***Original Research Article***

**Genetic Variability, Heritability and Genetic Advancement for Yield and Yield-associated Traits of Sunflower (Helianthus annuus L.)**

**ABSTRACT**

A field study was carried out at the Botany farm of the College of Agriculture, Pune, during the Kharif season of 2024-25. The experiment employed a Randomized Block Design with three replications to evaluate thirty-two sunflower genotypes. The primary objective was to assess the genetic variability present for seed yield and its component traits. The findings revealed a wide spectrum of variability for all the characters investigated. The estimates for the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from low to high. Notably, high magnitudes of both PCV and GCV were observed for seed yield per plant (35.17% and 33.13%, respectively), followed by plant height (15.80% and 15.07%), head diameter (14.65% and 13.04%), and 100-seed weight (15.22% and 12.76%). High heritability in conjunction with high genetic advance was recorded for plant height, seed yield per plant, days to 50% flowering, and days to maturity. This combination suggests the predominance of additive gene action for the inheritance of these traits, presenting an ideal scenario for effective selection. Consequently, these characters should be prioritized in future sunflower breeding programs for crop improvement.

Keywords: GCV, Genetic Advance, Heritability, PCV, Sunflower, Variability

1. **INTRODUCTION**

The sunflower (*Helianthus annuus* L.) is a globally important oilseed crop belonging to the genus *Helianthus*. Sunflower seeds are valued for their diverse applications, containing 40-54 percent oil and 16 percent protein (Velioglu & Beker, 2012). Characterized by a low saturated fatty acid content and high levels of polyunsaturated and monounsaturated fatty acids, the oil is extensively used for cooking, in margarine production, and for biodiesel (Heiser, 1976). In addition to its nutritional role, sunflower oil is recognized for its potential health benefits and its use as a dermo-protective agent (Speranza et al., 2021). Sunflower is the world's second most widely cultivated oilseed crop after soybean, and sunflower meal is the third most consumed oilseed meal (FAOSTAT, 2023).

Russia leads the world in sunflower seed production, followed by Ukraine and Argentina (USDA, 2025). According to the latest USDA (2025) data, global sunflower cultivation spanned 28.23 million hectares in 2024-2025, producing 52.45 million metric tons with an average yield of 1.85 metric tons per hectare. In contrast, India’s cultivation area was 0.18 million hectares, yielding 0.11 million metric tons at 0.63 metric tons per hectare, with Karnataka emerging as the leading producer, followed by Andhra Pradesh and Maharashtra with an area of 1.62 lakh ha.

The presence of ample genetic variability within a crop species is a fundamental prerequisite for the success of any plant breeding initiative. Evaluating the degree of variability present among various cross combinations offers critical insights into the available genetic diversity that can be utilized for selection. The estimation of heritability is essential, as it quantifies the proportion of phenotypic variation that is due to genetic causes, thus allowing breeders to efficiently identify superior inbred lines from a genetically heterogeneous population. Furthermore, heritability becomes a more robust indicator of the expected response to selection when analysed alongside genetic advance, as opposed to being considered in isolation. Within this framework, the current study was conducted to evaluate the genetic variability, heritability, and genetic advance among a collection of 32 sunflower (*Helianthus annuus* L.) genotypes.

1. **MATERIALS AND METHODS**
   1. **Location of Study**

A uniform piece of land was selected for conducting the trial. It was ploughed, harrowed and the stubbles of the previous crop were collected and finally the land brought to fine tilt. The present investigation was conducted at Research Farm, College of agriculture, Pune (MH) India during *kharif* season 2024-25. A total of 32 genotypes including two checks viz., DRSH-108, Phule Bhaskar were utilized for the study.

