



# Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.125>

## ASSESSMENT OF GENETIC VARIABILITY FOR YIELD AND ITS ATTRIBUTING TRAITS IN SUNFLOWER INBREDS

Shraddanjali Narasannavar<sup>1\*</sup>, Arjuman Banu<sup>2</sup>, Dattatraya Bhat<sup>2</sup>, Priyadarshini S.K.<sup>2</sup>,  
S.D. Nehru<sup>2</sup> and Karthik N.<sup>1</sup>

<sup>1</sup>Department of Genetics & Plant Breeding, UAS, GKVK, Bangalore, Karnataka, India

<sup>2</sup>AICRP on Sunflower, ZARS, UAS, GKVK, Bangalore, Karnataka, India

\*Corresponding author E-mail: [shraddabn@gmail.com](mailto:shraddabn@gmail.com)

(Date of Receiving-17-07-2026; Date of Revision-05-09-2026; Date of Acceptance-08-09-2026)

### ABSTRACT

An investigation was carried out to assess the extent of genetic variability for seed yield and its component traits in sunflower. The experimental material comprised 50 inbred lines along with seven checks, which were evaluated during the *rabi* seasons of 2018, 2019, and 2020 at the ZARS, GKVK, University of Agricultural Sciences, Bengaluru. The experiment was laid out in an augmented design. Analysis of variance revealed highly significant differences among the inbred lines for all the traits studied, indicating the presence of considerable genetic variability. For all characters, the phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) suggesting a lower influence of environmental factors on the expression of these traits. Result revealed that, high estimates of broad-sense heritability were observed for all the traits, reflecting the predominance of genetic control, particularly additive gene action. High heritability coupled with high genetic advance as a percentage of mean (GAM) was recorded for head diameter, plant height, test weight, and seed yield per plant. This indicates that these traits are mainly governed by additive gene action and that improvement through direct selection would be effective. In contrast, high heritability associated with low GAM was observed for days to 50 per cent flowering, volume weight, and oil content, suggesting a greater influence of environmental factors and non-additive gene action in the expression of these traits.

**Key words:** Genetic Advance; Genetic Variability; Genotypic Variation; Inbreds; Phenotypic Variation.

### Introduction

Oilseed crops hold a strategic position in Indian agriculture, forming the backbone of the edible oil industry and contributing significantly to the country's agricultural economy. India is the fourth largest producer of oilseeds in the world, cultivating about 26–27 million hectares with an annual production of 35–37 million tonnes and productivity around 1.3–1.4 tonnes per hectare. Sunflower (*Helianthus annuus* L.) has become an important edible oilseed crop in India due to its short growing season (85-100 days), wide adaptability, great yielding potential, low photosensitivity, cross pollination, and high market price. In India, Karnataka is the major sunflower producing states and mostly grown as arable crop with meagre irrigation support which is followed by

unified Andhra Pradesh, Maharashtra, Bihar, Odisha and Tamil Nadu. Karnataka has historically been the leading producer of sunflower, contributing a significant share of 50 per cent of sunflower area and 40 per cent of total production due to its suitable semi-arid climate and well-developed hybrid seed production base (Rao *et al.*, 2018; Reddy *et al.*, 2020). In Karnataka, during 2024–2025, sunflower was cultivated over an area of 0.75 lakh ha, with a total production of 0.75 lakh tonnes and an average productivity of 963 kg ha (Anon., 2025).

Sunflower has regained relevance in the state of Karnataka as a result of the government of India increasing the minimum support price to 7,721 Indian rupees per quintal during 2025-26 and providing support to the oil seed sector. The presence of genetic variability

is required before beginning any breeding programme. The goal of sunflower breeding in India is to develop hybrids or cultivars with high yield, oil content, and oil quality, as well as disease and insect resistance. Information on variability and heritability is essential to develop selection criteria any plant breeding activity. Heritability estimates in addition to genetic advance is a more reliable measure in estimating the expected progress/performance to be achieved during the process of selection. Hence, variability existing in a gene pool of any crop species is crucial to plant breeder. The coefficients of variation expressed at phenotypic and genotypic levels are used to compare the variability among different traits for identifying the trait association and selection of the superior genotype. The coefficients of variation reported at the phenotypic and genotypic levels are used to compare trait variability in order to identify trait associations and selection the superior genotype.

