Journal of Scientific Research and Reports

Volume 30, Issue 9, Page 551-559, 2024; Article no.JSRR.122890
ISSN: 2320-0227

Study on Genetic Diversity in 45 Elite Sunflower Inbred Lines (*Helianthus annuus* L.)

Y. Prudhvi Kumar Reddy [a], B.V. Ravi Prakash Reddy [b*], P. Shanthi [a] and K. Venkataramanamma [b]

[a] Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati, Andhra Pradesh, India.
[b] Department of Genetics and Plant Breeding, Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/jsrr/2024/v30i92382

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/122890

Original Research Article

Received: 27/06/2024
Accepted: 01/09/2024
Published: 05/09/2024

ABSTRACT

The present investigation aimed to study the genetic diversity of 45 sunflower inbred lines to identify genetically distinct parents for hybridization, facilitating the development of high yielding hybrid cultivars. The field experiment was carried out during the *Rabi* 2023-2024 at the Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India. Findings revealed significant differences among inbred lines for the studied traits. The inbred lines were grouped into six clusters using Tocher's method. Cluster I is the largest cluster with 34 inbred lines. Maximum intra cluster distance of 15.17 is associated with cluster I whereas maximum inter cluster distance of 79.75 is

**Corresponding author: E-mail: bvr.prakashreddy@angrau.ac.in;*

Cite as: *Reddy, Y. Prudhvi Kumar, B.V. Ravi Prakash Reddy, P. Shanthi, and K. Venkataramanamma. 2024. "Study on Genetic Diversity in 45 Elite Sunflower Inbred Lines (Helianthus Annuus L.)". Journal of Scientific Research and Reports 30 (9):551-59. https://doi.org/10.9734/jsrr/2024/v30i92382.*

found between cluster II and cluster V. Cluster VI recorded maximum means for six traits. Among the studied traits, seed yield (g/plant) (50.81) contributed maximum towards total diversity. Based on the significant genetic diversity observed among the 45 sunflower inbred lines, the study successfully identified genetically distinct parental genotypes for hybridization. This provides a foundation for developing superior hybrid cultivars with enhanced seed yield potential.

Keywords: Sunflower; genetic diversity; D2 analysis.

1. INTRODUCTION

Sunflower belongs to family Compositae (*Asteraceae*) and is diploid with chromosome number 2n = 34. It is one of the four most widely grown and consumed oil crops in the world [1]. Presently, it is cultivated in an area of 20.00 million hectares globally with production of 30.00 million tonnes and productivity of 1,500 kg ha^{-1} [2]. Sunflower seed oil is widely acclaimed in several countries compared to other vegetable oils owing to its easy availability and several health benefits including less serum cholesterol, low-density lipoprotein levels, antioxidants, regulating blood pressure, anti-inflammatory, skin protection, and pain relief [3]. Sunflower seed oil is characterized by a relatively high proportion of unsaturated fatty acids, especially linoleic acid and oleic acid, conferring high nutritional value [4]. Furthermore, the residual meal from sunflower seeds after oil extraction contains rich protein (40 to 50%), with a high nutritional value and balanced amino acid composition, thus rendering it a high-quality plant protein resource [5]. A substantial decline in sunflower cultivated area has been observed in recent years, primarily attributed to a limited availability of highquality hybrid cultivars. This scarcity underscores the significant potential for harnessing sunflower genetic diversity to identify superior accessions [6]. These elite accessions can serve as valuable resources for the development of advanced hybrid cultivars, thereby enhancing sunflower production and yield. Biometrical techniques like Mahalanobis's D^2 statistic offer a quantitative approach to assess genetic divergence among breeding lines and provides a valuable index of genetic diversity, allowing the grouping of genotypes based on D^2 values. The genetic diversity analysis in the studied inbred lines help in identifying most diverse and distantly related inbred lines which can be further crossed ensuring better manifestation of heterosis [7]. Present study aimed to significantly contribute to the identification of genetically diverse sunflower inbred lines, thereby facilitating the development of superior hybrids with enhanced yield potential. This research addresses the critical challenge of limited availability of high-quality hybrid cultivars.

