DoI: https://doi.org/10.58537/jorangrau.2025.53.1.04

J. Res. ANGRAU 53 (1) 38-47, 2025

GENETIC VARIABILITY AND DIVERGENCE STUDIES FOR YIELD AND ITS RELATED TRAITS IN SUNFLOWER

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Date of Receipt : 15-12-2024 Date of Acceptance : 11-02-2025

ABSTRACT

The development and cultivation of hybrids is the key to improving the productivity of sunflower crop. The present study evaluated 52 hybrids during *Rabi* 2023-24 for genetic parameters and genetic variability in relation to yield and its attributing traits. Among the experimental hybrids, the analysis of variance revealed significant differences in yield and its attributes. The traits seed yield (kg ha^{-1}) and oil yield (kg ha^{-1}) recorded the high GCV (26.5 and 27.8) and PCV (28.2 and 29.9) values, respectively. The traits seed yield (kg ha^{-1}), hundred seed weight and oil yield (kg ha^{-1}) recorded the high heritability (>60%) along with high genetic advance expressed as a percentage of mean (>20%). Accordingly, additive genetic effects play a major role in theinheritance of these traits with little influence from the environment.The assessment of genetic diversity grouped the 52 hybrids into six distinct clusters, with the majority (34 hybrids) falling into Cluster I. Among the clusters, the maximum intra-cluster distance was observed in Cluster II (12.14). The greatest inter-cluster distance (75.18) was observed between Cluster VI and Cluster II, suggesting that interbreeding among members in these two clusters could facilitate the production of highly desirable transgressive segregants. Based on a genetic divergence study, the hybrids SH 2876, SH 2883, SH 2896, SH 2904, SH 2895, SH 2878, SH 2886, SH 2899, SH 2884, SH 2922 and KBSH 78 were utilized in the sunflower inbred line development programme.

Keywords: Sunflower, Variability, Diversity, Cluster analysis

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is the fourth leading oilseed crop after soybean, mustard and groundnut in India. In India, sunflower is cultivated over an area of2.69 lakh ha with a production of 2.79 lakh tonnes and a productivity of 1037 kg ha^{-1}(IIOR, 2023). Karnataka, Odisha, Haryana, Maharashtra, Bihar, and West Bengal are the leading sunflower-producing states in India. Andhra Pradesh ranks eighth,covering 0.1 lakh ha area with a production of .085 lakh tonnes and productivity of 695 kg ha^{-1}.The advantageous features of sunflower crop include photo-insensitivity, thermo-insensitivity and short growth cycle that enables the well adaptation to various environments (Chen *et al.,* 2023). In addition to its major contribution in edible oil production, it is also employed as a raw material for the manufacturing of various

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industrial products, including pharmaceuticals, paints and biodiesel.

The performance of early introduced sunflower varieties in India was satisfactory in the beginning. On the other hand, a gradual reduction in yield and oil content due to inherent self-incompatibility problem (Debaeke *et al*., 2021). This led to a shift towards the production of hybrids. Exploitation of heterosis on the commercial scale is made possible owing to high cross-pollinating nature of sunflower (Mohan *et al.,* 2022). A survey of genetic variability determinants *viz.,*genotypic and phenotypic coefficient of variations (GCV and PCV) indicates the degree of variation exists among sunflower genotypes with respect to particular character and also detail about role of the environment in expression of the character. Broad senseheritability (h^2) and genetic advance as percent of mean (GAM) defines selection effectiveness and also nature of gene action in inheritance of particular character. Hence the study of these variability parameters is absolutely necessary to start an efficient breeding programme (Vamsi *et al.,* 2022).

Genetic diversity plays a crucial role in ensuring the success of breeding programs, particularly when aiming to produce hybrids through crosses involving genetically different lines with contrasting and complementary features (Reddy *et al*., 2024b). Breeders typically select genetically diverse parents with contrasting traits to maximize heterosis (hybrid vigour). Biometrical techniques like Mahalanobis D^2statistic offer a quantitative approach to assess genetic divergence among breeding lines. This method considers the interplay between various traits and their combined effect, enabling the classification of crop genotypes at both inter-varietal and sub-species levels. Mahalanobis D^2 statistic provides a valuable index of genetic diversity, allowing the researchers to group the genotypes based on D^2 values (Meena *et al*., 2022). The genetic diversity analysis in the studied hybrids helps in identifying most diverse and distantly related hybrids to be employed in getting desirable segregants for inbred line development programme in sunflower. The key to future improvement lies in exploiting a wider range of inbred lines to create even better hybrids. Hence, this study was conducted to assess the variability and genetic diversity in newly developed sunflower hybrids.

