited a significant difference among the genotypes for all the traits (Table 1), indicating the presence of considerable genetic variability among the experimental material under study. Thus, there is plenty of scope for improvement of different traits through selection. Tyagi and Tyagi

**Table 2.** Mean, range, coefficient of variation, heritability and genetic advance as per cent of mean for different traits in sunflower.

| Sl. No. | Trait | Mean | Range Minimum | Maximum | GCV (%) | PCV (%) | Coefficient of variation | Heritability (%) | SEm± | CV % |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Day to 50% flowering | 64.59 | 59.50 | 73.50 | 4.87 | 5.36 | 82.62 | 7.56 | 1.02 | 2.23 |
| 2 | Days to maturity | 94.65 | 89.50 | 103.50 | 3.31 | 3.64 | 82.62 | 7.52 | 1.01 | 1.51 |
| 3 | Plant height (cm) | 155.2 | 110.80 | 243.20 | 10.74 | 11.41 | 88.45 | 40.97 | 4.21 | 3.87 |
| 4 | Head diameter (cm) | 14.47 | 9.60 | 21.50 | 14.21 | 15.08 | 88.83 | 5.12 | 0.51 | 5.03 |
| 5 | Number of leaves per plant | 27.60 | 20.30 | 33.60 | 8.32 | 10.50 | 62.83 | 4.81 | 1.24 | 6.40 |
| 6 | Stem girth (cm) | 1.62 | 1.15 | 2.20 | 12.32 | 13.92 | 78.43 | 0.47 | 0.07 | 6.45 |
| 7 | Autogamy (%) | 72.37 | 42.30 | 93.40 | 47.32 | 47.34 | 99.92 | 90.38 | 0.68 | 1.33 |
| 8 | Seed yield per plant (g) | 41.54 | 7.28 | 71.32 | 38.23 | 40.35 | 89.80 | 38.64 | 3.70 | 12.59 |
| 9 | 100 seed weight (g) | 5.40 | 2.95 | 6.70 | 14.94 | 18.02 | 68.77 | 1.77 | 0.38 | 10.07 |
| 10 | Volume weight (g/ 100 ml) | 44.00 | 36.15 | 49.65 | 6.09 | 7.18 | 71.86 | 5.99 | 1.18 | 3.80 |
| 11 | Oil content (%) | 37.58 | 31.22 | 41.57 | 5.54 | 6.08 | 83.00 | 5.01 | 0.66 | 2.50 |

(2011) also reported significant differences for all the characters studied. The mean values, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean (Table 2) of all sixty seven genotypes were calculated for yield and yield attributes. For all the traits considered under the present investigation the values of PCV was greater than GCV for all the characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. 100 seed weight was the most affected by environment compared with the other characters. The variation observed in the characters studied in the present investigation were classified as, low (less than 10%), moderate (10-20%) and high (more than 20%) phenotypic and genotypic coefficients of variation (Deshmukh *et al.* 1986). The genotypic coefficient of variation (GCV) of different traits ranged from 3.64% for days to maturity to 47.34% for autogamy (%). Similarly phenotypic coefficient of variation (PCV) ranged from 3.31% to 47.32%, respectively for the same traits as GCV. Based on this classification, lowest PCV and GCV exhibited by days to maturity (3.31% and 3.64%) followed by days to 50% flowering (4.87% and 5.36%), volume weight (6.09% and 7.18%) and oil content (5.54% and 6.08%), respectively. A similar result was obtained by Satisha (1995). 100 seed weight (14.94% and 18.02%), head diameter (14.21% and 15.08%), stem girth (12.32% and 13.92%) and plant height (10.74% and 11.41%) exhibited moderate phenotypic and genotypic coefficient of variation. These results are in agreement with the report by Patil *et al.* (1996). Only seed yield per plant (38.23% and 40.35%) and autogamy % (47.32% and 47.34%) traits showed higher PCV and GCV. High estimates of PCV and GCV for these characters have earlier been reported by Virupakshappa and Sindagi (1987), Gangappa (1991), Suma and Virupakshappa (1994), Reddy and Reddy (2006), Kalukhe *et al.* (2010). The highest genotypic coefficient of variation was observed for seed yield per plant (36.03%) was observed by Baraiya *et al.* (2018). Characters those exhibited highest value of PCV and GCV, indicates that there is high level of variability and possibility of effective selection for the character improvement. The lowest GCV and highest PCV are indicating as the traits are influenced by environment. Moderate to low variability indicates

the need for improvement of base population.