2. MATERIALS AND METHODS

The experimental material comprised of 45 sunflower inbred lines, including five checks. The inbred lines used in the study were listed in Table 1. An Alpha Lattice Design with three replications is employed for cultivation of 45 sunflower inbred lines. The field experiment was carried out during the *Rabi* 2023-2024 at the Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India, geographically located at $15^0$29' north latitude and $78^0$29' east longitude at an altitude of 211.76 m above mean sea level. Each genotype was cultivated in two rows with a row length of 3m, with plot size of 3.0 × 1.8 m^2 per genotype maintaining a row spacing of 60 cm and plant spacing of 30 cm. All the agronomic practices recommended by Acharya N.G. Ranga Agricultural University were carried to raise a healthy crop. Data were collected on 11 traits, among which days to 50% flowering, days to maturity and final plant stand were recorded on plot basis. Plant height (cm), head diameter (cm), volume weight (g $100ml^{-1}$), 100-seed weight (g), seed yield (g/plant), seed yield (kg ha^{-1}), oil content (%), and oil yield (kg ha^{-1}) were recorded from five randomly selected plants per genotype in all replications.

Seed yield (kg ha^{-1}) and oil yield (kg ha^{-1}) were calculated as per the following formula.

$$\text{Seed yield (kg ha}^{-1}\text{)} = \frac{\text{Seed yield (kg/plot) x 10000}}{\text{Net plot area (m2)}}$$

$$\text{Oil yield (kg ha}^{-1}\text{)} = \frac{\text{Seed yield (kg/ha) x Oil content (\%)}}{100}$$

Analysis of variance (ANOVA) was conducted on the Alpha Lattice Design using the Variability package in R Studio. The collected data is subjected to statistical analysis employing Mahalanobis D^2 distance Mahalanobis, [8] and Tocher's method Rao, [9] to identify group

clusters. Statistical analysis was calculated using INDOSTAT 9.2 software and R Studio.

3. RESULTS

In the present study, genetic diversity among 45 sunflower inbreed lines was assessed using D^2 statistics of Mahalanobis [8] followed by clustering of genotypes using tocher's method. The mean values of 45 inbred lines were subjected to analysis of variance (ANOVA) and the mean sum of square for each trait was calculated and represented in Table 2. The analysis of dispersion based on the Wilk's criterion presented in Table 3 revealed highly significant difference (P= 0.00349 **) among inbred lines for 11 traits. Group constellation was carried out following tocher's method Rao, [9] and grouped 45 inbred lines into six clusters. The cluster composition is represented in Table 4 and Fig. 1. Cluster I was the largest comprising of maximum number of 34 genotypes followed by cluster II with seven genotypes the remaining clusters are monogenic with single genotype. Lakshman et al. [10] and Kumar et al. [2] also observed similar clustering pattern of genotypes among cluster as some clusters were unique having only single genotype.

The intra and inter cluster distance were displayed in Table 5 and Fig. 2. Maximum intra cluster value was observed for cluster I (D^2=15.17) followed by cluster II (D^2=15.13). Cluster III, IV, V and VI has zero intra cluster distance since they are monogenic clusters. The maximum inter cluster distance was found between cluster V and cluster II (D^2=79.75) followed by cluster IV and cluster II (D^2=70.78) and cluster VI and cluster V (D^2=57.87). Crossing between inbred lines of these clusters will result in higher hybrid vigour. Inter cluster distance was found minimum between cluster V and cluster III (D^2=9.39) suggesting close relation between them and low level of diversity. The inter cluster distances were greater than intra cluster except in some clusters and same is reported by Lakshman et al. [10] and Kumar et al. [2].