MATERIAL AND METHODS

Fifty-two sunflower hybrids including four checks namely NDSH 1012, KBSH 44, KBSH 78 and Tilhan Tech SUNH1 were evaluated at the Regional Agricultural Research Station, Nandyal during *Rabi* 2023-24. The details of hybrids employed in the investigation are detailed in Table 1. Analpha lattice design was employed to carry out the field experiment in two replications. Each replication consists of four blocks with 13 plots each. The genotypes were sown at a spacing of 60 cm between the rows and 30 cm between the plants within a row. All recommended agronomic practices and measures for plant protection were undertaken to ensure healthy, uniform, and stable crop growth.The data were collected from random sample of five plants of each hybrid in each replication for number of days to 50% flowering, hundred seed weight (g), plant height (cm), head diameter (cm), seed yield (kg ha^{-1}), oil content (%) and oil yield (kg ha^{-1}).

The data were subjected to analysis of variance (ANOVA) based on Alpha lattice design to test the significance as suggested by Patterson and Williams (1976). In this study, the genetic parameters including GCV, PCV, heritability in broad sense (h^2) and genetic advance as percent mean (GAM) were computed. The estimates of GCV and PCV were classified as low, moderate and high as <10%, 10-20% and >20%, respectively according to Sivasubramanian and Menon (1973). The estimates of heritability were classified into low, moderate and high as 0-30%, 30-60% and >60% according to Johnson *et al.,* (1955). The estimates of GAM were classified into low, moderate and high as <10%, 10-20% and >20%, respectively according to Johnson *et al.,* (1955). The analysis of genetic divergence was executed according to Mahalanobis D^2 statistic. The grouping of hybrids into different clusters was done by using Tochers method. The genetic divergence analysis using mean data of all traits over two replications was carried out by employingthe INDOSTAT 9.2 software.

RESULTS AND DISCUSSION

Genetic Parameters

The variance analysis showed significant disparities among the studied hybrids for all the traits,suggesting the adequate variability present in the studied material (Table 2). Further, no significant variation was observed among the blocks for any of the traits except number of days to 50% flowering. The summary statistics such as mean, range,GCV, PCV, GAM and heritability values of the studied traits were shown in Table 3. Seed yield (kg ha^{-1}) trait ranges from 316.1 kg ha^{-1}to 1447.1 kg ha^{-1} with mean value of 1091.1 kg ha^{-1}. Whereas, the trait oil yield (kg ha^{-1}) ranges from 104.9 kg ha^{-1} to 501.7 kg ha^{-1}with mean value of 357.5 kg ha^{-1}. The findings showed that the PCV estimates exceeded the GCV estimates for all traits, suggesting a significant environmental influence on their expression. Notably, seed yield (kg ha^{-1}) and oil yield (kg ha^{-1}) traits recorded the higher estimates of PCV and GCV values. The high GCV values enable the rewarding of direct selection for these traits. The research performed by Lakshman *et al*. (2021) showed a narrow gap between the estimates of PCV and GCV for head diameter, hundred kernel weight,hundred seed weight and yield traits indicating the low effect of environment and genetic factors majorly influence the expression of trait. Moderate PCV and GCV values observed for plant height (cm), head diameter (cm) and oil content (%) traits. The lower estimates of PCV and GCV was observed for the trait number of days to 50% flowering. Roja *et al*. (2021) reported low GCV values for number of days to 50% flowering,number of days to maturity, oil content and volume weight indicating the major environmental role in the trait expression. Further, the low GCV value implies that the direct selection is not rewarding for such traits.

The broad sense heritability ranged from 29.3% (oil content (%)) to 87.8% (seed yield (kg ha^{-1})). The heritability estimates were observed to be high for the traits number of days to 50% flowering, seed yield (kg ha^{-1}), hundred seed weight (g) and oil yield (kg ha^{-1}). The traits plant height (cm) and head diameter (cm) showed moderate heritability. Whereas, the heritability estimate was observed to be low for the trait oil content (%).Yasir and Abed (2024) reported high heritability for the traits seed yield, seed weight and disc diameter indicating the genetic progress through heritable gene action.The direct selection derived from the phenotypic values is effective for the traits with high heritability. The GAM values were varied from 6.2 (number of days to 50% flowering) to 53.1 (oil yield (kg ha^{-1})). The recorded GAM values showed higher estimates for seed yield (kg ha^{-1}), hundred seed weight (g) and oil yield