* 1. **Experimental Design and Procedure**

A total of 32 sunflower genotypes including two checks viz., DRSH-108, Phule Bhaskar were sown in a randomized block design with three replications for genetic variability studies for ten quantitative traits by using Analysis of Variance (ANOVA) viz., Days to 50% flowering (No.), Days to maturity (No.), Plant height (cm), Head diameter (cm), Seed filling percentage (%), 100 seed weight (g), Seed yield per plant (g), Hull content (%), Volume weight (gm/100 ml), Oil content (%). The experimental materials were sown in 32 lines of 4.5 m row length in three replications. Standard agronomic practices were performed uniformly for all the experimental units. Sowing was done with a maintained space of 60 cm x 30 cm between row to row and plant to plant, respectively. To maintain the optimum plant population, thinning was done after 15 days of sowing. At maturity five plants from each genotype were selected randomly for recording of data on yield and its related characters. The oil content (%) was estimated by using the Nuclear Magnetic Resonance (NMR) method this is inline with ISO 10565:1998. Oilseeds—Simultaneous determination of oil and moisture contents—Method using pulsed nuclear magnetic resonance spectroscopy.

**Statistical Analysis**

The mean over replication of each character was subjected to statistical analysis. The parameters, genotypic coefficient (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula given by Burton (1952), estimation of heritability in broad sense (h2) 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 Burton and Devane (1953), 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 Allard (1960). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized in the range of above 20%: High, 10-20%: Moderate, and below 10%: Low by Sivasubramanian and Madhavamenon (1973). Johnson et al. (1955) classified heritability (h²) estimates as Low: 0-30%, Medium: 30-60%, and High: Above 60%. The categorization of genetic advance as percentage of mean estimates as 20%: High by Johanson et al. (1955). All statistical analyses were performed by using INDOSTAT software.

1. **RESULTS AND DISCUSSION** 
   1. **Analysis of Variance**

Analysis of variance for the randomized block design (RBD) with respect to 32 genotypes of sunflower revealed significant differences among the material used in the present investigation for all the ten traits viz., Days to 50% flowering (No.), Days to maturity (No.), Plant height (cm), Head diameter (cm), Seed filling percentage (%), 100 seed weight (g), Seed yield per plant (g), Hull content (%), Volume weight (gm/100 ml), Oil content (%), indicating the presence of considerable genetic variability among the experimental material under study, which is essential for effective selection and hybrid development. Thus, there is plenty of scope for improvement of different traits through selection. Tyagi and Tyagi (2011), Dudhe et. al. (2020) and Mohan et al. (2022) also reported significant differences for all the characters studied. The results are displayed in Table 1.

* 1. **Range and mean of ten Traits**

The per se performance of sunflower genotypes revealed that there was a substantial variability among genotypes for all the characters. The range value of mean among 32 genotypes for ten quantitative traits is 5.2-139.20. The results were presented in Table 2 and Fig. 1. The value ranges from 46.33-63.67with a mean of 55.86 for days to 50% flowering. The results indicated that there is a variation for this trait and earliness can be created by selecting best genotype that will ultimately lead to early maturity. The mean value of plant height is 85-180.87 with a mean of 139.2 cm. The result indicated that there is great variation for this trait and dwarf genotype can be developed by selecting best genotypes. The head diameter was recorded as a mean of 16.78 with ranges from 11.03-21.87. The range values of mean for seed yield per plant (15.33-48.63), 100 seeds weight (4.08-6.92), oil content (29.70-41.47), days to maturity (76.33-93.67 days), Hull content (21.17-30.57), seed filling percentage (70.70-88.50) and Volume weight (37.86-50.40). These results are aligned with previous research by Neha et. al. (2024). Developing new hybrids requires a thorough assessment of parental lines. This evaluation should consider not only the actual performance of each parent (its own individual yield or quality), but also other key genetic parameters like Genetic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, and genetic advance.

* 1. **Phenotypic and Genotypic Coefficient of Variation**

Following the classification of Sivasubramanian and Madhavamenon (1973), both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were categorized into three groups: low (<10%), moderate (10-20%), and high (>20%).