Table 1. List of 45 inbred lines used in the study

S. No	Entry	Source	S. No	Entry	Source
1	NDSI-2	RARS, Nandyal.	24	RP-10	RARS, Nandyal.
2	NDLB-5	RARS, Nandyal.	25	CMS-249B	IIOR, Hyderabad.
3	NDSI-3	RARS, Nandyal.	26	NDI-47	RARS, Nandyal.
4	RP-16	RARS, Nandyal.	27	CMS 302B	PDKV, Akola.
5	OPH-74	PAU, ludhiana	28	RCR-39	RARS, Nandyal.
6	CMS- 30B	RARS, Nandyal.	29	PB-120	IIOR, Hyderabad.
7	CMS- 104B	UAS, Banglore.	30	IC-502039	VNMKV, Lathur.
8	RHA-1096	UAS, Banglore.	31	NDI-20	RARS, Nandyal.
9	R-106	UAS, Raichur.	32	NDLR-27	RARS, Nandyal.
10	NDLR40	RARS, Nandyal.	33	RHA 859	RARS, Nandyal.
11	RSFH 5	RARS, Nandyal.	34	PS2023B	IIOR, Hyderabad.
12	PB-110	IIOR, Hyderabad.	35	R X R -2-38	RARS, Nandyal.
13	NDLR1	RARS, Nandyal.	36	NDLR4	RARS, Nandyal.
14	RHA-172	RARS, Nandyal.	37	NDI-50	RARS, Nandyal.
15	NDLR-36	RARS, Nandyal.	38	RHA-1013	UAS, Banglore.
16	NDI-55	RARS, Nandyal.	39	ARM-243-B	IIOR, Hyderabad.
17	COSF-6B	TNAU, Coimbatore.	**Checks**		
18	COSF-7B	TNAU, Coimbatore.	40	R-64	UAS, Raichur.
19	EC-601829	IIOR, Hyderabad.	41	LTRR-341	UAS, Banglore.
20	RSFH-11	RARS, Nandyal.	42	RHA-95C-1	TNAU, Coimbatore.
21	NDI-43	RARS, Nandyal.	43	RHA 6D-1 (br)	UAS, Banglore.
22	EC-601768	IIOR, Hyderabad.	44	PM-81	UAS, Raichur.
23	NDLR-32	RARS, Nandyal.	45	KBSH-44	UAS, Banglore.

Table 2. Analysis of variance for yield and yield attributing traits in sunflower

S. No	Traits	Mean Squares			
		Replications (df:2)	Genotypes (df:44)	Blocks (df:24)	Error (df:64)
1	Days to 50% flowering	1.49	9.60**	1.98	2.63
2	Days to maturity	0.59	14.82**	5.97	6.04
3	Final plant stand	0.77	5.27**	3.28	2.64
4	Plant height (cm)	1.20	606.00**	57.80	75.40
5	Head diameter (cm)	1.15	8.67**	0.90	0.82
6	Volumetric weight (g $100ml^{-1}$)	2.55	92.19**	2.02	2.50
7	100 seed weight(g)	0.06	1.22**	0.15	0.14
8	Seed yield (g/plant)	0.29	30.96**	5.27	3.03
9	Seed yield (kg ha^{-1})	3947.00	109698.00**	26871.00	15457.00
10	Oil content (%)	2.53	8.17**	2.94	2.30
11	Oil yield (kg ha^{-1})	680.00	13364.00**	2724.00	1410.00

**, ** Significant at 1% and 5% levels, respectively*

Table 3. Analysis of variance for dispersion in sunflower genotypes

Source of Variations	DF	Mean Squares	Probability
Varieties	44	3.69**	0.00349 **
Error	87	1.87	
Total	131	0.048	

