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Exploring Genetic Variability for Yield and its Component Traits in Sunflower (*Helianthus annuus* L.)

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Abstract

The present study was carried out with 40 sunflower germplasm accessions to explore the extent of magnitude of genetic variance, heritability (broad sense) and genetic advance as *per cent* of mean for yield attributing characters. The analysis of variance revealed the existence of significant differences among the entries for all the traits studied. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied which implies that the characters were highly influenced by the environmental effects. High PCV, GCV and genetic advance as per cent of mean was recorded for seed yield per plant. High heritability coupled with high genetic advance as per cent of mean was noted for seed yield per plant, 100 seed weight and plant height indicating that these characters were under the control of additive gene effects. Selection based on these characters would be effective in designing future sunflower breeding strategy.

Key words **:** Sunflower, genetic advance, heritability, variability.

Introduction

Sunflower (*Helianthus annuus* L.) plays a pivotal role in global agriculture as a versatile oilseed crop belonging to Asteraceae family. In world, the countries like Russia, Ukraine, Argentina, China, France, USA, Spain and India contributed about 14% to 16 % of vegetable oils, 7% of the oilcake and meal produced from oil seeds. In India, Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Maharashtra and Punjab are the lead producing states of sunflower. The sunflower crop is occupied in an area of 2.41 lakh ha with a production of 2.79 lakh tonnes and productivity of 963 Kg/ha in India (1).

Presently, the area of sunflower crop is reduced due to the fact that unavailability of the good quality seed, bird damage, menace of diseases such as Alternaria, powdery mildew, sunflower necrosis and sunflower leaf curl virus disease and lack of attractive MSP at local market, shift in cropping pattern (2). In this context, sunflower breeders require genetic variability to isolate superior genotypes with high yielding potential.

The success of any plant breeding program depends on the genetic variability and selection skill of plant breeder (3, 4). Presence of high variability for yield and yield attributing traits offers much scope for crop improvement (5) and is essential for developing high-performing cultivars. Coefficients of variation indicated the extent of variability relative to the mean, and heritability estimates provided insights into the genetic basis of the observed variation (6). Heritability estimates along with genetic advance are also helpful in predicting the grain yield under selection. Knowledge on heritability and genetic advance of the character indicate the scope for the important of a trait through selection. Grain yield being a complex character is very difficult to improve by selecting the genotypes for yield *per se*, therefore identifying the characters which are closely related and have contributed to yield becomes highly essential.

The study was framed with an objective to trace out genetic variability in sunflower by identifying promising accessions with desirable traits for further selection and hybridization efforts.

Materials and Methods

The present investigation was carried out during *rabi*, 2022-23 with 40 sunflower germplasm accessions (Table-1) to examine the nature and magnitude of heritable variation for six yield attributing characters. The field experiment was conducted at an altitude of 211.3 m above mean sea level, latitude of 18.29 ° N and longitude of 78.29 °E at ANGRAU, Regional Agricultural Research Station, Nandyal, Andhra Pradesh. The experimental material sown with a spacing of 60 x 30 cm in a row of 3 m length in randomized block design (RBD) replicated thrice. Standard crop protection and production practices were followed to raise a healthy crop. Observations were recorded in five randomly selected plants per accession in each replication for the six quantitative traits *viz.,* days to 50% flowering, plant height, head diameter, 100 seed weight, seed yield per plant and oil content except for days to 50% flowering which recorded on plot basis.

The mean for each trait under each replication was subjected to statistical analysis. The data for various

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Table-1 : List of sunflower germplasm accessions utilized for the study.

S.No.	Entry	S.No.	Entry	S.No.	Entry	S.No.	Entry
1.	NDLB-2	11.	NDSI 3	21.	ARM243B	31.	CMS-249B
2.	NDLB-3	12.	CMS-21B	22.	HA243B	32.	IB-5
3.	NDLB-4	13.	CMS-65B	23.	ARM248B	33.	CMS-17B
4.	NDLB-5	14.	CMS-104 B	24.	CMS-265B	34.	CMS-67B
5.	NDLB-6	15.	CMS-105B	25.	CMS 302B	35.	CMS-72B
6.	NDLB-7	16.	CMS-107B	26.	CMS-597B	36.	CMS-110 B
7.	NDLB-8	17.	CMS-108B	27.	CMS-952B	37.	HA 250B
8.	NDSI-2	18.	HA-112 B	28.	CMS-1B	38.	CMS-335B
9.	CMS-2B	19.	CMS-148B	29.	CMS-248B	39.	CMS-30B
10.	CMS-11B	20.	CMS-243B	30.	NDSI-3	40.	ARM249 B

Table-2 : ANOVA for six yield and its attributing traits in 40 sunflower germplasm accessions.

