**Analysis of Genetic Variability, Heritability and Genetic Advance for Yield and Yield-related Traits of Sunflower (*Helianthus annuus* L.)**

**ABSTRACT**

A field experiment was conducted at Rajendranagar farm of ICAR-Indian Institute of Oilseeds Research, Hyderabad during *rabi*-2024-25. Thirty two sunflower genotypes were evaluated in Randomized block design with three replications. The aim of the experiment was to determine the genetic variability for seed yield and oil content. The results of the study recorded a broad range of variability for all the characters under study. Low to high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded. The traits seed yield per plant (54.4% and 56.3%) followed by linoleic acid (49.9% and 52.9%), oleic acid (46.7% and 49.5%), plant height (23.9% and 24.5%), head diameter (21.7% and 23.2%) and 100 seed weight (21.2% and 27.1%), respectively, recorded high phenotypic and genotypic coefficients of variation. high heritability coupled with high genetic advance as a percentage of the mean were recorded for seed yield per plant, plant height, head diameter, no of leaves per plant, seed length, 100 seed weight, volume weight, stearic acid, palmitic acid, oleic acid and linoleic acid, indicating the predominance of additive gene action for these characters and therefore, provides the most effective condition for selection and these traits should be used in future sunflower improvement programmes.

***Keywords*:** Diversity; genetic advance; heritability; sunflower; variability; yield

1. **INTRODUCTION**

Sunflower (*Helianthus annuus* L.), a member of the family *Compositae*, is a major oilseed crop primarily cultivated for its edible oil. The genus *Helianthus* includes 52 species encompassing 67 taxa (Schilling 2006; Stebbins et al. 2013). Sunflower was introduced to India in late 1960s (Meena et al. 2013). In India, sunflower is grown during the *kharif*, *rabi*, and spring seasons, making it one of the fastest growing oilseed crops. Karnataka, Andhra Pradesh, Maharashtra, West Bengal, Odisha and Punjab are the major sunflower growing states. Presently, it is cultivated over 2.69 lakh hectares, with an annual production of 2.79 lakh tons and an average productivity of 1037 kg/ha (Directorate of Economics and Statistics 2023). 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. Assessing the extent of variability helps breeders make informed decisions when selecting superior genotypes. The phenotypic and genotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations and to quantify and compare variability across different traits. Heritability estimates provide insights into the proportion of total variation that is genetically inherited, aiding in effective selection. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. When combined with genetic advance, these estimates become valuable predictors of expected improvement under selection. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection. Assessment of variability for yield and other characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement ([Kumar et al. 2019](https://www.sciencedirect.com/science/article/pii/S2096242820300403" \l "bib16)). Therefore the present study was carried out with the objective to identify genetic variability and [heritability](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/heritability) of the desirable traits among sunflower genotypes for future breeding program.

**2. MATERIAL AND METHODS**

***2.1 Location of study***

The present investigation was conducted at Research Farm, Rajendranagar of ICAR-Indian Institute of Oilseeds Research, Hyderabad, (India) during *Rabi* season 2024-25, which is located at a latitude of 17º 15' 16” N, longitude 78º 18’ 30” E and altitude 536 meters above MSL in Telangana State.

***2.2 Experiment Design and Procedure***

A total of 32 sunflower genotypes including 4 maintainer lines, 5 restorer lines, twenty F1 hybrids three checks (DRSH-1, KBSH-44 and TilhanTech-SUNH-1) were sown in a Randomized Blocked Design with three replications for genetic variability studies for fifteen quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), head diameter (cm), number of leaves per plant, seed yield per plant (g), seed width (mm), seed length (mm), 100 seed weight (g), volume weight (g/100 ml), oil content (%), oleic content (%), linoleic acid (%), stearic acid (%) and palmitic acid (%). The experimental materials were sown in 2 rows each of 3.0 m length. 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 accession were selected randomly for recording of data on yield and its related characters. The observations on days to 50 per cent flowering were recorded on plot basis. The oil content (%) was estimated by using the NMR method, while fatty acid profile was analysed using Gas Chromatography (GC).