Analysis of genetic parameters presented in Table 2 and Fig. 2 revealed that genotypic coefficient of variation (GCV) estimates were consistently lower than phenotypic coefficient of variation (PCV) values for all traits examined as presented in Table 2 and Fig. 2. Seed yield per plant exhibited the highest variability, with GCV (33.13%) and PCV (35.17%), followed by plant height (GCV 15.07%, PCV 15.80%) and head diameter (GCV 13.04%, PCV 14.65%). Moderate variability was observed for 100-seed weight (GCV 12.76%, PCV 15.22%) and hull content (GCV 9.54%, PCV 11.68%). Traits showing relatively lower variability included oil content (GCV 8.58%, PCV 9.96%), volume weight (GCV 7.41%, PCV 9.57%), days to 50% flowering (GCV 7.16%, PCV 7.84%), and seed filling percentage (GCV 5.76%, PCV 7.24%). Days to maturity displayed the most constrained variation, with the lowest GCV (4.42%) and PCV (4.90%) values among all traits studied.

The disparity between genotypic and phenotypic coefficients of variation was most pronounced for 100-seed weight (2.46%), indicating significant environmental influence on this trait. Subsequent differences were observed for volume weight (2.16%), hull content (2.14%), seed yield per plant (2.04%), head diameter (1.61%), seed filling percentage (1.48%), oil content (1.38%), and plant height (0.73%). In contrast, phenological traits showed minimal GCV-PCV differences: days to 50% flowering (0.68%) and days to maturity (0.17%), suggesting stronger genetic control over these developmental traits.

The consistent pattern of phenotypic coefficient of variation (PCV) exceeding genotypic coefficient of variation (GCV) for all traits demonstrates significant environmental modulation of phenotypic expression. Traits exhibiting wider PCV-GCV disparities (e.g., 100-seed weight, volume weight) showed greater sensitivity to environmental fluctuations, while those with narrower differences (e.g., days to flowering, maturity) manifested stronger genetic control. Notably, traits displaying both high PCV and GCV values (particularly seed yield and plant height) represent prime targets for selection-based genetic improvement, given their combined economic importance and genetic variability potential.

Consistent with findings by Manasa et al. (2024), our study observed higher PCV than GCV values across traits. Significant genetic variability was particularly evident for key agronomic traits including seed yield per plant, plant height, head diameter, and 100-seed weight, which exhibited both high GCV and PCV estimates. These results align with previous research: Makane et al. (2011) for plant height, Supriya et al. (2016) for seed yield per plant, 100-seed weight and plant height and Mohamed et al. (2018) for plant height, head diameter, seed yield per plant.\

* 1. **Heritability (H2bs) Genetic Advance and Genetic Advance as Per cent Mean**

Broad-sense heritability (h²) estimates were calculated for all traits and are presented in Table 2 and Fig. 3. The interpretation of these values followed the classification criteria established by Robinson et al. (1949), where heritability estimates were categorized as low (<30%), moderate (30-60%), or high (>60%).

Broad-sense heritability estimates ranged from 60.05% to 90.99%, indicating moderate to high genetic control across traits. Plant height exhibited the highest heritability (90.99%), followed by seed yield per plant (88.76%), days to 50% flowering (83.52%), and days to maturity (81.41%). Morphological traits showed strong heritability: head diameter (79.18%), oil content (74.26%), and 100-seed weight (70.27%). Quality traits demonstrated slightly lower but still substantial heritability: hull content (66.71%) and seed filling percentage (63.18%). Volume weight showed the most environmental influence with the lowest heritability estimate (60.05%).

Heritability estimates quantify the transgenerational transmission of traits, determining the reliability of phenotypic selection based on the heritable component of observed variation. These parameters enable plant breeders to identify superior genotypes with greater confidence. Consequently, the effectiveness of selection depends fundamentally on three key genetic parameters: (1) the magnitude of phenotypic variation, (2) heritability estimates, and (3) expected genetic advance - collectively determining the potential for genetic improvement in crop populations.

