



Study of Genetic Variability for Yield and Quality Parameters in Newly Developed Sunflower (*Helianthus annuus L.*) Interspecific Derivatives Over Two Seasons

Varshitha, V. ^{a*}, Prabhavathi, K. ^b, Meena, H. P. ^c and Praduman Yadav ^c

^a Department of Genetics and Plant Breeding, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad-500 030, India.

^b Seed Research and Technology Centre (SRTC), PJTSAU, Rajendranagar, Hyderabad-500 030, India.

^c ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500 030, India.

Authors' contributions

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

Article Information

DOI: 10.9734/IJECC/2023/v13i102990

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/106429>

Original Research Article

Received: 05/07/2023

Accepted: 09/09/2023

Published: 14/09/2023

ABSTRACT

The present investigation was conducted to study genetic parameters for sixteen characters viz., days to 50% flowering, days to maturity, plant height, head diameter, leaf length, leaf width, number of leaves per plant, 100 seed weight, volume weight, seed yield/plant, seed length, seed width, stem girth, leaf area index, chlorophyll content and oil content at ICAR-Indian Institute of Oilseeds Research during *kharif*-2022 and *rabi*-2022-23, respectively. The study included a total of 50 advanced (BC₂F₆) interspecific derivatives derived using five diploid annual compatible *Helianthus*

*Corresponding author: E-mail: varshithavaddempudi@gmail.com;

species along with three checks (ARM-243B, DRSF-108 and DRSF-113). Analysis of variance revealed significant differences for all the traits. High variation was observed for plant height and seed yield/plant and lowest was observed for 100 seed weight, oil content and head diameter. The difference between GCV and PCV was low for all the characters indicating less influence of environmental factors on the expression of these traits. High heritability coupled with high genetic advance in percent of mean was observed for plant height, leaf width, number of leaves/plant, volume weight, 100 seed weight, stem girth, leaf area index and chlorophyll content indicating additive gene action in the expression of these traits. Simple phenotypic selection may be effective for improving these characters. High heritability coupled with low genetic advance was observed for days to maturity and oil content suggesting involvement of non-additive gene action in the expression of these traits indicating little scope for further improvement through individual plant selection. The results showed that the experimental material used had a substantial quantity of genetic variability to be used in crop development programs in the future.

Keywords: Genetic advance; GCV; *Helianthus annuus*; heritability; PCV.

1. INTRODUCTION

“Sunflower (*Helianthus annuus* L.; $2n = 34$) is the fourth most important oilseed crop in the world following soybean, peanut and rapeseed” [1,2]. “It belongs to the genus *Helianthus*, family Asteraceae, tribe Heliantheae, sub tribe Helianthae, which includes 20 genera with 400 sub-species and originated in the USA” [3]. “It has recorded a production of 2.28 lakh tonnes from 2.25 lakh ha with the productivity of 1011 kg/ha according to the Directorate of Economics & Statistics” [4]. “It is a rich source of edible oil (40–45%) and because of the high concentration of polyunsaturated fatty acids with 55 to 60% of linoleic acid and 25 to 30% of oleic acid, which reduces the risk of coronary diseases by reducing blood cholesterol levels” [5]. “The requirement of high yield and quality edible oil is rising day by day and therefore, there is a need to increase the area, production and productivity of the crop which is possible through crop improvement strategies” [6]. “Developing genotypes with higher yield and oil content has become the ultimate objective of current sunflower breeding programmes. The seed yield of sunflower is a complex trait, which is highly influenced by environmental variations due to a narrow genetic base, while the production of superior hybrids which yield more for seed yield and oil content would become a great lacuna in the present scenario. These traits can be improved by finding a suitable source for higher yield among the vast germplasm of sunflower and making efforts to incorporate the variability into the cultivated sunflower. The success of a crop improvement programme depends on the extent and nature of available genetic variability, heritable variation and genetic advance present within the breeding population” [7]. “Greater the

