



Assessment of Genetic Diversity and Characterization of Sunflower Inbreds for Breeding Improvement

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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/ijpss/2025/v37i85614>

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://pr.sdiarticle5.com/review-history/140779>

Original Research Article

Received: 25/05/2025
Published: 22/07/2025

ABSTRACT

Aims: To assess the genetic diversity and characterize sunflower inbred lines based on morphological and quantitative traits, with the objective of identifying superior genotypes for future breeding programs and varietal improvement.

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Cite as: N.P.Sonawane, M.V. Dhuppe, S.P. Pole, V.R. Khandebharad, and P.S.Zade. 2025. "Assessment of Genetic Diversity and Characterization of Sunflower Inbreds for Breeding Improvement". *International Journal of Plant & Soil Science* 37 (8):101-12. <https://doi.org/10.9734/ijpss/2025/v37i85614>.

Study Design: Randomized block design.

Place and Duration of Study: Oilseeds Research Station, Latur during *kharif*-2024.

Methodology: Study included 42 sunflower genotypes along with two checks. The diversity analysis was carried out by using Mahalanobis D^2 statistic and characterization of sunflower accession by using DUS descriptors and IBPGR guidelines.

Results: The evaluation of 40 sunflower inbred lines and 2 checks revealed significant genetic variability across all morphological and yield-related traits. ANOVA showed highly significant differences for key traits, including days to 50% flowering, plant height, head diameter, 100-seed weight, seed filling percentage, and oil content. Cluster analysis grouped the genotypes into seven distinct clusters, with the highest genetic divergence observed between Clusters VI and VII. Head diameter contributed most to the genetic divergence, followed by oil content, volume weight, and seed filling percentage. Cluster VII genotypes were superior for early flowering and yield-contributing traits. Broad morphological variation was noted for leaf traits, ray floret number, seed length, and shape, indicating potential for diverse breeding applications.

Conclusion: The study revealed significant genetic variability among 40 sunflower inbreds and 2 checks, identifying promising lines for key yield traits. The observed diversity offers valuable potential for hybrid development and future breeding programs aimed at enhancing productivity and sustainability.

Keywords: DUS descriptors; genetic diversity; inbred lines; morphological traits; cluster analysis.

1. INTRODUCTION

Sunflower (*Helianthus annuus* L.) is a day-neutral, oilseed crop valued globally for its adaptability, short duration, high yield potential, and superior oil quality. Its insensitivity to photoperiod and temperature makes it a versatile crop for diverse agro-climatic conditions (Chen et al.2023). Introduced in India in 1969 as a "crop for all seasons," sunflower belongs to the family Asteraceae (Compositae) and is a diploid species with $2n = 34$ chromosomes (Sahin, 2023). The genus name is derived from the Greek words *helios* (sun) and *anthos* (flower). In India, it is commonly known as "Suraj Mukhi."

Sunflower is one of the four major global oilseed crops alongside soybean, mustard, and safflower (Khan et al. 2023). The crop originated in southern regions of the USA and Mexico (Lentz et al.2001). It was widely cultivated in the USSR during the 19th century before its introduction into Indian agriculture (Vossen and Umali, 2001). The plant height typically ranges from 50 to 300 cm, with a rough, hairy stem and ovate, serrated leaves (Seiler and Gulya,2004). Its inflorescence is a capitulum composed of sterile ray florets on the periphery and fertile disc florets in the center. The crop exhibits protandry, encouraging natural cross-pollination.

Sunflower seeds contain 42–46% edible oil, considered premium due to its light-yellow color, high smoke point (107°C), high linoleic acid (55–60%), and PUFA content. The oil's low

cholesterol nature and high vitamin content (A, D, E, K) make it beneficial for human health (Khan et al.2015). Globally, during 2024–25, sunflower was cultivated on 28.14 million hectares, producing 52.02 million metric tons with a productivity of 1.85 MT ha⁻¹. In India, cultivation covered 0.18 million hectares with a productivity of 0.63 MT ha⁻¹(USDA, 2025). Maharashtra contributed 1.24 thousand tonnes from 2.51 thousand hectares with a productivity of 494 kg ha⁻¹. Major sunflower-growing states include Karnataka, Andhra Pradesh, Maharashtra, and Tamil Nadu (Agriculture Department of Maharashtra, 2024).

