



Morphological Characterization and Character Association Studies in Sunflower (*Helianthus annuus* L.)

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Authors' contributions

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

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Abstract

Sunflower (*Helianthus annuus* L.) is an important oilseed crop, and the identification of genetically diverse and superior germplasm is essential for its improvement. The present investigation was undertaken to evaluate genetic variability, characterise sunflower germplasm using Distinctness, Uniformity and Stability (DUS) descriptors, and determine the association between seed yield and its contributing traits. A total of 46 sunflower genotypes, comprising 44 test genotypes and two checks, were evaluated during Kharif 2025 at the Oilseeds Research Station, Latur, Maharashtra, India. The genotypes were evaluated for ten quantitative traits, namely days to 50% flowering, days to maturity, plant height, head diameter, 100-seed weight, volume weight, hull content, seed filling percentage, oil content and seed yield per plant. Analysis of variance revealed highly significant differences among the genotypes for all the quantitative traits, indicating substantial genetic variability. The mean performance of the genotypes showed considerable variation for flowering, maturity, plant height, head diameter, seed characteristics, oil content and seed yield. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, head diameter, 100-seed weight, volume weight, hull content, seed filling percentage, oil content and seed yield per plant. Genotypic and phenotypic correlation analyses revealed significant positive associations of seed yield with head diameter, plant height, 100-seed weight and volume weight, with head diameter showing the strongest association. Morphological characterisation using DUS descriptors revealed variation among the genotypes for several qualitative traits related to hypocotyl pigmentation, leaf characteristics, head attitude, ray floret characteristics and seed traits. The evaluated genotypes differed for leaf colour, leaf shape, leaf serration, seed shape, seed coat colour and seed coat stripes, whereas some descriptors showed uniform expression across the genotypes. Based on quantitative performance and morphological characteristics, RHAGPR-3, RHA 274, 93 R, RCB-5, OPH-107, CMS-90-3B, 143 R and HOC-20R were identified as promising genotypes. The present study identified substantial genetic and morphological variability among the evaluated sunflower genotypes and provided useful genetic resources for selection and future breeding programmes aimed at improving seed yield and associated traits.

Keywords: *Helianthus annuus* L.; sunflower; genetic variability; morphological characterization; DUS descriptors; germplasm evaluation; character association; correlation analysis; seed yield; yield components.

1. Introduction

Sunflower (*Helianthus annuus* L.) is one of the world's most important annual oilseed crops belonging to the family Asteraceae. It is cultivated extensively because of its high-quality edible oil, desirable fatty acid composition, and wide adaptability to diverse agro-climatic conditions. Besides its use for edible oil production, sunflower serves as an important source of livestock feed, confectionery products, and industrial raw material, including biodiesel production. Owing to these attributes, sunflower contributes significantly to global vegetable oil production and plays an important role in ensuring food and nutritional security (Seiler *et al.*, 2017; Radanović *et al.*, 2018). Recent studies continue to emphasise sunflower's importance in sustainable oilseed production and genetic improvement.

India is one of the major oilseed-producing countries; however, the productivity of sunflower remains below the global average due to its narrow genetic base, susceptibility to biotic and abiotic stresses, and environmental fluctuations. Therefore, the development of high-yielding and widely adapted cultivars remains a primary objective of sunflower breeding programmes. The effective utilisation of genetically diverse germplasm is essential for broadening the genetic base and improving economically important traits such as seed yield and oil content (Allard, 1960; Falconer & Mackay, 1996; Johnson *et al.*, 1955; Radanović *et al.*, 2018; Seiler *et al.*, 2017).

Recent studies have emphasised the importance of assessing genetic variability and trait relationships for effective selection in sunflower breeding programmes. Sandhya Sree *et al.* (2021) reported significant variation among sunflower genotypes for economically important traits and observed high heritability coupled with high genetic advance for plant height, head diameter, 100-seed weight and seed yield per plant, indicating the usefulness of these traits for phenotypic selection. Vamsi *et al.* (2022) also observed significant variation among 67 sunflower genotypes for seed yield and associated agronomic traits, with substantial variability providing scope for selection and genetic improvement.

Morphological and genetic diversity assessment has also received considerable attention in recent sunflower research. Ibrar *et al.* (2022) evaluated 109 sunflower genotypes using morphological traits together with SSR markers and observed considerable variation for plant height, head diameter, 100-seed weight and seed yield per plant. The combined morphological and molecular analyses differentiated the germplasm into distinct groups, demonstrating the usefulness of diversity assessment for identifying potential parents and supporting hybrid breeding.

Characterisation using morphological and DUS descriptors provides an important approach for documenting and differentiating sunflower germplasm. Kumar *et al.* (2023) characterised 33 sunflower genotypes using DUS and related descriptors and reported considerable variation for several morphological characters, including seed and ray floret characteristics. The study also identified variation in quantitative traits and suggested the usefulness of selected genotypes for future breeding programmes. Gahukar and Fatak (2023) reported wide variation among sunflower inbred lines for several agronomic traits, with high genotypic and phenotypic variability for seed yield per plant, plant height and test weight, further supporting the scope for selection of superior genotypes. Neelima *et al.* (2023) likewise reported significant variability and heritability among sunflower inbreds and emphasised the importance of genetic parameters and association analysis for improving yield and its contributing traits.

Recent work by Reddy *et al.* (2025) demonstrated substantial genetic variability and diversity among sunflower hybrids, with high heritability coupled with high genetic advance for seed yield, hundred-seed weight and oil yield, indicating the potential for selection and genetic improvement. Recent studies have also highlighted the importance of improving sunflower tolerance to abiotic stresses, including drought, through physiological and biochemical approaches (Ameen *et al.*, 2024).