variability, more is the possibility of getting the desired plant genotypes. However, plant breeding efforts to develop varieties/hybrids with the desired economic characteristics are constrained by the narrow genetic base of the cultivated sunflower. Utilizing these crop wild relatives, numerous breeding efforts are made to create and characterize prebred lines, which are developed by crossing cultivated sunflower with various wild relatives followed by backcrossing for several generations, that can serve as a source of desirable compositions of different agro-morphological characters that have a positive influence on the seed and oil yield. For effective germplasm utilization, prior knowledge of genetic variation and genetic interactions among newly developed interspecific derivatives is essential. Sometimes phenotypic selection based on their performance may not be sufficient because these genotypes may perform poorly in further segregating generations, so it is essential to select the genotypes based on genetic worth of the genotypes i.e., based on heritability and genetic advance” [8]. Information on variability and heritability is useful to formulate selection criteria for improvement of seed yield and its component traits. So, taking all these aspects into consideration, the present study was conducted to evaluate the extent of genetic variability, heritability and genetic advance over mean for seed yield and its component traits in advanced sunflower interspecific derivatives for sixteen traits.

2. MATERIALS AND METHODS

2.1 Materials Used for the Study

The present investigation was carried out during *kharif-2022* and *rabi-2021-22* at ICAR-Indian Institute of Oilseeds Research, Rajendranagar,

Table 1. List of the genotypes selected for the present investigation

S. No.	Derived from	Generation	Interspecific derivatives
1	<i>H. annuus</i> (wild)	BC ₂ F ₆	PB-950, PB-954, PB-1007, PB-1010, PB-1015, PB-1027, PB-1054, PB-1203, PB-1209, PB-1213
2	<i>H. debilis</i>	BC ₂ F ₆	PB-884, PB-893, PB-895, PB-896, PB-910, PB-1136, PB-1139, PB-1148, PB-1162, PB-1170
3	<i>H. praecox</i>	BC ₂ F ₆	PB-1090, PB-1093, PB-1104, PB-1113, PB-1116, PB-1117, PB-1120, PB-1122, PB-1126, PB-1215
4	<i>H. argophyllus</i>	BC ₂ F ₆	PB-1338, PB-1340, PB-1359, PB-1369, PB-1371, PB-1372, PB-1392, PB-1398, PB-1400, PB-1401
5	<i>H. petiolaris</i>	BC ₂ F ₆	PB-1575, PB-1576, PB-1577, PB-1579, PB-1580, PB-1581, PB-1582, PB-1583, PB-1588, PB-1589
6	Cultivated sunflower	-	ARM-243B, DRSF-108, DRSF-113

Hyderabad located at a latitude of 17°22'31"N and longitude 78°28'27"E. Study material consisted of 50 advanced (BC₂F₆) interspecific derivatives derived using *Helianthus annuus* (wild), *H. debilis*, *H. praecox*, *H. petiolaris* and *H. argophyllus* as male parent and cultivated sunflower inbred ARM-243B as recurrent parent. The details of material are presented in Table 1.

2.2 Experimental Design

Each genotype along with three checks viz., ARM-243B, DRSF-108 and DRSF-113 was sown in two rows each of 3.0 m length following a spacing of 60 cm between the rows and 30 cm between the plants in an augmented block design (ABD) in five blocks. All the recommended crop production and protection practices were followed to raise the healthy crop successfully. At physiological maturity five plants from each accession were selected randomly for recording data on days to 50% flowering, days to maturity, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), leaf area index, chlorophyll content, head diameter (cm), stem girth (mm), 100 seed weight (g), volume weight (g/100 ml), seed yield/plant (g), seed length (cm), seed width (cm) and oil content (%). The traits days to 50% flowering and days to maturity were recorded on a plot basis. SPAD chlorophyll meter reading was recorded at the time of anthesis with SPAD 502 plus meter for upper, middle and lower leaves and an average of them was noted. Leaf area index was calculated by taking fully opened five leaves from each plant at anthesis and the area was measured by leaf area meter (LI-3000, Lincoln Nebraska, USA) and was calculated as per the method suggested by Watson [9]. Mean performance of the genotypes was calculated and the genotypic coefficient (GCV) and

phenotypic coefficient of variation (PCV) were estimated by using the formula given by Burton [10]. The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon [11]. Heritability in a broad sense (h²b) was estimated according to the formula suggested by Johnson *et al.*, [8] and Hanson *et al.*, [12]. Estimation of genetic advance was done following the formula given by Johnson *et al.*, [8] and Allard [13].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

A key requirement for crop development programs is selection, which depends on how much genetic variability is present in the breeding stock. Significant variations between the genotypes were shown by the analysis of variance, and these differences were further corroborated using genetic and statistical analysis of the data. The analysis of variance (p value at 1 and 5%) of 16 characters included in the present study revealed that the mean sum of squares due to treatments was found to be highly significant (P=0.01) for all the characters except for the trait number of leaves in *kharif* and seed length and seed width in *rabi* indicating sufficient amount of variation present in the material utilised. Whereas, variation was significant (P=0.05) for rest of the characters. The results pertaining to analysis of variance are presented in Table 2. These finding thus indicate that there is a remarkable amount of variability present in the advanced interspecific derivatives of sunflower. Which denotes that there is a large scope for selecting superior breeding material among the accessions under the current study. Similar significance for all the traits under study was reported by Reena *et al.* [14].