Yield improvement in sunflower remains a major breeding objective; however, seed yield is a complex quantitative trait governed by multiple component characters and influenced by environmental factors. The effectiveness of any breeding programme largely depends on the magnitude of genetic variability present in the breeding material and the nature of gene action controlling economically important traits. Sunflower inbred lines serve as the basic genetic resource for the development of superior hybrids, and systematic evaluation of their genetic potential is essential for successful hybrid breeding.

Estimation of genetic parameters such as phenotypic and genotypic coefficients of variation, heritability, and genetic advance provides critical insight into the relative contribution of genetic and environmental components to trait expression. These parameters help in identifying traits governed by additive gene action and in predicting the expected response to selection. Therefore, the present study was undertaken to assess the extent of genetic variability for seed yield and its attributing traits in sunflower inbred lines, with the objective of identifying key traits that can be effectively exploited for genetic improvement and development of high-yielding sunflower hybrids.

## Materials and Methods

## Plant material & experimental design

The field experiment was carried out during *rabi* season of 2018 to 2020 at Zonal Agriculture research station UAS GKVK Bangalore Karnataka, India. The experimental site is located at 12058' N latitude, 77035' E longitude and situated at an altitude of 930 m above the

**Table 1:** List of the inbred lines and checks used in the study.

| Sr. | INBREDS | Sr. | INBREDS  | Sr. | INBREDS               |
|-----|---------|-----|----------|-----|-----------------------|
| 1.  | GMU-324 | 26  | GMU-707  | 1   | LTRR 341              |
| 2.  | GMU-368 | 27  | GMU-711  | 2   | RHA 6D-1              |
| 3.  | GMU-379 | 28  | GMU-713  | 3   | RHA 297               |
| 4.  | GMU-411 | 29  | GMU-729  | 4   | RHA 95 C-1            |
| 5.  | GMU-420 | 30  | GMU-749  | 5   | CMS 17 B              |
| 6.  | GMU-450 | 31  | GMU-750  | 6   | CMS 234 B             |
| 7.  | GMU-426 | 32  | GMU-770  | 7   | CMS 1103<br>B (UAS B) |
| 8.  | GMU-428 | 33  | GMU-1000 |     |                       |
| 9.  | GMU-441 | 34  | GMU-1012 |     |                       |
| 10. | GMU-447 | 35  | GMU-1016 |     |                       |
| 11. | GMU-458 | 36  | GMU-1043 |     |                       |
| 12. | GMU-459 | 37  | GMU-1045 |     |                       |
| 13. | GMU-461 | 38  | GMU-1056 |     |                       |
| 14. | GMU-465 | 39  | GMU-1075 |     |                       |
| 15. | GMU-466 | 40  | GP6-451  |     |                       |
| 16. | GMU-475 | 41  | GP6-131  |     |                       |
| 17. | GMU-478 | 42  | GP6-374  |     |                       |
| 18. | GMU-480 | 43  | GP6-445  |     |                       |
| 19. | GMU-520 | 44  | GMU-756  |     |                       |
| 20. | GMU-523 | 45  | GPR-78   |     |                       |
| 21. | GMU-477 | 46  | GMU-266  |     |                       |
| 22. | GMU-597 | 47  | GMU-311  |     |                       |
| 23. | GMU-755 | 48  | GMU-434  |     |                       |
| 24. | GMU-714 | 49  | GMU-500  |     |                       |
| 25. | GMU-704 | 50  | GMU-505  |     |                       |

mean sea level. The experimental material for the present investigation comprised of 50 inbred lines obtained from IIOR, Hyderabad and 7 checks were sown for characterization using Augmented Block Design.

Each inbred was raised in two rows each of 3 m, adopting a spacing of 60 cm between rows and 30 cm between plants. At the time of sowing, half of the recommended dose of nitrogen, along with the full doses of phosphorus and potassium, was applied. The remaining 50 per cent of nitrogen was top dressed 30 days after