Narkhede *et al.* (2025) reported substantial variability among sunflower inbreds and positive associations of seed yield with head diameter, seed filling percentage, 100-seed weight and plant height, whereas Karthik *et al.* (2025) documented substantial variability in maintainer and restorer lines and high heritability coupled with high genetic advance for several yield-related traits. Complementary genomic studies have associated variation in sunflower agronomic traits with identifiable genomic regions, including salinity-response traits and shoot branching, while pan-genome analysis has further documented intraspecific diversity relevant to abiotic-stress response (McNellie *et al.*, 2024; Zhang *et al.*, 2024; Sun *et al.*, 2025).

Morphological characterisation is a fundamental step in germplasm evaluation and conservation. Characterisation based on Distinctness, Uniformity and Stability (DUS) descriptors provides an effective means of identifying and differentiating sunflower genotypes using qualitative and quantitative traits (Protection of Plant Varieties and Farmers' Rights Authority [PPV&FRA], 2009). These descriptors facilitate varietal identification, maintenance of genetic purity, germplasm documentation, and protection of plant varieties. Moreover, DUS characterisation enables breeders to identify genetically diverse parents for hybridisation and supports efficient germplasm management in breeding programmes (Ibrar *et al.*, 2022; Kumar *et al.*, 2023; Umarani *et al.*, 2020).

Seed yield in sunflower is a complex quantitative trait controlled by several interacting component characters. Traits such as days to flowering, days to maturity, plant height, head diameter, 100-seed weight, volume weight, hull content, seed filling percentage and oil content collectively influence final seed yield. Since seed yield is greatly affected by environmental factors, direct selection for yield alone is often less effective. Consequently, understanding the associations between yield and its component traits through genotypic and phenotypic correlation analyses provides valuable information for indirect selection and the development of superior cultivars (Johnson *et al.*, 1955; Hanson *et al.*, 1956; Dağüstü, 2002; Kaya *et al.*, 2009; Tyagi & Khan, 2013).

Several researchers have reported considerable morphological diversity and significant variation among sunflower germplasm for economically important traits. Genetic diversity assessment among maintainer and restorer lines is important for identifying diverse parental material and supporting hybrid development in sunflower (Ahmad *et al.*, 2022). Characterisation studies have demonstrated substantial variation in plant architecture, leaf morphology, head characteristics, flowering behaviour and seed traits, highlighting the availability of diverse genetic resources for crop improvement. Likewise, correlation studies have consistently reported positive associations of head diameter, plant height, 100-seed weight and other yield-attributing characters with seed yield, indicating that these traits can be effectively utilised as selection criteria in sunflower breeding programmes (Kumar *et al.*, 2023; Dağüstü, 2002; Ibrar *et al.*, 2022).

Although numerous studies have independently investigated genetic variability, morphological characterisation and trait association in sunflower, relatively limited information is available that integrates DUS-based characterisation with quantitative trait association under the agro-climatic conditions of Maharashtra. Simultaneous evaluation of qualitative descriptors and yield-related quantitative traits provides a comprehensive understanding of germplasm diversity and assists in identifying elite genotypes possessing desirable agronomic performance and distinct morphological characteristics.

Therefore, the present investigation was undertaken to characterise forty-six sunflower genotypes using DUS descriptors and to evaluate the associations between seed yield and its contributing traits through genotypic and phenotypic correlation analyses. The findings are expected to contribute to efficient germplasm utilisation and provide valuable information for the development of high-yielding sunflower cultivars suitable for future breeding programmes.

2. Material and Methods

The present investigation was carried out during the Kharif 2025 season at the Oilseeds Research Station, Latur, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India. The experimental farm is situated at 18°25' N latitude and 76°35' E longitude at an altitude of approximately 631 m above mean sea level. The region experiences a semi-arid tropical climate characterised by moderate rainfall, warm temperatures and deep black (Vertisol) soils, which are well suited for sunflower cultivation.

The experimental material consisted of 46 sunflower (*Helianthus annuus* L.) genotypes, comprising 44 experimental genotypes and two standard check varieties, collected from the germplasm maintained at the Oilseeds Research Station, Latur. The genotypes represented a diverse collection of breeding lines possessing considerable variation for yield and yield-contributing traits, making them suitable for morphological characterisation and association studies.

The experiment was laid out in a Randomised Block Design (RBD) with two replications. Each genotype was sown in two rows of 4.5 m length with a spacing of 60 cm between rows and 30 cm between plants. The crop was raised by adopting the recommended package of practices for sunflower cultivation. All agronomic operations, including land preparation, fertiliser application, irrigation, intercultural operations, plant protection measures and weed management, were carried out uniformly to ensure optimum crop growth and to minimise environmental variation among experimental plots.

Observations were recorded on five randomly selected competitive plants from each genotype in each replication. Data were collected for ten quantitative traits, namely days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), 100-

seed weight (g), volume weight (g 100 mL⁻¹), hull content (%), seed filling percentage (%), oil content (%) and seed yield per plant (g). Days to 50% flowering and days to maturity were recorded on a plot basis, whereas the remaining observations were recorded on individual plants. Oil content was estimated using Nuclear Magnetic Resonance (NMR) spectroscopy following standard laboratory procedures.