*** Significant at 5% level*

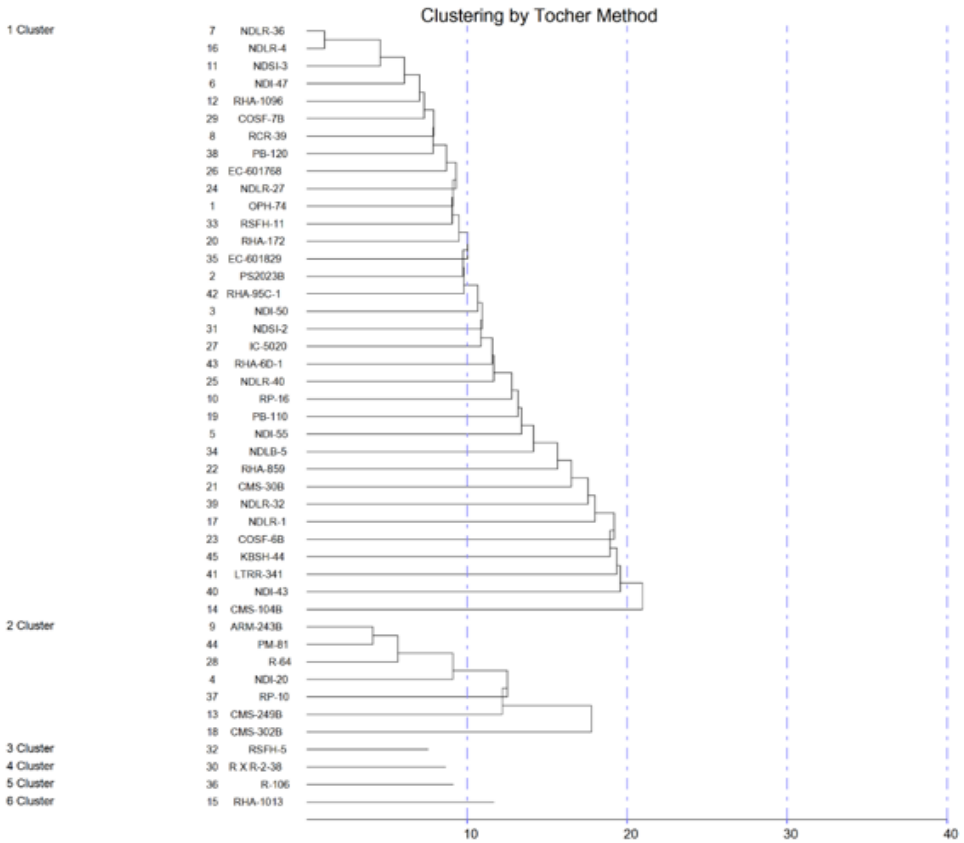

Fig. 1. Dendrogram showing relationship among sunflower genotypes in six clusters based on D2values

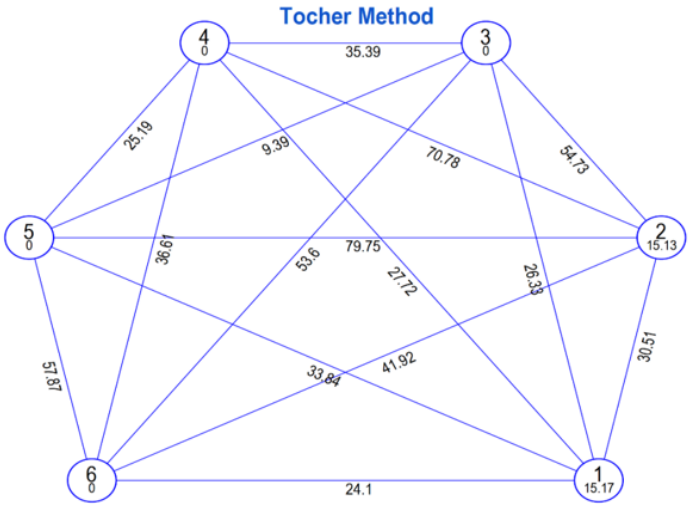

Fig. 2. Cluster diagram showing average intra and inter cluster distance for yield and its attributes of sunflower genotypes

A perusal of cluster means for 11 traits per cluster was presented in the Table 6. The Cluster VI reported maximum cluster means for the traits *viz.,* days to 50% flowering (56.67), plant height (117.87), head diameter (13.00), 100 seed weight (4.50), seed yield (g/plant) (26.87), seed yield (kg ha^{-1}) (1493.57). Highest cluster mean values for final plant stand (18.66) and volumetric weight (47.00) was displayed in cluster II. Cluster IV recorded desired highest cluster mean for oil yield (kg ha^{-1}). The desired values for days to 50 % flowering (52.67), days to maturity (86.33) *i.e.,* earliness was reported in cluster III and the same cluster exhibited higher value for oil content (37.80). Considering the mean performance of the clusters, the cluster VI had highest mean value for days to 50% flowering, plant height, head diameter, 100 seed weight, seed yield (g/plant), seed yield (kg ha^{-1}). Therefore genotypes from this clusterused as one of parents to get higher yield. Genotypes of this cluster can be used for generating variability.