## Heritability and genetic advance

Heritability provides an idea to the extent of genetic control for expression of a particular trait and the reliability of phenotype in predicting its breeding value (Tazeen *et al.* 2009). 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 (Gatti *et al.* 2005). Heritability estimates in broad sense and genetic advance as percent mean for different traits are shown on Figs. 1-3. Heritability is a good indicator of transmission of characters from parents to its progeny. According to Singh (2000), heritability values greater than 80% are very high, values 60–79% are moderately high, values from 40 to 59% are medium and values less than 40% are low. Therefore, the traits under study (Table 2) fall into the moderately high to high category since heritability >60%. The estimates of heritability for different traits help the researchers in selection of material from diverse genetic population. Therefore, high heritability helps in effective selection for a particular character. Most of the traits in this study were manifested moderately high to very high (62.83% - 99.92%), while lowest heritability (62.83%) revealed only for number of leaves per plant. The highest broad sense heritability value manifested for autogamy (99.92%) followed by seed yield per plant (89.80%) (Table 2) indicate that phenotypic expression is mostly due to genetic factors and selection for studied trait can be performed in earlier generations. Similar results were reported by Kalukhe *et al.* (2010), Supriya *et al.* (2016). Sridhar *et al.* (2006) reported high estimate (92.05%) of the broad sense heritability for head diameter. The information on heritability alone may not help in identifying characters for enforcing selection and heritability estimates in conjunction with predicted genetic advance is more reliable (Johnson *et al.* 1955, Panse 1957).

Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is another important parameter that guides the breeder in choosing a selection program (Hamdi *et al.* 2003). Johnson *et al.* (1955) classified genetic advance as a percentage of the mean; values 0–10%

are low, 10–20% are moderate and 20% and above are high. Based on this measure, the traits under study have high heritability value coupled with high-to-moderate genetic advance as a percentage of the mean (ranging from 0.47% to 90.38%) as shown in Table 2. Highest genetic advance as percent mean value was observed for autogamy % (90.38%) followed by plant height (40.97%) and seed yield per plant (38.64%) as compared to other traits under study. High estimates of genetic advance expressed as percentage of mean in sunflower have also been reported earlier for seeds yield per plant by Sultana *et al.* (2005), Reddy and Reddy (2006), Khan *et al.* (2007), Janamma *et al.* (2008). Among all the characters studied, autogamy % (99.92% and 90.38%, respectively) followed by plant height (88.45% and 40.97%) and seed yield per plant (89.80% and 38.64%) manifested high heritability coupled with high genetic advance as a per cent of mean indicating that these are simply inherited traits and expression of these traits are under the control of additive type of gene action and therefore, provides the most effective condition for selection. Traits like number of leaves per plant, stem girth, volume weight and 100 seed weight which has moderate heritability with low genetic advance as percentage of mean were predominantly governed by non-additive gene action and direct selection may not be possible because most of the variation is attributed to the environmental effects. High heritability values indicate that the characters under study are less influenced by environment in their expression. Therefore, the breeder may make his/her selection safely on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. Genetic advance as percentage of mean which coincide with high heritability is very useful than heritability alone in predicting the resultant effect during selection of best individual genotype, which was revealed in present study. High heritability characters coupled with moderate to high genetic advance in per cent of mean was offered scope of the traits for improvement through selection, so these characters could be improved more easily than the other characters. Generally, the breeder should adopt suitable breeding methodology to utilize in the future breeding program especially in case of sunflower.

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