The current study revealed high broad-sense heritability estimates for all evaluated traits, indicating predominant genetic control with minimal environmental influence on phenotypic expression.

Heritability estimates quantify the proportion of genetic variation contributing to total phenotypic variation, predicting both the potential for genetic improvement and the expected response to selection. These findings align with Thakur et al. (2021), who reported high heritability for key agronomic traits including seed yield per plant, 100-seed weight, and plant height.

Genetic advance estimates exhibited considerable variation across traits, ranging from 1.14 g (100-seed weight) to 44.31 cm (plant height). Plant height demonstrated the highest genetic advance (41.24 cm), followed by seed yield per plant (18.92 g) and seed filling percentage (7.60%). Moderate genetic advance values were observed for phenological traits: days to 50% flowering (7.54 days) and days to maturity (7.07 days). Quality traits showed intermediate values: oil content (5.41%), volume weight (5.19 g/100 mL), hull content (4.09%), and head diameter (4.01 cm). The lowest genetic advance was recorded for 100-seed weight (1.14 g), suggesting limited potential for selection-based improvement in this trait.

While heritability estimates quantify the proportion of phenotypic variation attributable to genetic factors, they do not elucidate the underlying gene action nor predict the expected genetic progress from selection. Reliable selection strategies require both high heritability and substantial genetic advance, which together indicate predominantly additive gene effects. Such traits are particularly responsive to selection, offering greater potential for genetic improvement in breeding programs.

High heritability coupled with low genetic advance suggests the predominance of nonadditive gene action (dominance/epistasis) in trait expression. Conversely, traits exhibiting both high heritability and high genetic advance (plant height, seed yield per plant, days to maturity, and days to 50% flowering) indicate primarily additive genetic effects, making them more amenable to selection. These findings are consistent with previous reports by Arshad et al. (2010) for flowering time, maturity duration, plant height, seed yield, and by Kalukhe et al. (2010) for seed yield and plant height, Supriya et al. (2016) reported high heritability for plant height Mamta et al. (2017) and Divya et al. (2019) for seed yield per plant.

Genetic advance expressed as percentage of mean ranged from 8.22% (days to maturity) to 64.30% (seed yield per plant). Four traits demonstrated high genetic advance (>20%): seed yield per plant (64.30%), plant height (29.63%), head diameter (23.90%), and 100-seed weight (22.03%). Moderate genetic advance (10-20%) was observed for hull content (16.05%), oil content (15.24%), days to 50% flowering (13.49%), volume weight (11.84 g/100 mL), and seed filling percentage (9.43%). Notably, days to maturity showed the lowest genetic advance (8.22%), indicating limited potential for selection improvement. Manasa et al. (2024) observed the maximum genetic advanced as per cent of mean for seed yield per plant, plant height and head diameter.

1. **CONCLUSION**

This study characterized 32 sunflower genotypes sourced from the Indian Institute of Oilseeds Research, Hyderabad, Oilseed Research Institute, Latur, Zonal Agriculture Research Institute, Solapur. revealing significant treatment differences across all evaluated traits. High genotypic (GCV) and phenotypic (PCV) coefficient of variation values were observed for key agronomic traits: seed yield per plant (33.1%, 35.2%), plant height (15.1%, 15.8%), head diameter (13.0%, 14.7%), 100-seed weight (12.8%, 15.2%), hull content (9.5%, 11.7%), oil content (8.6%, 10.0%), and volume weight (7.4%, 9.6% g/100 mL). These results demonstrate substantial heritable variation, making these traits particularly responsive to selection-based improvement in sunflower breeding programs. The study revealed distinct patterns of gene action through combined analysis of heritability (broad-sense) and genetic advance. Plant height (h²=90.99%, GA=41.24 cm) and seed yield per plant (h²=88.76%, GA=18.92 g) exhibited both high heritability and substantial genetic advance, indicating predominant additive gene effects that Favor direct phenotypic selection. Conversely, head diameter (h²=79.18%, GA=4.01 cm), 100-seed weight (h²=70.27%, GA=1.14 g), and oil content (h²=74.26%, GA=5.41%) showed high heritability but limited genetic advance, suggesting non-additive gene action predominates. For these traits, heterosis breeding would be more effective than direct selection for achieving genetic gains.