Morphological characterisation of the sunflower genotypes was carried out using the Distinctness, Uniformity and Stability (DUS) descriptors prescribed by the Protection of Plant Varieties and Farmers' Rights (PPV&FR) Authority, Government of India. Qualitative descriptors related to hypocotyl pigmentation, leaf morphology, head characteristics, ray floret traits and seed characteristics were recorded at appropriate growth stages to identify distinct morphological features and assess the diversity among the evaluated genotypes. Standard DUS descriptors provide a reliable basis for varietal identification and germplasm characterisation.

The recorded quantitative data were subjected to analysis of variance (ANOVA) for a Randomised Block Design to determine the significance of differences among genotypes following the procedure described by Panse and Sukhatme (1985). Genotypic and phenotypic correlation coefficients were estimated according to the method proposed by Johnson *et al.* (1955) to determine the magnitude and direction of associations between seed yield and its component traits. All statistical analyses were performed using R statistical software, and the significance of correlation coefficients was tested at appropriate probability levels. The analysis was used to identify traits exhibiting strong positive associations with seed yield for their effective utilisation in sunflower improvement programmes.

3. Results and Discussion

3.1 Analysis of Variance

The analysis of variance (Table 1) revealed highly significant ($P \leq 0.01$) differences among the 46 sunflower genotypes for all ten quantitative traits, namely days to 50% flowering, days to maturity, plant height, head diameter, 100-seed weight, volume weight, hull content, seed filling percentage, oil content and seed yield per plant. The significant differences observed among the genotypes indicate the existence of substantial genetic variability within the experimental material, providing considerable scope for effective selection and genetic improvement.

The treatment mean squares for all the studied traits were considerably higher than their corresponding error mean squares, suggesting that the observed variation was predominantly due to genetic differences among the genotypes rather than environmental influences. Furthermore, the non-significant replication effects for the characters indicated uniform experimental conditions and enhanced the reliability and precision of the recorded observations.

The presence of significant variability among the evaluated sunflower genotypes confirms the availability of a broad genetic base for crop improvement. Such variability is a prerequisite for the effective estimation of genetic parameters and the identification of superior genotypes possessing desirable agronomic traits. Similar findings have been reported by Rauf (2008), Kaya *et al.* (2009), Tyagi and Khan (2013), and Kumar *et al.* (2023), who observed significant genetic variation among sunflower genotypes for yield and yield-attributing characters, emphasising the potential for selection in sunflower breeding programmes.

Table 1. Analysis of variance (ANOVA) for ten quantitative traits in sunflower (*Helianthus annuus* L.)

Sr. No.	Characters	Replication (df=1)	Treatment (df=45)	Error (df=45)
1	Days to 50 per cent flowering	4.347826	37.75459**	2.547826
2	Days to maturity	9.1413043	82.34686**	4.3413043
3	Plant height (cm)	166.0539	944.8404**	42.13391
4	Head diameter (cm)	0.851332	8.652814**	0.578834
5	Hull content (%)	4.41767	29.22464**	6.719801
6	100 seed weight (g)	0.018	0.817689**	0.071097
7	Seed filling (%)	0.228283	145.7219**	10.2842
8	Volume weight (g/100ml)	0.104457	74.46494**	5.26765
9	Oil content (%)	3.3242	33.6133**	1.9105
10	Seed yield per plant (g)	26.08718	48.08291**	8.886908

*Significance at 5% probability level; **Significance at 1% probability level

3.2 Mean Performance of Sunflower Genotypes

The mean performance of the 46 sunflower genotypes for the ten quantitative traits is presented in Table 2. Considerable variation was observed among the genotypes for all the characters studied, indicating the presence of broad phenotypic diversity within the experimental material. The observed differences in flowering behaviour, maturity duration, plant stature, head diameter, seed characteristics and seed yield reflect the diverse genetic background of the evaluated germplasm and provide opportunities for identifying superior genotypes for breeding programmes.

The range, mean and performance of individual genotypes for each trait enabled the identification of promising genotypes possessing desirable combinations of yield and yield-contributing characters. Such information is useful for selecting parental lines in hybridisation programmes and for developing high-yielding sunflower cultivars adapted to diverse agro-climatic conditions.