S. No.	Characters	Mean Squares		
		Replications (df:2)	Genotypes (df:39)	Error (df:39)
1.	Days to 50% flowering	1.51	27.16**	4.28
2.	Plant height (cm)	9.8	813.48**	220.23
3.	Head Diameter (cm)	6.05	10.63**	5.35
4.	100 seed weight (g)	0.59	1.82**	0.25
5.	Seed yield per plant (g)	1.52	12.88**	0.50
6.	Oil content (%)	0.45	8.44**	3.60

Table-3 : Mean, Variability, Heritability, Genetic advance as per cent of mean for six yield and its attributing traits in 40 sunflower germplasm accessions.

Characters	General Mean	Range	PCV %	GCV%	Heritability (%)	Genetic advance	Genetic Advance as % of mean
DFF	57.66	47-63.5	6.31	5.86	84.20	4.39	11.09
PH	97.87	67.5-157.5	20.60	17.59	92.90	3.2	30.95
HD	11.53	7.9-17.5	20.00	14.09	49.60	2.35	20.44
HSW	6.99	4.55-8.45	13.66	12.66	85.90	1.69	24.18
SY/P	19.82	16.5-26.6	21.79	21.54	96.10	5.02	25.33
OC	35.52	29.22-38.38	5.78	4.37	57.31	2.42	6.82

Note: DFF-Days to 50% flowering, PH-Plant height (cm), HD-Head Diameter (cm), 100 SW-100 seed weight (g), SY/P- Seed yield per plant (g), OC%-Oil content (%)

characters were statistically analyzed for significance by using analysis of variance technique (7). The components of variances were used to estimate the genotypic and phenotypic coefficient of variance (8). Values of PCV and GCV for all the traits were divided into three categories, *viz.*, >20 % (high), 10-20 % (moderate) and <10 % (low). Heritability in broad sense was estimated as per the method described by (9) and traits were classified as high (<60%), moderate (30-60%) and low (0-30%) heritability as per the method of (10) and expressed as percentage of mean. Traits were classified as high (>20%), moderate (10-20%) or low (0-10%) genetic advance as per the method suggested by (11). The data analysis was carried out with WINDOWSTAT 9.2 version software.

Results and Discussion

The phenotypic variation manifested by the genotype has two components namely genotypic and environmental. The ANOVA (Table-2) for six yield and its attributes revealed highly significant differences among the sunflower germplasm accessions for all the characters under study, indicating adequate genetic variability in the genetic resources and the differences can be attributed to variations present in the genotypes as well as the environmental factors. The estimates of PCV were higher than GCV for all the characters under study (Table-3 and Fig.-1) indicating that the characters were less influenced by the environment. Higher amount of genetic variability was displayed by the traits *viz.*, seed yield per plant (21.79 PCV% and 21.54 GCV%), Plant height (20.60 PCV% and 17.59 GCV%) and head diameter (20.00 PCV% and 14.09 GCV%) implying that these traits attributed markedly to the total genetic variability. These results are in consonance with the findings of (12, 13, 14, 15, 16, 17, 18).

High heritability (>60%) coupled with high genetic advance as per cent of mean (GAM) (>20%) reveals that most likely the heritability is due to additive gene effects