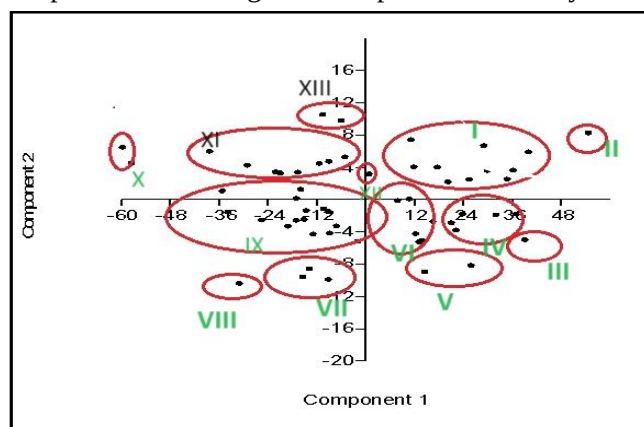


**Fig. 1:** Grouping of inbred into different clusters based on principal component analysis for genetic variability.

**Table 2:** ANOVA for seed yield and its attributing traits in fifty inbred lines and seven checks.

| Source of variation       | Blocks | Treatments | Checks  | Inbreds | Check Vs inbred | Error |
|---------------------------|--------|------------|---------|---------|-----------------|-------|
| Degrees of freedom (df)   | 4      | 56         | 6       | 49      | 1               | 24    |
| Days to 50% flowering     | 10.57  | 31.76      | 60.58   | 23.66   | 255.51          | 0.85  |
| Plant height(cm)          | 3.51   | 794.99     | 2000.37 | 663.42  | 9.61            | 0.67  |
| Head diameter(cm)         | 0.65   | 6.96       | 23.74   | 5.040   | 0.70            | 0.13  |
| Seed yield/plant (g)      | 1.15   | 226.43     | 728.66  | 166.26  | 161.48          | 0.25  |
| 100 seed weight (g/100ml) | 0.027  | 1.27       | 1.15    | 1.30    | 0.29            | 0.008 |
| Volume weight(g/100ml)    | 0.42   | 34.08      | 196.42  | 14.90   | 0.037           | 0.054 |
| Oil content (%)           | 0.35   | 27.96      | 36.89   | 19.75   | 376.48          | 0.026 |

**Table 3:** Genetic variability traits in 50 inbred lines and seven checks for seed yield and its attributing traits.

| Trait                      | Mean   | Range  |       | PCV<br>% | GCV<br>% | Heritability<br>% | GAM<br>% |
|----------------------------|--------|--------|-------|----------|----------|-------------------|----------|
|                            |        | Max    | Min   |          |          |                   |          |
| Days to 50% flowering      | 63.93  | 76.00  | 55.00 | 5.98     | 5.80     | 94.00             | 11.61    |
| Plant height(cm)           | 112.10 | 166.60 | 52.50 | 17.99    | 17.98    | 99.80             | 37.07    |
| Head diameter (cm)         | 10.58  | 14.20  | 5.00  | 16.67    | 16.31    | 95.00             | 32.87    |
| Seed yield/plant (g)       | 22.48  | 72.00  | 3.80  | 44.19    | 44.14    | 99.00             | 90.81    |
| 100 seed weight (g/100 ml) | 4.98   | 7.21   | 2.95  | 17.96    | 17.86    | 98.00             | 36.60    |
| Volume weight(g/100ml)     | 43.95  | 51.61  | 34.36 | 6.88     | 6.85     | 99.00             | 14.08    |
| Oil content (%)            | 38.82  | 50.69  | 29.55 | 8.84     | 8.83     | 99.10             | 18.17    |

sowing. The crop was raised under irrigation, following all the recommended package of practices to ensure good growth.

Five random plants from inbreds were used to record observation on yield and its contributing traits. Data was recorded for seven characters viz., days to 50% flowering, plant height (cm), head diameter (cm), 100 seed weight (g), seed yield per plant and oil content (%) and volume weight (g/100ml). To test the difference among the inbreds, the analysis of variance was performed individually for each character as per method suggested by Federer (1956). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton, 1952. Heritability ( $h^2$ ) in broad sense was calculated according to the formula given by Allard, 1960.

The experimental material for the present investigation comprised of 50 inbred lines obtained from ICAR-IIOR, Hyderabad and 7 checks.