Despite its importance, the sunflower area in India has declined due to limited availability of quality hybrids. To overcome this constraint, exploiting the existing genetic diversity becomes crucial for identifying superior genotypes (Reddy et al.2024). The selection of genetically diverse and agronomically superior parents is fundamental to a successful hybrid breeding programme (Arunachalam, 1981). Genetic divergence, especially measured through Mahalanobis's D^2 statistic, serves as a reliable tool for quantifying diversity among genotypes and guiding parent selection (Rangaswamy et al. 2014). Information on the nature and extent of variability present in a population due to genetic and non-genetic factors serves as a critical prerequisite for any systematic breeding programme (Rao, 2012).

The D^2 analysis helps in grouping genotypes based on genetic distances, identifying promising

combinations for heterosis and variability (Murty and Arunachalam, 1966). Greater divergence between parents increases the likelihood of obtaining heterotic hybrids with wider segregation. Genetic divergence estimates also help in understanding the structure of genetic variation within a population. Several studies (e.g., Murty and Arunachalam, 1966; Singh and Choudhary, 1979; Punitha *et al.*, 2010) have supported the use of D^2 statistics for parent selection in crop improvement.

In the current study, 40 sunflower inbred lines along with 2 checks were evaluated for morphological and yield-related traits. Characterization was done using IBPGR descriptors and UPOV guidelines. Traits studied included hypocotyl pigmentation, leaf shape, color, serration, ray and disc floret characteristics, bract shape, plant branching, pigmentation, flowering time, maturity, plant height, and head diameter. Such characterization enables the identification, selection, and classification of genetically distinct lines, which is vital for effective conservation and utilization of genetic resources in breeding programmes.

This study aimed to explore genetic variability, quantify divergence, and identify superior inbred lines for hybrid development, ultimately contributing to the improvement and sustainability of sunflower production.

2. MATERIALS AND METHODS

The present investigation was carried out during the *kharif* season of 2024 at the Oilseeds Research Station, Latur, affiliated with Vasant Naik Marathwada Krishi Vidyapeeth, Parbhani (Maharashtra), India. The primary objective of the study was to evaluate and characterize 40 sunflower (*Helianthus annuus* L.) inbred lines along with two standard checks, LSF-08 and SS-2038, for both morphological and agronomic traits.

The experiment was laid out in a Randomized Block Design (RBD) with two replications, maintaining a spacing of 60 × 30 cm between and within rows, respectively. Each plot consisted of a single row with 15 plants, and all standard agronomic practices were followed uniformly throughout the growing season to ensure healthy crop establishment and optimal plant performance.

For the assessment of quantitative traits, observations were recorded on five randomly selected competitive plants from each genotype

per replication, including the checks. The data were collected on Days to 50% flowering, Days to maturity, Plant height (cm), Head diameter (cm), Hull content (%), 100-seed weight (g), Seed filling percentage (%), Volume weight (g/100 ml), Oil content (%), Seed yield per plant (g).

Analysis of variance, following a randomized block design was performed to partition the variation carried out as per the standards of Panse and Sukhatme, (1985). The genotypic and phenotypic components of variance based on analysis of variance were estimated by using formula proposed by Johnson *et al.* (1955). The genotypic and phenotypic coefficient of variation were estimated using Burton and Devane (1953) formula. Heritability and genetic advance were computed according to Johnson *et al.* (1955). Genetic divergence among the genotypes was estimated using Mahalanobis's D^2 statistical method (Mahalanobis, 1936), which is a multivariate approach for assessing genetic diversity based on multiple quantitative traits. The clustering of genotypes was performed based on D^2 values to determine inter- and intra-cluster distances, aiding in the identification of genetically diverse parents for hybridization.