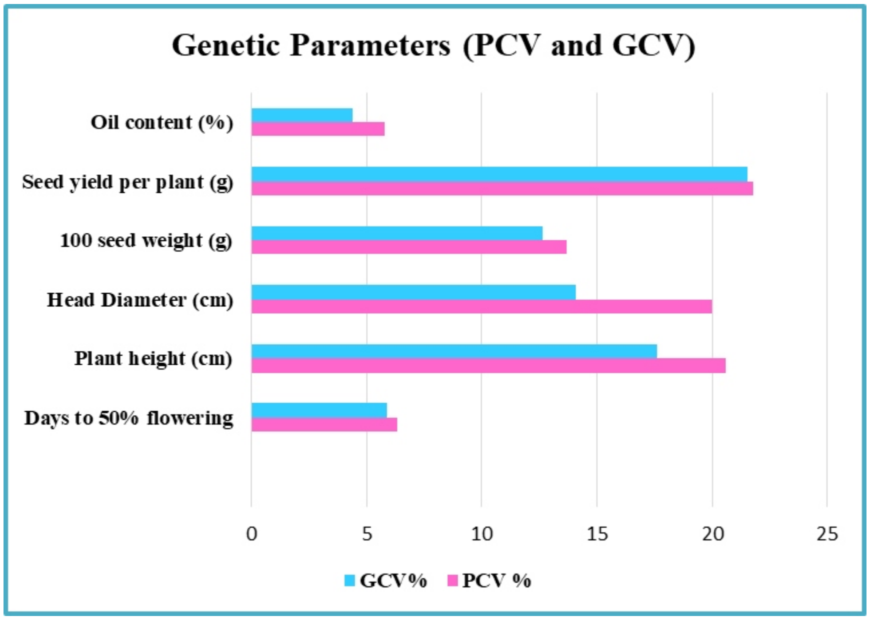

Fig.-1 : The Genotypic and Phenotypic coefficient of variation for the studied traits.

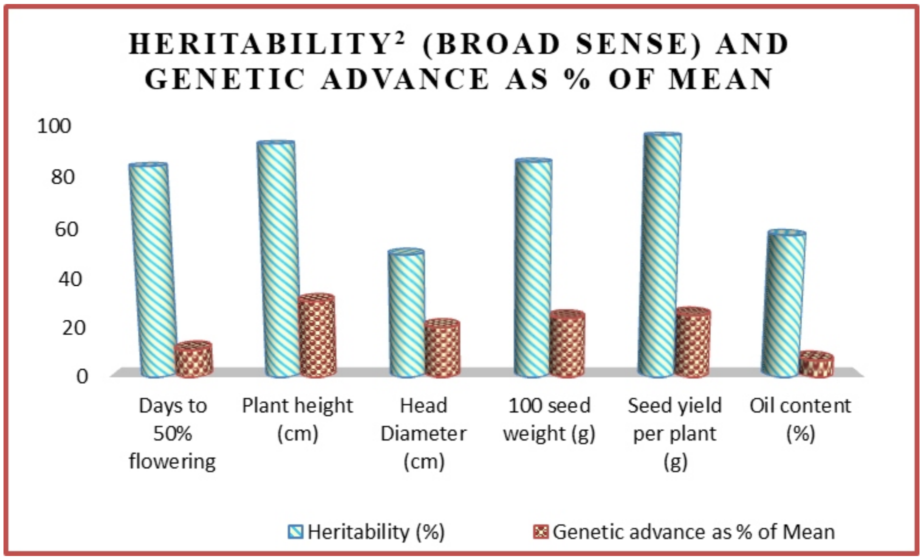

Fig.-2 : Pattern of Heritability and Genetic advance as per cent of mean for the analyzed traits.

and simple selection may be rewarding for improving a particular trait. In the present study high heritability coupled with high GAM was noticed for the traits, seed yield per plant (96.10% heritability and 25.33 GAM) and plant height (92.90% heritability and 30.95 GAM) indicated that predominance of additive gene action in the governance of these characters and hence selection of genotypes based on these characters would be more rewarding for target plant selection in early generation. (19, 20, 21, 22) also documented same kind of results for plant height and seed yield per plant in sunflower.

Conclusion

The experimental material chosen for present investigation differed in genotypic make up as evidenced for considerable variability that provides sufficient basis for selection by the breeder. The PCV for all the characters are higher than the GCV indicating that masking effects of environment on the variability. The traits *viz*., seed yield per plant and plant height exhibited high PCV and GCV, High heritability and GAM and were found as good gain traits which would help in transferring these traits through hybridization followed by recurrent selection.