Table 2. Mean performance of 46 sunflower genotypes for quantitative traits

Sr. No.	Genotypes	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Hull content (%)	100 seed weight (g)	Seed filling (%)	Volume weight (g/100ml)	Oil content (%)	Seed yield per plant (g)
1	DRSF-108	60.50	96.00	102.50	11.80	37.79	3.21	64.55	27.50	30.93	18.61
2	138-R	60.50	83.00	79.00	13.02	31.95	4.21	72.54	36.80	35.83	26.00
3	OPH-74	62.50	85.50	74.50	11.90	33.70	4.50	73.10	30.02	33.04	23.80
4	163 R	71.00	91.50	66.00	10.57	27.48	4.62	63.66	32.40	29.54	21.10
5	HOC-20R	64.00	88.50	87.50	13.72	24.32	3.75	82.00	34.66	39.05	28.00
6	OPH-107	60.00	84.00	101.50	14.84	35.53	4.36	83.30	28.64	38.11	30.80
7	93 R	57.00	83.00	96.00	14.98	29.33	5.44	77.79	34.77	38.03	32.20
8	EC661924	66.50	91.50	64.00	11.62	31.07	3.98	70.84	31.84	36.90	23.90
9	EC601757	58.00	82.50	72.00	10.88	30.98	4.98	60.73	42.65	31.91	22.40
10	COSF-12B	61.50	99.00	56.50	10.01	29.64	4.10	76.42	30.25	32.41	20.00
11	302 B	61.50	97.00	69.50	10.29	30.11	4.00	59.23	24.89	35.70	22.40
12	OPH-118	73.50	95.50	101.50	11.62	38.98	4.36	66.23	35.12	34.52	23.20
13	OPH-104	62.00	98.00	105.00	10.43	27.48	3.52	80.32	30.36	40.10	30.20
14	COSF-V5	62.00	96.00	76.80	13.02	32.03	4.78	75.32	34.23	32.40	26.00
15	OPH-105	64.50	93.00	77.50	12.88	30.82	4.21	71.32	35.10	34.85	25.80
16	IC-502617	61.00	96.00	96.00	15.68	33.98	4.67	70.61	30.00	31.75	19.60
17	MRHA 2-R	63.50	93.00	101.00	14.42	26.65	4.22	77.61	32.60	38.76	28.80
18	121 R	55.50	90.00	73.00	12.39	35.38	4.28	87.00	38.15	35.16	25.50
19	EC-601751	59.50	93.00	72.50	11.48	32.08	4.12	67.25	40.14	32.93	20.80
20	358 B	71.00	107.00	77.00	11.55	35.62	3.28	72.33	25.28	31.11	18.90
21	CMSMA X BKR-1	59.50	92.00	93.50	12.18	26.16	4.80	82.66	40.01	35.63	24.40
22	GMU689	57.50	90.00	70.00	9.66	31.57	3.12	83.97	28.25	36.70	17.50
23	OPH180	65.50	101.00	70.50	10.85	27.73	4.52	71.67	31.50	38.19	23.10
24	OPH109	61.50	96.50	78.50	10.15	28.98	3.79	59.65	32.31	37.64	21.70
25	CMS-90-3B	60.00	94.00	108.00	17.22	28.18	4.82	83.28	48.67	35.78	34.90
26	COSF-6B	63.00	98.00	81.00	11.62	34.73	4.11	70.59	32.45	34.80	23.90
27	RCB-5	71.00	106.50	120.50	14.70	24.85	3.25	88.50	26.80	43.15	30.80
28	R-630	61.50	96.50	61.50	11.90	30.39	4.27	78.54	36.70	25.22	24.50
29	RHAGPR-3	61.50	82.50	125.00	17.64	29.98	5.42	71.88	49.13	39.37	35.30
30	RHA 274	61.50	95.00	101.50	15.19	34.52	5.42	77.60	51.06	36.33	31.20
31	166 R	58.00	93.00	75.00	13.02	28.64	4.33	62.89	40.45	37.12	26.00
32	143 R	57.50	91.00	79.50	11.62	25.67	4.18	64.22	33.45	44.90	23.20
33	CSFI-99	68.00	102.00	79.00	10.43	33.42	4.25	67.62	34.22	36.70	22.40
34	GMU-502	71.00	108.00	111.00	13.72	26.66	5.13	78.16	29.40	36.87	27.40
35	RHA 1055	62.00	97.00	131.00	14.28	34.02	5.29	76.65	34.80	39.82	28.60
36	GMU 1031	55.50	89.00	78.00	12.95	38.10	4.67	74.02	37.30	31.41	25.90
37	159-R	61.50	96.00	90.00	10.85	25.21	4.03	61.35	32.00	40.81	29.40

Sr. No.	Genotypes	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Hull content (%)	100 seed weight (g)	Seed filling (%)	Volume weight (g/100ml)	Oil content (%)	Seed yield per plant (g)
38	GMU 500	63.00	98.00	155.00	14.70	34.42	4.89	72.67	38.80	32.03	26.00
39	GMU 324	63.00	98.00	68.50	13.02	32.88	4.11	59.66	36.23	28.11	23.80
40	GMU 258	61.50	96.00	65.00	10.50	32.47	3.97	56.48	33.88	31.25	21.00
41	PI-686644	58.50	92.00	58.50	9.24	29.95	3.32	69.74	29.11	29.47	17.50
42	USDA-112	59.50	98.00	64.50	10.22	30.77	3.79	79.78	31.25	33.70	20.40
43	PI-686806	55.50	88.00	81.00	11.76	29.07	4.18	65.33	39.20	34.11	23.50
44	USDA-121	56.50	108.00	61.00	8.82	36.22	2.88	66.38	23.18	27.05	12.60
45	PI-686543	64.00	100.00	78.50	8.96	37.05	3.11	87.82	25.62	31.98	14.00
46	LSF-08	60.00	95.00	127.00	13.02	26.04	4.15	86.34	36.96	38.79	26.50
	Grand mean	62.02	94.43	86.13	12.29	31.14	4.23	72.82	34.09	35.00	24.42
	SE (±)	1.13	1.47	4.59	0.54	1.83	0.19	2.27	1.62	0.98	2.11
	CD 5 %	3.21	4.20	13.07	1.53	5.22	0.54	6.46	4.62	2.78	6.00
	CV	2.57	2.21	7.54	6.19	8.32	6.31	4.40	6.73	3.95	12.21

3.3 Morphological Characterisation of Sunflower Genotypes

Morphological characterisation of the 46 sunflower genotypes was carried out using standard DUS (Distinctness, Uniformity and Stability) descriptors prescribed for sunflower. The evaluated genotypes exhibited considerable diversity for various qualitative traits related to plant, leaf, head, ray floret and seed characteristics, indicating the presence of a broad genetic base within the experimental material.