3.2 Variability and Heritability

“Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop” [15]. The assessment of heritability and variation through phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV) and genetic advance as percent of mean (GAM) is important to understand the heritable and non-heritable components of the total variability, which in turn aids to identify the suitable breeding method for improving a particular trait of interest. Wide range of variation was observed for plant height (75.0-162.0 cm and 99.7-161.7 cm, respectively) followed by stem girth (10.4-32.8 cm and 11.5-22.3 cm, respectively) and lowest for seed length (0.67-1.2 cm and 0.75-1.25 cm, respectively) followed by seed width (0.22-0.62 cm). Sandhya Sree *et al.* [6], Suttur *et al.* [16] and Reena *et al.* [15] reported the highest variation for plant height, Supriya *et al.* [17] and Latha *et al.* [18] for seed yield. It can be observed from the results that all the characters showed closer values of PCV and GCV (Table 3). PCV is higher than GCV for all the traits in both the seasons, which reveals the role of the environmental factors on all the characters, but the magnitude can be stated to be low, as the difference between PCV and GCV is very low, except for plant height in *rabi*, which showed equal estimates of PCV and GCV which indicates that there is least influence of environment on the expression of this trait. This was found to be similar to the findings of the study undertaken by Sandhya Sree *et al.* [6], except for plant height in *rabi*. Sivasubramanian and Madhavamenon [11] classified “PCV and GCV values as low (0-10%), moderate (10-20%) and high (>20%) values”. According to this classification, high PCV and GCV values were observed for volume weight, 100 seed weight and leaf area index in both the seasons. High PCV and GCV value for 100 seed weight was also reported by Seneviratne *et al.* [19]. The traits plant height, leaf width, number of leaves, head diameter and chlorophyll content exhibited moderate PCV and GCV values in both the seasons whereas characters like days to 50% flowering, days to maturity and oil content exhibited low PCV and GCV values in both the seasons. The expression of low coefficients of variation for these traits indicates that there was a low amount variation in the material evaluated, which requires search for variation in other material [18] or also due to presence of both

positive and negative alleles for those in the population [20]. Seed yield showed medium PCV and GCV in *kharif* (15.26% and 15.20%), where it was observed to be high PCV and GCV in *rabi* (25.21% and 25.16%). Stem girth showed high PCV and GCV in *kharif* (22.91% and 22.89%) but medium PCV and GCV in *rabi* (10.52% and 10.24%). Moderate PCV for head diameter by Reena *et al.* [15] and moderate GCV for plant height, head diameter and 100 seed weight by Kumar *et al.* [21] and Neelima *et al.* [20]. Further, low PCV for the characters volume weight, days to 50% flowering, days to maturity and oil content was also reported by Kalukhe *et al.* [22] and Makane *et al.* [23].

Robinson *et al.* [24] classified “heritability values as high (>60%), moderate (30-60%) and values less than 30% low”. Falconer and Mackay [25] classified “genetic advance as a percent of mean as low (0-10%), moderate (10-20%) and high (>20%)”. “The estimates of heritability ranged from 25.0% for days to maturity to 94.0% for leaf area index during *kharif*-2022 and 32.0% for days to maturity to 92.0% for leaf area index during *rabi*-2022-23 whereas, genetic advance as percentage of mean ranged from 8.1% for days to maturity to 57.0% for leaf area index during *kharif*-2022 and 5.9% for days to maturity to 57.6% for leaf area index during *rabi*-2022-23. Estimates of heritability and genetic advance as percent of mean (GAM) are essential selection parameters. The estimate of genetic advance is more useful as a selection tool when coupled with heritability estimates” [8]. Heritability coupled with genetic advance will help to predict the genetic gain under selection there by also gives information on the suitable breeding method for improving a trait. High heritability coupled with high genetic advance as a percent of mean was noticed for plant height, leaf width, number of leaves, volume weight, seed width, stem girth, leaf area index and chlorophyll content in both the seasons indicating that these characters are governed by additive gene action. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Sonu Kumar *et al.*, [26] recorded “high heritability coupled with high genetic advance for days to 50% flowering, days to maturity, plant height etc”. “High heritability and genetic advance noted for leaf area index, plant height, specific leaf area, the number of leaves per plant, oil yield, seed set per cent, seed yield, 100 seed weight, the number of seeds per head, head