In addition to quantitative characterization, the genotypes were also evaluated for qualitative traits based on internationally accepted guidelines. Morphological characterization was conducted following the IBPGR Descriptors for Sunflower (1985) and Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), India (2009), under the framework of Distinctiveness, Uniformity, and Stability (DUS) testing.

A total of 24 qualitative traits were recorded, including hypocotyl pigmentation, leaf shape, leaf colour, leaf blistering, leaf serration, leaf angle of lateral veins, the orientation of blade, leaf petiole pigmentation, stem pigmentation, ray floret number, ray floret colour, ray floret shape, disk floret colour, pollen colour, bract shape, bract pigmentation, plant natural position of closest lateral head to the central head, head attitude, head shape, plant branching, seed length, seed shape, seed coat strips and colour of seed coat stripes.

These traits were chosen for their relevance in sunflower breeding and utility in varietal identification, classification, and selection of diverse parental lines. The data collected were

statistically analysed to estimate the extent of variability and to identify superior and genetically divergent genotypes suitable for inclusion in breeding programs.

3. RESULTS AND DISCUSSION

Plant breeders aim to assess genetic variation in germplasm using quantitative and morphological traits, as the evaluation of morphological traits is relatively straightforward and does not require advanced techniques or costly equipment. In the present study, analysis of variance (ANOVA) revealed highly significant differences among the genotypes for all the traits evaluated, indicating substantial genetic variability in the experimental material (Table 1). A wide range of variation was observed for most of the traits studied. The quantitative traits analyzed included days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), hull content (%), seed filling percentage, 100-seed weight (g), volume weight (g/100 ml), oil content (%), and seed yield per plant (g), all of which showed significant genotypic differences. Similar observations were recorded by Dudhe *et al.* (2019), which supports the present findings.

The estimates of phenotypic coefficient of variation (PCV) were high for head diameter (28.31%), 100-seed weight (27.83%), and seed yield per plant (19.06%), followed by hull content (18.56%) and volume weight (14.89%) (Table 2). Similarly, genotypic coefficient of variation (GCV) was also high for head diameter (28.22%) and 100-seed weight (27.45%), followed by seed yield per plant (18.38%) and hull content (17.11%). In all the traits studied, PCV values were higher than their corresponding GCV values, indicating the influence of environmental factors on trait expression. The narrow gap between PCV and GCV for most traits suggested low environmental interference,

particularly for traits like head diameter and 100-seed weight.

High heritability estimates were recorded for all traits, with head diameter (99.4%), oil content (98.94%), seed filling percentage (97.71%), volume weight (97.58%), and 100-seed weight (97.25%) exhibiting very high heritability. High heritability coupled with high genetic advance as percentage of mean was observed for seed yield per plant (36.52%), head diameter (57.96%), 100-seed weight (55.76%), and hull content (32.49%), indicating that these traits are largely governed by additive gene action and can be effectively improved through selection. Moderate genetic advance as a percent of mean was observed for volume weight (29.94%), oil content (23.74%), and seed filling percentage (20.10%). Low estimates were recorded for traits such as days to 50% flowering (11.51%) and days to maturity (10.46%), suggesting limited scope for improvement through direct selection

3.1 Genetic Diversity Analysis

The genetic divergence among 42 sunflower genotypes was assessed based on ten quantitative characters using Mahalanobis's D² statistic (Mahalanobis,1936). The genotypes were grouped into distinct clusters following Tocher's method of clustering as outlined by Rao (1952) (Table 3). This multivariate technique enables effective classification of genotypes based on the degree of genetic diversity and assists in identifying genetically diverse parents for hybridization programs. The clustering pattern provides valuable insight into the extent of variability present in the germplasm and helps in selecting promising genotypes from divergent clusters to exploit heterosis and enhance genetic gain in sunflower breeding programs.