(kg ha^{-1}) traits, moderate for head diameter (cm) and plant height (cm) and low for oil content (%) and number of days to 50% flowering traits. Interestingly, the traits seed yield (kg ha^{-1}), hundred seed weight (g) and oil yield (kg ha^{-1}) showed higher estimates of

Table 1. Details of sunflower hybrids utilized in the study

S.No	Hybrid	Parentage	S. No	Hybrid	Parentage
1	SH 2876	ARM 248 A × HOCL 20R	27	SH 2916	CMS 30A × NDI 39
2	SH 2878	NDLA 2 × CSFI 99	28	SH 2917	NDLA 2 × NDI 39
3	SH 2883	NDCMS 30A × GMU 736	29	SH 2918	NDLA 3 × NDI 39
4	SH 2884	NDLA 2 × GMU 736	30	SH 2919	CMS 30A × NDI 43
5	SH 2886	NDLA 5 × GMU 736	31	SH 2920	NDLA 2 × NDI 43
6	SH 2888	ARM 248A × GMU 736	32	SH 2922	NDLA 2 × NDI 44
7	SH 2894	NDCMS 30A × TSG 27	33	SH 2924	NDLA 2 × NDI 49
8	SH 2895	NDLA 2 × TSG 27	34	SH 2926	NDLA 2 × NDI 50
9	SH 2896	NDLA 3 × TSG 27	35	SH 2927	NDLA 3 × NDI 50
10	SH 2897	NDLA 5 × TSG 27	36	SH 2928	NDLA 2 × NDI 51
11	SH 2899	ARM 248A × TSG 27	37	SH 2929	NDLA 3 × NDI 51
12	SH 2900	NDCMS 30A × OPH 137	38	SH 2930	CMS 30A × NDI 52
13	SH 2901	NDLA 2 × OPH 137	39	SH 2931	NDLA 2 × NDI 52
14	SH 2902	NDLA 3 × OPH 137	40	SH 2932	NDLA 3 × NDI 52
15	SH 2903	NDLA 5 × OPH 137	41	SH 2933	CMS 30A × NDI 55
16	SH 2904	NDLA 7 × OPH 137	42	SH 2934	NDLA 2 × NDI 55
17	SH 2905	ARM 248A × OPH 137	43	SH 2935	NDLA 3 × NDI 55
18	SH 2906	CMS 30A × NDI 24	44	SH 2936	CMS 30A × NDI 56
19	SH 2907	NDLA 2 × NDI 24	45	SH 2937	NDLA 3 × NDI 56
20	SH 2908	CMS 30A × NDI 32	46	SH 2938	CMS 30A × NDI 61
21	SH 2909	NDLA 2 × NDI 32	47	SH 2939	NDLA 2 × NDI 61
22	SH 2910	CMS 30A × NDI 34	48	SH 2940	NDLA 3 × NDI 61
23	SH 2911	NDLA 2 × NDI 34	49	NDSH 1012	Check
24	SH 2912	NDLA 2 × NDI 35	50	KBSH 44	Check
25	SH 2913	NDLA 3 × NDI 35	51	KBSH 78	Check
26	SH 2915	NDLA 3 × NDI 36	52	TTSUNH 1	Check

heritability and GAM. Mariyam *et al.* (2024) reported the high estimates of heritability and genetic advance forvolume weight, head diameter, seed filling percentage and seed yield suggesting the manifestation of traits is attributed to additive gene action and the influence of environment is least. Further, Baraiya *et al*. (2018) showed that the response to direct selection is effective with high heritability and high GAM.The trait number of days to 50% flowering exhibited high heritability coupled with low GAM value. Roja *et al*. (2021) reported the high heritability accompanied by low genetic advance for volume weight, number of days to 50% flowering and days to maturity indicating that the nonadditive gene action prevails, making selection potentially ineffective.