## Result and Discussion

The results of ANOVA (Table 1) carried out in the present study showed highly significant mean sum of squares for all the traits indicating presence of sufficient variability in the experimental material. Inbred lines of sunflower showed a wide range of diversity in yield and its contributing traits, as well as in oil content. Wide range of variation observed for plant height (52-166cm) followed by Days to 50% flowering (55 to 76days) Head diameter 5 -14(cm), Seed yield/plant 3.80-72(g), 100 seed weight 2.95 -7.21(g), volume weight 34-51ml, Oil content 29-

50(%) this result are in line with Neelima *et al.*, 2016 and Varalakshmi *et al.*, 2019. The estimates of phenotypic coefficient of variation were slightly higher than their corresponding genotypic coefficient of variation (Table 2) for all the traits under this study indicating the less influence of environment effect on the expression of these traits. The traits with almost equal value of PCV and GCV can considered as stable similar result in (Dimitrijevic *et al.*, 2017). High heritability coupled with high genetic advance as percent of mean (GAM) was noticed for head diameter, plant height, test weight and seed yield per these traits are governed by additive gene action and Directional selection could be more effective. High heritability coupled with low GAM was observed for days to 50 % flowering, volume weight and oil content, implying that the function of favourable environment rather than genotype and therefore, selection may not be rewarding. Low heritability coupled with high GAM indicates that it is regulated by additive gene effects and is heavily influenced by environments and therefore, selection would be effective. These results are in line with Madhavi Latha *et al.*, 2017.

**Table 4:** Principal components showing the eigenvalues.

| PC | Eigen value | % variance |
|----|-------------|------------|
| 1. | 626.33      | 90.635     |
| 2. | 26.4675     | 3.83       |
| 3. | 17.7818     | 2.5731     |
| 4. | 16.2699     | 2.3544     |
| 5. | 3.34474     | 0.48401    |
| 6. | 0.852197    | 0.1233     |

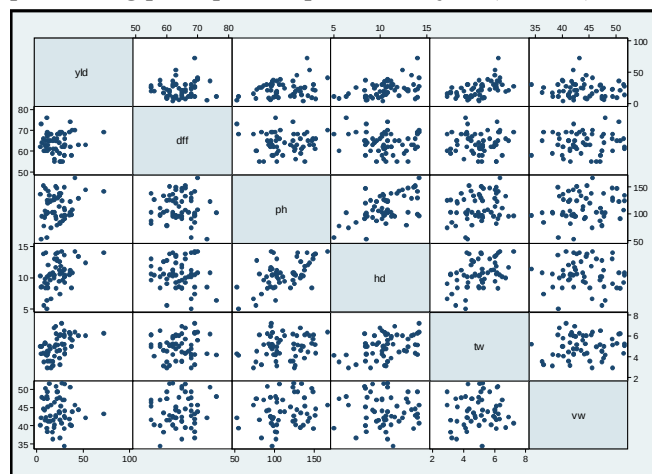
**Table 5:** Component analysis of traits under study using principal component analysis in 50 inbreds sunflower.

| Variable | Comp1  | Comp2  | Comp3   | Comp4   | Comp5   | Comp6   | Comp7   |
|----------|--------|--------|---------|---------|---------|---------|---------|
| Yield    | 0.47   | 0.0612 | -0.3970 | -0.2021 | 0.1538  | 0.7358  | -0.0674 |
| Dff      | -0.062 | 0.64   | -0.2666 | -0.3442 | -0.6100 | -0.1142 | 0.1036  |
| PH       | 0.45   | 0.08   | 0.4561  | 0.2831  | -0.4202 | 0.0591  | -0.5654 |
| HD       | 0.56   | -0.10  | 0.0753  | 0.2423  | -0.1861 | -0.1445 | 0.7409  |
| TW       | 0.48   | 0.11   | -0.2480 | -0.2492 | 0.3889  | -0.6335 | -0.2741 |
| VW       | 0.04   | 0.47   | 0.6675  | -0.3249 | 0.3978  | 0.1395  | 0.2023  |
| OC       | -0.07  | 0.57   | -0.2248 | 0.7309  | 0.2891  | 0.0208  | 0.0001  |

### Genetic diversity (Principal Component Analysis)

Principal component analysis was used to identify the most significant variables in the dataset. The relevance of a character to the PC can be shown in the Eigenvalues are the corresponding values. The principle component analysis of adjusted correlated and standardized of different inbreds and checks resulted in four major PCs which together explained 90.62% of variability in Table 3. The 59 inbreds and checks scattered in all the four quadrants of two dimensional graph (Fig. 1) Based on positioning, the 59 inbreds and accessions and checks could be grouped into 13 cluster. Of the 13 cluster, cluster IX with 14 accessions, cluster I with 10 accession, Cluster XI with 8 accessions, Cluster IV and VI with 5 accessions, Cluster VII with 3 accessions and the number of remaining clusters varied from 2 in cluster V, XIII and 1 in cluster II, III, VIII X similar result find in (Dudhe *et al.*, 2022).