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|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sr. No.** | **Characters** | **Mean sum of square** | |  |
| **Replication**  **d.f.**  **(2)** | **Treatments**  **d.f.**  **(31)** | **Error**  **d.f.**  **(62)** |
| **1.** | **Days to 50 % flowering** | **2.54** | **51.28\*\*** | **3.16** |
| **2.** | **Days to maturity** | **2.82** | **46.75\*\*** | **3.30** |
| **3.** | **Plant height (cm)** | **37.11** | **1365.41\*\*** | **43.60** |
| **4.** | **Head diameter (cm)** | **0.25** | **15.61\*\*** | **1.25** |
| **5.** | **100 seed weight (g)** | **0.08** | **1.51\*\*** | **0.18** |
| **6.** | **Hull content (%)** | **2.30** | **20.70\*\*** | **2.95** |
| **7.** | **Seed filling percentage (%)** | **18.20** | **77.30\*\*** | **12.57** |
| **8.** | **Oil content (%)** | **0.94** | **31.16\*\*** | **3.22** |
| **9.** | **Volume weight (g/100ml)** | **0.17** | **38.81\*\*** | **7.04** |
| **10.** | **Seed yield per plant (g)** | **25.98** | **297.44\*\*** | **12.04** |

**Table- 1. Analysis of variance for 10 Characters.**

**Table-2. Estimation of variability parameters for 10 different characters.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr.**  **No.** | **Name of Character** | **Range** | **Mean** | **G.C.V. (%)** | **P.C.V. (%)** | **Heritability**  **(h2) (bs)**  **%** | **Genetic advance**  **(at 5% K)** | **GA as % of mean**  **(at 5% K)** |
| 1. | **Days to 50 % flowering** | 46.33-63.67 | 55.86 | 7.16 | 7.84 | 83.52 | 7.54 | 13.49 |
| 2. | **Days to maturity** | 76.33-93.67 | 86.02 | 4.42 | 4.90 | 81.41 | 7.07 | 8.22 |
| 3. | **Plant height (cm)** | 85-180.87 | 139.2 | 15.07 | 15.80 | 90.99 | 41.24 | 29.63 |
| 4. | **Head diameter (cm)** | 11.03-21.87 | 16.78 | 13.04 | 14.65 | 79.18 | 4.01 | 23.90 |
| 5. | **100 seed weight (g)** | 4.08-6.92 | 5.21 | 12.76 | 15.22 | 70.27 | 1.14 | 22.03 |
| 6. | **Hull content (%)** | 21.17-30.57 | 25.49 | 9.54 | 11.68 | 66.71 | 4.09 | 16.05 |
| 7. | **Seed filling percentage (%)** | 70.70-88.50 | 80.63 | 5.76 | 7.24 | 63.18 | 7.60 | 9.43 |
| 8. | **Oil content (%)** | 29.70-41.47 | 35.54 | 8.58 | 9.96 | 74.26 | 5.41 | 15.24 |
| 9. | **Volume weight (g/100ml)** | 37.86-50.43 | 43.86 | 7.41 | 9.57 | 60.05 | 5.19 | 11.84 |
| 10. | **Seed yield per plant (g)** | 15.53-48.63 | 29.44 | 33.13 | 35.17 | 88.76 | 18.92 |  |

**Fig. 1. Mean and range for 10 traits in sunflower**

**Fig. 2. Phenotypic and genotypic coefficient of variation of 10 traits in sunflower.**

**Fig. 3. Heritability (broad sense) and genetic advance as percentage of mean for 10 traits in sunflower**