Variation was observed in traits such as hypocotyl anthocyanin pigmentation, leaf colour, leaf shape, leaf blistering, leaf serration, angle of lateral veins, orientation of leaf blade, head attitude, ray floret shape, seed shape, seed coat colour, seed coat stripes and stripe colour. The observed diversity in morphological traits facilitated the identification of distinct genotypes and provided valuable information for germplasm characterisation, maintenance of varietal identity and selection of diverse parents for breeding programmes.

Differences in plant morphology among the genotypes reflected the genetic variability present in the experimental material. Genotypes possessing unique combinations of morphological descriptors can serve as valuable genetic resources for future crop improvement programmes. Morphological characterisation based on DUS descriptors is an effective approach for distinguishing genotypes and supporting varietal registration and protection.

The DUS-based morphological characterisation revealed considerable diversity among the 46 sunflower genotypes for several qualitative traits. Leaf colour exhibited noticeable variation, with dark green leaves being the most frequent (21 genotypes), followed by light green (19 genotypes) and green (6 genotypes). Leaf shape was predominantly cordate (26 genotypes), while triangular and ovate leaf shapes were observed in 13 and 7 genotypes, respectively. Leaf serration varied among the genotypes, with medium serration being the most common (26 genotypes), followed by coarse (14 genotypes) and fine serration (6 genotypes).

Uniformity was observed for certain descriptors, as all 46 genotypes exhibited a half-turned-down head attitude and elongated ray floret shape, indicating limited variation for these characters within the evaluated germplasm. Seed shape showed moderate diversity, with elongated seeds predominating (25 genotypes), followed by ovoid wide (11 genotypes) and ovoid elongated (10 genotypes). Seed coat colour was predominantly black (39 genotypes), whereas brown, grey and white seed coat colours were represented by 5, 1 and 1 genotypes, respectively. Seed coat stripes were absent in 27 genotypes and present in 19 genotypes. These observations demonstrate the usefulness of DUS descriptors for distinguishing sunflower germplasm and identifying unique morphological features that can support varietal identification, germplasm conservation and parent selection in breeding programmes.

Similar observations of substantial morphological diversity among sunflower germplasm have been reported by Kaya *et al.* (2009), Radanović *et al.* (2018), Ibrar *et al.* (2022), Kumar *et al.* (2023), Delen *et al.* (2024) and Umarani *et al.* (2020), emphasising the importance of DUS characterisation in germplasm evaluation and breeding programmes.

3.4 Character Association Analysis

Character association analysis was carried out by estimating genotypic and phenotypic correlation coefficients among seed yield and its component traits. The results revealed varying degrees of association among the studied characters, indicating the complex nature of seed yield and the importance of component traits in determining overall productivity.

Generally, genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlations, indicating that the observed associations were predominantly governed by genetic factors and that environmental influence on trait expression was comparatively lower. Similar observations were reported by Johnson *et al.* (1955), Rauf (2008), Kaya *et al.* (2009) and Tyagi and Khan (2013).

3.4.1 Genotypic Correlation

The genotypic correlation coefficients among the ten quantitative traits are presented in Table 3. In general, the genotypic correlations were higher than the corresponding phenotypic correlations, indicating that the associations among traits were predominantly governed by genetic factors with comparatively less environmental influence.

Seed yield per plant exhibited a highly significant and positive genotypic correlation with head diameter ($r = 0.8579$ **), followed by 100-seed weight ($r = 0.6892$ **), plant height ($r = 0.6465$ **) and volume weight ($r = 0.6229$)**. These results indicate that genotypes possessing larger heads, heavier seeds, taller plants and higher seed density tend to produce greater seed yield. Similar positive associations between seed yield and these yield-contributing traits have been reported by Rauf (2008), Kaya *et al.* (2009), Tyagi and Khan (2013) and Kumar *et al.* (2023), emphasising their importance as reliable selection criteria in sunflower breeding programmes.

Plant height exhibited a highly significant positive correlation with head diameter ($r = 0.7208$ **), 100-seed weight ($r = 0.4194$ **) and oil content ($r = 0.4806$ **), while significant positive associations were also observed with volume weight ($r = 0.2915$ *) and seed filling percentage ($r = 0.3716$ *). These findings suggest that vigorous plants generally develop larger capitula and heavier seeds, ultimately contributing to enhanced productivity. Similar relationships were documented by Kaya *et al.* (2009) and Ibrar *et al.* (2022).

Table 3. Genotypic (r_g) and phenotypic (r_p) correlation coefficients for different characters in 46 sunflower genotypes

Characters		DF	DM	PH	HD	100SW	VW	HC	SFP	OC	SYPP
DF	r_g	1.0000	0.5103**	0.1995	0.0398	-0.0274	-0.2756	-0.0786	-0.0030	0.0741	0.0382
	r_p	1.0000	0.4553**	0.1555	0.0078	-0.0396	-0.2363*	-0.0114	0.0074	0.0629	0.0325
DM	r_g		1.0000	0.0318	-0.2866	-0.3922**	-0.4961**	0.0952	0.0383	-0.1186	-0.3503*
	r_p		1.0000	0.0317	-0.2626*	-0.3753**	-0.4259**	0.0079	0.0027	-0.1487	-0.3104**
PM	r_g			1.0000	0.7208**	0.4194**	0.2915*	-0.0563	0.3716*	0.4806**	0.6465**
	r_p			1.0000	0.6392**	0.3591**	0.2712**	-0.0865	0.3164**	0.4294**	0.5585**
HD	r_g				1.0000	0.6686**	0.5868**	-0.0815	0.3595*	0.3308*	0.8579**
	r_p				1.0000	0.6142**	0.5301**	-0.1086	0.2689**	0.3003**	0.7362**
100SW	r_g					1.0000	0.7086**	-0.0175	0.0361	0.1296	0.6892**
	r_p					1.0000	0.6490**	-0.1112	-0.0286	0.1815	0.5588**
VW	r_g						1.0000	-0.0364	0.0648	0.1011	0.6229**
	r_p						1.0000	-0.1468	-0.0322	0.0992	0.5284**
HC	r_g							1.0000	-0.2219	-0.5941**	-0.4481**
	r_p							1.0000	-0.0046	-0.4718**	-0.3219**
SFP	r_g								1.0000	0.2726	0.3684*
	r_p								1.0000	0.2316*	0.2467*
OC	r_g									1.0000	0.6489**
	r_p									1.0000	0.5278**
SYP	r_g										1.0000
	r_p										1.0000