Table 1. Analysis of variance of randomized block design for ten characters in Sunflower

Sr. No.	Characters	Mean Sum of Squares		
		Replication	Treatment	Error
1	Days to 50 per cent flowering	0.583	29.2395**	3.096
2	Days to maturity	3.048	45.819**	2.096
3	Plant height (cm)	393.300	235.79**	9.530
4	Head diameter (cm)	41.062	21.726**	0.066
5	Hull content (%)	62.820	31.947**	2.593
6	100 seed weight (g)	3.823	2.3127**	0.033
7	Seed filling (%)	325.700	86.62**	1.000
8	Volume weight (g/100ml)	178.209	66.753**	0.818
9	Oil content (%)	10.822	28.8848**	0.155
10	Seed yield per plant (g)	64.313	50.853**	1.837

* Significance at 5 % level and ** significance at 1% level

Table 2. Mean, range, variability, heritability (Broad sense), genetic advance and genetic advance as per cent mean for ten characters of 42 Sunflower genotypes

Characters	Mean	Range Min	Max	Genotypic variance	phenoty pic variance	Environme ntal variance	GCV (%)	PCV (%)	ECV (%)	Heritability in broad sense (H ²) (%)	Genetic Advance	Genetic Advance as % of mean
Days to 50 per cent flowering	58.48	50	67	13.07	16.16	3.09	6.21	6.91	3.02	80.85	6.69	11.51
Days to maturity	79.00	78	97	21.86	23.95	2.09	5.31	5.56	1.64	91.25	9.20	10.46
Plant height (cm)	123.91	102	172	113.13	122.66	9.52	8.48	8.83	2.46	92.23	21.04	16.78
Head diameter (cm)	11.43	7	17	10.82	10.89	0.06	28.22	28.30	2.20	99.40	6.75	57.95
Hull content (%)	22.58	14	32	14.67	17.26	2.59	17.10	18.55	7.19	84.99	7.27	32.49
100 seed weight (g)	3.75	2	7	1.14	1.17	0.03	27.44	27.83	4.62	97.25	2.16	55.76
Seed filling (%)	65.90	53	79	42.81	43.81	0.81	9.80	9.98	1.51	97.71	13.32	20.10
Volume weight (g/100ml)	44.15	24	48	32.96	33.78	0.81	14.71	14.89	2.31	97.58	11.68	29.93
Oil content (%)	33.65	23	40	14.36	14.51	0.15	11.58	11.65	1.20	98.94	7.76	23.74
Seed yield per plant (g)	30.18	17	40	24.50	26.34	1.83	18.38	19.05	5.03	93.03	9.83	36.52

Table 3. Composition of 42 inbred lines including two checks into seven clusters

Cluster	Total Genotypes	Inbred lines
Cluster I	6	RCB-5,25-2, RCR-63,64,65,68
Cluster II	6	RCB-5, RCMS-34B, USDA-42,63,126,128
Cluster III	7	RCB-19-25, RCR-71,74,75, RCMS-16B, USDA-126,164
Cluster IV	8	RCB-11,23-1,32, RCR-70,72, RCMS-96B, USDA-94, DRSF-113
Cluster V	10	RCB-6,16,47, RCMS-8B, USDA-8,65,104,110,188, PI-599977
Cluster VI	3	RCR-67, RCMS-76B, USDA-63
Cluster VII	2	LSF-08, SS-2038

Table 4. Intra and Inter cluster distances (D)

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	13.54	36.76	18.18	32.27	27.47	17.03	45.39
Cluster II		14.98	32.96	22.87	32.01	43.62	23.98
Cluster III			16.63	31.11	23.92	21.54	44.09
Cluster IV				17.28	37.75	36.03	27.94
Cluster V					20.92	34.81	43.28
Cluster VI						14.65	51.90
Cluster VII							12.13

3.2 Intra and Inter Clusters Distance

D² analysis is considered as one of the most effective methods to quantify the degree of genetic divergence among genotypes at both intra- and inter-cluster levels. In the present investigation, genetic divergence among 42 sunflower genotypes was assessed using Mahalanobis's D² statistic and clustering was done using Tocher's method. The results revealed that the inter-cluster distances were generally higher than intra-cluster distances (Table 4), indicating the existence of substantial genetic variability among the genotypes studied. The intra-cluster D² values ranged from 12.13 to 20.92. The highest intra-cluster distance was recorded in Cluster V (20.92), followed by Cluster II (14.98), Cluster III (16.63), Cluster IV (17.28), Cluster I (13.54), and Cluster VI (14.65). The lowest intra-cluster distance was found in Cluster VII (12.13), indicating less genetic diversity within that cluster.