Table 2. Analysis of variance for yield and its attributing traits in 52 sunflower hybrids

Variables	Mean sum of squares				
	Replication	Treatment (unadjusted)	Treatment (adjusted)	Block (adjusted)	Error
df	1	51	51	12.42	38.58
Number of days to 50% flowering	1.38	8.32***	-3855.58	3.08**	0.81
Plantheight(cm)	44.43	680.40	1703905.99***	111.08	218.45
Head diameter (cm)	0.24	11.19**	137.33***	3.47	3.88
Hundredseed weight (g)	0.21	2.69***	-232.05	0.36	0.16
Seed yield (kg ha^{-1})	24192.22	178296.02***	4857173.92***	8219.02	12604.38
Oil content (%)	7.09	20.34*	1149.03	17.57	9.03
Oil yield(kg ha^{-1})	440.11	21585.26***	1470112.36	761.89	1853.41

Table 3. Estimates of mean, variability, genetic advance as per cent ofmean and heritability (broad sense) for yield and its attributes in 52 sunflower hybrids

Traits	Mean	Range		Coefficient of Variation		Heritability (%)	GAM
		Minimum	Maximum	PCV (%)	GCV (%)		
Number of days to 50% flowering	52.75	45.0	56.5	4.2	3.5	71.8	6.2
Plantheight(cm)	133.5	80.7	167.9	15.6	11.7	55.9	18.0
Head diameter (cm)	16.8	8.1	21.0	16.3	11.5	49.5	16.6
Hundredseed weight (g)	5.7	3.6	8.0	21.2	19.6	85.3	37.3
Seed yield (kg ha^{-1})	1091.1	316.1	1447.1	28.2	26.5	87.8	51.1
Oil content (%)	32.8	27.1	36.7	12.0	6.5	29.3	7.3
Oil yield (kg ha^{-1})	357.5	104.9	501.7	29.9	27.8	86.3	53.1

Genetic diversity

The 52 sunflower hybrids were classified into six clusters using Tocher's method with criterion that average intra cluster distance estimates were lower than inter cluster distance estimates (Table 4 and Fig.1.). Further, the spread of hybrids to these six clusters is at random only. The highest number of hybrids was grouped into cluster I (34 hybrids). The cluster II and cluster III had ten and five hybrids each, respectively. Clusters IV, V and VI are having single hybrid each. The all check

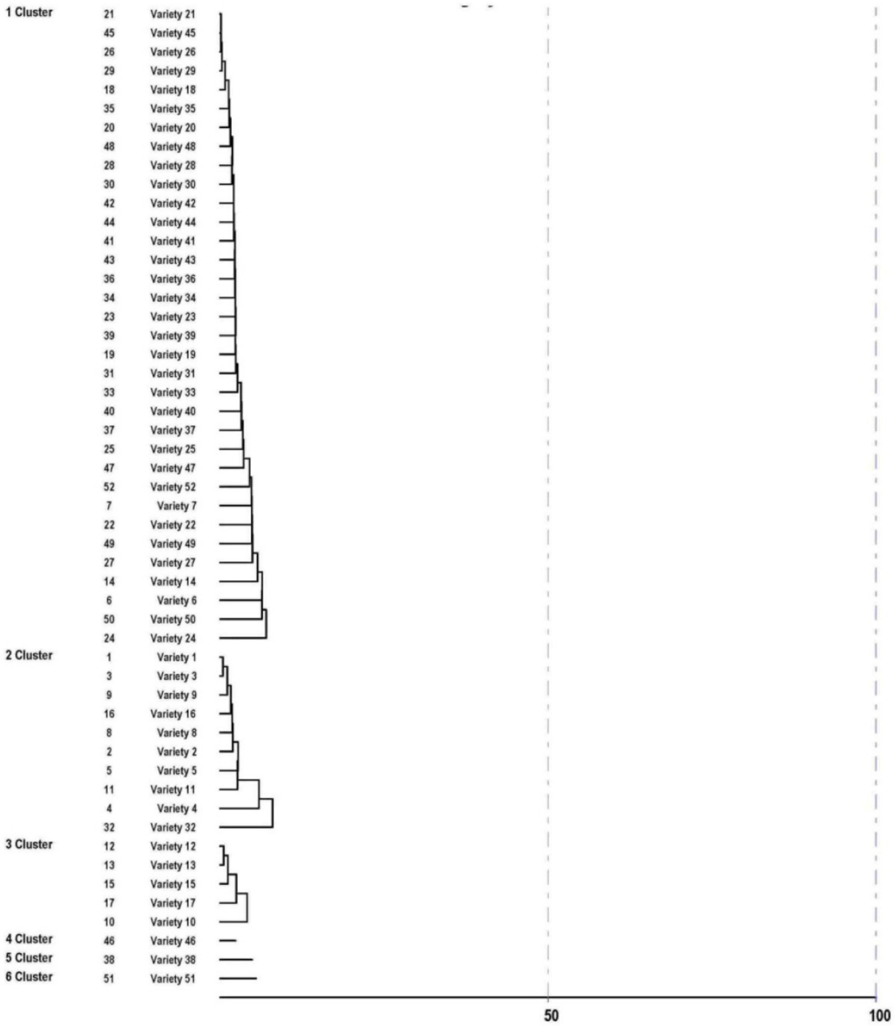

Fig. 1. Dendrogram showing relationship among 52 sunflower genotypes in six clusters based on D² values