Head diameter also exhibited significant positive correlations with 100-seed weight ($r = 0.6686$ **), volume weight ($r = 0.5868$ **), seed filling percentage ($r = 0.3595$ *) and oil content ($r = 0.3308$ *), indicating that larger heads are associated with superior seed development and increased oil accumulation. Comparable observations have been reported by Yasin and Singh (2010), Radanović *et al.* (2018), Dudhe *et al.* (2020), Kumar *et al.* (2023) and Sri *et al.* (2025).

A strong positive association was observed between 100-seed weight and volume weight ($r = 0.7086$ **), suggesting that heavier seeds generally possess greater density. Similar findings were reported by Rauf (2008) and Tyagi and Khan (2013).

Among the negative associations, days to maturity showed significant negative correlations with 100-seed weight ($r = -0.3922$ **), volume weight ($r = -0.4961$ **) and seed yield per plant ($r = -0.3503$ *), indicating that early-maturing genotypes tended to produce heavier seeds and higher seed yield under the present experimental conditions. Likewise, hull content exhibited a highly significant negative association with oil content ($r = -0.5941$ **) and seed yield per plant ($r = -0.4481$ **), suggesting that reduced hull content is desirable for improving both oil recovery and seed yield. Similar inverse relationships have been reported by Dağüstü (2002), Arshad *et al.* (2007), Kaya *et al.* (2009) and Tyagi and Khan (2013).

Overall, the results indicate that head diameter, plant height, 100-seed weight and volume weight are the most important traits associated with seed yield and therefore can be effectively utilised as indirect selection criteria for improving productivity in sunflower breeding programmes.

3.4.2 Phenotypic Correlation

The phenotypic correlation coefficients largely followed the same trend as the genotypic correlations, although their magnitudes were generally lower, indicating the influence of environmental factors on the expression of these characters.

Seed yield per plant exhibited highly significant positive phenotypic correlations with head diameter ($r = 0.7362$ **), plant height ($r = 0.5585$ **), 100-seed weight ($r = 0.5588$ **) and volume weight ($r = 0.5284$ **),. These results confirm that these characters play a major role in determining seed yield and may therefore be considered reliable selection criteria under field conditions. Similar findings were reported by Rauf (2008), Kaya *et al.* (2009) and Kumar *et al.* (2023).

Plant height exhibited highly significant positive correlations with head diameter ($r = 0.6392$ **), 100-seed weight ($r = 0.3591$ **), volume weight ($r = 0.2712$ **), seed filling percentage ($r = 0.3164$ **) and oil content ($r = 0.4294$ **), indicating that increased vegetative growth is associated with improved reproductive performance.

Head diameter maintained significant positive associations with 100-seed weight ($r = 0.6142$ **), volume weight ($r = 0.5301$ **), seed filling percentage ($r = 0.2689$ **) and oil content ($r = 0.3003$ **), reinforcing its importance as one of the major yield-contributing traits.

Among the negative relationships, days to maturity exhibited significant negative correlations with head diameter ($r = -0.2626$ *), 100-seed weight ($r = -0.3753$ **), volume weight ($r = -0.4259$ **) and seed yield per plant ($r = -0.3104$ **),. Similarly, hull content was negatively associated with oil content ($r = -0.4718$ **) and seed yield per plant ($r = -0.3219$ **), indicating that lower hull content contributes to improved oil accumulation and seed productivity.

The close agreement between the genotypic and phenotypic correlation coefficients suggests that the observed associations are stable and largely under genetic control. Consequently, head diameter, plant height, 100-seed weight and volume weight may be considered the most effective traits for indirect selection in sunflower improvement programmes.

3.5 Breeding Implications

The present study revealed substantial variability for both qualitative and quantitative traits among the evaluated sunflower genotypes. Morphological characterisation facilitated the identification of distinct genotypes, while character association analysis identified important yield-contributing traits useful for indirect selection.

The positive associations of head diameter, 100-seed weight, volume weight, seed filling percentage and oil content with seed yield suggest that these characters should receive greater emphasis in selection programmes. Furthermore, superior genotypes such as RHAGPR-3, RHA 274, 93 R, RCB-5, OPH-107, CMS-90-3B, 143 R and HOC-20R may serve as valuable parental lines in future sunflower breeding programmes aimed at improving seed yield and oil productivity. Similar findings were reported by Seiler *et al.* (2017) and Dudhe *et al.* (2020).