The main objective of component analysis is to explain as much variance as possible in a data set by utilizing the smallest number of components and items or variables within each factor. Component analysis, which divides associated features into independent clusters, can be used successively to identify traits that can be used as a selection criterion (Kaya *et al.*, 2002). The Varimax method was used to rotate temporary factors after performing principal component analysis (Table 4).

**Fig. 2:** Principle component axis.

Component 1 indicated the highest factor loading value head diameter 0.56, followed by test weight (0.48) yield 0.47. Negative loading observed in days to 50% flowering -0.62. In Component 2. The largest factor-loading value was positive for features like days to 50% flowering 0.64, followed by oil content (0.57) and volume weight 0.47, while negative loading was found in head diameter -0.10. The highest component loading value was positive for volume weight 0.66, plant height (0.45), and head diameter (0.075) in factor 3. yield -0.39, dff -0.26, and oil content -0.22 had negative loading. In Factor 4, the highest positive factor-loading value was possessed by the oil content (0.73), followed by head diameter (0.24) and plant height 0.283. more number of negative loading was possessed by yield -0.2021 dff -0.3442, test weight -0.2492 and volume weight -0.3249. In component 5 the highest positive value was observed volume weight 0.39 for 100 seed weight (0.38), and yield 0.15 Negative value observed in days to 50% flowering (0.61, plant height -0.42 and head diameter -0.18. The highest factor-loading value was positive for yield 0.73. and volume weight 0.13 negative loading was possessed by head diameter -0.14 followed by dff -0.11 and test weight -0.63. In Factor 6 In component 7, The highest factor-loading value was positive for traits like head diameter (0.74), followed by Oil content (0.001), volume weight 0.20, negative loading value was yield -0.06 and test weight -0.27.

The first six components explained 95.30% of the total variation (Table 5). The first component, determining 31.75% of the variation. If the third component explained 15.17% proportion variance while the fourth component justified 12.39% of the total variance. The present findings are comparable with those Meena *et al.*, (2022), who worked on sunflower germplasms.

**Table 6:** Principal components axis.

| Principle component axis   |       |       |       |       |       |       |      |
|----------------------------|-------|-------|-------|-------|-------|-------|------|
| Eigen value                | 2.22  | 1.24  | 1.06  | 0.86  | 0.78  | 0.48  | 0.32 |
| Proportion of variance (%) | 31.75 | 17.75 | 15.17 | 12.39 | 11.25 | 7.00  | 4.70 |
| Cumulative variation (%)   | 31.75 | 49.50 | 64.67 | 77.05 | 88.30 | 95.30 | 100  |

## Conclusion

The present investigation revealed the presence of substantial genetic variability among sunflower inbred lines for seed yield and its attributing traits, indicating ample scope for genetic improvement through selection. The close correspondence between phenotypic and genotypic coefficients of variation for most traits suggested minimal environmental influence and greater genetic control over trait expression. High estimates of broad-sense heritability for all characters indicated the predominance of genetic factors in governing these traits. The traits such as head diameter, plant height, test weight, and seed yield per plant exhibited high heritability coupled with high genetic advance as a percentage of mean, suggesting the involvement of additive gene action. These traits can therefore be effectively improved through simple and direct selection.

In contrast, traits showing high heritability with low genetic advance, such as days to 50 per cent flowering, volume weight, and oil content, indicated the influence of non-additive gene action and environmental effects, suggesting the need for alternative breeding approaches. Overall, the findings provide valuable insights into the genetic architecture of yield-related traits in sunflower inbreds and offer useful guidance for the selection of parental lines and formulation of effective breeding strategies aimed at developing high-yielding and stable sunflower hybrids.