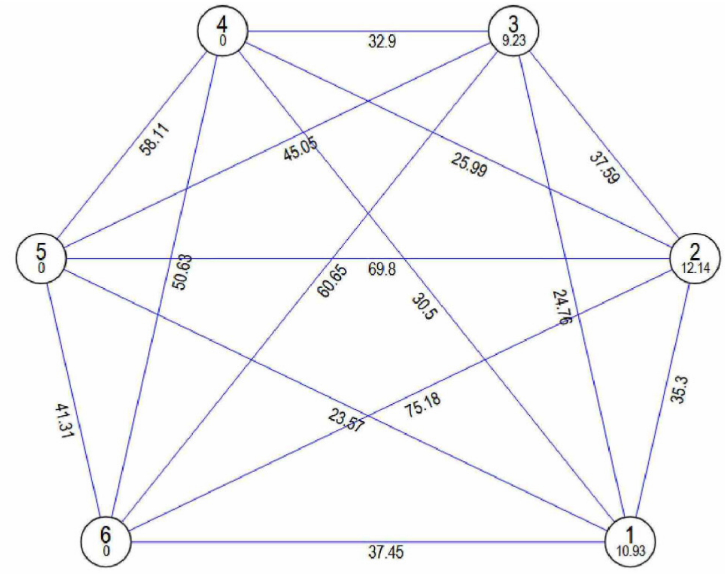

Fig. 2. Cluster diagram showing average intra and inter cluster distance

Table 4. Clustercompositionof52sunflower hybrids basedon Tocher's method

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	34	SH 2909, SH 2937, SH 2915, SH 2918, SH 2906, SH 2927, SH 2908, SH 2940, SH 2917, SH 2919, SH 2934, SH 2936, SH 2933, SH 2935, SH 2928, SH 2926, SH 2911, SH 2931, SH 2907, SH 2920, SH 2924, SH 2932, SH 2929, SH 2913, SH 2939, Tillhan Tech SUNH 1, SH 2894, SH 2910, NDSH 1012, SH 2916, SH 2902, SH 2888, KBSH 44, SH 2912
2 Cluster	10	SH 2876, SH 2883, SH 2896, SH 2904, SH 2895, SH 2878, SH 2886, SH 2899, SH 2884, SH 2922
3 Cluster	5	SH 2900, SH 2901, SH 2903, SH 2905, SH 2897
4 Cluster	1	SH 2938
5 Cluster	1	SH 2930
6 Cluster	1	KBSH 78

Table 5.Averageintraandinterclusterdistancesforthe 52 sunflowerhybrids

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	10.93					
Cluster 2	35.30	12.14				
Cluster 3	24.76	37.59	9.23			
Cluster 4	30.50	25.99	32.90	0.00		
Cluster 5	23.57	69.80	45.05	58.11	0.00	
Cluster 6	37.45	75.18	60.65	50.63	41.31	0.00

hybrids were placed in cluster I except KBSH 78, which is grouped into cluster VI. Lakshman *et al*. (2021) reported the presence of single genotype in five clusters and highlighted the role of solitary clusters in harnessing heterosis in hybrid development in sunflower.

The mean intra cluster and intercluster distances are provided in Table 5 and Figure. 2.The intra cluster D^2 values varied from 0 (cluster IV, V and VI) to 12.14 (cluster II). The Cluster II with large intracluster distance suggests a substantial variation in genetic makeup among the genotypes within that cluster.The genotypes which were stocked under the same cluster may show minimum variation from one another as the aggregate of the measured trait. The inter cluster distance was ranged from 23.57 to 75.18. The greatest inter-cluster distance was noted between Cluster II and Cluster VI (75.18), followed by Cluster II and V (69.80), Cluster III and VI (60.65), and Cluster IV and V (58.11), highlighting substantial genetic diversity within these clusters. Further, cluster I was nearest to cluster V (23.57) and farthest to cluster VI (37.54). The cluster II was nearest and farthest to cluster IV (25.99) and cluster VI (75.18), respectively. The cluster III was nearest to cluster I (24.76) and farthest to cluster VI (60.65). The cluster IV was nearest and farthest to cluster II (25.99) and cluster V (58.11), respectively. The cluster V was nearest to