Table 2. Analysis of variance for different characters in sunflower interspecific derivatives over two seasons

S. No.	Characters	Mean squares					
		Blocks (df: 4)		Genotypes (df: 52)		Error (df: 8)	
		<i>Kharif-2022</i>	<i>Rabi-2022-23</i>	<i>Kharif-2022</i>	<i>Rabi-2022-23</i>	<i>Kharif-2022</i>	<i>Rabi-2022-23</i>
1	Days to 50% flowering	90.25**	68.13**	17.93**	12.14**	2.28	0.40
2	Days to maturity	58.21**	66.23**	21.57**	19.88*	0.53	3.97
3	Plant height	746.96**	257.35**	353.95**	215.77**	3.11	0.12
4	Leaf length	14.5**	20.72**	3.47**	4.77**	0.68	0.48
5	Leaf width	22.51**	18.24**	4.34**	4.83**	0.17	0.15
6	Number of leaves	206.44**	115.56**	28.27*	21.17**	6.18	0.73
7	Head diameter	1.27**	0.54**	5.64**	3.07**	0.08	0.06
8	Volume weight	90.16**	715.81**	87.55**	44.14**	0.57	0.05
9	Hundred seed weight	1.12**	1.08**	0.74**	1.28**	0.04	0.03
10	Seed length	0.01*	0.01	0.02**	0.01*	0.00	0.0
11	Seed width	0.01**	0.01*	0.01**	0.01*	0.00	0.00
12	Seed yield	2.74**	29.41**	7.54**	44.75**	0.07	0.18
13	Stem girth	46.47**	1.36**	184.2**	3.57**	0.03	0.16
14	Leaf area index	5.25**	3.34**	0.87**	0.97**	0.06	0.07
15	Chlorophyll content	37.73**	11.85**	11.20**	17.19**	1.43	0.13
16	Oil content (%)	4.88**	18.87**	2.95**	2.00**	0.04	0.03

* $P \leq 0.05$; ** $P \leq 0.01$

Table 3. Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for different characters in advanced interspecific derivatives of sunflower over two seasons

Character	Mean		Range		Coefficient of variation				Heritability (%)		Genetic advance as percent of mean	
	Kharif	Rabi	Kharif	Rabi	PCV (%)		GCV (%)		Kharif	Rabi	Kharif	Rabi
					Kharif	Rabi	Kharif	Rabi				
DFF	63.35	63.33	51.13-71.80	56.13-71.8	7.02	6.29	6.60	6.21	86.0	92.0	11.4	11.4
DM	96.63	98.70	84.40-107.07	90.00-106.33	4.52	4.23	4.46	3.72	76.0	74.0	8.1	5.9
PH	128.63	132.12	75.02-162.08	99.78-161.71	15.89	11.60	15.83	11.60	69.0	76.0	29.3	21.5
LL	19.81	19.85	14.77-26.02	13.45-24.88	10.57	12.72	9.72	12.23	51.0	59.0	16.4	21.8
LW	17.18	17.41	11.64-22.14	10.36-22.14	13.95	14.12	13.74	13.95	66.0	82.0	25.2	25.7
NL	34.46	33.62	26.87-56.53	26.53-53.87	19.51	16.64	18.13	16.44	81.0	72.0	30.8	30.1
HD	13.13	12.72	9.98-16.77	10.35-18.41	17.11	11.84	16.97	11.69	25.0	32.0	43.3	18.5
VW	36.98	40.44	24.31-51.05	19.64-58.55	22.87	24.55	22.78	24.54	83.0	77.0	31.4	21.6
HW	3.77	4.42	2.40-5.59	2.36-7.26	22.52	23.23	21.87	22.87	69.0	57.0	18.1	11.7
SL	0.96	1.01	0.67-1.24	0.75-1.25	11.99	10.54	10.87	8.28	52.0	59.0	31.6	27.9
SW	0.43	0.43	0.22-0.62	0.22-0.62	19.85	21.03	18.44	17.99	69.0	71.0	42.8	45.7
SY	18.47	26.10	14.95-24.71	12.80-49.49	15.26	25.21	15.20	25.16	49.0	51.0	39.7	42.3
SG	17.38	16.65	10.04-32.88	11.55-22.35	22.91	10.52	22.89	10.24	88.0	76.0	28.2	46.3
LAI	3.52	3.40	1.63-6.25	1.68-6.39	32.25	32.76	31.52	31.87	94.0	89.0	57.0	57.6
CC	31.87	36.18	27.45-44.28	29.56-46.76	10.79	11.18	10.14	11.13	67.0	76.0	29.8	20.7
O	34.97	36.70	31.90-38.06	31.21-39.87	4.90	5.17	4.87	5.15	75.0	79.0	8.9	9.5