Among the inter-cluster distances, the maximum average divergence was observed between Cluster VI and Cluster VII (51.90), indicating the presence of maximum genetic divergence between genotypes of these two clusters. This was followed by Cluster I and Cluster VII (45.39), Cluster III and Cluster VII (44.09), and Cluster II and Cluster VI (43.62). The minimum inter-cluster distance was recorded between Cluster III

and Cluster IV (31.11), suggesting that the genotypes in these clusters are genetically more similar.

Cluster-wise Intra and Inter-cluster Divergence Summary:

- i. Cluster I showed maximum divergence with Cluster VII (45.39), followed by Cluster II (36.76), Cluster IV (32.27), Cluster V (27.47), Cluster III (18.18), and minimum with Cluster VI (17.03).
- ii. Cluster II exhibited highest divergence with Cluster VI (43.62), followed by Cluster I (36.76), Cluster IV (32.96), Cluster V (32.01), Cluster III (22.87), and lowest with Cluster VII (23.98).
- iii. Cluster III had highest divergence with Cluster VII (44.09), followed by cluster II (32.96), Cluster IV (31.11), Cluster V (23.92), Cluster VI (21.54), and lowest with Cluster I (18.18).
- iv. Cluster IV displayed maximum divergence with Cluster V (37.75), followed by Cluster VI (36.03), Cluster I (32.27), Cluster III (31.11), Cluster VII (27.94) and minimum with Cluster II (22.87).
- v. Cluster V showed highest divergence with Cluster VII (43.28), followed by Cluster IV (37.75), Cluster VI (34.81), Cluster II (32.01), Cluster I (27.47) and minimum with Cluster III (23.92).

- vi. Cluster VI exhibited maximum divergence with Cluster VII (51.90), which was also the highest inter-cluster distance overall, followed by Cluster II (43.62), Cluster IV (36.03), Cluster V (34.81), Cluster III (21.54) and minimum with Cluster I (17.03).
- vii. Cluster VII had its highest divergence with Cluster VI (51.90), followed by Cluster I (45.39), Cluster III (44.09), Cluster V (43.28), Cluster IV (27.94), and lowest with Cluster II (23.98).