Table6. Cluster means with respect to yield and its at tributes among 52 sunflower hybrids

S. No	Character	Cluster number						Contribution %	Times ranked 1st
		I	II	III	IV	V	VI		
1.	Number of days to 50% flowering	52.88	52.30	54.50	52.00	52.50	45.00	15.16	201
2.	Plantheight (cm)	130.66	146.33	143.13	92.90	148.20	80.70	4.75	63
3.	Head diameter (cm)	17.33	17.32	15.02	8.10	16.80	14.10	6.26	83
4.	hundred seed weight (g)	6.26	4.58	3.97	4.80	7.10	5.85	31.83	422
5.	Seed yield (kg ha^{-1})	1192.31	581.22	1336.75	856.60	1441.45	1400.75	35.14	466
6.	Oil content (%)	32.99	32.23	31.88	30.74	49.63	34.72	2.41	32
7.	Oil yield (kg ha^{-1})	397.07	186.07	423.26	263.95	34.72	486.55	4.45	59

cluster I (23.57) and farthest to cluster II (69.8). The cluster VI was nearest and farthest to cluster I (37.45) and cluster II (75.18), respectively. Based on these studies, crosses made between cluster II (SH 2876, SH 2883, SH 2896, SH 2904, SH 2895, SH 2878, SH 2886, SH 2899, SH 2884, SH 2922) and cluster VI (KBSH 78) followed by cluster II and cluster V (SH 2930) provide the greatest opportunity to break the undesirable linkages and releases the hidden variability to give desirable transgressive segregants.Lagiso *et al*., (2021) suggested that hybridizing clusters with large inter-cluster distances would be a logical approach for recombining desirable traits in sunflower hybrid development programs.

The average values for seven quantitative traits across clusters were recorded and showed in Table 6. The cluster mean values for number of days to 50% flowering range from 45.0 (cluster VI) to 54.5 (cluster III). For the traits, plant height (cm) and head diameter (cm), the cluster mean values range from 80.7 (cluster VI) to 148.2 (cluster V) and 8.1 (cluster IV) to 17.33 (cluster I), respectively. The cluster mean values of hundred seed weight (g) and seed yield (kg ha^{-1}) range from 3.97 (cluster III) to 7.1 (cluster V) and 581.22 (cluster II) to 1441.45 (cluster V), respectively. Whereas, the oil content (%) and oil yield (kg ha^{-1}) showed cluster mean values ranging from 30.74 (cluster IV) to 49.63 (cluster V) and 34.72 (cluster V) to 486.55 (cluster VI). The wide range of cluster mean values indicates a significant variation between the genotypes and can be exploited in future breeding programmes in sunflower (Reddy *et al*., 2024a). Among the studied traits, the trait seed yield (kg ha^{-1}) showed the highest contribution (35.14%) towards total divergence followed by hundred seed weight (g) (31.83%), number of days to 50% flowering (15.16%), head diameter (cm) (6.26%), plant height (cm) (4.75%), oil yield (kg ha^{-1}) (4.45%) and oil content (%) (2.41%). The traits hundred seed weight (g), seed yield (kg ha^{-1}) and number of days to 50% flowering are the main contributors which accounted for 82.13% of total genetic divergence. Neelima *et al*. (2016) observed that hundred seed weight played a most significant role in total genetic diversity after that plant height and days to maturity and highlighted the role of classifying the genotypes based on diversified traits in sunflower hybrid development programmes.

CONCLUSIONS

The present investigation showed the interrelationship between the yield and its attributing traits with the occurrence of significant variability and diversity among the hybrids. The traits seed yield (kg ha^{-1}) and oil yield (kg ha^{-1}) recorded the high GCV, PCV, heritability coupled with high genetic advance as percent of mean. Further, the trait seed yield (kg ha^{-1}) showed the maximum contribution to the overall genetic divergence. The highest inter cluster distance was noted between cluster II and VI followed by cluster II and V, cluster III and VI and cluster IV and V. Based on the genetic distance and *perse* performance for yield and its contributing traits, the hybrids SH 2876, SH 2883, SH 2896, SH 2904, SH 2895, SH 2878, SH 2886, SH 2899, SH 2884, SH 2922 and KBSH 78 were exploited in future breeding programmes to get the desirable segregants for inbred line development in sunflower.

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