4. Conclusion

The present study revealed considerable morphological diversity and significant variation among the 46 sunflower genotypes, highlighting the availability of valuable genetic resources for sunflower improvement. DUS-based characterisation effectively distinguished the genotypes based on qualitative traits, facilitating germplasm identification and utilisation. Character association analysis indicated that head diameter, plant height, 100-seed weight, and volume weight were positively and significantly associated with seed yield, suggesting that these traits can serve as reliable selection criteria for improving productivity. The superior genotypes RHAGPR-3, RHA 274, 93 R, RCB-5, OPH-107, CMS-90-3B, 143 R, and HOC-20R were identified as promising parental lines for future breeding programmes aimed at developing high-yielding and high-oil sunflower cultivars.

5. Limitation of the Study

The present investigation was conducted with two replications, which may limit the precision of the estimates compared with experiments involving a greater number of replications. Nevertheless, the significant variation observed among the genotypes for the studied traits provides useful information for preliminary evaluation and selection of promising sunflower germplasm. Further evaluation of the identified genotypes across additional replications, seasons and environments would strengthen the reliability and broader applicability of the findings.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

The authors declare that they have no known competing financial or non-financial interests, personal relationships, or affiliations that could have influenced the work reported in this manuscript.

References

- Ahmad, H. M., Wang, X., Mahmood-Ur-Rahman, Fiaz, S., Azeem, F., & Shaheen, T. (2022). Morphological and physiological response of *Helianthus annuus* L. to drought stress and correlation of wax contents for drought tolerance traits. *Arabian Journal for Science and Engineering*, 47(6), 6747–6761. <https://doi.org/10.1007/s13369-021-06098-1>
- Allard, R. W. (1960). *Principles of plant breeding*. John Wiley & Sons. <https://books.google.com/books?id=zYw5PwAACAAJ>
- Ameen, M., Zia, M. A., Najeeb Alawadi, H. F., Naqve, M., Mahmood, A., Shahzad, A. N., Khan, B. A., Alhammad, B. A., Aljabri, M., & Seleiman, M. F. (2024). Exogenous application of selenium on sunflower (*Helianthus annuus* L.) to enhance drought stress tolerance by morpho-physiological and biochemical adaptations. *Frontiers in Plant Science*, 15, 1427420. <https://doi.org/10.3389/fpls.2024.1427420>
- Arshad, M., Ilyas, M. K., & Khan, M. A. (2007). Genetic divergence and path coefficient analysis for seed yield traits in sunflower (*Helianthus annuus* L.) hybrids. *Pakistan Journal of Botany*, 39(6), 2009–2015.
- Dağüstü, N. (2002). Correlations and path coefficient analysis of seed yield components in sunflower (*Helianthus annuus* L.). *Turkish Journal of Field Crops*, 7(1), 15–19. Official university publication record
- Delen, Y., Palali-Delen, S., Xu, G., Neji, M., Yang, J., & Dweikat, I. (2024). Dissecting the genetic architecture of morphological traits in sunflower (*Helianthus annuus* L.). *Genes*, 15(7), 950. <https://doi.org/10.3390/genes15070950>
- Dudhe, M. Y., Mulpuri, S., Meena, H. P., Ajjanavara, R. R. G., Kodeboyina, V. S., & Adala, V. R. (2020). Genetic variability, diversity and identification of trait-specific accessions from the conserved sunflower germplasm for exploitation in the breeding programme. *Agricultural Research*, 9, 9–22. <https://doi.org/10.1007/s40003-019-00406-w>
- Falconer, D. S., & Mackay, T. F. C. (1996). *Introduction to quantitative genetics* (4th ed.). Longman. <https://www.pearson.com/en-gb/subject-catalog/p/introduction-to-quantitative-genetics/P200000004168>
- Gahukar, S. J., & Fatak, S. U. (2023). Genetic variability and heritability studies in sunflower inbred lines. *Journal of Oilseeds Research*, 40(Special Issue), 322–323. <https://doi.org/10.56739/4m0fv851>
- Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespepeza. *Agronomy Journal*, 48(6), 268–272. <https://doi.org/10.2134/agronj1956.00021962004800060008x>
- Ibrar, D., Khan, S., Mahmood, T., Bakhsh, A., Aziz, I., Rais, A., Ahmad, R., Bashir, S., Nawaz, M., Rashid, N., Irshad, S., Alotaibi, S. S., Dvorackova, H., Dvoracek, J., & Hasnain, Z. (2022). Molecular markers-based DNA fingerprinting coupled with morphological diversity analysis for prediction of heterotic grouping in sunflower (*Helianthus annuus* L.). *Frontiers in Plant Science*, 13, 916845. <https://doi.org/10.3389/fpls.2022.916845>
- Ibrar, D., Khan, S., Mahmood, T., Bakhsh, A., Aziz, I., Rais, A., Ahmad, R., Bashir, S., Nawaz, M., Rashid, N., Irshad, S., Alotaibi, S. S., Dvorackova, H., Dvoracek, J., & Hasnain, Z. (2022). Molecular markers-based DNA fingerprinting coupled with morphological diversity analysis for prediction of heterotic grouping in sunflower (*Helianthus annuus* L.). *Frontiers in Plant Science*, 13, 916845. <https://doi.org/10.3389/fpls.2022.916845>
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47(7), 314–318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Karthik, N., Uma, M. S., Nehru, S. D., Ramesh, S., Srinivasa Reddy, K. M., Satish, H., Rath, B., Ganiger, S. S., Prashantha, V., & Malipatil, S. S. (2025). Genetic variability, heritability and genetic advance as percent of mean for yield and oil traits in maintainer and restorer lines of sunflower (*Helianthus annuus* L.). *Plant Cell Biotechnology and Molecular Biology*, 26(11–12), 1–9. <https://doi.org/10.56557/pcbmb/2025/v26i11-129906>