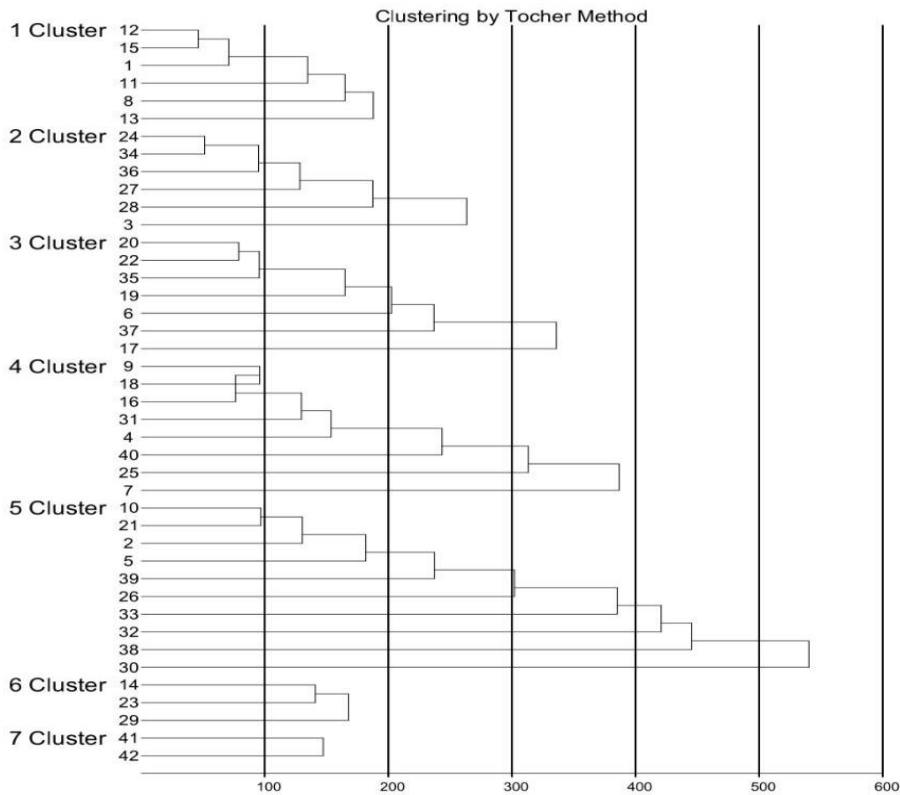


Fig 1. Clustering pattern of 42 genotypes in sunflower by Tocher’s method

Table 5. Contribution of different character to genetic diversity in sunflower genotypes

Sr. No.	Traits	No. of times appearing 1st in ranking	Contribution towards Divergence %
1	Days to 50 per cent flowering	2	0.23%
2	Days to maturity	3	0.35%
3	Plant height (cm)	5	0.58%
4	Head diameter (cm)	397	46.11%
5	Hull content (%)	3	0.35%
6	100 seed weight (g)	33	3.83%
7	Seed filling (%)	54	6.27%
8	Volume weight (g/100ml)	103	11.96%
9	Oil content (%)	240	27.87%
10	Seed yield per plant (g)	21	2.44%