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, LL: Leaf length, LW: Leaf width, NL: No. of leaves, HD: Head diameter, VW: Volume weight, HW: 100 seed weight, SL: Seed length, SW: Seed width, SY: Seed yield, SG: Stem girth, LAI: Leaf area index, CC: Chlorophyll content, O: Oil content (%)

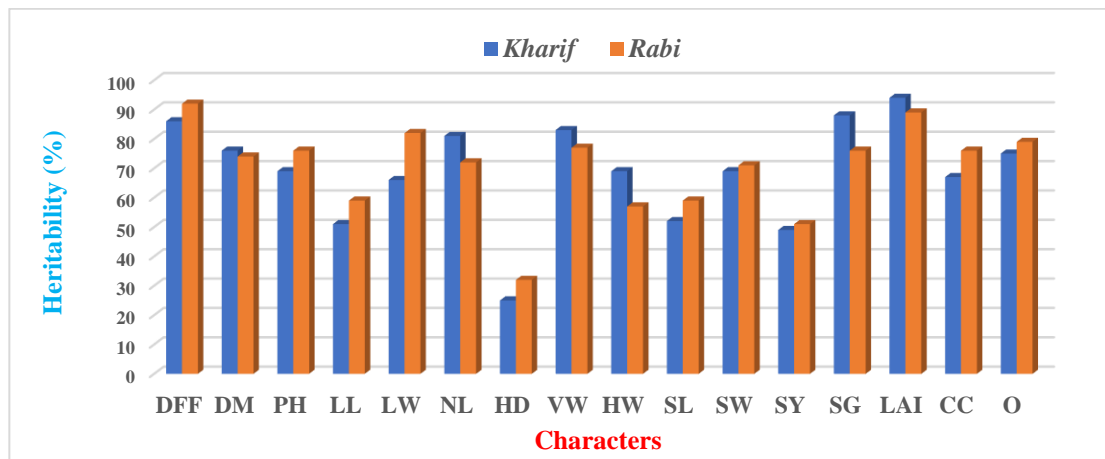


Fig. 1. Heritability (%) of different traits during *kharif-2022* and *rabi-2022-23* seasons