- Kaya, Y., Evci, G., Durak, S., Pekcan, V., & Gücer, T. (2009). Yield components affecting seed yield and their relationships in sunflower (*Helianthus annuus* L.). *Pakistan Journal of Botany*, 41(5), 2261–2269.
- Kumar, S. P., Singh, L., Dudhe, M. Y., Praveen, S., Gupta, P., & Surendra, T. (2023). Characterization and evaluation of new sunflower genotypes. *International Journal of Plant & Soil Science*, 35(8), 109–118. <https://doi.org/10.9734/ijpss/2023/v35i82887>
- McNellie, J. P., May, W. E., Rieseberg, L. H., & Hulke, B. S. (2024). Association studies of salinity tolerance in sunflower provide robust breeding and selection strategies under climate change. *Theoretical and Applied Genetics*, 137, 184. <https://doi.org/10.1007/s00122-024-04672-3>
- Narkhede, T. A., Pole, S. P., Singh, G., Zade, P. S., & Mirkad, S. B. (2025). Studies on variability, heritability, genetic advance and character association for yield and yield attributes in sunflower (*Helianthus annuus* L.) inbreds. *Journal of Advances in Biology & Biotechnology*, 28(7), 1487–1496. <https://doi.org/10.9734/jabb/2025/v28i72665>
- Neelima, S., Venkataramanamma, K., Prabhakar, K., & Venkateswarlu, N. C. (2023). Genetic variability and association studies in sunflower inbreds. *Journal of Oilseeds Research*, 40(Special Issue), 95–96. <https://doi.org/10.56739/jor.v40iSpecialissue.145258>
- Panase, V. G., & Sukhatme, P. V. (1985). *Statistical methods for agricultural workers* (4th ed.). Indian Council of Agricultural Research.
- Protection of Plant Varieties and Farmers' Rights Authority. (2009). *Guidelines for the conduct of test for distinctiveness, uniformity and stability on sunflower (Helianthus annuus L.)*. Government of India.
- Radanović, A., Miladinović, D., Cvejić, S., Jocković, M., & Jocić, S. (2018). Sunflower genetics from ancestors to modern hybrids—A review. *Genes*, 9(11), 528. <https://doi.org/10.3390/genes9110528>
- Rauf, S. (2008). Breeding sunflower (*Helianthus annuus* L.) for drought tolerance. *Communications in Biometry and Crop Science*, 3(1), 29–44.
- Reddy, B. V. R. P., Reddy, Y. P. K., & Venkataramanamma, K. (2025). Genetic variability and divergence studies for yield and its related traits in sunflower. *The Journal of Research ANGRAU*, 53(1), 40–49. <https://doi.org/10.58537/jorangrau.2025.53.1.04>
- Sandhya Sree, G., Roja, V., Meena, H. P., Vishnuvardhan Reddy, A., & Ramesh, D. (2021). Genetic variability, heritability and genetic advance studies for economically important traits in sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research*, 38(1), 92–95. <https://doi.org/10.56739/jor.v38i1.137005>
- Seiler, G. J., Qi, L. L., & Marek, L. F. (2017). Utilization of sunflower crop wild relatives for cultivated sunflower improvement. *Crop Science*, 57(3), 1083–1101. <https://doi.org/10.2135/cropsci2016.10.0856>
- Sri, B. K., Suresh, G., Toprope, V. N., & Pole, S. P. (2025). Understanding the contribution of yield components in sunflower (*Helianthus annuus* L.) through correlation and path coefficient analysis. *Journal of Experimental Agriculture International*, 47(5), 744–751. <https://doi.org/10.9734/jeai/2025/v47i53463>
- Sun, Y., Wang, Y., Bai, J., Guo, J., Li, G., Yang, X., Tian, Q., Huang, Y., Lv, S., Cao, H., & Liu, L. (2025). Integrative GWAS and transcriptomic analyses reveal regulatory genes controlling shoot branching in sunflower. *Frontiers in Plant Science*, 16, 1674383. <https://doi.org/10.3389/fpls.2025.1674383>
- Tyagi, S. D., & Khan, M. H. (2013). Correlation and path coefficient analysis for seed yield in sunflower (*Helianthus annuus* L.). *International Journal of Agricultural Research, Sustainability, and Food Sufficiency*, 1(2), 7–13.
- Umarani, E., Saritha, A., & Ramanjaneyulu, A. V. (2020). Evaluation and characterization of sunflower (*Helianthus annuus* L.) germplasm lines. *Journal of Oilseeds Research*, 37(Special Issue), 58. <https://doi.org/10.56739/jor.v37iSpecialissue.139461>
- Vamsi, D. M., Meena, H. P., Sandhya Sree, G., & 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. *Environment and Ecology*, 40(2A), 451–457.
- Yasin, A. B., & Singh, S. (2010). Correlation and path coefficient analyses in sunflower. *Journal of Plant Breeding and Crop Science*, 2(5), 129–133. <https://doi.org/10.5897/JPBCS.9000032>
- Zhang, C., Li, H., Yin, J., Han, Z., Liu, X., & Chen, Y. (2024). Pan-genome wide identification and analysis of the SAMS gene family in sunflowers (*Helianthus annuus* L.) revealed their intraspecies diversity and potential roles in abiotic stress tolerance. *Frontiers in Plant Science*, 15, 1499024. <https://doi.org/10.3389/fpls.2024.1499024>

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