Relative contribution of different traits in the present study is represented in the Table 7 and Fig. 3. Among the traits studied, seed yield (g/plant) (50.81%), contributed maximum to the total variation followed by seed yield (kg ha^{-1}) (12.02%) and head diameter (11.92 %). The traits that contributed least to the genetic diversity were final plant stand (0.2 %) and days to maturity (0.3 %). Rani et al. [11] reported that seed yield (g/plant) contributed maximum towards diversity in their study. Lakshman et al. [10] reported that head diameter contributed maximum towards diversity in their study.

Table 4. Cluster composition of sunflower genotypes based on Tocher's method

Cluster Group	No. of Genotypes	List of Genotypes
Cluster I	34	NDLR-36,NDLR-4,NDSI-3,NDI-47,RHA-1096,COSF-7B,RCR-39,PB-120,EC-601768,NDLR-27,OPH-74,RSFH-11,RHA-172,EC-601829,PS2023B,RHA-95C-1,NDI-50,NDSI-2,IC-502039,RHA-6D-1,NDLR-40,RP-16,PB-110,NDI-55,NDLB-5,RHA-859,CMS-30B,NDLR-32,NDLR-1,COSF-6B,KBSH-44,LTRR-341,NDI-43 and CMS-104B
Cluster II	7	ARM-243B, PM-81, R-64, NDI-20, RP-10, CMS-249B and CMS-302B
Cluster III	1	RSFH-5
Cluster IV	1	R X R-2-38
Cluster V	1	R-106
Cluster VI	1	RHA-1013

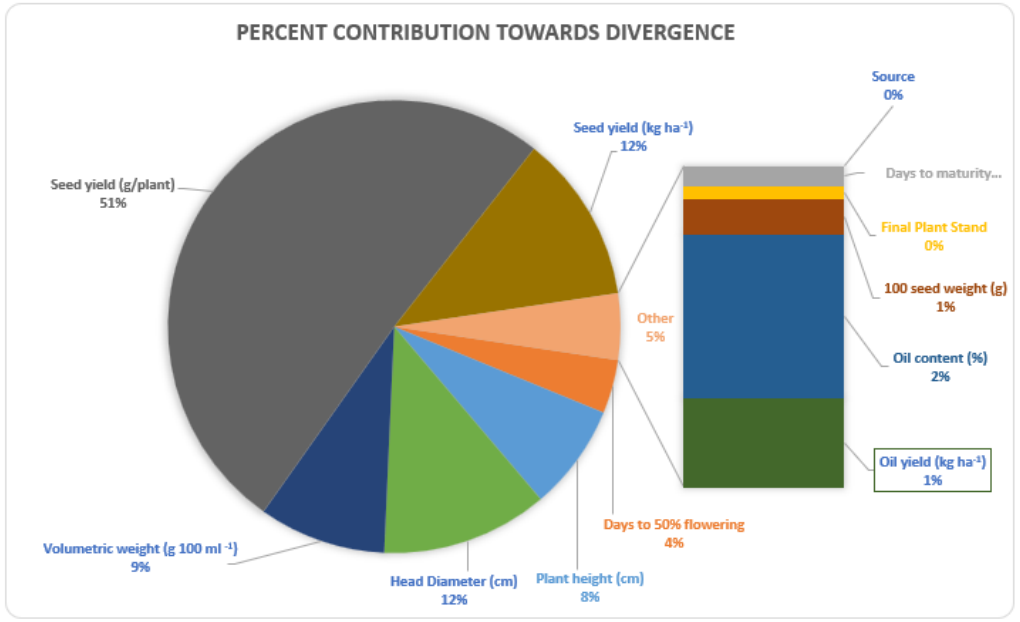

Fig. 3. Relative contribution of 11 traits to total genetic diversity in sunflower genotypes