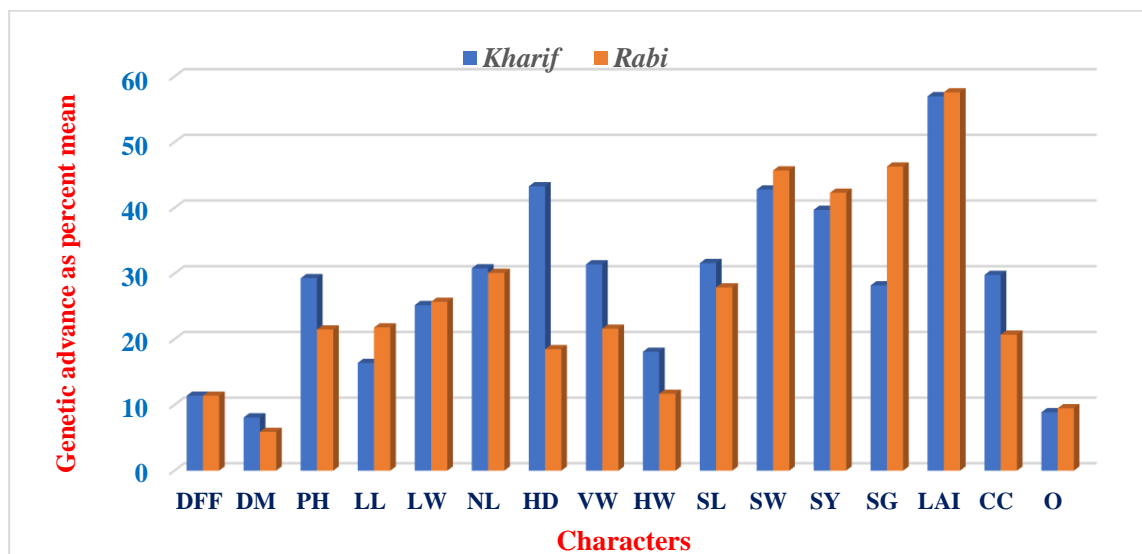


Fig. 2. Genetic advance as percent of mean of different traits during *kharif-2022* and *rabi-2022-23* seasons

diameter and autogamy per cent” by Varalakshmi et al., [16]. “High values of phenotypic and genotypic coefficient of variability, and high heritability with high genetic advance were observed for seed yield/plant, oil yield/plant. plant height, head diameter, oil content and test weight” by Mohan and Seetharam [27]. High heritability coupled with medium genetic advance as a percent of mean was observed for days to 50% flowering in both the seasons indicating involvement of both additive and non-additive gene action in the inheritance of these traits and population improvement by reciprocal recurrent selection can be useful. On the contrary high heritability with low GAM was found for days to maturity and oil content in both *kharif* and *rabi* seasons indicating that the role of a favourable

environment rather than the genotype and the selection is not rewarding. Madhavi Latha et al. [28] for days to 50% flowering, days to maturity and plant height and Supriya et al. [17] for days to 50% flowering. Medium heritability with high GAM was found for the trait seed length and seed yield/plant in both the seasons. For the trait leaf length medium heritability and GAM was observed in *kharif* whereas medium heritability with high GAM was found in *rabi* indicating that leaf length cannot be improved through selection. Head diameter showed low heritability with high GAM in *kharif* but medium heritability and GAM in *rabi*. 100 seed weight showed high heritability with medium GAM in *kharif* but medium heritability and GAM in *rabi*. The estimates of genetic advance help in understanding the type

of gene action involved in the expression of various quantitative characters [29-31].

4. CONCLUSION

The analysis of various genetic parameters in the present investigation reveals higher values of GCV, PCV, heritability and genetic advance as per cent of mean for the traits viz., leaf area index and volume weight. As a result, seed output in segregating generations can be used as a criterion for selecting a single plant and promoting to the next generation. Moderate values of PCV, GCV coupled with high heritability and genetic advance were recorded for plant height, leaf width, number of leaves per plant, 100 seed weight and chlorophyll content. Low values of GCV, PCV coupled with high heritability and low genetic advance for days to maturity and oil content.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Shamshad Md, Dhillon SK, Kaur, G. Heterosis for oil content and oil quality in sunflower (*Helianthus annuus* L.). Current Advances in Agricultural Sciences. 2016;8(1):44-48.
2. Yamgar SV, Dhone PU, Pathare SM, Karande GR. Cytoplasmic diversity studies in sunflower (*Helianthus annuus* L.): A Review. International Journal of Current Microbiology and Applied Sciences. 2018;7(2):36-41.
3. Heiser Jr CB. Taxonomy of *Helianthus* and origin of domesticated sunflower. Sunflower Science and Technology. 1978; 19:31-53.
4. DES; 2021. Available: <https://eands.dacnet.nic.in>
5. Joksimovic J, Jovanka A, Marinkovic R, Jovanovic D. Genetic control of oleic and linoleic acid contents in sunflower. Helia. 2006;29(44):33-40.
6. Sandhya Sree G, Roja V, Meena HP, Vishnuvardhan Reddy A, Ramesh D. Genetic variability, heritability and genetic advance studies for economically important traits in sunflower (*Helianthus annuus* L.). Journal of Oilseeds Research. 2021;38(1):92-95.
7. Vivek Singh, Sharad Pandey, Gideon Synrem. Study of genetic variability, heritability and genetic advance for yield and its contributing traits in Toria [*Brassica campestris* (L.) ssp. Toria)]. The Pharma Innovation Journal. 2023;12(6):2374-2378.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
9. Watson DJ. The physiological basis of variation in yield. Advances in Agronomy. 1952;4:101-145.
10. Burton GW. Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress, Pennsylvania State College, USA: 1952.
11. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agricultural Journal. 1973;60:1093-1096.
12. Hanson GH, Robinson HF, Comstock RE. Biometrical studies of yield segregating population of Korean lespedeza. Agronomy Journal. 1956;48:268-272.
13. Allard RW. Principles of Plant Breeding. John Wiley and Sons; 1960.
14. Reena M, Sheoran OP, Sheoran RK, Chander S. Genetic variability, character association and path analysis for agronomic traits in sunflower (*Helianthus annuus* L.). Annals of Agri-Bio Research. 2017;22(1):31-35.
15. Reena R, Sheoran RK, Sharma B. Studies on variability, heritability and genetic advance for quantitative traits in sunflower (*Helianthus annuus* L.) genotypes. Research Environment and Life Sciences. 2016;10(6):491-493.
16. Varalakshmi K, Neelima S, Narasimha Reddy R, Sreenivasulu KN. Genetic variability studies for yield and its component traits in newly developed sunflower (*Helianthus annuus* L.) hybrids. Electronic Journal of Plant Breeding. 2019;11(1):301-305.
17. Supriya SM, Kulkarni VV, Shankar Goud I, Lokesha R, Govindappa MR. Genetic variability studies for yield and yield components in sunflower (*Helianthus annuus* L.). Electronic Journal of Plant Breeding. 2016;7(3):737-741.
18. Latha KM, Prasad AVSD, Neelima S, Maheswari PU. Genetic variability studies for yield and its attributes in sunflower. Bulletin of Environment, Pharmacology and Life Sciences. 2017;6(2):117-120.