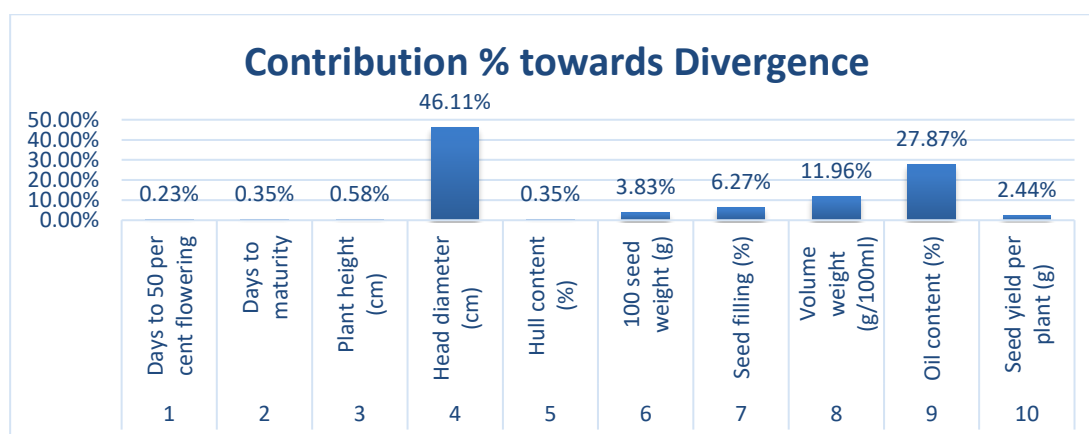


Fig. 2. Contribution of each character towards divergence

Table 6. Morphological characterization of sunflower genotypes

No.	Characteristics	Category	No. of genotypes
1	Hypocotyl: Anthocyanin Pigmentation	Absent	15
		Medium	22
		Strong	1
		Lanceolate	2
2	Leaf size	Small	16
		Medium	19
		Large	6
3	Leaf: Shape	Lanceolate	3
		Rounded	37
4	Leaf: Color	Light green	19
		Green	8
		Dark green	13
5	Leaf: Blistering	Absent	42
		Medium	0
		Strong	0
6	Leaf: Serration	Fine	1
		Medium	6
		Coarse	33
7	Leaf: Angle of lateral veins	Acute (<90)	29
		Obtuse (>90)	11
8	Leaf: Orientation of blade	Erect	10
		Drooping	30
9	Leaf: Petiole anthocyanin pigmentation	Absent	38
		Present	4
10	Stem: Pigmentation	Absent	38
		Present	4
		Elongated	26
11	Ray floret: Shape	Ovate	13
		Rounded	0
		Light yellow	31
12	Ray floret: Color	Yellow	11
		Orange	0
		Purple	0
13	Ray floret number	Medium	20
		Many	13
14	Disk floret: Color	Yellow	42
15	Disk floret: Anthocyanin pigmentation of stigma	Absent	38

No.	Characteristics	Category	No. of genotypes
		Medium	0
		Strong	4
16	Disk floret: Pollen colour	White	0
		Yellow	42
17	Bract: Shape	Elongated	42
		Rounded	0
18	Bract: Anthocyanin pigmentation	Absent	42
		Present	0
19	Plant: Natural position of closest lateral head to the central head (end of flowering- branched)	Above	32
		Below	10
20	Head: Attitude	Inclined	0
		Vertical	3
		Half turned down	39
		Turned down	0
21	Head: Shape of the grain side	Concave	3
		Flat	0
		Convex	39
		Irregular	0
22	Plant: Branching	Absent	29
		Present	13
23	Seed length	Basal	0
		Short	26
		Medium	15
		Long	1
24	Seed: Shape	Elongated	12
		Ovoid elongated	11
		Ovoid wide	19
		White	0
25	Seed coat: Stripes	Absent	24
		Present	18
26	Seed coat: Color of Stripes	White	6
		Grey	11
		Brown	0
		Black	0

3.3 Contribution of Different Characters to Genetic Diversity in Sunflower Genotypes

The number of times that each of yield component characters appeared in first rank and their respective percentage contribution towards genetic divergence are presented in (Table 5). The results showed that head diameter contributed the most towards genetic divergence (46.11%) by taking 397 times ranking first, followed by oil content (27.87%) by taking 240 times, volume weight (11.96%) by taking 103 times, seed filling percentage (6.27%) by taking 54 times, 100 seed weight (3.83%) by taking 33 times, seed yield per plant (2.44%) by taking 21 times, plant height (0.58%) by taking 5 times, days to maturity and hull content each (0.35%) by taking 3 times and days to 50 per cent flowering (0.23%) by taking 2 times.

3.4 Morphological Characterization

The distinctiveness, uniformity and stability (DUS) study evaluated 26 morphological traits to determine their variation among 42 genotypes taken for analysis (Table 6.). At the seedling stage, only 1 genotype exhibited strong hypocotyl anthocyanin pigmentation, 24 had medium pigmentation and the remaining 17 showed no pigmentation. Out of 42 genotypes 6 genotypes showed large leaf size, 20 was recorded as medium size and 16 have small leaf size. For leaf shape 39 genotypes were identified as having rounded leaf shapes and remaining 3 genotypes have lanceolate shaped leaves. Leaf colour of 19 have light green colour, 13 genotypes recorded for dark green colour and remaining 8 genotypes have green coloured leaf. Coarse leaf serration was predominant in 33 genotypes, medium serration was seen in 6 genotypes, while only one genotypes showed