Table 5. Average intra and inter cluster distances for the sunflower genotypes

	Cluster Distances					
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**
Cluster I	15.17					
Cluster II	30.51	15.13				
Cluster III	26.33	54.73	0.00			
Cluster IV	27.72	70.78	35.39	0.00		
Cluster V	33.84	79.75	9.39	25.19	0.00	
Cluster VI	24.10	41.92	53.60	36.61	57.87	0.00

Table 6. Cluster means with respect to yield and its attributes among sunflower genotypes

S. No.	Character	Cluster means					
		I	II	III	IV	V	VI
1.	Days to 50% flowering	53.78	54.57	52.67	56.33	54.67	56.67
2.	Days to maturity	88.08	87.19	86.33	92.00	87.00	91.33
3.	Final plant stand	18.10	18.66	17.94	18.00	18.54	17.86
4.	Plant height (cm)	94.66	97.18	70.07	103.40	72.53	117.87
5.	Head diameter (cm)	9.76	9.51	6.38	9.27	5.43	13.00
6.	Volumetric weight (g $100ml^{-1}$)	37.03	47.00	33.60	29.67	27.57	34.93
7.	100 seed weight (g)	3.78	4.03	2.97	2.70	3.63	4.50
8.	Seed yield (g /plant)	22.61	23.24	14.77	25.80	18.73	26.87
9.	Seed yield (kg ha^{-1})	1256.03	1290.54	820.43	1433.37	1040.67	1493.57
10.	Oil content (%)	35.52	36.46	37.80	37.53	37.37	30.73
11.	Oil yield (kg ha^{-1})	446.54	469.78	310.00	539.33	388.27	459.80

Table 7. Contribution of yield and its attributes towards total diversity in sunflower genotypes

S. No.	Source	Contribution %	Times ranked 1st
1	Days to 50% flowering	3.84	38
2	Days to maturity	0.30	3
3	Final Plant Stand	0.20	2
4	Plant height (cm)	7.58	75
5	Head Diameter (cm)	11.92	118
6	Volumetric weight (g $100ml^{-1}$)	9.09	90
7	100 seed weight (g)	0.51	5
8	Seed yield (g/plant)	50.81	503
9	Seed yield (kg ha^{-1})	12.02	119
10	Oil content (%)	2.42	24
11	Oil yield (kg ha^{-1})	1.31	13

4. DISCUSSION

The significance of mean sum of squares across all studied traits indicates presence of variability in these traits and also suggests a focus on these traits for further improvement [12]. Malik et al. [13] in their study identified cluster VII and cluster VIII as most diverse (D^2= 156.01) and suggested for hybridization between these two groups to harness high magnitude of heterosis. Their finding supported this study, where similar conclusions were drawn for cluster V and cluster II based on inter cluster distance (D^2=79.75). Revanth et al. [14] in their study obtained high mean value for head diameter, 100 seed weight, seed yield per plant and oil content in cluster VI. They suggested for selection of genotypes belonging to cluster VI for use of parents in hybridization programmes aimed to increase seed yield. Similar kind of parent selection from cluster VI based on cluster mean is recommended in this study. Neelima et al. [15] in their study identified 100 seed weight contributed maximum towards total divergence. In order to select genetically diverse parents, they suggested classification of material based on traits like 100 seed weight, plant height, days to maturity and seed yield per plant. This study emphasised more on traits seed yield (g/plant), seed yield (kg ha^{-1}) and head diameter for selection of most diverse parents.

5. CONCLUSIONS

The present study exhibited high differences among the genotypes for seed yield and almost all the yield components which may favour selection and its utilization in recombination breeding programme. Cluster analysis revealed that clusters V and II were most diverse therefore, more emphasis should be given on cluster V and II in selecting inbreds for development of high-quality hybrid cultivars. Cluster VI exhibited superior mean values for most traits. Genotype (RHA-1013) from cluster VI can be a promising parent for increasing yield and generating genetic variability. Seed yield (g/plant), seed yield (kg ha^{-1}) and head diameter were considered to be important traits contributing toward genetic divergence. Further research and validation of these findings across diverse environments and genotypes will be crucial for the successful implementation of breeding programs aimed at enhancing sunflower productivity.