## Reference

- Bentur, M.G., Parameshwarappa K.G., Malligawad L.H., Chavan R.D., Toprope V.N., Jagtap P.K., Aglave B.N., Srinivas T., Reddy A.L., Rajesh A.P. and Umamaheshwari P. Genetic variability and association studies in Sunflower Inbreds. *Journal of Plant Breeding*, **7(4)**, 953-959.
- Burton, G.W. (1952). Quantitative inheritance in grasses. In: Proceedings of the 6th international grasslands congress, **1**, 227-283.
- Dudhe, M.Y., Mulpuri S., Meena H.P., Ajjanavara R.R., Kodeboyina V.S. and Adala V.R. (2020). Genetic variability, diversity and identification of trait-specific accessions from the conserved sunflower germplasm for exploitation in the breeding programme. *Agricultural Research*, **9**, 9-22.
- Dudhe, M.Y., Mulpuri S., Meena H.P., Ajjanavara R.R., Kodeboyina V.S. and Adala V.R. (2020). Genetic variability, diversity and identification of trait-specific accessions from the conserved sunflower germplasm for exploitation in the breeding programme. *Agricultural Research*. **Mar. 9(1)**, 9-22.
- Federer, W.T. (1963). Procedures and designs useful for screening material in selection and allocation, with a bibliography. *Biometrics*, **19**, 553-587.
- Federer, W.T. (1963). Procedures and designs useful for screening material in selection and allocation, with a bibliography. *Biometrics*. **Dec. 1**, 553-87.
- KSDA (2025). Area, production and productivity of crops in Karnataka. <https://agriculture.karnataka.gov.in/statistics>
- Lakshman, S.S., Chakraborty N.R., Debnath S. and Kant A. (2021). Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. *African Journal of Biological Sciences*, **3(1)**, 129-145.
- Lakshman, S.S., Chakraborty N.R., Debnath S., Kant A. (2021). Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. *African Journal of Biological Sciences*. **Jan. 3(1)**, 129-45.
- Latha, K.M., Prasad A.V., Neelima S. and Maheswari P.U. (2017). Genetic variability studies for yield and its attributes in sunflower. *Bulletin of Environment, Pharmacology and Life Sciences*. **6(2)**, 117-20.
- Madhavi Latha, K., Durgaprasad A.V.S., Neelima S. and Uma Meheshwari P. (2017). Genetic variability studies for yield and its attributes in sunflower. *Bull. Env. Pharmacol. Life Sci.*, **Vol 6 Special issue (2)**, 117-120.
- Neelima, S., Ashok Kumar K., Venkataramanamma K. and Padmalatha Y. (2016). Genetic variability and genetic diversity in sunflower. *Electronic Journal of Plant Breeding*, **7(3)**, 703-707.
- Neelima, S., Kumar K.A., Venkataramanamma K. and Padmalatha Y. (2016). Genetic variability and genetic diversity in sunflower. *Electronic Journal of Plant Breeding*. **Nov 9, 7(3)**, 703-7.
- Ram, J.J., Singh U.K., Singh S.K. and Krishna B. (2018). Study of genetic diversity in sunflower (*Helianthus annuus* L.). *Int. J. Curr. Microbiol. App. Sci*, **7(5)**, 2266-2272.
- Ram, J.J., Singh U.K., Singh S.K. and Krishna B. (2018). Study of genetic diversity in sunflower (*Helianthus annuus* L.). *Int. J. Curr. Microbiol. App. Sci*. **7(5)**, 2266-72.
- Reavanth, T., Manivannan N., Sasikala R. and Rajendran L. (2021). Assessment of genetic diversity among the maintainer and restorer inbreds of sunflower (*Helianthus annuus* L.). *Electronic Journal of Plant Breeding*, **12(3)**, 800-803.
- Reavanth, T., Manivannan N., Sasikala R. and Rajendran L. (2021). Assessment of genetic diversity among the maintainer and restorer inbreds of sunflower (*Helianthus annuus* L.). *Electronic J. of Plant Breeding*. **12(3)**, 800-3.
- Sujatha, H.L. and Nandini R. (2002). Genetic variability study in sunflower inbreds. *Helia*, **25(37)**, 93-100.
- Sujatha, H.L. and Nandini R. (2002). Genetic variability study in sunflower inbreds. *Helia*. **25(37)**, 93-100.
- Varalakshmi, K., Neelima S., Reddy R.N. and Sreenivasulu K.N. (2020). Genetic variability studies for yield and its component traits in newly developed sunflower (*Helianthus annuus* L.) hybrids. *Electronic Journal of Plant Breeding*, **(1)**, 301-305.
- Varalakshmi, K., Neelima S., Reddy R.N. and Sreenivasulu K.N. (2020). Genetic variability studies for yield and its component traits in newly developed sunflower (*Helianthus annuus* L.) hybrids.
- Virupakshappa, K. and Sindagi S.S. (1988). A note on germplasm collections in sunflower. *J. Oilseeds Res*, **5**, 119-120.
- Virupakshappa, K. and Sindagi S.S. A note on germplasm collections in sunflower.