19. Seneviratne KGS, Ganesh M, Ranganatha ARG, Nagaraj G, Devi KR. Population improvement for seed yield and oil content in sunflower. *Helia*. 2004;27(41):123-128.
20. Neelima S, Kumar KA, Venkataramana K, Padmalatha Y. Genetic variability and genetic diversity in sunflower. *Electronic Journal of Plant Breeding*. 2016;7(3):703-707.
21. Kumar P, Dhillon SK, Sao A. Genetic analysis of sunflower genotypes under water stress environments. *International Journal of Farm Sciences*. 2014;4(4):26-35.
22. Kalukhe VK, Moon MK, Magar NM, Patil SS. Genetic variability in sunflower (*Helianthus annuus* L.). *Bioinfolet*. 2011;7:197-200.
23. Makne VG, Shinde CA, Mohrir MN, Shaikh Md, Shoyab Akhil, Md Ab Majid. Genetic variability studies in new versions of sunflower (*Helianthus annuus* L.). *Bioinfolet*. 2011;8(1):44-51.
24. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*. 1949;41:353-359.
25. Falconer DS, Mackay TFC. *Introduction to quantitative genetics*. 4th ed. UK: Longmans Green, Harlow, Essex; 1996.
26. Sonu Kumar, Chauhan MP, Amit Tomar, Ravindra Kumar Kasana. Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza Sativa* L.). *Journal of Pharmacognosy and Phytochemistry*. 2018;7(3):2161-2164.
27. Mohan GS, Seetharam A. Variability studies in sunflower lines derived through interspecific hybridization. *Indian Journal of Plant Genetic Resources*. 2004;17(2):121-124.
28. Madhavi Latha K, Durga Prasad AVS, Neelima S, Uma Maheshwari P. Genetic variability studies for yield and its attributes in sunflower (*Helianthus annuus* L.). *Bulletin of Environment, Pharmacology and Life Sciences*. 2017;6(2):117-120.
29. Hamouda FE, Bashirand SGE, Ginaro MK. Phenotypic and genotypic coefficients of variation and other growth attributes in sesame genotype under rainfed conditions. *Advances in Agriculture Science*. 2016; 2(3):79-84.
30. Rao TV. Variability studies for yield and yield components in sunflower (*Helianthus annuus* L.). *International Journal of Applied Biology and Pharmaceutical Technology*. 2012;3(2): 0976-4550.
31. Suttur DS, Ghodke MK, Pole SP. Genetic variability, heritability and genetic advance in sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research*. 2010;27: 55-56.

© 2023 Varshitha et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/106429>