6. FUTURE LINE OF WORK

- Genotypes from the most genetically distinct clusters, V (R-106) and II (ARM-243B, PM-81, R-64, NDI-20, RP-10, CMS-243B, and CMS-302B), could serve as promising parental candidates for hybridization programs aimed at exploiting heterosis.
- The genotype RHA-1013, a member of cluster VI, could serve as a valuable parental source for enhancing yield and genetic diversity in breeding programs

ACKNOWLEDGEMENT

The author is thankful to Acharya N. G. Ranga Agricultural University and ICAR- Indian Institute of Oilseed Research, Hyderabad for providing assistance in conducting the research work.

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 manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Li Z, Xiang F, Huang X, Liang M, Ma S, Gafurov K, Gu F, Guo Q, Wang Q. Properties and Characterization of Sunflower Seeds from Different Varieties of Edible and Oil Sunflower Seeds. Foods. 2024;13(8):1188-1195.
2. Kumar PS, Dudhe MY, Sabesan T, Saravanan K. Study on genetic diversity in sunflower (*Helianthus annuus* L.) 33 elite genotypes. Plant Archives. 2024;24 (1):259-264.
3. Holgado F, Ruiz-Mendez MV, Velasco J, Marquez-Ruiz G. Performance of olive-pomace oils in discontinuous and continuous frying. Comparative behavior with sunflower oils and high-oleic sunflower oils. Foods. 2021;10(12): 3081-3097.
4. Yang L, Chen H, Yin C, Song S, Zhang Y, Liu X and Hu Z. Research on

mechanical-structure properties during sunflower seed extrusion-oil extraction. Journal of Food Processing and Preservation. 2022;46(1):16158-16170.
5. Subasi BG, Vahapoglu B, Capanoglu E, Mohammadifar MA. A review on protein extracts from sunflower cake: Techno-functional properties and promising modification methods. Critical Reviews in Food Science and Nutrition. 2022; 62(24): 6682-6697.
6. Reddy BVRP, Amarnath K, Reddy BC, Venkataramanamma K, Prabhakard K, Venkateswarlu NC. Discerning genetic diversity among sunflower germplasm accessions through multivariate analysis. Electronic Journal of Plant Breeding. 2024;15(1):194-200.
7. Tomkowiak A, Bocianowski J, Kwiatek M and Kowalczewski PŁ. Dependence of the heterosis effect on genetic distance, determined using various molecular markers. Open Life Sciences. 2020;15 (1):1-11.
8. Mahalanobis PC. A statistical study at Chinese head measurement. Journal of Asiatic Society of Bengal. 1928;25:301-307.
9. Rao CRV. Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York. 1952;236- 272.
10. Lakshman SS, Chakraborty NR, Debnath S, Kant A. Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. African Journal of Biological Sciences. 2021;3 (1):129-145.
11. Rani R, Sheoran RK, Sharma B. Studies on variability, heritability and genetic advance for quantitative traits in sunflower (*Helianthus annuus* L.) genotypes. Research in Environment and Life Sciences. 2016;10(6): 491-493.
12. Mariyam N, Kulkarni VV, Sujatha M, Tembhurne BV. Assessment of Genetic Variability and Character Associations in Sunflower (*Helianthus annuus* L.) Yield Related Traits. Asian Journal of Soil Science and Plant Nutrition. 2024;10(1): 320-327.
13. Mallik M, Manivannan N and Chandirakala R. Genetic diversity in sunflower (*Helianthus annuus* L.) Journal of Oilseeds Research. 2016;33 (4): 243-249.
14. Reavanth T, Manivannan N, Sasikala R and Rajendran L. Assessment of genetic diversity among the maintainer and restorer inbreds of sunflower (*Helianthus annuus* L.). Electronic Journal of Plant Breeding. 2021;12(3): 800-803.
15. Neelima S, Kumar KA, Venkataramanamma K and Padmalatha Y. Genetic variability and genetic diversity in sunflower. Electronic Journal of Plant Breeding. 2016;7(3):703-707.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/122890