***2.3 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 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). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (PCV) were categorized in the range of 20%: High, 10-20%: Moderate, and 20%: High by Sivasubramanian and Madhavamenon (1973). Johanson 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 R-software.

**3. RESULTS AND DISCUSSION**

***3.1 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 fourteen traits *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), head diameter (cm), number of leaves per plant, seed yield per plant (g), seed length (mm), 100 seed weight (g), volume weight (g/100 ml), oil content (%), oleic content (%), linoleic acid (%), stearic acid (%) and palmitic acid (%) except seed width (mm), 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), Dasari Mohan Vamsi et al. (2022) and Zade et al. (2025) also reported significant differences for all the characters studied. The results are displayed in Table 1.

**Table 1. Mean sum of squares and their significance from analysis of variance (ANOVA) of fifteen plant characters in sunflower**

|  |  |  |  |
| --- | --- | --- | --- |
| **Characters** | **Mean sum of squares** | | |
| **Replication** | **Treatments** | **Error** |
| **2** | **31** | **62** |
| Plant height (cm) | 128.82 | 1451.55\*\* | 38.49 |
| Head diameter (cm) | 0.70 | 16.79\*\* | 1.14 |
| No of leaves per plant | 151.60\*\* | 26.87\*\* | 5.43 |
| Seed length (mm) | 0.02 | 0.045\*\* | 0.01 |
| Seed width (mm) | 0.01 | 0.02 | 0.02 |
| Days to 50% flowering | 0.39 | 16.77\*\* | 1.20 |
| 100 seed weight (g) | 0.44 | 2.77\*\* | 0.67 |
| Seed yield per plant (g) | 0.42 | 372.49\*\* | 12.94 |
| Days to maturity | 0.39 | 20.66\*\* | 0.71 |
| Volume weight (g/100 ml) | 0.01 | 44.83\*\* | 1.02 |
| Oil content (%) | 0.10 | 20.43\*\* | 1.45 |
| Stearic acid (%) | 1.57\* | 1.90\*\* | 0.28 |
| Palmitic acid (%) | 1.63\*\* | 0.55\*\* | 0.15 |
| Oleic acid (%) | 409.61\* | 1075.15\*\* | 63.0 |
| Linoleic acid (%) | 429.42\* | 975.96\*\* | 58.67 |

***3.2 Range and Mean of Fifteen Traits***

The per se performance of sunflower genotype revealed that there was a substantial variability among genotypes for all the characters. The range value of mean among 32 genotypes for fifteen quantitative traits is 0.3-177.6. The results were presented in Table 2 and Fig 1. For days to flowering, the range values from 49.0-59.5 with a mean value is 53.8. The results indicated that there is a variation (37.5 days) 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 50.8-177.6 with a mean of 114.2 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 12.9 with ranges from 3.3-17.1. Number of leaves per plant was recorded range values from 16.1-33.9 with a mean of 23.1. The seed length was recorded as a mean of 1.0 mm with ranges from 0.8-1.4 mm. On the other hand, the range values of mean for the number of seed yield per plant (4.0-53.4), seed width (0.3-0.9 mm), 100 seeds weight (1.8-6.7), oil content (28.9-41.4), days to maturity (77.5-89.5 days),stearic acid (3.5-7.2), palmitic acid (2.6-4.5), oleic acid (22.6-86.4) and linoleic acid (6.5-68.2) with mean values of 24.7, 0.5, 4.8, 35.3, 83.9, 5.3, 3.5, 48.2 and 42.9, respectively. This shows as there is great variation among the studied genotypes for various traits, so higher seed yielding and higher oleic content hybrids can be developed through selection. Comparable results were found in the study by Mohan et al. (2020) for majority of the traits.