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References

1. Directorate of Economics and Statistics, Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and Framers Welfare, Government of India. (2022-23). *Agricultural statistics at a glance*.
2. Dudhe M.Y., Sujatha M., Meena H.P., Ranganatha A.R.G., Varaprasad K.S. and Vishnuvardhan Reddy A. (2019). Genetic variability, diversity and identification of trait-specific accessions from the conserved sunflower germplasm for exploitation in the breeding program. *Agric Res*., 3: 9-22.
3. Adhikari B.N., Shrestha J., Dhakal B., Joshi B.P. and Bhatta N.R. (2018). Agronomic performance and genotypic diversity for morphological traits among early maize genotypes. *Int. J. Appl. Biol*., 2(2): 33-43.
4. Patel A.A., Patel J.M., Patel R.M., Gajjar K.D., Chaudhary D.R. and Soni N.V. (2023). Combining ability and gene action analysis for yield and yield attributing traits in kharif maize (*Zea mays* L.). *Frontiers in Crop Improvement*, 11(1): 31-36.
5. Chaudhary D., Anand Singh Jeena, Usha Pant, Rohit and Sonali Gaur (2023). The performance of advanced clones of sugarcane (*Saccharum sp.* complex) for yield and its attributes in multi-environmental conditions. *Frontiers in Crop Improvement*, 11(1): 37-40.
6. Lohani P., Usha Pant, Anu Singh, Jeena, A.S., Singh N.K. and Singh S.P. (2023). Estimation of genetic variability parameters for seed yield and its component traits among accessions of *Brassica rapa* var. yellow sarson. *Frontiers in Crop Improvement*, 11(1): 55-59.
7. Panse V.G. and Sukathme P.V. (1967). Statistical method for agricultural workers. ICAR, New Delhi. pp. 381.
8. Burton, G.W. and Devane, E. H. (1993). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron J*. 45: 478-481.
9. Lush J.L. (1940). Heritability of quantitative characters in farm animals. *Proceedings of 8th Congress of Genetics.Heriditas,*35: 356-375.
10. Robinson H.F., Comstock R.E. and Harvey P.H. (1949). Estimates of heritability and degree of dominance in corn (*Zea mays*). *Agron. J.,* 41: 353-359.
11. Johnson H.W., Robinson H.F. and Comstock R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.,* 47: 314-318.
12. 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. *Electron. J. Plant Breed.,* 11(01): 301-305.
13. Farooq M.U., Uma M.S., Nehru S.D. and Manjula C.P. (2021). Genetic analysis of yield, its attributing traits and oil content in multi-headed sunflower (*Helianthus annuus* L.) restorer lines. *Mysore J. Agric. Sci.,* 55(4): 371-377.
14. Hilli H.J. and Immadi S. (2021). Variability and correlation studies in sunflower lines (*Helianthus annuus*). *J. Pharmacogn. Phytochem*., 10(3): 221-223.
15. Vamsi M.D., Meena H.P., Sandhya S.G. and Payasi S.K. (2022). Assessment of genetic variability, heritability and genetic advance in sunflower (*Helianthus annuus* L.) genotypes for seed yield and other agronomic traits. *Environ. Ecol*., 40(2A): 451-457.
16. Anuradha B., Manivannan N., Sasikala R., Harish S. and Senthivelu M. (2023). Genetic variability and association studies in BC_3F_1 population of sunflower (*Helianthus annuus* L.). *Electronic Journal of Plant Breeding,* 14(3): 923-927.
17. Varshitha V., Prabhavathi K., Meena H.P. and Yadav P. (2023). Study of Genetic Variability for Yield and Quality Parameters in Newly Developed Sunflower (*Helianthus annuus* L.) Interspecific Derivatives Over Two Seasons. *Int. J. Environ. Clim. Chang*., 13(10): 3226-3234.
18. Mariyam N., Kulkarni V.V., Sujatha M. and Tembhurne B.V. (2024). Assessment of Genetic Variability and Character Associations in Sunflower (*Helianthus annuus* L.) Yield Related Traits. *Asian J. Soil Sci. Plant Nutr*., 10(1): 320-327.
19. Sandhya Sree G., Roja P., Meena H.P., Reddy V.A. and Ramesh D. (2021). Genetic variability, heritability and genetic advance studies for economically important traits in sunflower (*Helianthus annuus* L.). *J. Oilseeds Res*., 38(1): 92-95.
20. Aboelkassem K.M., Ahmed A.A.E.H. and Abdelsatar M.A. (2021). Evaluation of some sunflower genotypes for agronomic traits and oil quality. *Helia.* 44(74): 43-57.
21. Lagiso T.M., Singh B.C.S. and Weyessa B. (2021). Evaluation of sunflower (*Helianthus annuus* L.) genotypes for quantitative traits and character association of seed yield and yield components at Oromia region, Ethiopia. *Euphytica,* 217(2): 27.
22. Umarani E., Saritha A. and Ramanjaneyulu A.V. (2022). Estimation of Genetic Parameters in Sunflower (*Helianthus annuus* L.) Germplasm Lines for Yield and Its Contributing Traits. *Int. J. Environ. Clim. Chang*., 12(12): 936-942.