fine leaf serration. Among the 42 sunflower genotypes evaluated, the majority (30 genotypes) exhibited an acute angle of lateral veins and the remaining 12 genotypes showed an obtuse angle of lateral veins. Out of the 42 genotypes evaluated, 32 genotypes exhibited a drooping leaf blade orientation and remaining 10 genotypes showed an erect leaf blade orientation. A large majority of the genotypes 38 out of 42 showed absence of pigmentation on the leaf petiole and remaining four genotypes exhibited pigmentation on the leaf petiole. For stem pigmentation 38 genotypes showed absence of pigmentation and remaining 4 genotypes showed the presence of stem pigmentation. Variation in ray floret number was recorded among the genotypes, a medium number of ray florets (30–40) was observed in 23 genotypes, higher number of ray florets (>40) was recorded in 17 genotypes and only two genotypes showed a lower number of ray florets. Ray floret colour was predominantly yellow, noted in 31 genotypes and for light yellow colour 11 genotypes was observed. Ray floret shape varied distinctly among the genotypes. For ray floret shape elongated ray florets were observed in 28 genotypes indicating a predominance of this shape. In contrast, ovate-shaped ray florets were recorded in 14 genotypes. Ray floret shape determines the overall appearance and pollination efficiency. In disc floret colour Yellow colour were uniformly observed across all 42 sunflower genotypes evaluated reinforcing the uniformity of this trait among cultivated sunflower lines. A majority of the genotypes 38 out of 42 exhibited an absence of pigmentation in disc florets while strong pigmentation was observed in only four genotypes. All 42 sunflower genotypes uniformly exhibited yellow pollen colour indicating a genetically stable and non-variable trait among the sunflower lines studied. All 42 genotypes showed elongate round bract shape this uniformity suggests limited variation for this trait, which influences head protection and seed cover during development. None of the genotypes exhibited pigmentation on the bracts, showing a total absence of this character across all 42 genotypes. This suggests pigmentation is not a common trait in cultivated sunflower lines studied. In 32 genotypes, the position of the closest lateral head was found to be above the central head. In contrast, 10 genotypes showed the lateral heads positioned below the central head. This trait reflects plant architecture and potential for branching. A majority of the genotypes, 39 out of 42, exhibited a half-turned down head orientation indicating that this is the

predominant head attitude among the studied genotypes while, only three genotypes exhibited a vertical head orientation. Head attitude affects seed filling and protection from sun or birds. A Convex head shape was predominantly observed in 39 genotypes, making it the most common head shape among the studied genotypes. In contrast, only three genotypes exhibited a concave head shape. Head shape can influence water retention and seed development. Branching was absent in 29 genotypes, indicating a predominantly non-branching growth habit. In contrast, 13 genotypes exhibited branching. This trait is important for seed yield and plant structure. Seed length showed considerable variation among the genotypes. A total of 26 genotypes exhibited short seed length, 15 observed for medium seed length and only 1 exhibited for long seed length. Seed size influences market preference and oil content. Variation in seed shape was observed among the sunflower genotypes. A total of 12 genotypes exhibited elongated seed shape, ovoid-elongated seeds were found in 11 genotypes and the remaining 19 genotypes exhibited ovoid-wide seed shape. Seed shape is an important market and breeding trait. Absence of seed coat stripes was recorded in 24 genotypes and remaining 18 genotypes exhibited the presence of seed coat stripes. Striped seeds are often preferred in confectionery sunflower. Grey-coloured seed coat stripes were observed in 11 genotypes and White stripes were recorded in six genotypes. Stripe colour influences seed marketability and classification.

4. CONCLUSION

The present study revealed significant genetic variability among sunflower inbred lines for key agronomic and quality traits. Several superior genotypes were identified for traits such as early flowering, seed yield, oil content, and head diameter, which can serve as valuable parents lines in future breeding programs. High heritability coupled with high genetic advance for most traits indicates the predominance of additive gene action, suggesting effective improvement through direct selection. Morphological characterization showed wide diversity, and cluster analysis grouped genotypes into seven distinct clusters with maximum genetic divergence between Cluster VI and VII, indicating potential for heterosis breeding. These findings provide a strong foundation for genetic enhancement and hybrid development in sunflower.

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 this manuscript.

ACKNOWLEDGEMENTS

The author gratefully acknowledges the guidance and support of Dr.M.V. Dhuppe, Oilseeds Specialist, Oilseeds Research Station, Latur for valuable suggestions and encouragement during the course of this research. The facilities provided by the Oilseeds Research Station, Latur, are also sincerely acknowledged. Special thanks to all staff and fellow researchers who contributed directly or indirectly to this study.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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