**Fig. 1. Mean and range for 15 traits in sunflower**

***3.3 Phenotypic and Genotypic Coefficient of Variability***

The genetic variability parameters for different traits *viz.,* genotypic coefficient of variation (GCV) and phenotypic coefficient variances (PCV) are displayed in (Table 2 and Fig. 1). For all the traits considered under the present investigation the values of phenotypic coefficient of variation is slightly higher than the genotypic coefficient of variation 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. The variation observed in the characters studied in the present investigation were classified as, low (<10%), moderate (10-20%) and high (>20%) phenotypic and genotypic coefficients of variation (Deshmukh et al. 1986). The highest GCV was recorded for seed yield per plant (54.37%), linoleic acid (49.87%), and oleic acid (46.67%) followed by plant height (23.94%), head diameter (21.67%), and 100 seed weight (21.16%). These values indicate that these traits are genetically variable and potentially under additive gene control. Moderate to low GCV was observed for traits such as days to 50% flowering (5.19%) and seed width (13.54%). These results are consistent with the earlier reports of Reddy and Reddy (2006) and Kalukhe et al. (2010). The highest GCV and PCV values were found particularly for seed yield per plant (54.4% and 56.3%) followed by linoleic acid (49.9% and 52.9%), oleic acid (46.7% and 49.5%), plant height (23.9% and 24.5%), head diameter (21.7% and 23.2%) and 100 seed weight (21.2% and 27.1%), respectively (Table 2). 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 highest genotypic coefficient of variation was observed for seed yield per plant (36.03%) was observed by Baraiya et al. (2018). Moderate GCV and PCV were recorded for stearic acid (16.9% and 19.6%), number of leaves per plant (14.2% and 17.4%), seed length (13.6% and 16.0%), volume weight (13.5% and 13.8%) and palmitic acid (12.9% and 17.0%), respectively. Moderate GCV and high PCV (13.5% and 28.8%, respectively) revealed the seed width, which indicates that the trait is more influenced by the environment. Low GCV and PCV for days to maturity (3.8% and 3.9%), days to 50% flowering (5.2% and 5.5%) and oil content (8.7% and 9.4%), respectively, indicating less variability exists in these characters and highly influenced by the environments. Moderate to low variability indicates the need for improvement of the base population. The results of both phenotypic and genotypic coefficients of variation were similar with Mamta et al. (2017). Reena et al. (2019), Lakshman et al. (2021), Sandhya sree et al. (2022), Anuradha et al.(2023) and Mohan et al. (2022).

**Fig. 2. Phenotypic and genotypic coefficient of variation of 15 traits in sunflower**

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

Heritability is a good indicator of the transmission of characters from parents to their offsprings. 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). The estimates of heritability help the plant breeder in selection of genotypes from diverse genetic population. Therefore, high heritability helps in the effective selection of a particular trait. Heritability in the broad sense ranged from low to high. 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 low to high category since heritability >22%. Most of the characters in this study were manifested moderately high to very high (57.4% - 95.6%), while lowest heritability (22.04%) revealed only for seed width. The highest broad sense heritability value manifested for volume weight (95.56%) followed by plant height (94.83%), seed yield per plant (93.28%), days to maturity (93.33%), oil content (86.71%), days to 50% flowering (86.68%) and oleic acid (88.93%) (Table 2 and Fig. 2), indicate that phenotypic expression is mostly due to genetic factors and selection for studied traits can be performed in earlier generations. Recently, Narkhede et al. (2025) recorded high broad sense heritability for days to 50% flowering, days to maturity, head diameter, 100 seed weight, volume weight, oil content (83.48%) and seed yield/plant. Similar results were reported by Kalukhe et al. (2010), Supriya et al. (2016). On the contrary, seed width showed the lowest heritability (22.04%). These observations confirm that traits with high heritability can be reliably selected in early generations. This result is in accordance with Makane et al. (2011).

The genetic advance is a useful indicator of the effective and efficient selection progress that can be expected as a result of exercising selection on the base population. 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. In this study, high heritability coupled with high genetic advance as a percentage of the mean (>20) were recorded for seed yield per plant, plant height, head diameter, no of leaves per plant, seed length, 100 seed weight, volume weight, stearic acid, palmitic acid, oleic acid and linoleic acid, indicating the predominance of additive gene action for these characters and therefore, provides the most effective condition for selection. Similar results were matched with Neelima et al. (2016), Mamta et al. (2017) and Mallik et al. (2020). High heritability coupled with high genetic advance was recorded for seed yield per plot, yield per hectare, oil yield, seed number per plant head and yield per plant head by Mola et al. (2024). On the other hand, high heritability with low genetic advance as percentage of the mean was revealed for days to 50% flowering and days to maturity which indicates that these traits were governed by non-additive genes. Only oil content was recorded high heritability coupled with moderate genetic advance as percentage of the mean indicating the significance of dominance and epistatic effects in the inheritance of this character and selection for this trait would be less effective. It suggests that these traits can be improved by selective breeding efforts. Further, low heritability coupled with low genetic advance as percentage of the mean was revealed for seed width indicating that improvement of this trait is not possible with any of the breeding methods. These results are in line with Varshitha et al. (2023) and Mariyam et al. (2024).

**Fig. 3. Heritability (broad sense) and genetic advance as percentage of the mean for 15 traits in sunflower**

**Table 2. Estimation of genetic variability parameters**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Range** | | **Mean** | **Variability** | | **Coefficient of variability** | | **H2** | **GA** | **GAM** |
| **Min** | **Max** | **GV** | **PV** | **GCV** | **PCV** |
| Plant height (cm) | 50.8 | 177.6 | 111.0 | 706.5 | 745.0 | 23.9 | 24.5 | 94.8 | 53.3 | 48.0 |
| Head diameter (cm) | 3.3 | 17.1 | 12.9 | 7.8 | 8.9 | 21.7 | 23.2 | 87.2 | 5.4 | 41.7 |
| No of leaves per plant | 16.1 | 33.9 | 23.1 | 10.7 | 16.1 | 14.2 | 17.4 | 66.4 | 5.5 | 23.7 |
| Seed length (mm) | 0.8 | 1.4 | 1.0 | 0.02 | 0.03 | 13.6 | 16.0 | 70.2 | 0.2 | 23.6 |
| Seed width (mm) | 0.3 | 0.9 | 0.5 | 0.01 | 0.02 | 13.5 | 28.8 | 22.0 | 0.1 | 13.1 |
| Days to 50% flowering | 49.0 | 59.5 | 53.8 | 7.8 | 8.9 | 5.2 | 5.5 | 86.7 | 5.3 | 9.9 |
| 100 seed weight (g) | 1.8 | 6.7 | 4.8 | 1.05 | 1.7 | 21.2 | 27.1 | 60.9 | 1.6 | 34.0 |
| Seed yield per plant (g) | 4.0 | 53.4 | 24.7 | 179.8 | 192.7 | 54.4 | 56.3 | 93.3 | 26.7 | 108.2 |
| Days to maturity | 77.5 | 89.5 | 83.9 | 9.9 | 10.7 | 3.8 | 3.9 | 93.3 | 6.3 | 7.5 |
| Volume weight (g/100 ml) | 28.0 | 54.0 | 34.8 | 21.9 | 22.9 | 13.5 | 13.8 | 95.6 | 9.4 | 27.1 |
| Oil content (%) | 28.9 | 41.4 | 35.3 | 9.5 | 10.9 | 8.7 | 9.4 | 86.7 | 5.9 | 16.7 |
| Stearic acid (%) | 3.5 | 7.2 | 5.3 | 0.8 | 1.1 | 16.9 | 19.6 | 74.7 | 1.6 | 30.2 |
| Palmitic acid (%) | 2.6 | 4.5 | 3.5 | 0.2 | 0.3 | 12.9 | 17.0 | 57.4 | 0.7 | 20.2 |
| Oleic acid (%) | 22.8 | 86.4 | 48.2 | 506.1 | 569.6 | 46.7 | 49.5 | 88.9 | 43.7 | 90.6 |
| Linoleic acid (%) | 6.5 | 68.2 | 42.9 | 458.6 | 517.3 | 49.9 | 52.9 | 88.7 | 41.5 | 96.7 |

**4. CONCLUSION**

The present study reveals that there is a significant amount of variability among all the genotypes for all the traits studied. The highest seed yield per plant followed by linoleic acid, oleic acid, plant height, head diameter and 100 seed weight, respectively. Low GCV and PCV were recorded for days to maturity, days to 50% flowering and oil content, indicating less variability exists in these characters and highly influenced by the environments.. High heritability values indicate that the characters under study are less influenced by environment and breeder may make his/her selection on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. High heritability traits 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 traits. Generally, the breeder should adopt suitable breeding methodology to utilize in the future breeding program especially in case of sunflower.

**DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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